

LOCUS: contig_1 ClWae19 7032512 bp DNA linear 20-MAR-2024

DEFINITION as Genus species strain: *Paenibacillus amylolyticus* ClWae19

ACCESSION: The data is retrievable at the National Center for Biotechnology (NCBI) as SUB14651639, BioProject PRJNA1145425, BioSample SAMN43065443 with a Localid as ClWae19_contig_1 with Accession CP168019 as *Paenibacillus amylolyticus* ClWae19

KEYWORDS: genomics; probiotic; canine; antimicrobial; *Paenibacillaceae*

SOURCE: North American Gray wolf (*Canis lupus*) GI tract

ORGANISM: *Paenibacillus amylolyticus*

COMMENT: Annotated using prokka 1.14.6 from <https://github.com/tseemann/prokka>

FEATURES: Location/Qualifiers

source 1..7032512

/organism= "*Paenibacillus amylolyticus*"

/mol_type="genomic DNA"

/strain="strain ClWae19"

rRNA 159..1709

/locus_tag="EFAGFIKM_00001"

/product="16S ribosomal RNA"

rRNA 2018..4939

/locus_tag="EFAGFIKM_00002"

/product="23S ribosomal RNA"

tRNA 5009..5084

/locus_tag="EFAGFIKM_00003"

/product="tRNA-Asn"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Asn(gtt)"

tRNA 5088..5179

/locus_tag="EFAGFIKM_00004"

/product="tRNA-Ser"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Ser(gga)"

tRNA 5189..5260

/locus_tag="EFAGFIKM_00005"

/product="tRNA-Glu"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Glu(ttc)"

tRNA 5328..5403

/locus_tag="EFAGFIKM_00006"

/product="tRNA-Val"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Val(tac)"

tRNA 5421..5494

/locus_tag="EFAGFIKM_00007"

/product="tRNA-Met"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Met(cat)"

tRNA 5522..5599

/locus_tag="EFAGFIKM_00008"

/product="tRNA-Asp"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Asp(gtc)"

tRNA 5695..5770

/locus_tag="EFAGFIKM_00009"

/product="tRNA-Phe"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Phe(gaa)"

tRNA 5791..5866

/locus_tag="EFAGFIKM_00010"

/product="tRNA-Thr"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Thr(tgt)"

tRNA 5876..5961

/locus_tag="EFAGFIKM_00011"

/product="tRNA-Tyr"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Tyr(gta)"

tRNA 5968..6041
/locus_tag="EFAGFIKM_00012"
/product="tRNA-Trp"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Trp(cca)"

tRNA 6071..6145
/locus_tag="EFAGFIKM_00013"
/product="tRNA-His"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-His(gtg)"

tRNA 6167..6241
/locus_tag="EFAGFIKM_00014"
/product="tRNA-Gln"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Gln(ttg)"

tRNA 6246..6320
/locus_tag="EFAGFIKM_00015"
/product="tRNA-Gly"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Gly(gcc)"

tRNA 6327..6400
/locus_tag="EFAGFIKM_00016"
/product="tRNA-Cys"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Cys(gca)"

tRNA 6406..6486
/locus_tag="EFAGFIKM_00017"
/product="tRNA-Leu"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Leu(caa)"

CDS 6669..7349
/locus_tag="EFAGFIKM_00018"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTNGKNVSDTDLLFDLSVWEEAWKNRPRSSKYKKKSVPSNTEEA

FERWARDYHAQSFTTEEGKQRSERIMGWIENQGVFAGLSILDIGAASGIFTIPFAEKG

ASVTAVEPSELLVSLMKETIPSALESKIEIVNEREYEEISIQDKGWEKKYDFAFASMCP

AMSDWEAIEQAINCARKYVYISTMAGQKEHTLMHELKDV LGVTSSYKAGDMGYIQQLL

YLK GILIR"

CDS 7346..7594

/locus_tag="EFAGFIKM_00019"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIITREVNSFEVPVEEIIIEKLPEWLNTYELPSDEDSLRLAEDYI

SDTYKDSTVTFSRGGFRFGKILIQLEQPNMKT VGTKDKR"

CDS complement(8029..10419)

/gene="yesS_1"

/locus_tag="EFAGFIKM_00020"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31522"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator YesS"

/db_xref="COG:COG2207"

/translation="MRPISYLHKMIIFGILLSTLPILLTGIAAFIYSSNQTELHRTQA

NRQLLEQM QSNVEHKLATVSYMLDQAVRSPVTLRSLSDSSSVQGNGPLLADKLQSEFQ

NMRSWEPLLDITLVNQSQNWLIDHAGLYRNTDFPLALPMKELISDTLTSGWQLSPSSV

FSNDERSPGTGCIYHIALARSIPNLNTSSDAALIAGIPACSLQNTLGEASLGNAASGL

IILNREQRILVHPDPVYIGQPLSAIGLQDRDTEANITKLSPITFSTGF EKREVKIADT

HYSLTYPSTLKGWTVVLISPTNILTQEYIDIGLHTLYISIFLLLLSLLLAWLGSKRM

HVPIRKLLTQLGDNHLSKEGNTLAQQSPFSDFEQIRAGVSQLSASRSQLENTLNVH
LLQIRNHFMNLFQGKIPVHTLHDTLNEYGYTHQVREWQQIAVITLQADLVNHTKYRA
SDRDLLLFAIQNILEETVVHNQQLLPIVLEHTVVTVIGTVEQDQFIFSQQLYVLTDQL
QQQMDKILALQVSIGFSQSHSSLHHIPQAYTEALEALRHRMKLGTGIIFQYENIDHYT
PTWSMTYPESLEYSLIQAIQNADEVQASALLKQLLEVIFGMEVTPEEYEVALTRLLTH
ILQMTQESGIRLGQISQSRGSMFHELHGLQYAAEVEDWFKYQVILPVIQVFKARQYAQ
YQHISEKMIAMIHQDYDKDLTLEECAVKLHYNANYLSSVFRKETGCAFSEYLTKYRFN
IAKKWLDESDLTVKDIAARLRYNPNQNFIRSRKWEGITPGQYRERKQKAEVSNRN"

CDS 10975..11283

/locus_tag="EFAGFIKM_00021"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRLNKGNGWAIVLIALGALLLFGKLTPLLGHLMGYLIPVLMIAL

GYYGVKRGNVMLGWIVLIIGIISLMGKLAWLIGPIAIGLIIFGISMLSNNRSRRGRY

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CDS 11319..11990

/gene="liaH_1"

/locus_tag="EFAGFIKM_00022"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32201"

/codon_start=1

/transl_table=11

/product="Protein LiaH"

/db_xref="COG:COG1842"

/translation="MSVFRRMRDITVANLNEHLEQSQDPVKLIDQFLVSTRQDIGEAE

KLRHQYASHTRQMKQQADQAAGMVNKREEQASMALKAGEEHLAKLALQEKILHEEKME

QYNELYAQSYAALQELDEQIDQLKVEYQNVYSKRQYYYARMQTIQLQQRMNQRGNHNG

QNVPRMFNRLDDQVSDLEYEAQSLRDIRRMNQDGSQVTGSMSSSTLDKELERLRQKLN

NDRKE"

CDS 11996..12229

/locus_tag="EFAGFIKM_00023"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKLYRSARNRMLTGLIGGISENLGLSTLLRIIFFISIFATGG

TSLLIYFIAALVVPKESNHVDPYAYDSNVRGYK"

CDS 12247..12756

/locus_tag="EFAGFIKM_00024"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKLYRSTRDRMLTGLCGGISETIGMDSTLLRIIFVISIFVTGG

TSLLIYFIAALVVPKEPYPPYDPYGYGPGQGPGPGRGYDNYDHQPPRGPFQNNHNQQG

PGNFGPGPGFNRPQSGPRSYDNNAYGAGAPQESELDSMMKDIEKKALKKEVEELRQK

LSRYEKGEK"

CDS 12758..13465

/gene="liaH_2"

/locus_tag="EFAGFIKM_00025"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32201"

/codon_start=1

/transl_table=11

/product="Protein LiaH"

/db_xref="COG:COG1842"

/translation="MGVFKRIKDMTKASVNDMLDKVEDPIVMLNQYLRDMEAEIHEAE

VTVAKQMANERRMKQRLDEAERTSVQRESQAEAAALSNGQEEVARKLLEEKIYFDQKIT

EYSELHAQSEAQAKDLLQLHDMKDEFYKMRNKRNELVSRAQMAKAKKQMSSINSLHS

IESGGASLGFHRMEEKIMQLEAEADVARAPYRNTSSSTYTNPVDVEKQFKVDQQLQALK

NKMGNGSKNEANGTSKE"

CDS 13616..14263

/locus_tag="EFAGFIKM_00026"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNQKSKWLAVVIMIIGTMMLLNDNINFLTAAALILLTVGMLQVR
NGDTRKGHRYLGIGAALLLLDNLMIIVFLIVLASLAYFYSKNKKIHLDEGVMKKQNFMA
RYYWDQSSWTLRSMWLWHAIGEVDNADLSLSIPEEKQTIVLLQGVMGNVRLTLPEDYGV
EIEASVLFGRINLLGEQDSGMMNKLWVRTPGYESSEHKAKFVISYIVGDLNISNP"

CDS 14295..15410

/gene="liaS_1"
/locus_tag="EFAGFIKM_00027"
/EC_number="2.7.13.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32198"
/codon_start=1
/transl_table=11
/product="Sensor histidine kinase LiaS"
/db_xref="COG:COG4585"
/translation="MKTKRHTDMVTRSMGEGILLVFIVLAVVLYVLYTYGYLAPFTGW
RHLIQSGLALLLLLIGIGAVFGFYQSYRVKRIELLRETLWLWEKGSLSRTVPDLGDD
DVGRLLSEQLGRIGKKWEDQISSLQRLSTHNAQLAEQARITAIVEERQRLARELHDAVS
QQLFASMTATAVGRKMEKDFERAQRQVALIEEMASVAQSEMRALLHLRPVYLEGKH
LEQGLRDLVMEKTKVPMDIVLEMDDEDIDLIKGIENHLFRIVQEAMSNTLRHAKAEKM
EIRIQRRTDAIRVLIRDDGQGFDLDENKQASYGLANMRERVTEIGGAIQFVTAPGKGT
RIEITPLMNDESEEEHVNGTGSRNVDGNVDQSIARG"

CDS 15352..16020

/gene="liaR_1"
/locus_tag="EFAGFIKM_00028"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32197"
/codon_start=1

/transl_table=11

/product="Transcriptional regulatory protein LiaR"

/db_xref="COG:COG2197"

/translation="MEPEVETETETSIKVLVDDHEMVRIGLAAVLDTEDGIEVVGEA
GSGEEGIRLAQEYKPDVVLMDLVMEGMDGIEATRQVLKMYPECKVIVLTSYLDDEKMY
PVIEAGAFSYLLKTSRANEVADAIRAAARGQSVLESQVASKMMNRFRQPQAAAPLHDE
LTDREMDVLRLLAKGKSNQDIADDLIIGIKTVKFHVTNLLAKLGVDDRTQAAIYAYKN
GLAE"

CDS 16470..17219

/locus_tag="EFAGFIKM_00029"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLNRWMTAGILAIIIILIGVTQVYAEKNESKVAQLEQLIYTAD
SVIDNVDRLLVIKWQGEKGDAQEQAVALASHLGLLEPPMQVRQTSHNVYRSEVVVG TAN
GGVGMLVNVVDTGANGYYAIVQLSGDAHTDRKALMTLHEEVDQLLVDSGMKATWNMSV
QGTAVTATEHDASQQLLEIEEQLSTKVDIASVERYTDAGTASVSYKAAELPLSIKSGS
HMLNMQLAVHQVGDEVNDRITVGFPVITIEY"

CDS 17435..18985

/gene="zwf_1"

/locus_tag="EFAGFIKM_00030"

/EC_number="1.1.1.49"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54547"

/codon_start=1

/transl_table=11

/product="Glucose-6-phosphate 1-dehydrogenase"

/db_xref="COG:COG0364"

/translation="MVEKQLQDEVQTPGAVFFIFGATGDLARRKLFPAIYSLYREGKL
AEDFAVIGVARRPRSPPEEFREDIYESIKEFCRYPAGEPDEWNAFVEHFYKALDINN
EGFKELRAQTEHLESKFNTPGNRLFYLALAPELFGSVSYSLRDGGMLESQGWNRLVIE

KPFGYDLQSAEHLNEQIREVFREEEYRIDHYLGKEMVQNIEVIRFGNAFFEPLWNNK
HIANVQITLGETVGVEERGYYDHSGALRDMGQNHMLQMLTMIAMEPPSRLFPEDIRD
EKVKVLRSLRAFTSDEEVSNNVVRGQYSEGEYRGKQLPGYRQEDKVD PQSNTETYFAA
RVFVDNFRWAGVPFYIRTGKRLPVKTTEIVVEFKSMPNNVYLGKKYKLEPNLLVIRVN
PMEGIYIKINAKKPGSDSEIQPLAMDFCQSCMIGINSPEAYERLLHDAAEGDSTYFTR
WDEVATAWSFVDRIAAAWGQNQGELHTYPAGTWGPEATDKLLEQDGFHWWPVNGQDED
SVIWQVNG"

CDS 19355..19756

/gene="mhqP_1"

/locus_tag="EFAGFIKM_00031"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P96694"

/codon_start=1

/transl_table=11

/product="Putative oxidoreductase MhqP"

/db_xref="COG:COG2259"

/translation="MMLDVGLLLIRLVIGLSFMAHGAQKLFGWFGGYGIKGTGGWFES

MGMKPGALVALLAGLAIEFGGGLLLALGLLTPVGGILIALTMVIAIVKVHGANGYWSTQ

NGFEYNLAILVIGVALALTGGGQYALDALIF"

CDS 20078..21691

/gene="prfC"

/locus_tag="EFAGFIKM_00032"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q99V72"

/codon_start=1

/transl_table=11

/product="Peptide chain release factor 3"

/translation="MNERTKGIKPMKAANDILQQEVDKRRTFAIISHPDAGKTTLTE

KLLLFGGAIRLAGTVKARKASKHATSDWMEIEKQRGISVTSSVMQFDYLDHRVNILDT

PGHQDFSEDYRTLTAAADSAVMLIDVAKGVEAQTIKLFQVCAKRGIPITFINKLDRE

GKSPFDLMEELNVLGIRSVPMNWPIGTGRELCGVYDRMKNQVELFQGDDHSTIKVQK

VDGYKDPIIREMAGEYLHDQLCQDLELLDIAGDQFDMEKVQRGELTPIFFGSAINNFG
VQTFLENFLELAPKPEPRRSTAGEIQPTNEKFSGYVFKIQANMNPAHRDRIAFLRIVS
GKFQRGMSVKHTRVGKEIKLSQPQQFLAQDRDIVEEAYAGDIIGLFDPGIFRIGDSLS
QGSEVVFEELPTFSPEIFAKVTVKNALKHKQYQKGIDQLTEEGTIQVFQTVSFDETIL
GVIGQLQFEVFEYRMKGEYGVQDVQLQRMQYQFARWIVDENLDPSKFRINSALVKDKKG
NYVVLFFENEYAMRTAMDKNPTAQFLETAP"

CDS complement(21920..22153)

/gene="sspl"

/locus_tag="EFAGFIKM_00033"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00669"

/codon_start=1

/transl_table=11

/product="Small, acid-soluble spore protein I"

/translation="MPITLSLREAIVHKVHDKSDDLREMIIEGSVDGPEAALPGLGAI

FEMIWKNTTEPAKQEELIQIAQEHLHTIPVQPLI"

CDS 22321..22983

/gene="ktrA_1"

/locus_tag="EFAGFIKM_00034"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32080"

/codon_start=1

/transl_table=11

/product="Ktr system potassium uptake protein A"

/db_xref="COG:COG0569"

/translation="MAKKQYAVIGMGRFGSSVANALSGMGFDVLDAIDAEQRTQEMSN

VVTHAVSADSTDEEALRALGIRNFDVWVAIGEDIQASILTTLILKDMGVPVLIVKAQ

NELHGKVLQKIGADKVIYPERDMGLRVAHHLTSPNILDYIELSEDYSILEMRASEQMI

GKNLMELNIRARFGCNVMAIRSGNSMNISPYAEDRIEAGDVLIIVGHKDHCLKMELAY

PK"

CDS 22983..23798

/gene="aviRb"

/locus_tag="EFAGFIKM_00035"

/EC_number="2.1.1.208"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9F5K6"

/codon_start=1

/transl_table=11

/product="23S rRNA (uridine(2479)-2'-O)-methyltransferase"

/translation="MDADGKDGKMDIVSPQNTRVKEWAQLLEKKHRTRQHKYIIEGIH
LVQEALRAGADLECIVYDGEQGVPSLEGGLENPLQRVEWVSVSPAVIAKCTDTMTPQP
VFAIVRKGSEPLESLITGARGLVVLDGVQDPGNVGTIIRSADAAGAAGVVLGAGCAD
VYNPKTIRSTMGSLFHLPIVEGQLESLLPEAKAAGVKLVSTSLQAEHSCYSYDFTQSV
WLVIGNEGKGISDARLVDDAITIPMQGQAESLNAAMAATILLFEAMRQRMV"

CDS 23934..24278

/locus_tag="EFAGFIKM_00036"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MILGGDIFMAKKGQTFQTYTEEFKLNAVRSYVEGSSSYKVVAER
EGIRNCSQLKVWVKWKNGEAFDERKNSVPNPLKGRPRTAFGSVEEERDYLQAQVDYL
KKRYPNLVKEKR"

CDS 24443..25138

/locus_tag="EFAGFIKM_00037"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISBth8"

/codon_start=1

/transl_table=11

/product="IS3 family transposase ISBth8"

/translation="MMAIHFANREFGYPRMTTALWEAGLNVNHKKVWRIMRELSIQSV
IRKKRKKSSYTPSVIYPNRLKRQFHATAPQQKMVTDITYISDGSFVYLSVIQDLFNN
EIVAWQLSKRNDVQLVLDTVEQWTQKRDVSEAVLHSDQGFQYTSQAYNSRLEAFGVKG
SHSRKATCLDNACIESFFSHLKTEKLYLNQCNSEAEIRQAVEDYMYNRYRRFQAKLK

QRAPIEYRCALAA"

CDS 25406..26101

/gene="walR_1"

/locus_tag="EFAGFIKM_00038"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37478"

/codon_start=1

/transl_table=11

/product="Transcriptional regulatory protein WalR"

/db_xref="COG:COG0745"

/translation="MNNAKILIEDEAPIADLLSYGLSLEGFQTKVATNGAEGLENEIR

LFQPDLLLLDWMLPDQSGLDICKKVTSEYNIPIFMITAKSDITDKVLGLEFGADDYIT

KPFDLREVIARIRTIILRRVEQASNVDPSIAIHFQDIEIYLEERVVKHKNNSELT

PKEFDLLITLARNPGRTFTRSELLDLVWGYHFAGDTRTVDTHIQLRKKLDAADYITT

VFGIGYKFKKTGG"

CDS 26109..27569

/gene="sasA_1"

/locus_tag="EFAGFIKM_00039"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"

/codon_start=1

/transl_table=11

/product="Adaptive-response sensory-kinase SasA"

/translation="MVNKISTKFLLGFLIFSFSVLLNQTVKEFTRTGNQNLITSEL

VGLKNNNSVYVRQAFLINHFSNNELYFGEMAEELGNTLNHSTGNSVGVTYVNGELLYA

SDQSLFSEAKENDIQEAIEGKTAYSINYNDNKTSVLFSPVVMGDSKVGILRFYKDFT

LLYQQSGKILEIILYITLAIFSVAFLFSYILSRHVTPLGKLARASSEVKDGNLDVRI

HFKRKDEIGRLAENFNDMINQIGLQIRIIEKDRDQLRELHKQEKLFDDNITHELKTPL

TSILGYAELIKANGERDREFFEKGTTHIIEESRRLHAMVIKLEVSRQHVNELERVEV

GAILRDVCESMSIRAQRYKKNIVVNIESELYLLAQTDSIRQLFINLLDNAIKYSLAFA

EISVRGVQEEGKVRIYIGNPSDPIDADELTKLFQPFYLAHPKDSEAGSVGLGLSIVKS

IVEELEGSIIVSQNNYMVVTVFEFDSLKSDRGEEQL"

CDS 27569..28693

/locus_tag="EFAGFIKM_00040"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKNYLQRPWTLLFMLFLTSCSVGHQSETIISSNDAEDIQHP
GSSPVQVQKIYRLPDEYMGQWLGWSSSHSIIGSYKTASIPERSILTRLDQPFQSNNI
KELSTNNVQTILSPDGKYITEMYNTNLDVNIKILSLADGQEATVDTVNTKDKFLQDVS
WSNNGKYLSYLVLDSSGSDKASRLRYNMESRTLQVYEFQDIDEGGTLGGMNVSEDGRS
VLFESMHSGKTNVLLGKINNKTIEKRYVRQIGREQNPAWISNDQFVFLGTDGTLYEYD
QRNSELIIILERSVIFEISQDKKFIAYSLRDEDVVYVGKMQGRNILEPVPYHGIVPT
TMYWNTDSSRLLIQNQKSYTHSEPGQVDFAAAGPSFIIEFK"

CDS 28861..30645

/gene="oatA"

/locus_tag="EFAGFIKM_00041"

/EC_number="2.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A3D6"

/codon_start=1

/transl_table=11

/product="O-acetyltransferase OatA"

/translation="MNGKNNLTIKRYMPGIDGLRAISVLAVIAYHFDFKWAQGGLLG
GIFFVLSGYLITDQILLEWKMHKNIFLWNFWIRRLRRLLPAMISMLMFVALWLIVTDP
TRLLSLSGDFISSVFYVNNWYLIFHNVSFYDSFGPPSPIGHLWLSLIEEQFYLVWPVV
LLLAI RFAPRRGRMLMVYIAVLASISATAMAVMYEPGTDPSRVYYGTDTRAFAIFIGAA
LAVGWPSWKLNRISPTARTLLDCVGGLGLLILLILIYRTNEYDDSLYRFGFLYLSII
SAIVISVLAQPASRLAKLLGCKPLAWIGKRSYSLYIWHYPVITLMHPTGNERLNILQI
MIQLIITFILSILSYTWIEEPIRKVGKVAQLRFIRSHHWFKPAIIFTFTLLALFRVES
WITNETKVRSESVQPVIVQEVTSSNNQQELNTDNTTEEIPAPVPMVKGEGITVIGDSLAL
NVA SVLEEKLP GIVVDGKVGRQMSQAQSVIEDLRAKDKLGDRIVIALGTNGAFNQSSL

SSLLDSLQGEKKIYLVTRVPKNWQNTVNEALKDVTREYPNVKIIDWYAASENKNDLF

YHDGVHLTPEGAQFYASVLVEHIQEDQG"

CDS 30684..31382

/locus_tag="EFAGFIKM_00042"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKNKARKAWMVWGLALLIMILGYMGFRSLDTTNAQQEESDAQA

MGATKYISNQTQPEQSNNASSNDSQKTDVLSTEGEGVTIIGDSVTVGIEPYLKEKLPK

INVDGKVGRQMSQAESTVSELKAQGKLGDRIIIELGTNGPFSKKHLQHLLTALSDAKQ

VIVVTTRVPKGWQDSVNSTINDVAQEFDNAQVVDWYAASEGKGDYFYKDGVHLKPDGG

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CDS 31425..32444

/gene="tagU_1"

/locus_tag="EFAGFIKM_00043"

/EC_number="2.7.8.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01140"

/codon_start=1

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/product="Polyisoprenyl-teichoic acid--peptidoglycan

teichoic acid transferase TagU"

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KLVDVGGVDFYVEKDMNYESKADNYEYDINLKEGQQHLDGKTALQYVRF RHDAMSDY

SRTKRQRELMNEIVEQMKNNTSLVKLPVILEEVSPYIDTNLSVNDMWKLAS VGYQSKI

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IHQDK"

CDS 32460..35849

/locus_tag="EFAGFIKM_00044"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
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WKTFEQQDYTGPSFIRVSHEKVSQRQFTADITFDLVYGTTNLAEPQLQRPLFASLMGT
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VEGRDIYLTIVAKDKNTIDKYENVTHPAMLNDPKRLQADIKSGAFGDYAVPIWVNNIH
PNESPGVDAIFNYFKSTSLDEKVTFRITSTDGKPKVSNVDDALNNVFFIFVYTNNP
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TPPHDPNMEYDLLIDRMLEQAKVMGEAGIANTKYDYYHIPYEENRKAEDPTYVSRGT
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SKPSGKELQSLTVSALGESAFVLEGLGFNVTDQDQDKADILVNTFESSAFVEKGKPYIA
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HSQHQRLLANSIFSAPHETSESSGSDVKFSDLKNVESWAGREIRELVDADVLQGTGK
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GGDRFEPGLSITREEMAQIVANTLKLKQEVSTSNTEVLEQFTDKDLIAPYARDSVAY
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CDS complement(36284..37492)

/locus_tag="EFAGFIKM_00045"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MSLKFQSPDESGHENEDKVDQIQSRSQKKNKDTQIKKGDSRGS
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TAVSLTVLAPPLMLLGQSAFSGSFLLADITGGPMSSIALAPAFVAGMAIGRLDLTRKR
VSLSLAFGGLVMLVISKSLASKVLPELGRSFETWLVSVQGVAAQPDYPYAIWPLNVDSP
MWHMLLWTAPHSASTFQMTMTGLGIALLVIGLAFLIPKKVNVLLQPFAAVGRVALTMYA
IQFVFWILSLSGINYSYGELPFGDLLVVIVTLILGWLISRLGTGPLESMLRYFDRIF
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CDS 37786..38544

/locus_tag="EFAGFIKM_00046"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKYTVITGASSGIGYETALAFARGKNLILVARRLDKLEDLKST

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ETMLRVNIESLTILSTLYVRDYANVEGTQLINVSSALGYAIAVGSVAYSASKYYVSAF

TEGLAKELELKGAALKAKILAPAITETEFVQKSIDAEGFDYKANMPKYHTAKEMAGFM

IDLYDHNEVVVGIVDQNYEFQLTGAIYPVISELN"

CDS 38605..39690

/gene="nemA_1"

/locus_tag="EFAGFIKM_00047"

/EC_number="1.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77258"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG1902"

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AAAIEAGADGVEIHGANGYLINQFLGENSNTRTDEYGGSIENRARFAIEVTKAIVVEI

GAERTGFRISPGTPLGGIQDGEQGPELYRYLVKELAQLDLAYLHVMHLRDEQQLQDIR

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PTFFGLGSKGYTDYPTLEELKSNEGKH"

CDS 39866..40864

/gene="tdh_1"

/locus_tag="EFAGFIKM_00048"

/EC_number="1.1.1.103"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00627"

/codon_start=1

/transl_table=11

/product="L-threonine 3-dehydrogenase"

/translation="MRAAQIQKYSKKIQVEINNIEIPQIHSREVLVRVKAAGVNPLDI

LNMNGSVRMIADYTLPLTLGNELSGVIEAVGDDVLNFKVGDSVYTRLPLNKIGAFAY

AAVHEDALSMMPENLSFIEAAVPLTALTAYQALHDVLRAPNKKLFIPGGTGGFGAM

APIAKSMGLTVITSGSERGRSRTLSIGADQFINYKKENYADILSDIDYVIDTLGAEE

IKAELSILKPQGKLVSLKAGPNYRFAADSHFPMWKKALFGLVGARLDSMARKNQNEYR

FMFVHSSGSQLENITTLEKNDIKPSIDSTYRFDEIEKALIKVSTGHSQGKVILTF"

CDS 40920..41498

/gene="comR_1"

/locus_tag="EFAGFIKM_00049"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P75952"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional repressor ComR"

/translation="MARSKEFEESVVLKAMRLFWEQGYEKTSMRDLVNHMGIHRKSL

YDTFGDKHTLFLKTVLDYDHKISSALAAGVERSKTATEALQFIFCSLIHGEESPASGC

FIVNSTVELAARDKDMNNRSTEMFGNTEKLIKDIMVWGQQEGEFTTEYNAEVLAEYLH

NVSIGLRGMAKTSMTKEKLLRIAMLSMDLILR"

CDS 41588..42370

/locus_tag="EFAGFIKM_00050"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRKTVLITGVSGGIGKELADRFAKGGHHIVLVARSEGKIQDLAQ
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QEVNMIDVNIKALTVMTKLFLPDMIQRGHGGVMNVASLVGFFPGPMMSVYYATKAYVL
SFTEALENEVSGTGVTVTALCPGLTSTGFVDRSGMGVSKMLQGPIMEAGQVAQEGYQG
FLRGKTLIMPGARNRFIAFMPRLLPRKMMTRMIRSSQDKTGH"

CDS complement(42375..42953)

/gene="olsG_1"
/locus_tag="EFAGFIKM_00051"
/EC_number="2.1.1.344"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:L0D9B6"
/codon_start=1
/transl_table=11
/product="Ornithine lipid N-methyltransferase"
/translation="MKTSEPLLFLQGFLRNPKRVGSLLPSSKFLARKIVQSVRWDEV
SIAELGPGTGAVTRLMRAHLPKSATVFLFERDPKMRSNLKRIYPEFMFHSNASYLLKR
INQEYIHQLDSIICGLPFFNFSREMRQNILSQIHTALRPEGTLVLYQYSLHMKQRLAE
LFEIEKIQFVPLSFPPVFVYVCRKRQDEGHTL"

CDS complement(42988..44088)

/gene="rcsC_1"
/locus_tag="EFAGFIKM_00052"
/EC_number="2.7.13.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00979"
/codon_start=1
/transl_table=11
/product="Sensor histidine kinase RcsC"
/translation="MIKRLPQFKKKIQINILYQMLISLLISFVGSVGVNNMLIIAAAK
ISERFNWPSLLYIFPYVLTPIFIVIFTLIFLFFTRKIVRDLITLEQGLQIISEGNLNY

RVPVNRQDELGRVASNINHMTEQLKQQIAKERELEQSKMDLITGISHDLRTPLTSIIG
YIELLKSESFQDKAEYDRFIQNTYNKATHLKKLLDDLFEYTRLNEVNTQLDLKNVDLC
QLLDQLLFEFEPLAQEHGIRIEKTLGNAPIMVSLDSDKIARAIDNLLMNALKYSFKPG
TIHVRMSVQHNHVTIEVENKGIPLTIEQKNRLFDRFYKVDYSRNSEGIQSGSGLGLSI
ARNIADLHQGTTLKHTRNVFIFQLSLPSNIQ"

CDS complement(44081..44761)

/gene="srrA_1"

/locus_tag="EFAGFIKM_00053"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9L524"

/codon_start=1

/transl_table=11

/product="Transcriptional regulatory protein SrrA"

/db_xref="COG:COG0745"

/translation="MNTVLVVDDEPDIRDVIHVYLRNEGYQVIEAANGEEALNIIKTT
SVQLVILDVMMPIMDGIKACFKIREVSSTPIIMLSAKEEDIDKITGLTTGADDYMKP
FNPLELLARVKAQLRRQTLIGKPESNSLILIKDLVIDTSKHSVKLKDNDISLTPLEFS
ILVLLASHPGQVFSSEKIYETVWKEPYGYSDNTVMVHIRNLREKLELNPREPQYIKTV
WGVGYKID"

CDS complement(44819..45385)

/gene="olsG_2"

/locus_tag="EFAGFIKM_00054"

/EC_number="2.1.1.344"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:L0D9B6"

/codon_start=1

/transl_table=11

/product="Ornithine lipid N-methyltransferase"

/translation="MNSNEPILFLKSFLQSPKHVGSII PSSRFLASKMVKQASWLEAK
AVAELGSGTGPI TRYIHQQVQDSTKVLLFEMNETMRNTLKTAYQEFSCYPDAARLVES
MNQEGVQQLDYIFSGLPFFNFEPELRNTLVDQIYKALKPGGLFI AFQYSLQMKKTLSE
HFIIEKIELVPLNIPPAFVYVCRKKETI"

CDS complement(45430..45933)

/locus_tag="EFAGFIKM_00055"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MISNTILELLHQYGYLIFYFAFSLGPFGIIPNEITIISGAILS
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WAMCIGLFIPIVRYVLPLLIGMSGVQYRKFALISYSSALLWTITYFTAGTYFGGPILS
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CDS 46798..47385

/gene="sigW_1"

/locus_tag="EFAGFIKM_00056"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q45585"

/codon_start=1

/transl_table=11

/product="ECF RNA polymerase sigma factor SigW"

/db_xref="COG:COG1595"

/translation="MSEQDEYIELVTLIRTGHEEAYGELYEKTVTRIYQTVRFLIKDK
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SDVGMEYDFSTDLINKLANRPLLEQVHRLPYKLQQVVTLHYLNEYTQEEIAGILEIPL
GTVKSRIHAALAKLRQKEKMNPRLRGKAEDLHETR"

CDS 47372..48121

/locus_tag="EFAGFIKM_00057"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLDEQLRTAYQEETKDWSVPARIKHKMMDGIRSDSHIRKNRKK
WLVTGILAAVLIPTGAYAGYTYLADGIYGSQENITAMGGTAEDYMRLEAKLQTAKAH
FSEEEFVKYMDLLKQLGQMAVKYADSQGNMHPEQWNTVEQERYNLLVAELEPFFEKLE

AVSVGSSKKLMDEQQFWTEQLEQAektftKEQYLEFKSVYEQMKKYKVMVMDKDGSIQ

EERLSAEQKDDLRLQLERRLIPYLKRLGLDVR"

CDS complement(48196..49071)

/gene="rhaR_1"

/locus_tag="EFAGFIKM_00058"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MKSIFLGEQFNLVCRRTSNTTSREVFHAHSQLEITYIHEGYGQL

ITEGQVFSLEPGMLMIFRPFQLHHIQVSRQQPFIRNVLMVELDLLKAHWPQFIVTH

DFIQDLLEEQSPIQPIRLAATSPLVQRMEQYADTYPGLLPHEIEEDTLLFLLDLLAQL

RYLWQDGQQRCSEDVFSSANVLHPHAEAIMQWIEQHYQEPFRLEHIADTLHLSPYHL

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GSTPHQYRLKVQGRK"

CDS 49180..50337

/gene="gfo_1"

/locus_tag="EFAGFIKM_00059"

/EC_number="1.1.99.28"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q07982"

/codon_start=1

/transl_table=11

/product="Glucose--fructose oxidoreductase"

/translation="MLKVAIIGAGAIISGAHISAYLAFPERCQIVAVVDIYVEKAQKRI

NEYGLEGAQAVMDYTDLLAQNIDLVSVCPTPYTHAPIACDFMQAGAHVLVEKPMASSL

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YYDLWWRGTWKEGGGCTLNHAVHHIDAMLWMMGPPVELQAMMANTAHDNAEVEDISM

AMLRFAQEGELGMITSSVVHHGEEQQLIFQGKEARVSAPWKVVASTARNNGFPEPNREL

EHQIQKLADLDPDVTHVGHAGQVENVLNAIETGSPLLVDGQSGRNTLELIVGIYKSAS

TGEKVVFPPLGAEDAFYTREGIMQHAVHFYEKKTVDNFEDSSITLGRKLDF"

CDS 50949..51881

/locus_tag="EFAGFIKM_00060"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLFANAGMALMPHKLMSAYMFFISLYAAGMIIAQIGIFRLYYNK
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YFMVTILFAMQLLLHLGSAFTGYELLAELSLILSVFVSFIVFTMIFEKIIGVMQAATY
TSTRDEVTGLFTQKHFIHQANQALSKGKTVGVLYIEIQNPTHISSEESFKRAGRAVGR
ALEGSGFAGRYQSDVIVALITSSNLPLAELANSIRMKIDVEASSTVLIGYIDTKPEFT
LDDHIREAKEGAIRTKQSGLNRIFDLDDQSKILAD"

CDS 51896..53155

/locus_tag="EFAGFIKM_00061"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNAVISSKASTLVHEAIGNTDVSFEKVGRFESGQFIEFCEAVA
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VVTSPGTPKPSIIPALRNLLPNQSEVTGNGQEDWESTDSDLEKIKDRIYRYTAKLTS
AGSFDSSDVMDELDPVPIQERIILKDRIIGTILVGVMGVESKVGSTHQSILIANYLK
RKGYSVGLVEANSSSDFTSIENAYEGTQDFKSNNIHFSIEGVEYYKNNNKLDINHLIT
AGHDYLILDIGSFEESDWSKEFYRASVNIVLGAGSEWRQGKIRRFRLHKKMDQSNWV
YCVPFVENLSIQDIRKDLPGNLVYRIPPHADPYKHQGDTSVLNKLKMSYMGDSKKIS
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CDS 53188..54222

/locus_tag="EFAGFIKM_00062"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKIRFRQKQLLLSASIGGAILFVCVIAGYFIIDYIQGRYVER
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EIVGKRIKIDVQKNSIITPMLFEDGITPNDLRNQEFSLVQLPLKLLKDEFVDVRIRF
ATGQDYIVLSKKKVEDLNNGTIWYKMTEKEILTMSSAIVDAYINDASIYALSYVDPYM
QDGAIIINYPSPKVLDLIESNPNIIVGLATTALERQVRACLEQDLQSMSDEDRQKYISG
RNTTEMNSREYITETEGQGNGTTSQQDNLSLMNENSTDMNQSQNTGNTPNATSDSGSIF
KDSNTREPAQ"

CDS 54237..54920

/locus_tag="EFAGFIKM_00063"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKQILVMGHYDKTDFMMYLGKLLSMDHRVLIVDATQNKDYEFVF
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YVVTSYENPVIQKNVNLIRAYFQGEKLSSVNLPVTKVIYEVSNHLDEKYMDSLLDELP
LSWKESLVYYPDERDQTLKIINQYKNTVMVKRMSSSYKLVIKQAIEFILGLETSKVNA
LWKRAERSN"

CDS 54922..55761

/locus_tag="EFAGFIKM_00064"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGKIALWGMQHGLGVTSATAALAAFIGLEYDVRTLVSQPQRTDG
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QNISVLEKYFDNQRKHWPEVLEEKPHLLMTQYDPMSKYKIKNIANKYKLKAPILTIP
YNTSFKDHLNDGDIKGFFARNRFVGGSSHENHYFIQEVGRAAKTILHEIGINTKLKRIE
RGN"

CDS 55763..57670

/locus_tag="EFAGFIKM_00065"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGLNFTINFLAILIVAVLIAYLFLKLNRPKGQVGTRQKNENEE
RFQFDYLLEYVKTMINEYVNSNLLDMGMTSEEYNRRLGVVAELRSAMKNATSGDIQEK
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LIDKYQLDQPKKVIDGTVD SYVITGDEIDSIFVKEARGSLFDDKLAIVVQRVYQHY
KGFGVIDEIRDMSIDGVSGGVSGVPTNMQIVEDEISLLQGMKQYKYPGYQSVWIFFRG
KSIHLSFLSFETDLELKRVCQNIYKYDNPGQLTETNGFKVNEMKDGSRVVVVRPPFAE
SWAFFVRKFDLPNMKLDHLISSKDAVNAELARDMIKYLKGAQVTAFTGPQGSGKTSL
VMASVKIYATLTLRIQEMTFELHLRRLYPQRNSLALREteniAGQAGLDLQKKTdGS
VNILGEVATDPVAAWMIQMSQVASLFTIFTHHATSARELVWSLRNSLLKTGVFQNERI
AEEQVANAVQWDVHMRKEMNGKRYIERITEITPVRFESDTLEHEEVLSKGDsIESKLD
ALVNLQREVYRRNSGRVWNARNIIEYRNGEYVAVSPISPEKIEKMLFNMNEEDRENFG
QFLNAHWGQAQ"

CDS 57667..59739

/locus_tag="EFAGFIKM_00066"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNKWIWIFAiAGGALLISGGILLYLILKDRKRKNRENvWPSSK
NVTGKTprQLLVfyQkSYHQLIKVPIVKSQILKIRKRLTAINTYDEYSLRKETMRITY
LTLGSIIGLIVLAIISKSWMALFFGALAAIVINELCIDIFVNRVEDRLLKQFSNVLE
DDRHHYQEVrmVDEALYQAAQSSPHDIKLQTERIHEVLTskDPARELEKYYAVAPNRY
LKVfSGVSHLIMEYGDRNVQKGSmyLNAINKFVQEIRYDLmRRQKLRYKLGGTLlLAL
IPILLSfPLQRWAENYFPITTEfyDSRIGFLVRMFIYASAVICYLLIRKLSenDEAKY
VAKGPRKEWEKKAYSWSWVKWIVDRLVPSPNTRKHhRTNMLLKEANSHLTleWLYIHR
IVISVSAFIGVIVFSVFLHYNSVHHIFSKPTSEATNILGYMNADELERANQVTMDNQ
IIEDLRtnKDLTREQVVQSIETHSNEPLTDVAMNNTVnRIIGKVTVVNNEYLkWWELL
IAIGFGVTGYyITIWILQFQRRLRALEMQNEVDQFHVLI SILCEFERISVETVLEWME

RYSIIFRPALQKCLLNYSGAEEALKMLKSDAPFDSFGRIVKRLMQAVDKLSLREAFD
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CDS 59758..60243

/locus_tag="EFAGFIKM_00067"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEENTGVGIRVAAGIFLTIMLITIVVIITISSQDAAKQGQTKMA

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CDS 60277..60657

/locus_tag="EFAGFIKM_00068"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSETVEKFILVAAEISILIVACMFALGGIQSQDAAVNITHKSAV

NEERRLFTSLEITEQVTYTGAEVLQSIRQMKTLDANIRVVNKYFYSSDDIESIDVSGV

DLNRTYVVSYIRDSQGKVQTIVFT"

CDS 60671..61219

/locus_tag="EFAGFIKM_00069"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MENSFSKILGIFIAIVLLFLYPLFQQAQRQDDLQIIVHSVTT

FVDSARTKGYITPEMYLEFNQKLGATGNQYDIQMEHLHKKYNPEYTDPANPATFRDSF

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GITDGNVKVYVPYGGMVINEDY"

CDS 61206..62189

/locus_tag="EFAGFIKM_00070"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS 62221..66225

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CDS 66354..66623

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/inference="ab initio prediction:Prodigal:002006"

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CDS 66698..67447

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CDS 67466..67747

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CDS 67786..69144

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CDS 69166..69975

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CDS 69976..70251

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CDS 70264..70623

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/codon_start=1

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CDS 70636..75453

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CDS 75456..76013

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CDS 76963..77499

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CDS 78339..78641

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CDS 78616..78765

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CDS 79502..80758

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CDS 80771..84265

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CDS 84450..89357

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CDS 89434..89850

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CDS 90619..91461

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CDS 91481..92266

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CDS 92448..93704

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CDS 93720..94061

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CDS 94505..95041

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CDS 95250..96104

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CDS 96106..96741

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CDS 97938..99173

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/inference="ab initio prediction:Prodigal:002006"

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IPVKEAFSPGISQSKAPYIAVAMGTGIMTGFPDHSFGLSKTTTRAEASVILLRIANME

GKKASSFEALNEIRSVGVAKSNFKEITPFEFTTGRDFSDASEKKVTFSNKSGLVLHR

TIAVDASDWNKKGVYAPFFISESEKDWYQSTAKRKNIVAVFQEITIYPSKKGFNLDD

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GLVARFKTDDGSGVSIYGR"

CDS 99170..99790

/locus_tag="EFAGFIKM_00096"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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YEPGNEKPRFTQGDKFIEINVFTGYPKPFSEEKEYGTRPDDKKNKGK"

CDS 99805..102552

/locus_tag="EFAGFIKM_00097"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHIDYIAHVYETKEIRVNSDNILQEGETVQLAAEVREIDYQGNT

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LYGNVFSRDYLFHTFVQMTGTCTYQFEVEKIWTLKWDPKKKETDAEGNEREVPDPQE

AEEPVSKQYTVERP YAWTIDT LSVYSLDEATLIN YAFGSGQITLQPEG YVPPDFQAE
TTGDYPPPNPVKVTAPP GKTGGKDRPSPD EDLQSLAEEAVPDVEVENDAFYFNGG
TVMDPQRSPESGPQPGEIPDPVQIDENVLYSPYNYIPISKANKQDTISEGTIRYTLMD
NSVNGGDDQEFDIYGINTVTVHTPVVNYSLVSDDQPHNQKTVPNMNR SALILERPFTV
RIPTSGQHLDAGSYPGYGDRDYAKYYRIKQVRFPFDVYSADRSQFYPRNTWIDVQVPV
LDTTFYLPVWVDEGDYQVEFRNIAENVPTHFSSEPEIDAQPDANTDLYYHAASDEVSV
EVIGRLYDFEITDIADYNWELVFRRFKNSLAPT WISYWTGTQDIDGDKRGNKPQFTVP
IRPGSHPLQGYQNAVKTGYPFKFDFTKGNMFGPRDGIRLTPTFDVSKDGSTRVPV
ELYYSTNQRFIRIGSTEDQVKRFVILNDRLRQVPSEQLRDTATYKYNRYGEIHPGMM
SERAYQEYYRDKFTKMKTPVGGYSLLLMPEQLRTFIGPKTNIPTTASADVL RANAAIQ
QWYGEYSLPAEPYVVQAGTNLVEYGRTHGGLDAKSPIFLK DGYIVVNFNFESIREGNL
AAPHLQYIHAPLMNQWLLEGFQREVEDSYGNSFTLRDGDVVFYHADRSSRDDFSAQVP
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CDS 102727..103014

/locus_tag="EFAGFIKM_00098"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDTKDKDQEIIDRSEAIQYLKDTYDL DVKITRKQM QPKMAMS

WVTFYGYVSQH EEQSFNVSYNIEENRTESFSFSPELEEVLLNEGYPYKLE"

CDS 103036..104331

/locus_tag="EFAGFIKM_00099"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKESSNNREITDLVYKKMSQEAYKDYETGKKIGVLP GWEVL DQ

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VTNFIHPGDFIASGMLGGYERHVGSTLVIDKNYDDFNASYGAVDKIKDTLGGPSYHDM

KHYSFDDDDGYIDNTLYDEITGERVSFSPRKPSDHNILDHAREAWDTLSKGFKSVNVV
GGYSAGTIELTSEELKEIAGKWSRQAQDMSRTFERIQRNFFEYTESSHSQRLVPIVWD
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CDS 104363..104638

/locus_tag="EFAGFIKM_00100"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSGSSIAMDLQQLLQAEQELDLILSELRENEREARVLYGKLNTW

KGQSADKLRIKVEVFFYQLDTRTQLLLKQKQEMLDAIKRIKDADGSY"

CDS complement(104825..105874)

/gene="ugl_1"

/locus_tag="EFAGFIKM_00101"

/EC_number="3.2.1.179"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9RC92"

/codon_start=1

/transl_table=11

/product="Unsaturated glucuronyl hydrolase"

/translation="MKEHIGDKCPHFAGKDGKYDNINTDWWASGFWPGMLWIMYDMTG

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QDERFLNTAKRIAPYFIAALPEDHVPYWDFRLPTLEGQSRDSSAAAIAASGLLELA

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CDS 106093..106458

/locus_tag="EFAGFIKM_00102"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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IVVNNHTYPIGQGMLFFFQPYQLHHVYVEVHPNTPYERNIFYVEPIVMDRYLEAFPH
RRSFFRGCGMGAISSKFLT"

CDS 106467..107024

/locus_tag="EFAGFIKM_00103"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDQVDWMYESYNQSRSRVGGEEESVLFLLQLLSVLDQQKEGAD
EALSQLTDSRHFHRHLEKMMWWIKKHLDYEIRLDQIAADVHLYKSYASRIFHEETGRSI
TDYVTARRLKKAYLLLETTSLWVKRRGRRRARFPNGCISSSYFANLPGRARCIIGNNLN
GAASIILVCKIIALLRLYTQLVFTV"

CDS complement(107140..107460)

/gene="yodB_1"
/locus_tag="EFAGFIKM_00104"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34844"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator YodB"
/db_xref="COG:COG1733"
/translation="MSDDENAKQICTKVEQSYQIIGRKWVALIIHALMEEPKRKFSEIH
AYIPDLSKRVLNERMKELEEEGLVVRHVVTERPVRTEYMLSRKGTTELGRALSAVERWA
DKWL"

CDS 107876..109330

/gene="zwf_2"
/locus_tag="EFAGFIKM_00105"
/EC_number="1.1.1.49"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54547"

/codon_start=1
/transl_table=11
/product="Glucose-6-phosphate 1-dehydrogenase"
/db_xref="COG:COG0364"
/translation="MDAMTFVLFGATGDLAKRKIYPALYNLYMDQKMPKSFSVIGLGR
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QREQELNIPENRMFYMSVAPEFFEPIALNIQESGLGNTKGWKKLIEKPFQGHDLQSAR
DLNEKLSNTFAEEEEYRIDHFLGKPMVQNIETLTYPVIALWSNRYIANVQITASE
TVGVEERAAYYDQSGALRDMFQNHMLQLLMMIGLHLPKRCTPEEIQFKKQKIAEALRP
LTKENIASEVVRAQYAAGELKGSSVVGYLDEPGIPAGSQNETYVAARLWIDDPFWSEV
PFYIRTGKRLAEKSTRIVVEFKAPLKTGHESSENTTEPNLLTIEIGPGESISLQLNAKN
PLNHDEVEPMHMTFN SGKRNIP EAYENLIFDAMRGDSTFFAHWNEVELAWQWVQPIQE
AFEAGSVPLDTYSAGSHGPESADRLTAADGFRWW"

CDS 109915..110808

/locus_tag="EFAGFIKM_00106"
/EC_number="1.1.1.343"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:G5EBD7"

/codon_start=1
/transl_table=11
/product="6-phosphogluconate dehydrogenase,
NAD(+)-dependent, decarboxylating"
/db_xref="COG:COG1023"
/translation="MKLGLVGLGKMGLNLGRNLIDHKHEVVAFDLNAEAVNEMKEYGA
EGVSSYAEMVASLESPRVLWIMVPHNVVDAVLAEVSPLLSKGDIIIEAGNSHYKESIR
RYEEMKPKGIHYMDAGTSGGMEGARNGACYMIGGDPEAWAIVEPAFKDTSVENGYLYA
GKAGSGHFLKMVHNGIEYGMMA SIGEGFDVLEKSGFD FDFEQVARVWNNGSVIRSWLM
ELTERAFSKDANLDEIKGVMHSSGEGRWTVETA FDLQTATPVIALSLLMRYRSLETDT
FTGKVVAALRNEFGGHAVEKN"

CDS 110895..111539

/gene="tal_1"
/locus_tag="EFAGFIKM_00107"

/EC_number="2.2.1.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P19669"
/codon_start=1
/transl_table=11
/product="Transaldolase"
/db_xref="COG:COG0176"
/translation="MKFFLDTGNVEEIKRIERLGLVDGVTTNPSLIAKEGRVFKEVIQ
EICGVVKGPVSAEIVIGLKAEDMLKEAYEIAEWAPNVVIKLPMTEDGLYACHELTQKGI
KTNVTLIFSAAQGLMAAKAGATYISPFVGRLLDDIAVDGMKLIRDRLILDMYDLPSEI
IAASIRNIKHVEDAALSGAHATIPGSLLPTLWKHPLTDSGIERFLKDWESVVK"

CDS 111804..112682

/gene="yunB"
/locus_tag="EFAGFIKM_00108"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32131"
/codon_start=1
/transl_table=11
/product="Sporulation protein YunB"
/translation="MMRRKWRSRRRRKPPSGKRKMWLIILLVTAFCLMQGFAYVDKKM
KPPIMHLAKIRVKQIATEAINKAITAQVADGKTNEGLIDWKTDTTGKVSGFMLNYNEH
MRITASTMNIVQSTLQNVHMLKEKIPLGQALGSPVLASFGPSIPVRIEPQGAVKVDLN
TRQQNAGINMILVEVYIHIIAEVAVVVPFDMETVDTEIPISYLLVGDVPMYYYYDN
QGKPVGSNGSNAPAIALPSGHTGVSNGNGVTTNPPSQNQQTTPSDHLQGNELEIEPDE
LPDVNGGLQLNKDAHP"

CDS complement(112770..113840)

/gene="lytH"
/locus_tag="EFAGFIKM_00109"
/EC_number="3.4.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32130"
/codon_start=1

/transl_table=11
/product="L-Ala--D-Glu endopeptidase"
/db_xref="COG:COG0739"
/translation="MQQRLTFRHTYRFWIKTLLAGTLLLPFLPVEVYSEPAQAAPKPQ
ATELKPAEIFAARRHLYETIGQMTQIPWYRLAAIDQYERTITRAHPKDRKHPERLTGI
FMTPPAWRGWLNPDQHPESILFFKGYGRDGS DGIADANNDQDVLYSMASVIQGY
GNKQEDFNIALWEYYHNSRAVQRIQQFAKLYEHFDNLDLFGHAFPVPLGTNYSYRSTW
GKRSWGGYRIHEGTDIFAPHGLPVRSTCYGVVEIKGWNPFGGWRIGIRDLNNHYHYY
AHLSGFDQSARIGEVVPGQVVGWVGSSGYGKPGTQGKFPPHLHYGIYRDSGLHEWSF
DPYPQLKHWEQDERKQKNKKSK"

CDS 114081..114980

/gene="lipA"
/locus_tag="EFAGFIKM_00110"
/EC_number="2.8.1.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32129"
/codon_start=1
/transl_table=11
/product="Lipoyl synthase"
/db_xref="COG:COG0320"
/translation="MAKRVKEPKPDWIRIKLTGDNYQEMKTMMSKTLHTVCEEARC
PNIYECWANRTATFMILGDICTRACRFCAVNTGLPTELDLQEPERVAEAAEQMNLQHC
VITSVARDDLKDGGATIFAETVKAVRRRLPLCSVEVLIPDFLGDLESLQIVMDAKPDI
LNHNIETVERLSDKVRAKAKYKRSLELLARAKEMQPNIPTKSSIMLGVGEEYNEILST
MDDLRAVNCDIMTIGQYLQPSEKHLYVEKYYPPEEFAALKQEGLKRGFSHVESGPMVR
SSYHAHEQVKSATKHAEQAATHA"

CDS 114977..115402

/locus_tag="EFAGFIKM_00111"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MMGDTGLEEEKITEQIQDQLQEPVQDSVVESVEEKPKEPVIVQI
GGKNYEIVQNHKEGWNPEVFRDRYSEVLERYDYIIGDWGYSQLRLKGFYRDNHPKATK
DSTIASMVDYINEYCNFGCAYFVLQKSKDQPQAKAKSGS"

CDS complement(115430..116233)

/gene="ppnKA"
/locus_tag="EFAGFIKM_00112"
/EC_number="2.7.1.23"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31612"
/codon_start=1
/transl_table=11
/product="NAD kinase 1"
/db_xref="COG:COG0061"

/translation="MRYVYVQDRGDQLSIDLSQQFHAKKEEGFKLDAESPEIVISIGG
DGTMLQAFHNFIDRIPDIAFVGVTGHLGFYADWKKEELRELVRLMSGKGDPERLKPR
IVQYPLLELEIRKKSGNSSYIALNEFTLKGVDGTVAQVDINDVTFEMFRGDGICVST
PSGSTAYNKALGGAMVHPTIEAIIQAEIASINNRVYRTLGSPPVILPKHHHCDFSRKD
QRLLMTIDHVNVMVEDLISVRCQVSSHKVSFARFRPYPFWNRVRTAFLD"

CDS complement(116338..117591)

/gene="yIbJ_1"
/locus_tag="EFAGFIKM_00113"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34765"
/codon_start=1
/transl_table=11
/product="Sporulation integral membrane protein YIbJ"
/db_xref="COG:COG3314"

/translation="MAASQRLTHVLVTLALLILCVLMVLYPAETWHAGVRGLSIWWDV
LFPSLFPFLVLSSELLGFGIVHFLGTLLNPLMRPLFRVPGSGGFVFAVSCASGYPTGA
KLTAQLWAQKLVTREEGERLVAFTTSSDPIFMIGAVSVGFFHNVAIAPVLVASHYAAA
FLVGMLMRFHGGTAKGSHQDISSASPSEGIPRNRLVRAIYAMHEARKADGRAFGELLR
QAVSSSLRLIIIVGGLVVFFSVMMELLVQTGWLGGLYGITEQLLRHSGLPSPSLV

GGLFEVTLGNKEAGSAGASIPLVFKVAAAAFVLSWGGLSVHAQIMSVLSNTPMRYGPF
LFARAIHALIAPVLVLLLWTPMMGRSSSPVLMEPGFAPSLSTYTPDWGLIFLCGMIVF
VSLIVLLLFLAILSSILKPRRHAKK"

CDS 118152..118529

/gene="yjbl"

/locus_tag="EFAGFIKM_00114"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31607"

/codon_start=1

/transl_table=11

/product="Group 2 truncated hemoglobin Yjbl"

/db_xref="COG:COG2346"

/translation="MNPSLSIYDNLGGEKGVRLVEAFYPIVQQNEQLAPLPEDIQP

VIDKQYMFLSQFFGGPGLFSEAFGHPMMRRARHMHFEVTVRAEAWLACMDQALTQIGV

EEPLHAFILQRLSGPAHHFVNTP"

CDS 118573..119304

/locus_tag="EFAGFIKM_00115"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MELEPLYKVKVTCHYCETHEYTSRVRPSLKRPYRTDSDFCAYYK

LENPDFYVVRICPQCGFATTENATEHLNDVQRKAFKEQIGNRWVKRDYSGARTLEQAL

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CDS complement(119317..119550)

/locus_tag="EFAGFIKM_00116"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIPFENSWPYDIVMGDIYVQQCPYCHASNVLPLKPKELVLIRE
GKKKLLVFPCCNTSMTVIDNDSYLLSSRPVRN"

CDS complement(119547..119717)

/gene="yycC"

/locus_tag="EFAGFIKM_00117"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37481"

/codon_start=1

/transl_table=11

/product="putative protein YycC"

/translation="MKPLQVSADTAVKLAESLGVPLEHLMHMPQHILMQKIAELAKQE
ASKPSAPEGEQE"

CDS 119836..121635

/gene="pepF1_1"

/locus_tag="EFAGFIKM_00118"

/EC_number="3.4.24.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54124"

/codon_start=1

/transl_table=11

/product="Oligoendopeptidase F, plasmid"

/translation="MKTPLHPVWDLESIFSGGSSSETFAAYLIEEEDVRKLQHLLNE
TPAPTSLEETAAFDPILELLQSCYMRVSEGSAFVSCLSQNQKDKKATQLQGAISSLG
AMLNGSKSKFDNTLSQTSDLVWDAWIAREDIQPLAFVLNESRTLAREKLSPELEGLAL
DLGVDGYHGWGKFYNTIVSKVNIPFEQDGETVMLSAGQAANKLSDSDRNVRETVFANW
EQAWTDVEDFCADTLNHLAGFRLKLYEKRGWDDILKEPLAINRMSRQTLDTMWVDVING
AKPALVQYLERKAELLGVDKLSWSDVDAPVGKSSGKITYDEAAINIVEQFAKFSPKLS
SFAEMAFEKRWIEAEDRPGKRPGGFCTSLPLSKATRIFMTFSGTPSNVSTLAHELGHG
YHQHIMEELPALNQRYAMNVAETASTFAELIVADALVQAATDEQEKLALLEDKIQRSV
AFFMNIHARFLFENRFYEQRKKGLVNADELSKLMVEAQQAFCGVLASDHPHFWASKL
HFYLTGVFPFYNFPYTFGYMFSAGIYARAQQEGTAFADKYDDLRTGRMTVEELAQKH
LGTDLTQPEFWQNAADLVIADIEQFLQMTATEK"

CDS 121910..122320

/locus_tag="EFAGFIKM_00119"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKIDELSLARQLDLVFKELDHESGLDSGVVQIRNNVIGKFG
IRHNPIAGRDGQMAVEEGGLNETQRTSFRAMALETLKFKRNWTHGEISYDFTVRQGM
LVDATMESNYNMASLMIRYPRTNTYKDSDMESTS"

CDS complement(122406..122639)

/locus_tag="EFAGFIKM_00120"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P22065"

/codon_start=1

/transl_table=11

/product="Small, acid-soluble spore protein alpha"

/translation="MYGNQNQGSGSRNNLVQPATAALQQLKIEAAQELGVTIPQDG
YYGNYTSRETGSLGGYITKRLVQIAEQQLSGRS"

CDS complement(122845..123819)

/gene="galM_1"

/locus_tag="EFAGFIKM_00121"

/EC_number="5.1.3.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39840"

/codon_start=1

/transl_table=11

/product="Aldose 1-epimerase"

/db_xref="COG:COG2017"

/translation="MKQVTKGQWNGYDTYLHSRELEITLLPRLGNNIISIRDLVQDR
DVVRRPDEDDLAFYLQKPYHFGVPLLIPPGRHGRGQFEYEGVRYQFDQNTANDNHIHG
LHRTQSWCVSDIEEDEDGCAITTELLTENEHWMQAQFPIPLKLEMTFSLQNAVFSQRL
RVTNLSSTPAPFGMGYHTWFLLDGKPADWTLQLPVSGIYGQNEEQLPTGELESLGECS"

ALNEGInLQGLNWDtLLKATEGELATAYLRRQDGyTLKysADEAFFKHwVLfTKGESD
QFLCIEPYTWLPDAPNLALSDEQTGLIRLEPEQPVELFSRIEVIPTD"

CDS 124409..125401

/gene="trpS"

/locus_tag="EFAGFIKM_00122"

/EC_number="6.1.1.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P00953"

/codon_start=1

/transl_table=11

/product="Tryptophan--tRNA ligase"

/translation="MKTVLSGIQPSGKLTGNYIGAikNFVKLQHDYQCHFMVVDLHA
ITVAQEPAALREQSEAVAALFIAAGIDPSKSNVFLQSHVPQHAELGWLMTTLTSMGEL
ERMTQFKDKSSGKDSVGAGLFVYPSLMAADILLYNADLVPVGEDQKQHLELTRDLAGR
FNHRYGEYFTIPDPYIPQVGARVMSLDDASSKMSKSNPNAGSYIALLDPPDVIRKKIS
RATTDSGREVVYDPANKPEVSNLMSIYAECAGMTLKEVAERYEGKMYGPFFKELAEV
VSVIEPLQQRYNEIRESGELADVLDTsARRAEEVAAQTLDaVKERMGFVPRRKQ"

CDS complement(125516..125716)

/locus_tag="EFAGFIKM_00123"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKGLSLWFAFSSIVLLTVSAIMISYSGWFAALLFVLSIANIGW
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CDS 125837..126055

/locus_tag="EFAGFIKM_00124"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P22065"

/codon_start=1

/transl_table=11

/product="Small, acid-soluble spore protein alpha"

/translation="MAQGSRSNNLVVPQANSALQQLKIEAAQELGVTIPQDGYGNYT
SRETGSLGGYITKRLVQIAEQSLAGSGK"

CDS complement(126173..127153)

/gene="yfhP"

/locus_tag="EFAGFIKM_00125"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31583"

/codon_start=1

/transl_table=11

/product="putative protein YfhP"

/db_xref="COG:COG1988"

/translation="MDTSTHFVMGIGLAGLAYVDPVVAASPMLAAVMIGTIAGSQAP
DIDTALRLKSNSLYIRNHRGLSHSLPFLLLWVLLITGVIALIFPGVPIGHVATWTAVA
VGFHVFTDLFNTYGTQAARPFTERWIAWNIIHIFDPFLFTTHVIAILLWAFDLIAPAP
LFVTLYSLTGLYYIWRTIARAQAVRKVRRLDNSPEQARYIVIPTISWNRWHVVKRVED
GSYVIGKMDGSNLVWSLHASSSTHAAVAASRKSPESAFLYFTSYAVAEVEELPAGYK
VRWADVRYRHRKQYPFVAVIVMDRNFETIDTYVGWLSDEKMDKKLLSARP"

CDS 127576..128187

/gene="ypmQ"

/locus_tag="EFAGFIKM_00126"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54178"

/codon_start=1

/transl_table=11

/product="SCO1 protein"

/db_xref="COG:COG1999"

/translation="MLKKYKWTWMLLGLALIMAVYLMWGTVFASKEKLPEIREIQSFS
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VSISFDPKVDTREKIKTFADRFHADYSGWYFLRGDMDKTKQLARDSFQILIEGENKDD
FAHMNMIGLVDENNQLRKVYNFNTEDVVPVAVIAEDIRNLIKE"

CDS complement(128256..128603)

/gene="rnmV_1"

/locus_tag="EFAGFIKM_00127"
/EC_number="3.1.26.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01469"
/codon_start=1
/transl_table=11
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/translation="MPIHVIVEGKNDRSKLKRLVGPEINILCTFGTLNSLKLETLRKQ
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CDS complement(129135..130310)

/gene="mdtG_1"
/locus_tag="EFAGFIKM_00128"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01528"
/codon_start=1
/transl_table=11
/product="Multidrug resistance protein MdtG"
/translation="MKTAIWLYLFLFLAVFDLHAQYPILTPFAISLGAAPTFIGWMMG
IYSLTHLPGNLIAGTQIDKHGSRRYIVFSLLGAGFILLQAYVQTPWQLLALRSISGF
VLAFLSPACLALLAQLSSDPVKQGKYSMSGHGVVHTLASVVSPAAGAIIVGSMGFSATF
SGLGYLLILTGVIAFMTMPRGIVKQHEKVTVPAKPDASPADATSAFLPVSWRYFALPL
VIACAQGILFFELPLRGGGQSSIMSTGLLFSIISIGALFTLSMLFLNRYSPKLRLVAG
VLLMSLCFFVMAAIPQVPLSTVLFVLGMSKGIIFPAMATLFIRLSGGSKLGRIFSLQS
IATSIGSGFIGPITAGQLRIGLSPYFIAFVLLMIGMLLLPYTSRREASLSDPKSILN"

CDS 130501..130983

/locus_tag="EFAGFIKM_00129"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNSNTEGVVMNIEVKEFVMQNWLVIVVALIILFFVLNVVKTVL"

KWAIAIIIIAALLIYSGISIDQIKQTVTDVQSSTMETLKKEATSMMLKEASKAKYVKG
QDGAFTITSPNVEIKGRTQSDKVDVTFRGISLGEWKLDNETIRTFVEQAQENKTAPAS
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CDS 131002..132147

/locus_tag="EFAGFIKM_00130"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLQNWLDLSELNGITIMLLLIVAASLLQGWSRGASRSAGRLFG

YLMGIMAVIGILLSIGLTLWLAPYVQQWLSEYASAMPNRELNRWEQMYITLVTAIAD

FPLMRFAVLFLVLSYGLIRLILGFLSSIFSSRQRSAEESAPKGMFSRLTGAFITIG

SVRGMIVIAVLFMIVSLYPGSMFSRYVEASPIYMQGAKSVIEPLSGTFIKDKLPVFTQ

AVQQELGGILQRKYEVIDHNIPTDIESAASEIVKGQSTDEAKARALYDWWGSRIQYDF

GKVDDYEQKGIWHEQNPQNTFDTRKGVCIDYARLYAVMARSQGLEVKVVTGLGYNGQG

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CDS 132253..134292

/gene="mrdA_1"

/locus_tag="EFAGFIKM_00131"

/EC_number="3.4.16.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AD65"

/codon_start=1

/transl_table=11

/product="Peptidoglycan D,D-transpeptidase MrdA"

/db_xref="COG:COG0768"

/translation="MKKHSNEKDELTDKRRFSYRMNVFFASFVIFSIIIVRLAFLQF

VEGPELSQEEASNITKDVLPPVRGTIYDSTGEVKLAYSKPIQSLYLTLYKNYGDVGG

QPSPNIGEVQDIATRLHDVFEQYKLKDSEPLTVEKIIEMDLNSRKANGFMPRIKSD

LSEEEVAYFLQHKDEFKGIQIVEESVRFYDPDTVAVQTIGYLKKFRSSKSLNKYKEVD

EANKTQTDPLVYTENEFGVFDGLELQYQDALRGKSGYTSVDVDLRNLPEGVAGSTPP

QKGYDLISSINKNVQVKTEQAILDQLNWLHRNPVSGKLHLNAKTGFAVAMEVDTGKIV

SAASMPDYDTNVWRTGGISSEDYDNIKIYQNGTIRGFPPDDSGKRAESVLLGSTIK
PLSVLIGLKEGFFTNTVYSDRGSTTFGGDNRRVQNSSGHVYGAMYPRDAIRHSSNVF
MIDEIGKKLYSKYGAKGVDVWDEYMEKFGLGISTGVDLPNEFLGRKEYGEDSIESSLT
KLVYASFGQQGKYTTMQLAQYTTMLANKGKRMEPQLVREFRDSEGNVVEKVKPKVLST
VEFNDAWNEVQRGMATEVSAFSGFPYDFARKTGTSTQVVGKPPVDNGVFIAYAPRNN
PKLAVAVVIPEGGFGSSSAAPVARAIFDAYDEEFGLDGVPKKDKNKDSSESQTQ"

CDS 134661..136634

/gene="mrdA_2"

/locus_tag="EFAGFIKM_00132"

/EC_number="3.4.16.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AD65"

/codon_start=1

/transl_table=11

/product="Peptidoglycan D,D-transpeptidase MrdA"

/db_xref="COG:COG0768"

/translation="MFNRLRKPMTEEDTPVNKPSTARLNLFFFAAFVIFSILIFRLA
FVQFVEGPELTYMETSRTNKDIPLAPVRGPYDATGEVALAYSEPVQSLYVLLYEDYR
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STKEIAFFMEKKTEYPGVMVLEENIRKYDPDGVAVQVVGYTREFKRAPDSIAKYKAIR
EGASTQRDPGLVYHEEEKVGFGLQYQEELRGRSGYQSIDIDARNLPDGTMLQTPP
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NDWDYDKIKYVFRNGTTESFPNDAPKPSRAESVLLGSGVIKPLSVLIGLKEGLFTAGQ
TYHDQGYAILGKDGRQVKNSHSAYNGSITARAEKSSNAFMIDMVGKRLLSKYGSEG
IDIWDKHMKEFGLGVSTGVDLPNEFLGRLEYTNKDESALTRLAFASFGQQAKYTTMQL
AQYTTMLANKGKRMEPHLVKEIRDADGNVVEIKPKVLNEVDFADAHWNEVHKGMVTK
VSADFDFPYDYARKTGTSEQGTGPNKKENGVFIAFAPRDNPKLAVAVVPEGGFGSVS
ASPIARKIFDAYDEVYGLDGTGPKGKKGEGKDKE"

CDS 136873..137817

/gene="mntA"

/locus_tag="EFAGFIKM_00133"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34385"

/codon_start=1

/transl_table=11

/product="Manganese-binding lipoprotein MntA"

/db_xref="COG:COG0803"

/translation="MVKMRSIQRGFITLAALVLVVLTACSSDAETSSGGKLQVTATT

GMIADVAREVGGAYVDVTGLMGPVGVDPHLYKASQGDIRKLEQAKVIFYNGLHLEGKMT

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EADPDHAAEYKAQAEAYLAKLEALDAEVREKILEIPEASRVLVTAHDAFGYFGQAYGM

KVMGLQGISTAAEYGAKDVSELRDYLVDNHIKAVFVESSVPAKAMEAIAGAAQKGHT

VSIGGELFSDAMGAEGTEEGTYIGMIRHNVETIVEALK"

CDS 137848..138669

/gene="mntB"

/locus_tag="EFAGFIKM_00134"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34338"

/codon_start=1

/transl_table=11

/product="Manganese transport system ATP-binding protein

MntB"

/db_xref="COG:COG1121"

/translation="MEDTTLLKQTPTKLNNSHLQGTQPTSAPLSVRDLAVAYHKKPVL

SSVSFDIPEGQLIGILGPNGAGKSTLIKAVLGLVPKMHGEVRIFGQSYREQRRRIGYV

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QLSGGQQQRVFLARALVQDADLYFMDEPFAGVDATTEKAIISLLEQLKKQGKTVLVVH

HDLATVEEYFDHVLLNGLRVAGGPTSEVFVPDTLQETYGGRIAMIGSRTEKGQV"

CDS 138673..139632

/gene="mntC"

/locus_tag="EFAGFIKM_00135"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O35024"

/codon_start=1

/transl_table=11
/product="Manganese transport system membrane protein
MntC"
/db_xref="COG:COG1108"
/translation="MWNWIVAILSDPNTRWILLGCLLLGFSSGIIGSFTFLRKQSLMG
DTLAHAALPGICIAFMLTETKSVGLFLFGALVAGIVATFGISWITRYSRIKQDAAMGI
VLTVFFGVGVWMLTRIQH GASGSQSGLDKYLF GQAASMVM TDVYVMGGVCLVLLIACL
AWFKEFKLVSFDPGFARGMGLPVAMLEQLILLTVIAVVAGIQAVGVVLVAALLVTPA
AAARCWTDSLALMVVLGIFGALSGATGTIFSTLVPNLPTGPVTVLAATVLFAGSALL
APRRGLLARRLRISIQAKSAYMREERATLQTLATQRNQQERGEM"

CDS 139632..140504

/gene="mntD"
/locus_tag="EFAGFIKM_00136"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34500"
/codon_start=1
/transl_table=11
/product="Manganese transport system membrane protein
MntD"
/db_xref="COG:COG1108"
/translation="MATFWIILTAVLVSSACAILGCFLILRRMALVGDAISHAVLPGI
AIAFLWSGSRDSLWMLLGATVFGLLTVFFIQSLQAGGLSSDASIGIVFTALFAVGVL
ISLNAQHIDLDCVLFGEIAYVQWDTLTGGTDVGPRAVWMLGITLLVILVVIGLFY
KQFKLCAFDPALAAACGIPVVLFH YLLMGLVSM TSVASFESVGSILVVGMLIVPAATA
YLLTDRLGKMILYAVLIGAASSVGGYIMAYALDASIAGCMVAVAGILFVLALLLSPKH
GIVFRYARRKFAAR"

CDS 140816..141565

/gene="ycsE"
/locus_tag="EFAGFIKM_00137"
/EC_number="3.1.3.104"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42962"

/codon_start=1
/transl_table=11
/product="5-amino-6-(5-phospho-D-ribitylamino)uracil
phosphatase YcsE"
/translation="MSELKYKLLALDMDGTLLNDNHEITQETAKWQIAIRRGVHVCL
STGRAVFHAMPYAVQLGLETMPMTVNGSEVWKAPHDLYMRHLMDPALIRKMQEIGEKY
NSWYWAYSVEELFNRDRWTDNIEGLEWLKFGFNTEVDEVRHQIMMELQQMGGLQMTNS
SPVNIEINPAGVSKASGVAEVCKLLGIEMSEVVAVGDSLNDLAVIEAVGLGVAMGNAQ
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CDS 141569..142060

/locus_tag="EFAGFIKM_00138"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLATVAWILIVLLFAVGMAGTVYPILPGAVAIFFAFLVYGWFFS
FDPFGVWFVIIQILIVVVLVADYVVSAGVKKFGGSKLSTTLSTIGVIIGPFVIPAF
GLVLGPFIFAGIFELIGGSSPSKASKVGFSGSVGLFTSTVMKILQIVMIVLFIIWVV
RFA"

CDS 142122..143750

/gene="murJ_1"
/locus_tag="EFAGFIKM_00139"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_02078"
/codon_start=1
/transl_table=11
/product="lipid II flippase MurJ"
/translation="MSKKETFIRGTLILAAAALIARVLGLVQRVPLEHILGDIGNASF
TISNTVYLMLLTVATAGIPSTLSKMVSERYALGRASEAQIYRAALIFAAGVVMMSA
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EQFARVGTAIIVAYVMLQWNYDDQTIAAGASFGGVLGSGVAFGVMLYFTLKLRRSDRA
AQLNYERAEQLPMRGIYSDFKLSIPIVLSSLAVPAINFIDSSLVPLLSGQIGLEEA"

TGVLAILGAKAQSIAGIPPILAIALSQLVPVISAAFARKDEAHLKSQVTLALRISIL
TGMPIVIALCAAAYSVNGLLFTNLDGTPIIALLTFGTIFQITMMTTNSILLGVGKPRI
TMISVAAGVVIKLIASLILAPIFGIYGIIATALCFLVITYLNLRVLRKIVDFSIMGD
RWKGFIIITVLLAAGVGFATNWIGNAIFGLFLPARVSFLTCLVVGVLVVVVYLVLMVV
LRVLRKDELGSYPRIHQKILRPLMRLQRGAGQRG"

CDS complement(143949..145235)

/locus_tag="EFAGFIKM_00140"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTSTRDSSSEQHHGSLLQMVR SIPGAAREIWRGKQA AWHASQA

LRHPLREIEWDTDTAAALQSEVERLLPASNKS FIRTDQVQSALVCEEDCIILEEIKTL

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REHMYRLLERCNALIFQDAYPQLLLYMNSRRIGRSCFHLLSHFHVSAFMTPFWERFWL

ERCSSLLSVALINEQNYIESRVVQHPYFQKEVLSKPAFHLHNLAGLNHIVFPLGRGA

GLAGRVIEHFGKLDERIMFGKGLYALLFGVEQVHTQVLEFARSVPHRGSRAEYWPDLF

TNREDEAGDHTLYAQGLLDEEWLPEGQRLYSPELLAVWGDTPYEPITRQDWLQTRDSL

GYLTAPRRPWLFEMSHEHRYGMLKTALAHDAKAITH"

CDS 145378..145722

/gene="ytpP"

/locus_tag="EFAGFIKM_00141"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34357"

/codon_start=1

/transl_table=11

/product="Thioredoxin-like protein YtpP"

/translation="MEQITSKPAFDVAIQSPRLTIAVFKADWCGDCKYIDPFMPEVEE

KYTRELT LIEVDVDQVGTVSEEQNILGIPSFVAYTDGRELVRYV NKLKRSREEIEQFL

DRAVEVYNTIHK"

CDS 146274..147212

/gene="ctaA"

/locus_tag="EFAGFIKM_00142"
/EC_number="1.3.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P12946"
/codon_start=1
/transl_table=11
/product="Heme A synthase"
/db_xref="COG:COG1612"

/translation="MKHLTLFKWLTCLVLMFLATFGGGIVTKTESGLGCGTEWPLC
NGKLVPAAHTVASLIEYSHRAVSALAGLLSIASFVAFLRFGKSRRDLQLFSLTLVFVI
VQGIMGAFAVVFSSAVMALHFGFALIAFASSLMMALGIRQEAKDGGLERLNKYPRV
SKKFRNLVWFSTIYTYLVVYTGA FVSHTDSAGGCSGFPLCNGQIPELSSGGVAVAFAH
RAAAASLVIVIAILGHFAYRNHPDNKEMRTLGVVSVVLILMQVVIGIFMMVTMNRPEV
YMFVALAHMLDIAILFGVLTYSFLVYKLHRPANRF"

CDS 147378..148094

/locus_tag="EFAGFIKM_00143"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"

/translation="MLRTLLGEKPRINEGKLKVAMDSMAHTLELFQRQMHVDHDP
YRKLYVWTQGLISSLDELEQSCFAAAHFRKKVVAGSTDDMTATEKAEYARYVYFYKDG
FIRCFAILDKVGTVLNEIFQLNTSNTKAHFSYFTVLRQFDYAREHHDALQLIQIKDS
YREPMSKLRKRRNMEIHVMNSEMHDLDLWQLHQTQGGKVKLEDLNQHVQEMRQGVDMVC
ETLTASYSYINKIWKRNNSL"

CDS 148486..149526

/gene="metN2"
/locus_tag="EFAGFIKM_00144"
/EC_number="3.6.3.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q831K6"
/codon_start=1

/transl_table=11
/product="Methionine import ATP-binding protein MetN 2"
/db_xref="COG:COG1135"
/translation="MRLIELKGLTKTYGKGAKSTTALSELNLSIQKEIYGVIGHSGA
GKSTLIRCINLLERPTEGEVWVDGINLTELSKTELQQRRKIGMIFQHFNLLSSATVY
DNVAFPLKLVNTPKEAIDRKVKEMLALVGLEHHSSKYPACLSSGGQKQRVGIARALASD
PNVLLCDEATSALDPQTTNSILKLLLDINEKYNLTIVLITHEMHVIQNICDKVAVIHQ
GGIVEQGPVTDVFLKPQHAITRDFMMRDHEAGLALEETALANAGVELQAGAASKLVKI
SFLGNKTYEAILSRTVRKTGVDFAILQGTISTIKQVPYGGQLTVRFEGDSNAIDRTISE
LTAEGLDVEVLR"

CDS 149527..150186

/gene="metI_1"
/locus_tag="EFAGFIKM_00145"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P31547"
/codon_start=1
/transl_table=11
/product="D-methionine transport system permease protein
MetI"
/db_xref="COG:COG2011"
/translation="MDFSTVRWEEVGKASIELTLQILGVSGLFTVILGLPLGVLLFMTA
RSASIKSRAVYTILSLIVNILRSVPFIILIVALIPFTRILVGTATGVLGVIPPLVISA
APYFARLVETTLREVDRGVIEAAQSMGASTGQIVRRVLLPEALPGLLAGITITIVTLV
SYTAMAGMVGGGGLGLTAINYGYFRYQNEIMIISVSMIILVQILQMAGDRLVTFFTR
K"

CDS 150262..151101

/gene="metQ_1"
/locus_tag="EFAGFIKM_00146"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32167"
/codon_start=1
/transl_table=11

/product="Methionine-binding lipoprotein MetQ"
/db_xref="COG:COG1464"
/translation="MKKWSFALLSLMLIAVLAACGNNKDADSGADNSAGAPRTVELKV
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ENKERGFNLVSVTPVHVPEFPGGYSKKIKSLDELADGAKVAIPNDPSNGGRALLLLAKE
GIITLKDNTNITSTIQDITANPKNLDIIEIDAAMMPRQLDEADLVFINANYALEANLN
PANDALLIEDLQGNPYANILVSREDNKDADAIQKLAAALHSEEVKTFIKERYKGAVEP
ATE"

CDS complement(151229..152227)

/locus_tag="EFAGFIKM_00147"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKNKRWISFLTLLMSLFTLSSALQVSAASENEQAPDEYDWITG
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EYVKTGHIHDDDQNLNAEELLSSYIRGTEEDNRELDPEYRTYITGWEIEPAYDSTKHQ
LVYSLGFKNADQQSMVNYNVKLLTREGYITAILVTDANFQQSRQFEETVLNQLSIN
AGYTYEEYNASTDKTSTIGLNSLLMGGIGYTASQKFSALLLLKKGWALILVVVLGLIG
WIRYRIKSSHGEEELSPSERTYLQEADEQQYADQNELSYRQSGHPSDVKPGKL"

CDS 152401..153180

/gene="fabG_1"
/locus_tag="EFAGFIKM_00148"
/EC_number="1.1.1.100"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P99093"
/codon_start=1
/transl_table=11
/product="3-oxoacyl-[acyl-carrier-protein] reductase FabG"
/translation="MKGKIALITGSAKGLGKMTALSLADQGCHIALNYVHSRTEAEAL
KAQIIAKGVRCIAIQADISKVEDISSLVEQVEGNLGSIDILVNNAGPFVRERRLFADY
SEAEVQMLVQGNLLGPMLLDQRVLPERRKQWGRIIHFGFSHAGEARSWPHRAVYAAA"

KVGLVSFTKTLAVEEAPYGITVNMVCPGDIRGANKEKTIDEMAGITDEETPRGRPGSG

EDIARVITYLCLDHSDFITGNIMDVSGGLDPIRPTIQREDT"

CDS complement(153319..153564)

/gene="nfuA"

/locus_tag="EFAGFIKM_00149"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01637"

/codon_start=1

/transl_table=11

/product="Fe/S biogenesis protein NfuA"

/translation="MSENAQSTMYDEVIDVLDKLRPFLQRDGGDVELVDVEDGIIKLLK

LVGACGSCPSSTITLKAGIERALLEEVEGVQEVVQVF"

CDS 153643..153897

/locus_tag="EFAGFIKM_00150"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRPIIEFCANNMHFGTDEVMDQLEENPDYDVIEYGCLTNCGQCS

MTPFALVNGEVVITDKVEDLYNAILAKIGEADAWDELDLD"

CDS complement(153894..155027)

/gene="yjlD_1"

/locus_tag="EFAGFIKM_00151"

/EC_number="1.6.99.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80861"

/codon_start=1

/transl_table=11

/product="NADH dehydrogenase-like protein YjlD"

/db_xref="COG:COG1252"

/translation="MLLHSCSTVYSPISVGLMQKGSVMKNFVILGGGYGGLTIKEL

LEGKIPSDTQIILVDRSPFQGLKTEYYALAAGTVSDYDLRIQFPVSDKVITYRYGEVTS

INLEQRQIEFEGQDPLVYDKLVIGLGCTDRFHNTPGAENYSCTIQSFSKTRETYLRNLN
EVKAYGNVHIVGGGLSGVEIAAELRESRPDLNISILDRGERVLSAFPQRLSVYVHEWF
NEHQVETRGHIAISRVEPNAINRDEQILTDAVVWTAGIQPVKVVQDLDTKDPQGRV
VLNEYQIPEYTDVYVVVGDCASVPYAPSGQAAEVQGEQIAHIQHALWKGEKPNPHPLK
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CDS complement(155190..156296)

/gene="mqnE"

/locus_tag="EFAGFIKM_00152"

/EC_number="2.5.1.120"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5SK48"

/codon_start=1

/transl_table=11

/product="Aminodeoxyfutalosine synthase"

/db_xref="COG:COG1060"

/translation="MSTLVTPFTDKRMAEIVEKVQNGVRLNVEDGVLYETDDLTLG
QLANEANLRKNGKKVYFIENMSLYFTNVCEAHCAFCNFRKDQGEESYTLSGQEMIDY
VEQHIHPGVREFHIVGGHNNHVPFQYYVDSLRLNEKYPDVTLKAYTAAEIDFFTRIS
GLSIKEVLQELQKAGLKTLTGGGAEILSDEYRKMRVDKANVDRYLEVHRTAHNLGMR
THTTMLYGSIESYEDRVNHMVQIRELQDETNGFMVFIPLSMQPKSKNASIMRRNSAYE
DLKTIAISRLMLDNIDHIKAYFINIGPQLAQVALGFGASDAHGTIVRERISHAAGALT
PEGLTRKELIWLIKAGRIPVERDTFYNEIQVYE"

CDS 156926..157282

/locus_tag="EFAGFIKM_00153"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O67709"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/db_xref="COG:COG0316"

/translation="MINISETAADRLKEMLAQQETPGMFLRLGVAPGGCTGFSYAMGF
DDKESDEDLYMDIQSMKVVEKENLKYLDGLEIDFEESGMTGGFTIHNPNAVATCGCG

SSFRTKEDAGVPDKDC"

CDS 157502..158146

/locus_tag="EFAGFIKM_00154"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMNIAIIGATGKAGSVILKEAADRGHKVTAIVRNASKLEDKSLN

TLEKDVFDLTAEDLKAFDVVVNAFGAPAGKENLHVEVGQALINILKDAPNTRLIVVGG

AGSLFTDESKTLRVFESPGFPDAYKATATNQGGQNLQDLQASSGIQWTFLLSPAGFFNPE

GVRTGKYQAGNDVILVNSEGNSYISYADYAIALVDEIENPQHKNERFTVVGEVK"

CDS 158402..158797

/locus_tag="EFAGFIKM_00155"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKMYSKGVILLIFAVFMISVSSGSGLSQYTNVKNKMNQFHITSL

YPKNKNGQTYGSAAYATSPETEPDLILATGVDGTDGYLLKKDLDGEQPKTPEEAIAIQ

NSRSPDGRDIPLYDKDGETVIGVFHVGGK"

CDS 159143..159721

/locus_tag="EFAGFIKM_00156"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEKCLKRIITLIFFISTVFFISNAQDVNALSCAESGGPQEQLI

YDGAVYGEVKQVKVDMKQEGFTGTKEKIRYILVEVERSWNTEVDSQLIATNFTWGF

FKEGNKYLIYFSEADGELSSSPCSLTIEMNHLNQATELFGEGFPKQQVNVEHKMWFM

FEQDNDLFIVGVAVFAAIFIFFMRVRKKKRKA"

CDS 159874..160752

/gene="rarD_1"

/locus_tag="EFAGFIKM_00157"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P27844"
/codon_start=1
/transl_table=11
/product="Protein RarD"
/db_xref="COG:COG2962"
/translation="MNSGLINAIAYIMWGVLPYWKLFENVPAGEILSHRVVWSFVF
MGIFVAVQRRWSDMKRILTSRSTLLSLTVSGLLIANWLIFIWAVNNGHVETSLGYY
LNPLLNVLLAVVFLHEKPNRGQWLAIAIAGVAVLIIAIDYGRFPWVAISLAVSFGLYG
LAKKKIKQDASVGLFSETAVVLPVALGYWIYLA VVGKATAWTL PAPMFFELL LSGVVT
ALPLLFFARAAARMSLSTLGFVQYIGPTIMLILSVFVKETVSPVLLVGFALIWTALI
VYAAASIRATRLAKVS"

CDS 160947..161288

/locus_tag="EFAGFIKM_00158"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MMVNNRYRKRPFFVKKAVVQILFQFAVSAIIGSIYGFMVNET
IAGYINKLLPSTDGPDHLHLYLPVVITVFIYSCLIQKRQRILLEKISFSCLHILVALLG
CISSVVLLVI"

CDS complement(161297..161752)

/locus_tag="EFAGFIKM_00159"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSFLKGFQQLAGEVTGKVLGGSVRVVGEIAGSPFIKEIGNGVEK
ATINTGKTVGQLASGTYYLASGAIRKDDTAIDAGLADIGGAVSNTAKGVAISAKYVYN
SGKDVVVG MKEEDKDRVKLGAKNLLAAAVTTLAVGVDAVDGVEGVDT"

CDS complement(162507..163556)

/gene="ganB_1"
/locus_tag="EFAGFIKM_00160"
/EC_number="3.2.1.89"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q65CX5"
/codon_start=1
/transl_table=11
/product="Arabinogalactan endo-beta-1,4-galactanase"
/db_xref="COG:COG3867"
/translation="MFKNVRGFKTSIMLAFVLLFTSIMLPAGQHASAAPSFAGKADIS
WVPGMEAQGYKWKDKNGVQRDIIDILKKDYQINSVRIRVFVNPSNDYGNNGYMNKDRAA
ALAQRAKNAGMSVMLTLHYSDSWADPGQQTCPAAWKNYTFQQLMDAVWNHTRDVMTAM
QSKGVTPDWVQIGNETSNGMLWEDGKASTNMKNYAWLVNTGHNAVKSLSSGKTIVHL
AGGDDNALYVWNIGGLINNGANFDMIAMSLYPSASGWNTAVTNTVNNAKDMINRYGKE
IIISEIGMDNNQAAAGKSFAAMKNQIRNLPNGKKGKGVFYWEPQATPGYNSGYGKGAW
QSNMMPTVVMEGFID"

CDS complement(163904..164131)

/locus_tag="EFAGFIKM_00161"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKSINKPRTLQKNIEFFTAALSQCMVSAWQEDPAGVYCEVGCGIV
ERISEDVRIRNNDGTSKYARDITMFQTEK"

CDS 164380..166461

/gene="ppk"
/locus_tag="EFAGFIKM_00162"
/EC_number="2.7.4.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P9WHV9"
/codon_start=1
/transl_table=11

/product="Polyphosphate kinase"
/db_xref="COG:COG0855"
/translation="MHRDVKTGNYVNRDLSWVEFNRRVLQEAQDPTTLLERMRLGI
VASNLDEFVSVRVAETKEKIKAGFTQKDFTGYTPSGLYRRLIKRTGTMVAEQYKTYRE
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LSVMLQKEGEQEGEPFMAIVQVPSNLPRVVQAPIRANSKKKT FILIEDLIKHHIHTLF
SGYISLAAQEFRVTRNADLFINEEEAGDLLEAIEKELRRRRRGAPVRLEVCKDFRPDA
LLELQDEFDIHDPVYEIDGPLDLSFLAGFVDSLESFSLKYSPVKPVYPLEFLPRESH
FELLRKRDVLVHHHPYESFEPVTD FILEASEDPRVLAIKMTLYRVNGDSRLIPALALAA
ESGKQVTVVVELKARFDEERNIAWARKLEKAGCHVVYGLVGLKTHAKIILVVRREQQG
LRRYVHVGTGNYNESTAKVYTDVGLFTSNPIIGEDASELFNEITGYSGPKALQAFRVA
PDGMKDELFALIRRETEHALKGKPSRIIAKINSLSHQEMIDELYEASQAGVQIDLIVR
GVCCLRPGVEGLSENIRVISIVDRFLEHSRLFYFENSGNPDVYISSADWMTRNLNRRI
ELMCPVFDPELKKMLVDILNLSLMDNVKARELMPGGNYVFVENEKPPLRSQTEAMGII
PWKPAEWSALT"

CDS complement(166421..167950)

/gene="gppA"
/locus_tag="EFAGFIKM_00163"
/EC_number="3.6.1.40"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P25552"
/codon_start=1
/transl_table=11
/product="Guanosine-5'-triphosphate,3'-diphosphate
pyrophosphatase"
/db_xref="COG:COG0248"
/translation="MTHTNETLGIIDIGSNSIRLVIIYELDQNEAYRIIHEDKYAARLS
SVVESDGTILRHSLDKAITLSQFKATCEAYQTKLIRAAATAAIRNASNVLEIIEWLE
TETGLTIECVSGDREAYYGFLGVTQSIDLADGYVVDIGGGSTEITVFRNRKRLHSISL
PIGAVNSHARYGGEDQWTEANANALCNEVIEALRGQDWIREHPGLPLIGLGGTMRTLA
KVEQKRTQYSLPVSHHYEISEEAMENIARSLPHL TSAQRKKVPGLAKDRADIIVPGVL
ILRTVFQLIQGDRYVVGAGLRDGLLRDYMAGGQPVVPDALKDSIRNFIHFGPPIPEK

RLQRIHQDMVTLYTALQGTPPDQADARILYAASMLHMAGKQINYFRYTQHSAYWTMNS
SIYGLSHRETILSASAADYHPKKRTPQLLNKHQDILKNSDERHAHRIGSLLRVAEAIN
RSESIAAIEATKENDSLQVQFTCTAEPLLELDGLEEAVKDLKEAWGVTLTHSIQQASK
G"

CDS complement(167977..168231)
/locus_tag="EFAGFIKM_00164"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEAFFKSLYGVAIFYFAMSIVLVAVTVLLFVTGIRLFMQKRNRGFA
VSCLIFACFIVFIIVVMLTTPFSATPPGSPEAMAALLHFG"

CDS 168470..169129
/gene="yheD_1"
/locus_tag="EFAGFIKM_00165"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07545"
/codon_start=1
/transl_table=11
/product="Endospore coat-associated protein YheD"
/translation="MSRQLASKWRKTAALMKYPVAAVHIPQTKAFNSGNLLQMLSRYG
MVVVKPIVGGGGYGIVRVASGGAYRYTHMKTTTSFASFSQMYRSLVRVKARRKYLIQ
QGIHLATIQGRPVDYRVKVKVTQRGWVFRSLVGRLARPGLCVTNLSKGGTMLSGRRAL
GLSLPHISGRHKRREMRSLTLCTYIMESQFPGVGQLGFDYGLDYSGKIWILEVNTRP
Q"

CDS 169490..169627
/gene="sda"
/locus_tag="EFAGFIKM_00166"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7WY62"
/codon_start=1
/transl_table=11

/product="Sporulation inhibitor sda"
/translation="MLSDEMLLD SYHKAIELNLERDFIALLLAEIHKRKLGTDVSAIL
H"

CDS complement(169977..170978)
/locus_tag="EFAGFIKM_00167"
/EC_number="1.18.1.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q816D9"
/codon_start=1
/transl_table=11
/product="Ferredoxin--NADP reductase"
/db_xref="COG:COG0492"
/translation="MTAQNSSHDMDLLIIGGGPAGLFAAFYGGMRQASVTLVESMPQ
LGGQLAALYPEKYIYDVAGFPKVTAQELVNNLVEQMSHFNPNIIRLEEKVVSVEKKDEQ
HFIVKTDENEYHAKAVIITAGVGAFEPRRLELEGAAKFEKSNLHYFISDLNAFAGKKV
LISGGGDSAVDWALMLEPIAEQVTLIHRRDKFRAHEHSVENLMNSKVNVTPTTEITEL
HGDDTITKVTLSHVKTKETQEIEVDDVIVNFGFVSSLGPIAEWGIEIDSNSIVVDSRM
ETSIPGIFAAGDITTYPGKLKLIAGVGGEAPTAVNNAKVYFDPDAKLSPGHSSNMKR"

CDS complement(171320..171511)
/locus_tag="EFAGFIKM_00168"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTTNVNFANLFKRLHQFHNSLKMDFMKLDIDVSNRFDLYLDLIE
ATKGFMKLIRLHASRFLK"

CDS 171606..172799
/locus_tag="EFAGFIKM_00169"
/EC_number="1.6.99.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q2FZV7"
/codon_start=1

/transl_table=11
/product="NADH dehydrogenase-like protein"
/db_xref="COG:COG1252"
/translation="MSSIPKIVILGAGYGGILTAQRLQKELNYNEADVTLVNRHDYHY
ITTHLHMPAAGTDITIEHARVPISKLIDEFKIDLVKSSVKEIRLQDRKIILEDGTLSYD
YLIIGLGGEPETFGIPGMLDHAMTIRSINSVRLIREHIEYQFAMYKNDNKRNRIRFVW
GGAGFSGVEFVAELADRIPLCKEFDVNP KDVHIYNVEAAPSALPGFDPELVEHAMNV
LKKKGVTFKIGVPIKQCLPDGVIVGEGEKLDAATV VWTGGIRGNSLLEQAGLEV MRGR
VKVDEYLRAPGHEHVYVIGDNSLVFNAEGRPPPTAQIAMQQGVNCAKNVVASIRKKQ
PQPFVFTSKGTVASLGKGEAIAVVGGKKYKGWKA AQLKKLVDLRYLFIIGGIPLVLKK
GRFFG"

CDS 172796..173050

/locus_tag="EFAGFIKM_00170"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRHCSVQVRGLLTREELDRYNALMQVGGYLEEQDQYDLAYIVQK
EVDILIMPAIERLKEKGRDRDRATAEFLESLKAVDDEDEE"

CDS complement(173202..173948)

/locus_tag="EFAGFIKM_00171"
/EC_number="1.11.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q5KUD5"
/codon_start=1
/transl_table=11
/product="Putative heme-dependent peroxidase"
/db_xref="COG:COG3253"
/translation="MNEAASTLEGWYALHDFRSINWAAWKAADDEERAVALDELEEFW
KEWKEVENSSQGSTVVYTVVGQKADLCMMHLRETLEDLKAVENAFNKT MFAQYTTKSY
SYVSVVELSNYLGKEGEDPMQNPEIARLKPVL PQRQYICFYPMNKKRELNDNWYMLS
MDERRTMMRSHGMIGRSYAGKVKQIITGSGVGFDDWEWGVTLFADDALQFKKLVYEMRF

DEVSARYGEFGSFYVGSLLEETLEDMLKL"

CDS 174223..174516

/locus_tag="EFAGFIKM_00172"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQFIPVLVLMVLFVMMFGIGFILNMLMKTTFPSYLFIIIVLP

VVYSLWDHSSSLMSHLGSFQLVDYMTGIAGLAGAVISGWTIQKLRLGGYRMF"

CDS 174899..176434

/gene="dnaB"

/locus_tag="EFAGFIKM_00173"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P07908"

/codon_start=1

/transl_table=11

/product="Replication initiation and membrane attachment
protein"

/db_xref="COG:COG3611"

/translation="MRMKNLHHYTEHHRYCVYREFGLSALDDRMLTGAYQPMVGAFV

GLYRLLFQHLPGEQVGYSPLQRRFLMTLGLPSEKGRKYLLEQTSKLEAVGLLQTS

RLYIPENDDIYIYELQPPLSPAEFFRTQHLLTLLRDKIGKFAVLSLRSGFSAVEND

APYPAANKENISVPFYDIFELNTHVIDYELEQALSEVSTTAQRTGTNDAAEENSLNYA

DIILRFPRESVNRRHVEQLRFDHEQLGIVNYVVKFNLSVQDVCRLLEDDEDDIFSPQGQ

LILDDLQHKASMQRQTKKRHEQQTVQAAKVVALRQHMEEPERKEDSGEPPVEHGVQM

EYYVEVPPQFMTKCDIHQYNMMLRNPEPYTRLLQTFFPGAVPDNLIDIFEKIDLSYKLP

GEVINVLIIHYLMALLVSGGEQRINRNFVEAIASNMLLKQVNSYEKAVQYIRDQAKVKG

KQAAGAAGTRTRTYGKGTKAKPEIIVQDISTGDVSEEEFEEMMRFAQQMMAKQK

GTS"

CDS 176681..176947

/locus_tag="EFAGFIKM_00174"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTQDFIEGTTEEAIHNLEIPTFEQLDNDTWDFETMKDFQFSFLF
VEFVVQQYGIDHLNKLIRDPQDFNGIFQCSEKELHQMMEFISK"

CDS 177071..177631

/gene="ydaF_1"
/locus_tag="EFAGFIKM_00175"
/EC_number="2.3.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P96579"

/codon_start=1
/transl_table=11
/product="Putative ribosomal N-acetyltransferase YdaF"
/db_xref="COG:COG1670"
/translation="MNPIMIDFPDEFFTERLLIRMPKPGDGKVVCEAVIASVDELKPW
MKWAQDKHTEYNSELGIREAHIKFLSRENRLLLVFLKDTGQLIASASLHSIDWEVRKF
EIGYWIDTRYSGKGYMTEAVQGITDFAFNHLNANRIEIRCDTKNTKSKMIPERLRFDL
EGVIRNEDLSVDGSELRDTNIYALVK"

CDS 177769..178434

/locus_tag="EFAGFIKM_00176"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKTHYYFSWFNHHFFPEKLVHCLQEDIENRKSLVMISADPSGYKD
EQVNFDDVSEWRWLNQANIIFDEYHFIDFRMQKEDAQRFIQNASVIFLCGGYPVLQND
FLAEYELSDVIKNSNAIMGASAGALNMAAKWLSLNNTDEVETSTIYDGIGFDHFAYE
SHSQRDYATFVQGYLFPLSEEIDIYAAEQESAIRVKDGKIEIMGPVYLISHSKIQLV
ETL"

CDS 178849..179388

/gene="tadA_1"

/locus_tag="EFAGFIKM_00177"

/EC_number="3.5.4.33"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00972"

/codon_start=1

/transl_table=11

/product="tRNA-specific adenosine deaminase"

/translation="MDKHYQNLLLAEEAEKARDEGTFPIGAIIVDADGSVVSRRNR
VFSSCDSTAHAEVDAIRKAGNVILHLESKKFIPKNELTYTTCEPCPMCTGTIVLSLI
KKVWWAANDKDIGAFKKFKELNSELPIYNDLFHDIEFVAAPYRDLELRQRKMLAEWNN
SRGYTDNHWNDELVNEIVQ"

CDS complement(179791..181437)

/locus_tag="EFAGFIKM_00178"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDSIGKNGKEAAEAIRSYVKPIFGFALNRVKHRAEAEDLAQEIM
LQLLKSFSGVRDIRSLDAYVWTVARYTWVNWLKKRAHAPQAIEINGMSELSAAPSREP
LDRLLVTEAYRELRRREVAFLSDIHRRIVMHYYDELKIGDIAIALNIPVNTVKWHLSE
AKKKLRKGMKMRATGTLSPVSMGEMGHSGSAGSLGETNDFLGRALAQNIVYAAHY
KARTVHQIAEELGMPPSLLEGEVRHLADYNFLIQTSPGKYQSNTIVWDLFELAVAGHQ
FWQDCAAEEVADVHFDALMEVRRQVVD SGVYVPEGDYNFLLWTLLPKNIEEQSWRSM
PA GENFDAIAPMRKDGGQYIAYAALNRSHYADPGFDMSSYVTFGPSLRYVEDTPLYLWQF
NTYWSDRQMDWRFLEYRNVEICHAFFQQGELPDNEENSEQYSFLEKGYIRKTEEGYKF
NAVWMDSPQTLDRNLKAMPDLSAVYAPAVGKLYDKMLNLFQNPQKHLEPQLAYMVRG
NTGGGRLVAYILKHLIDNGKLPPLPHQQKTISTWMGPVK"

CDS complement(181939..182454)

/locus_tag="EFAGFIKM_00179"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MEVIIIKVNKMYFIFSIVALFLLSACAGGVTGSSQQNELGEPYR
MALEELISTDTALNENMEYISLDFDKGIPLKDSKKSIEDYLH SKYNV KIYNLT YEEL
IEEGLSEQSENTLKGILLKIEKQEQSDNNIAIEVSKYRANEGSLSAKITLT YEEGKW
KVATHPTRES"

CDS 182717..184312

/gene="lcfB"
/locus_tag="EFAGFIKM_00180"
/EC_number="6.2.1.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07610"
/codon_start=1
/transl_table=11
/product="Long-chain-fatty-acid--CoA ligase"
/db_xref="COG:COG0318"
/translation="MLLSERLPIAASMYPEEPALMRYGQTMSYGELYGLVERLSHGLY
DEGLRAGDRFALLGDPDPQLVVAFYAAVGIGAIPSPMLTVP ELAAIFQDAEPH MV
IHDNQHAKAAIATVKLLGYCPKLF TTDEEGTSSSLAALLQQEPAFSPKDHFKRNVDD
TAVLIYTGGTTGRPKGVMHSHRGMAAWNQLTPSAGFGHDFKRRVLVLNLSHLVGQFQL
WATMAAGGCLVFLDEYPTDVHRIMEAVERDQITQLSTVGQLLRDLTREASVGGRNLKS
LSLIGCGGSIISPDTLQEVVSQFPEALIVNNYSQAECGMSISRLFPAQHMGDPHRLRS
VGRPADLAAQGEQGFEVRILDTDGSETVTGEAGEIVVRGAQTMLGYWRQLEATAETMP
DGWIRTGDVGCLDVEGYLYVFDRLKDMVIVGGSNVFCAEVEHVIVSHESVSEAAVIGH
PHPDEGEELVAFIVLRDGENMDLTRVRTFCEPHLAPYKWPTRLFIVDTLPRTAVDKID
KKHLRKHLSSISSEDIYANGNAVK"

CDS complement(184437..187265)

/locus_tag="EFAGFIKM_00181"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTRKCLKPKGIIPKVTAMVLTTALLGQVVASSVYAGDTLPYTGES"

AKGVNQPYQHGYTSAQILNWTPESDIHGDLLRAHVPLQPRNEAFAATQAYPELSPDTQ
LFTMSGDYGNAFFDSTPYTNEFSQYLFNWQYTDYYSYWHGMASAGVPEELYDPSKEW
TEKYFEFGILNIPNPAYTNAAHKNVKSIAIFFSDNDRGPQTYKQMLIQDENGFPV
AEKLAEMAEYYNYDGYFFNQEEVARGVAPEDIASYKKFMKYLRDKGLYVQWYDSTINT
TGKIQYQNQFNGLNSPFVQDSVLGRVSDSIFLNYVWNHKMLRDSRDHALSLGLDPLET
VFAGVEGGHDKFGRWKQSYDLRHNLDENGHPMNSIATLGADFTHNALDEEMGDGSTNH
RAEDEYQWMTFVRDRAWWSGPNQDPTDARRNASADLSDVYASGANWDGIAAYLTERSV
INGSNFATSFNTGHGLKYYEDGAVSNDKEWSNINIQDIPVTWQWWMDSKGDKLSVDFD
YGPSYEKGVRNYDSIGAFNGGSSLVNGTLNAENFLRLYKTDLSVNGQSKLELTYNK
PSTSDASSLHVGLIFEDDPSNVNVNPNAGQHTTGWKTSLDLSAYQGKTIAAMGLS
FDPHGMEIKNYQMNIGEIRISDGSAAVPDAPTGFHIAKALTNTDELVVAWDMKDYSEV
KQYNLYENGAYVGGVYDSTFYIKSLKQPSGELSIRAVGADGTESEATVLPYDLNAAVQ
NMDVKFKKNGDAIVSWKKPKKAKESGKDKDKDQNTDKDKDKNKGKGNESIQTLTQT
EYTKEPFTKSLQVKKGKQSAVLTGLPTNGEHYVLNIAIGGQNPVTHTGQLADLQITPY
AKEKVTVKDGKYLALPDLEDWYKIYVYENGVPREFGVTVVSQKFPYIIRGRTLSEL
TFTPSSNNSSLKLVIEDYAGNQASTILR"

CDS 187478..189307

/locus_tag="EFAGFIKM_00182"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKIVSVYNNFFKNNMFMKMLLIFSMISIVTIITLSYIIFLSVSD

STIRRELAIQKAAMEHVDRIYHQQYESVQNMVRDMHQNEALSANITYLMNHSYAEYVQ

HMTNGYYANQDDYSADVLKHFQNMIDRNSQINQLMLYSAEQQDLSTFNQHKQFRKLDA

NVAHSYIPDVMAMETPNISAPNYWIRKEINQWDPALYSIRVPINNTQTLRNLGQFLVF

FDSEGIGNALDNYESNLKGEIVVLSAKGTVLFDSSNNHYGKKYPYVNVADSLFDQDTM

DSMKKEQNMYVNKFVSADQGYVVIGTVPVEEMAETYAGIRNTIISIVCILFAVLVP

AFFIINFATRRIIRFTQKVYGNLTARIDDPDDELGQISHSFNDMLDELNLYIER

VYKAEIKQKETELVALQARINPHFLYNTLEVIRMRAISQGARDVGEMIYSLSVLFKSL

VQQKKNYTLKDEMEACRLYLELFRIRYKDFIYTIQIDAAYYQHPVVKLSLQPIENY

VVHGIQTERSDNRLSIVVEETDDVVQVEVKDNGKGIDPARLTEILEELERPEESGQMF

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CDS 189300..190823

/gene="rssB_1"

/locus_tag="EFAGFIKM_00183"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00958"

/codon_start=1

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/product="Regulator of RpoS"

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CDS 191105..192577

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CDS 192655..193584

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CDS 193608..194528

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CDS 194562..196919

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CDS 196924..200148

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CDS 200406..201725

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CDS 201722..204901

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CDS 204898..207681

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CDS 207857..208894

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CDS complement(209075..209230)

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CDS 209493..209810

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CDS 210284..212371

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EEKFRLIERNEERTSKAAEGLGRFIGLDQLHRIEAFDNSNIQGTNPVSAMIVFTDGKP
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CDS complement(212340..214037)

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CDS 214645..215985

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/locus_tag="EFAGFIKM_00197"

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DIVFFRYRLVQERIFKALTITLLALLFIIAVTMALSTTEDASFMMILFETTSAFGTVG
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CDS 216040..216711

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CDS complement(216772..217695)

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CDS 217940..218659

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AIYMISVVAASYHFANGLWSFLVSWGITVGPRAQRVSSYVCMSLFAIVSIMFIASLFA
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CDS 218703..220445

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CDS 220900..221664

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CDS 221840..222814

/gene="cpdA_1"
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/inference="protein motif:HAMAP:MF_00905"

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YRGGQQNEVTTMFREAGFTLLRNEHVVIEQGGERLAIAGLDDALTGRPDPAQAIKGLD
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CDS 222873..223604

/locus_tag="EFAGFIKM_00204"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
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CDS 223773..224405

/locus_tag="EFAGFIKM_00205"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLTRKMLVQGLPALWTERLVLRSLRQSDYSTLSELFSDPQVIRY
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CDS complement(224855..225664)

/gene="hisK_1"
/locus_tag="EFAGFIKM_00206"
/EC_number="3.1.3.15"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34411"
/codon_start=1
/transl_table=11
/product="Histidinol-phosphatase"
/db_xref="COG:COG1387"
/translation="MKFDLHTHHFRCGHADGNIRDYLEAGIKVGLQAIGISDHTPYFG
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IDAMKGNYPFSEIADQAI DETLQVIAESNVAIEINTSGKTKLGGWYPSDAILER A
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CDS complement(225695..226597)

/gene="cmpR_1"
/locus_tag="EFAGFIKM_00207"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q55459"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator CmpR"
/translation="MNISQLETITISK TMSFRKAGELLNLTQPAVSAQIKSLEDEFS
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YDTFELVSPSHPLAKKKHAAVDVLRSTPLILLSPDTVGRRTETIFKKHNIENIVM
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LNSAMQQFISDLKGM PETQFISSE"

CDS 227054..227512

/gene="cheX"
/locus_tag="EFAGFIKM_00208"
/EC_number="3.-.-"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9X1V3"
/codon_start=1
/transl_table=11
/product="CheY-P phosphatase CheX"
/db_xref="COG:COG1406"
/translation="MKAEVINPFLESARNVFEQLIQVSPSTGSLGVKNVEYIADHVWI
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CDS 227569..228342

/locus_tag="EFAGFIKM_00209"
/EC_number="1.-.-."
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7A3L9"
/codon_start=1
/transl_table=11
/product="putative oxidoreductase"
/translation="MLKDQVVFITGASSGIGALCAQMLIEEGAIPILAARSRDKLEEI
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DEMMDVNYMGIVRCKAVLPQMLERGKGQIVNVASMAGKIGTAKSASYTATKHAVLGF
SNALRQELRKTGVMVTTINPGPIDTPFFHRADPSGNYVNNVRWMLKPEGVAGHMIRA
MKKRKEEVNLPRLASAGIWLYQLFPRLADRLSHGVMNQK"

CDS 228738..230111

/gene="deaD"
/locus_tag="EFAGFIKM_00210"
/EC_number="3.6.4.13"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00964"
/codon_start=1
/transl_table=11
/product="ATP-dependent RNA helicase DeaD"
/translation="MTNQTFASIGVEQDLEAVLAKHGINEPSPVQAQTIPVILEGRDV"

VSKSQTGTGKTLAYLLPLLQSIKMDIKGTQKLIIAPTQELAMQIVREAQRYAEERKIG
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HYYFVEENRNKIDMLRRLVRQYNPDRAIVFNATEDIGEVEAKMNHGLSAAALYGDA
DKVTRSNVLSAFRNGKLQLLIASEVAARGLDIEGLPMVINYPDFDSEHYVHRAGRTG
RMGRSGIVLSIVDETQIFIMRKFARELGIELSERVLFGGKVLEADPRPDTRPEGHSFS
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CDS 230139..230891

/gene="ecsA_1"

/locus_tag="EFAGFIKM_00211"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P55339"

/codon_start=1

/transl_table=11

/product="ABC-type transporter ATP-binding protein EcsA"

/db_xref="COG:COG1131"

/translation="MENVQSPVLQISGLSGGYSAKRPVLHGIDLEVGRGEMVGLIGLN

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CDS 230894..232111

/locus_tag="EFAGFIKM_00212"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDLKLLWKQRRTGFWNGILPYLGYVIQSGVAMVFLFLVIAFSAW

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IQVEQQAGRVMRTLGWFDVPSSGQKVSSRRWLSKWGSGLPWNAGKAYRYLITKTFI
RTEVFSIVLRLVVLGMLLSWWTAGSYFGVGVLFFLLLAGVQLGALRRSHSESWIMI
YPISGESRRSQVLGFIFHLHALAALLMWLPMLAAGASGLTVTGAALILGILVIVIMRR
SQGNKWLKEEEDF"

CDS complement(232675..233973)

/gene="hisC_1"

/locus_tag="EFAGFIKM_00213"

/EC_number="2.6.1.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01023"

/codon_start=1

/transl_table=11

/product="Histidinol-phosphate aminotransferase"

/translation="MNPLAEQLNESIQTGSSHVYSMLSQLGKEIYFPKEGILSQSAEA

ASLAKTHNATIGIALEGGVPMHLQVIQEKLSAFQPKDLYPYAPPAGKPELRTVWRDKM

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TILQAAEAGVNVAVTDDAYFGLFFEDSIHESLFGKLANIHPRVLTVKVDGATKEEFV

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CDS complement(234152..234769)

/locus_tag="EFAGFIKM_00214"

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/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRRKEFTVDEEQEITAFLDQCSFGFLGTVSPDGQPRVTPLNFVY

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FGQAEPVKDLDIKGKVLQRFMEKLQPQGGYVSIDATDSRYTGNLKAVAVVRIVPERIS

AKFKFGQNLSSERFDHISSQLEQRNEGRDAETAEMMRKYCPFHQQ"

CDS 234925..236382

/gene="gabR_1"
/locus_tag="EFAGFIKM_00215"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94426"
/codon_start=1
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/product="HTH-type transcriptional regulatory protein
GabR"
/db_xref="COG:COG1167"
/translation="MELWLPMDTYELQHRYKYEALYHALRDAIHAGTLVGGTRLPSTR
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LAWASKRNAVIEDDYDSEFRWGGRIEPLKVLDRQVRVYVGSFSQTMVASFRLGYA
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CDS 236561..237346

/gene="rhaR_2"
/locus_tag="EFAGFIKM_00216"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01533"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaR"
/translation="MLQASPSSFVILPAVAKIVCEPGWKWKREKPMQNYDLFYVWSG
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EVQETVEFEHLLARYVRLFLSDVYGRDEESRLILKQLMIHLLRADTEEPVEKKVSNQL
SDVIQEVANYVRQHPGITHRVEDLAARAGLSPRYFSIKFKELVGSSVQSYIIRMRIER
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CDS complement(237173..237694)

/locus_tag="EFAGFIKM_00217"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSPYANKEDGAAPVTRYCAILFMNSYSSIYTCNTKLRSVVIGLL
SSPQNHTSCKSSAGLKRRRRFRKILHPFVEHPRLRTRRFPFITSSPFWSSGMLDNYP
IPDLKRFPVFLIRILTNLGRAFAGILLELTTEENIPVAQSIRHFGHIHAGMHQQMFR
PFNTHADNIRLHR"

CDS complement(237694..238485)

/gene="psd"
/locus_tag="EFAGFIKM_00218"
/EC_number="4.1.1.65"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39822"
/codon_start=1
/transl_table=11
/product="Phosphatidylserine decarboxylase proenzyme"
/db_xref="COG:COG0688"
/translation="MAKTLLRLMTELSSRKWISRTVGAFSKSRGSKAFIPYFVRTYDI
PVQEAEKDWKEYRSLNDFTRKLKPGMRPLESEHALISPVDARITAAGPISAGTLLN
VKGQNYTLAELLNHSPHLEKYKHGYGFVLYLSRPDYHRIHAPVSGRKIESEHIKGVY
PVNDFGLTHMRSVLSRNERLITYIAHDYGEVAVVKVGAMNVSSIYADTDSTWAQGD
DLAYFEFGSTVLLTQSGTFEPNPGLQLGDSVKMGALLGRLKPKT"

CDS complement(238571..239701)

/gene="yheD_2"
/locus_tag="EFAGFIKM_00219"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07545"
/codon_start=1
/transl_table=11
/product="Endospore coat-associated protein YheD"

/translation="MLQETIGIMFDSRMYRGIPAGRTGQESLANYEQAAASYGLTPCF
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VFNVRNRYRKDHIHDMHLHQDLALREHLPRAVKATPESLAYMMEQYDDLVIKPCSGSIG
HGIMRVFERDGQWKLTCETKAARKGWATFRLSKGQLPSATLRRIFRHAYLIEERIPLV
RYEGRPVDLRVSVQRGSDGLWGITGMFAKAAPAHTFVSNIAQGGKVMKLAELGLGES
GFDLARLEYRIGLVALRIAQNLAASLPHLADLGLDLGITRSGQIYFIECNGRDQRYGF
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CDS 240218..245431

/locus_tag="EFAGFIKM_00220"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKNGKKKVPTPKLRHVSPKYKELELTDRRADKMNSGFTVNREE
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TESKLAPFSVDASKLKPDAVGSEALQDYAVTSIHIADGAIVSAKLAEASVSEEHLIDG
SVSGHKIRNASIAGEKIRDGSITSQKLGNAIDSAKIADGSISTRHLRMLVTEELIK
NHAVTGDKIAISGVDTRHLTGGAVNTSKLADDAVTTTKIREAAVTGSKIEEHSIESHH
IQAGAVKQTHLAEGSVGRSQQLLNGSIGSDQIEDGSIQTRHLAEGSLSGRHLLDGSIGS
SQIRAHSVGKEQIGNGEVGSEHLTEGAVTSSKLADQSVGTAKLLEQSITASKISDQSV
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SVSGDALADDVWCERHLAESAVGTIELQDAAVTDVKLADGSVTTEKLTASVSSRALA
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IARAAVTTDKLAIDSVTSAQLAGGSIFPPHLTDHAVTSPKLSPESVATDKLADFAVTS
AKLADGSVTSSKIMAESINAKHIPAGTIRGYHLKQHAVSLEHLSEEIRSPELFADGSI
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VVSSQHLKPDIIHEEHIAEQVVTSHHLAPGSVETDHLAPLSITAHLQPGLISGLHLQ
AESTSAVHLQQGAVHSRHIQDGEILPHHHIHERSIGTSHLEEEAVSTIILQDESVTRSK
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VHLQNGSVTSAKLADGSINGSKLLEGTVSGIHIASESVQSGHIQADAIHADHIQERSI
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VILSDHIQEHSIGMLHLEQEAVSAIHLQNGAVTSTKLADGSVTGSKLLEGAVSDIHIA
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LSWIAAGPSQG"

CDS complement(245602..247167)

/locus_tag="EFAGFIKM_00221"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKFAKVMPTILGGALLLASVSSATAAPVSDQSIPLQAPYASEEG

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DGDGTTFRSLSGDLVDVGHELTGVIETANLEYRNEPGALNEAFADIFGNTIQSKNW

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CDS 247936..248892

/locus_tag="EFAGFIKM_00222"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MRKTRTTARYATRSNVTRRKTVLKKRRWKSGHKKGTKAYTFVIP
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DIPIPAEHLAPYVKAVLKGTDVALNDYHGPVTHHPVHPVVEAKHMLNSILARSDLRGA
SMTAIPHAISRKGLEVMGISSLEVPPLAQAKAVIGGLRVRAVHHVPVGRMNAVRIKKR
SGPDPLSQVVLNDHMAAIKWITDTLGPRGGYTDLQVRNLR"

CDS 248895..250046

/locus_tag="EFAGFIKM_00223"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSHRMMQHAGGEEMKGRSGVVHRRRTTNRRTTARRTVMNKRHRN
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KRLPLTDIIVVLNGTTDDSLKQVLRQPGLTVIYEPDRAGHDVGRALGAKMTDAETVLF
VDGDMVVSAEQLAPFLFAVDRGQDVALNNLTSLPAFVGQDEVSRKAYLNRTLGRAD
LGSNSMTAVPHALSRRMIQTVKPASLAVPPKAQSLAIQHGMNVSAPSQVDVIRSNRLR
PGNTGSGNDVAKLIIGDHLEALATLLGTGWNPAQAHTLSRVEVAYRRNA"

CDS 250046..250819

/locus_tag="EFAGFIKM_00224"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
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/translation="MTLTSMIIPTYNGLDLIRPCIDAIRQYSGDPASYEIIIVDNGST
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CMLMKRDVVESVGLLDEAYSPGHYEDDDYCYRTRLQGYRLLVCGDVLVHHQGSASFQK
TDPVAWKQLLERNRSIFMNKWHVDPLEYMDISDEGGNVE"

CDS 250816..251547

/gene="rmlA"

/locus_tag="EFAGFIKM_00225"

/EC_number="2.7.7.24"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39629"

/codon_start=1

/transl_table=11

/product="Glucose-1-phosphate thymidyltransferase"

/db_xref="COG:COG1209"

/translation="MKGVILAGGTGTRLYPLTRLINKHLLPVGKHPMIMYGIDRLRQA
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EEKPSQPKTSYCVTGIYMYDDHVFNLIRNIAPSARGELEITDVNNHYASAGGLEYDIL
QKYWSDAGTFESLQEAAVRMKGQLP"

CDS 251676..253094

/locus_tag="EFAGFIKM_00226"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MRVVTRTGAARASVSGKPRGIHPAVFMGSGTPTAAGTGSAGVRG
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THPKGVPAGRGGAAAGAKAGSAKGLPPPPAEHTVQAEAVPGGYAEGYRDGVFAGGEAL
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RAPTFQGLLFPVLRHFGIDWSRLKLTSSITINYSLHQSGLVPLLLQGRRVLLIGSQAPE
LAALLHNRGIHVTGIIDSVAGVMDIPRVMQQTAEHAFDIALVAAGIPAVILCRRIAGE
LGKVALDFGHLADKLVTGELQL"

CDS 253161..254888

/locus_tag="EFAGFIKM_00227"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNTPDQQRGEGRHGRNNKVNARNVIRRNIGNIHHNITPNISTHSD
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FIHHFGSVSMKALGEQDFAVVNKDNEQFYSQKWGDPHALVAETSRLARQQTSCTPSGQ
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NIPVPRGISPVQVAKPDLLAIPAGEALISAGDVQGWPREQQVHTTAVHGSHHGLAEG
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PPQLLNPD"

CDS 255240..255518

/locus_tag="EFAGFIKM_00228"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSSSTKKVVLWSKTGCHFCGEVKAFLTERNQPFENIEVQGNDVL
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CDS 255841..257184

/gene="moxC_1"

/locus_tag="EFAGFIKM_00229"

/EC_number="1.14.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34974"

/codon_start=1

/transl_table=11

/product="Putative monooxygenase MoxC"

/db_xref="COG:COG2141"

/translation="MTAKRSLKFGAIIHGVGGSNTTWRHPEVLSDASVNFIFYKRQAL
KAEKGKFDLVFIADGLYTEKSIPHFLNRFEPISILSALAAVTSRIGLVGTLSTSYSD
PFTVARQFGSLDQISDGRAGWNVVTSPLEGTAKNYSKSSHPHPERYIAAEYLQVTK
GLWDSWEDDAFVRDKERGVFFDPSKLHTLNHEGEFFSVQGPLNIARSRQGQPVIFQAG
SSEDGKTLAAQEADAVFTGHDTIEDAQAFYKDVKTRAASYGRSAQDIVILPGINPIVG
RTEEEAEQKYQEIASLVTIDKALDYLGRFFEHHDFSQYPLDEPFPELNGIGSNSFRSG
TDKIKKDAKEQGLTLREVALRAATPRSKFLGTPEQVADKIQEWFETEAADGFIIASEL
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CDS 257354..258997

/gene="gsiB_1"

/locus_tag="EFAGFIKM_00230"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P75797"

/codon_start=1

/transl_table=11

/product="Glutathione-binding protein GsiB"

/db_xref="COG:COG0747"

/translation="MNRSISWMKYMALAAVLVMSVLSGCGAAGGSTNSTAQASGGGQAG
QAEAGNLTFALATSPDTLDPHRSGLAVTVRAIRTIYDNLVVQLPDGSIKPWLATEWSV
SKDGKSYTFKLREGVKFHDGTPFNAEAVKYNLDRVIDPATKAANSLALIRPYSSSEVI
DEYTIKVNLESPSQAFGLNLSQALLGIVSPTAAQKYGDQLGKNPVGTGPYTFVKWDEN
ADIVVAKNKDYNWGPETVENKAAPHVDITFKIVPEEATRIGSVQSSQVLAAETVPPQ
NIAALKNDPNQQLQANTVGLPYTLFFNLKAPWDDVKVRQAVQSAVDVESIVKTLYL
GNYERAWSALSPGILGYDASLEGSINPDINKANQLLDEQGWVKGADGIRAKDGQKLT
RYVDGSPNREKRNDIAAIIQQQLKQVGIAVEVEITKDIATVIYQNWYDLYGNSQVNS
DPNALYAFYHTSAEGERPTLSGLSDPKIDELLEQGAVETDPDKRVQIYNQIQYQYLIEQ
AVILPIYVFPYTVAASKKVEGIKFDLSGLYPLFNDVRIQP"

CDS 259259..260191

/gene="gsiC_1"

/locus_tag="EFAGFIKM_00231"

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/inference="similar to AA sequence:UniProtKB:P75798"

/codon_start=1

/transl_table=11

/product="Glutathione transport system permease protein

GsiC"

/db_xref="COG:COG0601"

/translation="MVQTILSRLATSLLVIFGASVLVYCIMYLLPGDPVLLMLDPSSA

TPEMIENLRVQLGLDQPFYIQFANYFGDMLRGDFGKSMINSDPVLPKILEHFPATLAL

TALSSIIAITIGITLGVLSAIHRNGVIDFVARLVGLFGISMPTFWTGILLILLFSVQL

GWFPAMGSDGFSSVLPAATLGLVGAGFIVRMVRNSMLEVINEPFIVALRAKGLSERA

IMYGHALRNALIPAVTVIGMLIGDLLAGTVVETVFSRQGIGRIIADALMAKDLPVVQ

GVVFFTSIIYVVLNLLVDISYSYIDPRVRRVRT"

CDS 260252..261169

/gene="gsiD_1"

/locus_tag="EFAGFIKM_00232"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P75799"

/codon_start=1

/transl_table=11

/product="Glutathione transport system permease protein

GsiD"

/db_xref="COG:COG1173"

/translation="MSMKPLAGDKKAWAGSVGRIHLWNRRPWRYRVSFVSRFFFYAA

LLVVVFTVACAIVPGWIAPYDPTQMMDVILQAPSAAHLFGTDYFGRDIFSVVHGSR

DSLLIGFASVLVGGIVGSALGIISGYAGGVVDITMRAVDILMAVPGVLLALSVAAL

GPGLMNIALAVAVSSIPGYARVMRGQVISVKGLPFITATRSLGGSNARIFWKHVLPHS

LSPLLVMATLGVGTSILTGSGLSFLGLGVLEIPDWGALLSQGRGYLTVAWWICTFPG

LAITLFLAVNLIGDDIRDRLDPKVKGAA"

CDS 261292..261840

/gene="ssuE"

/locus_tag="EFAGFIKM_00233"

/EC_number="1.5.1.38"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80644"

/codon_start=1

/transl_table=11

/product="FMN reductase (NADPH)"

/db_xref="COG:COG0431"

/translation="MSHVVIIAGSPSKRSRLTGLTDYSSQKLTEAGITVEVIHVVDLP

AEDLVQARFDSSFIRDALAVVEAADAVIVATPVYKASYSGVLKFLDLIPQEGLRGKL

TLPLVIGGSIAHLLAIDYALKPVLAALGGRHILGGVYAVDQGIERLDDGKFVLSADIT

TRLDRSLDELLLTLEKDGITIS"

CDS 261910..262782

/gene="cmpR_2"

/locus_tag="EFAGFIKM_00234"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q55459"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator CmpR"

/translation="MNIENIEAFVYINHYGSFNKAAEVLFLSQPSVTARIQSLERELG

CKLFDRLGKQIVLTEGRKFLPYAQQVLQVIQKGKQKIQRRSTPDALRLGSTVSVSN

YVIPDFLPKIKEAYPEINIKLTATTDQLIAKLLGQEIDLAFVRKVMHPAIRTVAFYE

DPIQLYVYKGHPFIESGHVSMEAIRNEQLVFFECGSLDWLRIHRAFDLSLEHPPNITYH

VDNSETAKKLVMMQGAGIAFLPGLTVKKEVQNQELFPIQVHEVAGVSLQISVVTLKEEY

SPLAEPFGELLRKL"

CDS 263023..264081

/locus_tag="EFAGFIKM_00235"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSIRVGILDQTPIYEGETAVDAFRHTIELAQRAEQLGFHRFWVS

EHHDSGHVAGSSPEVLISHLLAHTKRIRLGSGGVMLQHYSKYVAENFNILAAALGPGR

VDLGIGRAPGGLPRSTQALQEGIQEASSLKEKIVQVKRYIHNEPLEDPSHPLAGLSAS
PLSDIPAELYVLGASVDSAGMAAELGLPYVFSLFINSNIEVALQAIRVYREQFDRSQG
REPYAALAISLIVAESEEEAEGLASEHMLVKIHLESGKVLTVGSVEQAEEFGRQSNET
YRIEILEPSVTRGTKESVGQALLKFQQEFAVEEFIVTTATRDFTKRIRSFELLREILA
EQGLSEFALESKEEAAIG"

CDS 264132..265358

/gene="scmP_1"

/locus_tag="EFAGFIKM_00236"

/EC_number="3.5.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54955"

/codon_start=1

/transl_table=11

/product="N-acetylcysteine deacetylase"

/db_xref="COG:COG1473"

/translation="MKSDLEQPKQHSDQQVQGPEHELHGERAEFVERLITIRRHHR
NPELSGEEKETAAIRSWLEEEGVHIADEYALRTGLVAEVGQGNGPVVALRADIDALP
IQEETKLEFASQVDGKMHACGHDAHTAILIGAARLLKQRESILPGKVRLIFQPSEEKA
TGARQVIQSGALSDVRAVFGLHNKPDQLQVGTVGIREGALMAAADGFVVKVEGVGTHAA
VPEAGIDPIVVAAHIVTALQAIVSRNVGAQESAVISVTKLHSGTAWNVIPDEAILDGT
VRTFDEKVRARIRERFNQVVAGVAAAYGTRATVRWIIQGPPAVVNDESLASAAEQVASQ
IGLNSIRPLPSPAGEDFSFYQKEVPGLFLFLGTSGPHEWHHPGFDVDERALPLGAHLL
AALAEKALHNVQAHQE"

CDS 265687..266547

/gene="cntK"

/locus_tag="EFAGFIKM_00237"

/EC_number="5.1.1.24"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0A0H3JU78"

/codon_start=1

/transl_table=11

/product="Histidine racemase"

/translation="MKQEIDFIKFSPTQNMILVKTDHAAEKYNHIATRLMSYDNVYA
EQVGFIETRPEAVARLEMAGGEFCGNACMALAAHHASEAGMAQQESMEIMLEVSGT
DQLIMCHVKKQQNEYDCQVTMPIPKQIEQRTIRYEGIELDMVIIRYAEFIHIVIEVDD
FDDTMKKRAQTLARLLGLTQGDKLIGILLYQSHLEEMAPLIYVPELDSLIWERGCGSG
TASVGAYLAWSQQREITQYIKQPGGAIKVAAQWNGAELGSITIEGSVGIVAQGKAFIE
APAEWSVVNA"

CDS 266591..267385

/gene="cntL"
/locus_tag="EFAGFIKM_00238"
/EC_number="2.5.1.152"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A0A0H3JXA8"
/codon_start=1
/transl_table=11
/product="D-histidine 2-aminobutanoyltransferase"
/translation="MIILVHFQTCLSEFAEKFDKLASKYDHTIQHSAELEAVINDYSR
FVTDQDNKAAWEQLERSELEELDSLWALRNKSAQCVAIMEKYRALKLENGDVKIADY
FKNIEECIDKEFGSFHVTSKSVLLVSGSGFPMTPLLIAKRTGAQVVGIDIDEESIRL
GQKVETLGAGLKIRLEPTLLENLEYTKEATHIIFSSTVAPKYELLDQLHALTNAQVV
VAMRYGDQLKSLFNYPMRATDSSKWKLVDQILRPDDVFDIALYQKA"

CDS 267452..268753

/gene="cntM"
/locus_tag="EFAGFIKM_00239"
/EC_number="1.5.1.52"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A0A0H3JT80"
/codon_start=1
/transl_table=11
/product="Staphylopine synthase"
/translation="MSNLQRILILGTGPASIQLAATLKDHLNCCIGIAGRQSVRSASV
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LEQMNDDEFIKQKCIILISPTFGSNRLVTHYMRERNAAPEVISFSTYLGDRWMHEHP"

SNHVITGKKVYIGSTRYPSEQVSKLCQVYERLDVALEVMRSPLEAETRNLISLVH
PPLFMNDFSLEAIFGASDTQRYVYKMYPEGPITEVLIREMRAQWQEIMNITERLHIQG
VNLLQFMTDDNYPVRLESISRQDIENFNQLQVIHQEYLLYIRYTSLLIDPFSEPNSEG
KYFDFSAVPFRQTFMNREGELDIPRMPKEDYYRIKIIQGIARHLDVSCPTIDQFIKY
EAKIQEVADANPDQRLSDAFVIQSFDEDIRMICIGLVSSRV"

CDS 268971..270608

/gene="cntA"

/locus_tag="EFAGFIKM_00240"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2FVE7"

/codon_start=1

/transl_table=11

/product="Metal-staphylopin-binding protein CntA"

/db_xref="COG:COG0747"

/translation="MKKGLTFTSILLVSAIALFAGCAQSTTEKESAQTTPANSQVQT
ELIYASAKDINDMNPPLYTGSMAPAQGMVYESLVENTPDGIKPLLAESWDISEDGKTYT
FHLRQDVKFRDGEFPAEAVKQNIQANAEKHAWIKLSTKITSVKVIDEHTVELTL
SEAYYPALVELSMTRPYVFISPKDFKDGKDGVSFGHGTGPYKLTDHKVEENATFEA
NEDYWGGAPAIKKITSKVLPAGETTFLALQKGEINFTDDRGADSIDVEAIDQLAES
GGYQVVRSEAMNTNMIVANSSRENSPVQETAVREALWVGIDRETISKDIFNGTQTVAD
TLFSANVNYAKVDLKKREYDPEMAKKLLDQAGWTLADGEGVRTKNGQPLAMKLYYDSN
SSSQKIQAELIQYSMKELGIQLEILGEESTSIANRRATGEYDLLFNQTWGLAYDPQST
IAAFTSDSAYKHTTSGIAEADELYKKIDAVMISTDEASRQSLYADIMKIVHDEAVFIP
ITNGRVTVVAPENLDGISFKQTQYELPFKMNFKYIN"

CDS 270800..271732

/gene="cntB"

/locus_tag="EFAGFIKM_00241"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2FVE8"

/codon_start=1

/transl_table=11

/product="Metal-staphylopin import system permease"

protein CntB"

/db_xref="COG:COG0601"

/translation="MGSYIVKRILLAIPLLIIISFITFVLINLSPLDPAVVVLQAQEV

PQITDELIAQTNKALGFDQPFMIQYANWIMAVVQLDFGNSYVSGEPVWSLMGPAFMNT

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VKDLLPTSGMDSYRSYILPVIVITVSYTGIIYFRTVRSSMLSNMNEDYVLYARASGLS

EKKVTLHILRNSLQVAVSIFCMAIPIVLGSTVVIENVFAWPGLGRLSVKSILSRDFPI

IQAYVLMMLAVTFVLNLTSLDIINAAMNPRLRKEF"

CDS 271732..272628

/gene="cntC"

/locus_tag="EFAGFIKM_00242"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2FVE9"

/codon_start=1

/transl_table=11

/product="Metal-staphylopin import system permease

protein CntC"

/db_xref="COG:COG1173"

/translation="MRILKNLSKDKLALTSLVIMVAIMAGVLAPLIAPHDPGQVNMK

LRYASSSWDYLLGNDHLGRCVLSRLIYGIRPSVLWVLVALSLSVLIGAIVGFVAGYFK

GKVDWIMRVCDIMLSFPGYVMTLAVVGILGAGLENILIAFVCMKWAWFARVIRTSVM

QFSDMDYVKFAKASGTPNLRITKHIVPVTFADIAVIASGSMCSMMLQISGLSFLGLG

IQAPHAEWGMMLNEAREVMFSRPELMLAPGLAIVVVSAFNFLSDALQVALDPKLMTS

QGKSDKSYESEVRKAAYEYSRG"

CDS 272609..273418

/gene="cntD_1"

/locus_tag="EFAGFIKM_00243"

/EC_number="7.2.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2FVF0"

/codon_start=1

/transl_table=11

/product="Metal-staphylopin import system ATP-binding

protein CntD"

/db_xref="COG:COG0444"

/translation="MNIVEVEHLKVWDTNTDKVIIHNSSFVKKQGSMAIVGESGSGK
SVTCRAIMRLNKPWIRQTGTMLFQGEDLNQLSEPEMRRKRGKHLQMILQNGMSAFDPS
CVIGVHIRETLQQHFGWNTREIERKIINAMESVMLRHPCEILNQYPHQLSGGMLQIRM
IALALVLEPDLIIADEPTTALDTISQYEVVEQLIQLRERMGCMMFISHDLGVVQKVA
DDVMVMKDGNIVERGNMHSVLTPEKHAYTQYLVSTRLELSNHFALMQGDL"

CDS 273419..274171

/gene="cntF"

/locus_tag="EFAGFIKM_00244"

/EC_number="7.2.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2FVF1"

/codon_start=1

/transl_table=11

/product="Metal-staphylopin import system ATP-binding

protein CntF"

/db_xref="COG:COG1124"

/translation="MLKVESIEKSYNQGGFLSKHRQQVLKQVTFECQQGECLGIIGES
GSGKSTLGRLLGIERPDLGTLLDGQDVQNRVRMGNL SAVFQNYTSSINPFLT VET
AIMEPMQAQQKLRRKHQGNSEKVDLLNQVGLGPSYRSKYPHELSGGEAQRVCIARAIS
TAPKLIVFDEAISSLDVSVQIQVLQLLKEIKLSYVFITHDIQAAAYICDRVIIF
REGQVVEIVPTKQLKDVQSDYAKRLKHLITF"

CDS 274186..275379

/gene="cntE_1"

/locus_tag="EFAGFIKM_00245"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0A0H3JTK0"

/codon_start=1

/transl_table=11

/product="Staphylopin export protein"

/translation="MSGAMSWPFLRLYLVLVLYFSANAILNVIPLQGESLGASGTTI
GLIMGAYMFTTMFFRPWAGRRIQKHGPIKILRLILIINGFALILYTFTGLGGYLVARI
LQGVSTAFFSMALQIGIIDALPEKDRSQGISYYSLSFSYIPGIVGPVIALGIWQTGGMD
YFTVVLIGIAVCTGVFGYTAKMEPSKEQPAVNPSEQNVSMWESFGQLVKNPYLFRCVS
LMLAASVVFGAITTFIPLYASQVPNGNAGVYLMQAGTVVLARIMLRKRIPSDGSWHS
PFIMGTMCLLAVAAQCVSFAVTGGVFFYVGAVFMGIGQAILYPTLTLYLSFVLPKLN
RNVLIGLFIAMADLGISLGGVIMGPLADFSSYSFMYMMCAILGAVMIVFAYERRRRPVT
GTSVS"

CDS 275376..276641

/gene="cntE_2"
/locus_tag="EFAGFIKM_00246"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A0A0H3JTK0"
/codon_start=1
/transl_table=11
/product="Staphylopine export protein"
/translation="MTARRESGDERLKPSMDATSNGLKNPVSFSEFIRFYMLAFLFFAA
NSALTILPLRSEAAGLNQAEIGLMMGAYMFTCMLLRPFAAQLLGKYGPLRVMQWLLL
LHAGTLLLFFVFGVETYLWLRALQGVATAFFSMTMQAGIVEKLEDKDRAQGGLSMYTLF
TMVPSLVIPIAIQIWENASDLAFTLLMIGLAALPLLIGYNVDLPRSTVQNKFYTLGD
MFRSFSGIWRSTPLLISSVVMLFASCVFGATATFLPLYMVSTGMASAGIFLTIQGLVV
ILCRFILRKKIPSDGSWNTWLMAGLMLCAALGTQLLSLVEIIGPLVYLSAVFSGFALA
LLYPTLTLYLSFVLPVDSRYVLMGIFMSSYDLGFSLGGLAMGFIVQVSSYSTMFMICT
LLSVAATILVLVFRQRMEAGNKARSMVSV"

CDS 277216..278412

/gene="yciC_1"
/locus_tag="EFAGFIKM_00247"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94400"
/codon_start=1
/transl_table=11
/product="Putative metal chaperone YciC"

/db_xref="COG:COG0523"

/translation="MTQKQVPVTVLSGYLGSGKTTVLNHVLNNRQGLKVAVIVNDMSE
VNIDAALVKGEATLSRTEEKLVELSNGCICCTLRDDLMQEIEKLVNEGKYDYILIEST
GISEPVPVAQTFTYADEESGIDLTRLARLDCLVTVVDANRFWHDFGSEQSLDRNQAT
GDEDTRDVVDLLIDQIETCDVLLLNKCDLVDETELNKLEGIIRKLQPNAKIIRTENGQ
VNPSEILNTGRFDFEKVSMAGWIQELEKESHTPETEEYGIGSFVYRRRKPFHPSRLA
EFMSYWPEEVVRAKGLVWLAAEGDVAASLSQAGPSIQFGPAGHWVAALPEADKEEILR
NEPDVLEKWDVQWGDRQTELMIGIEMERASIEDELQCLLSDEEMLADWGHFDNPLP
WPVEAV"

CDS 278693..278962

/gene="rpsN2"

/locus_tag="EFAGFIKM_00248"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31587"

/codon_start=1

/transl_table=11

/product="Alternate 30S ribosomal protein S14"

/db_xref="COG:COG0199"

/translation="MAKKSKVVREKQRQAIVAKYADLRRELKEKGDYEALQKLPRNSS
PTRLKNRCEVTGRPRGYLRKFKVSRIKFRELAHQGHIPGVTKSSW"

CDS 279078..279452

/locus_tag="EFAGFIKM_00249"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLDSFTLRRIQSVMNGYIHEKVPAPLRMTMVKLTIELNNNELILT
EERPAEERYQWDKMHIARFYWEENQWKVYARDEQSSWNPVDVITPCSDFENVLEQVER
DEAGCSGVRERDRLRVHFIREN"

CDS 279691..280167

/locus_tag="EFAGFIKM_00250"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKRGTTIFLKLAVLLIGVPILALCIFGIPWLANNPVNPNYAGAL
YPIVIIMYVSVIPFIVALYQAFRLLSYIDKNEAFSLMSVKSLKTIKYCAIVISSLYFV
MLPFVYVVAEKDDAPGLIIMGMPVVFASLVIASFSAVLQRLQEAIDIKSENDLVV"

CDS 280177..280410

/locus_tag="EFAGFIKM_00251"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAIIINIDVMLAKRKMTVTELAERVEITIANISILKTGKAKAIR
LSTLDAICKALDCQPGDILEYKADEDEDTNEHI"

CDS complement(280490..281341)

/gene="btr_1"
/locus_tag="EFAGFIKM_00252"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P40408"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator Btr"
/db_xref="COG:COG0614"
/translation="MKEHIFLPKPVFPRHVCFPDFIGGYSDFPKHHVNREYRTKEINL
DQCYNLHLVLEGKGFLLDTGTTRYELTRGQGFLYGPGLRQTYSDLDDPWSIRWIHFYG
IRLEEELLNGKGVDEPWLFQCSNFPVVTALMDRLLLELGRGYQVEDEHSVAATLYELLTR
LQSAASQINVSLNHTSERIREAGNYIRSHSNEHITLDHAAGIAGYSTTYFSRKFSQTF
GISFPEFLLESRLHLSKQLLATNLSIKQITLETGFSQSSYFIRCFKTQENVTPMQFR
MMHNHSL"

CDS 281523..283595

/gene="bgaA_1"
/locus_tag="EFAGFIKM_00253"

/EC_number="3.2.1.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:D9SM34"

/codon_start=1

/transl_table=11

/product="Beta-galactosidase BgaA"

/db_xref="COG:COG1874"

/translation="MAKSIQMDELKMGVCYYPEHWSEALWEDDFRRMKEMNITVIRMA
EFAWSIFEPEEDQFDFSFFQKALDLAHQYGLSVILGTPTATPPAWLTSKYPEVLNANK
DGVLYQHGMRRHTNYSSPIFRQQCDKIVRNMVIAYKDHPALIGWQIDNEFNCHMDVFY
AEADHVAFREWLKDRYESLENLNQAWGTIFWSQTYTDWEQVHLTRNMVSQSPNPHLAL
DEKRFISANTISFAKLQVDIIRELDPKHWITTINGTFGHLDNHEMTEDLLDFFSYDSYP
QFATIFPGTDGNSLQDRAWSMKLSNVRNMSPNFCVMEQQSGPGGWVDSIGMGTPRPGQ
IRLWSYQSVLHGTDLLVYFRWRTATFGTEMYWHGINDYHNQPNRRVREVAQVGEEFAK
IGRVIAGTTYQADVAILQDYDNIWDGELDEWHGPLQQQSVRSWYKQLQYRHIPTDMVT
LQPTTTLEELSEYKVIIYAHPAIMTDETAELLQAYVSQGGTLFFGARTGYKDIKGHCY
MRPFPGAVAELCGVTVEDFTLIKGTVPAAKLQWSGASERLQEGTSTAGFNEVLHVEHA
DVQVVAEYASEYYSGSPALTKRTVGQGQVWYYGAAYNEPVVDALLDEIGLSSPVGDLV
EVPSEVELGIRSGKD KAYVLLNYSQQVPIKLLKQAKELLSGTTLQNEINMPAYGVF
IFEIDLPH"

CDS complement(283740..284783)

/locus_tag="EFAGFIKM_00254"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTEEQSYTTEEISKLLKISKLTVDLIKKGDLVAYRVGKQMRID
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ASSAHAMTAVPRHLVITGQDVSLDILMRHMEKQTRDIRPLRSFMGSLDGLISMYRGES
DLVSTHLLDGGDTGEYNLPYIRKILTGRSYVVVNLLSRPAGLYVQRGNPQNLQNWTDLS
KPELRLANREIGSGARVLLDEQLRLHGIPAAGLIGYTEETSHMGVAAKVSSGEADV
VGIEKAARLVGQVDFIPLTQERYDLVMLRKQGNEAWTGSVLRILQSQEFRQELQSFE

YDVSRTGEILYEA"

CDS 285021..285893

/gene="modA"

/locus_tag="EFAGFIKM_00255"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37329"

/codon_start=1

/transl_table=11

/product="Molybdate-binding protein ModA"

/db_xref="COG:COG0725"

/translation="MRKKIGYVLGMSLGLALVLAGCGANTGTTDTSTGAEQTTSTPA
ASGETSSAGNTDPQETVDLTISAAASLTDAMKEIETNYELANPYIELNFNFGASGALQ
QQIEQGAPADIFVSAATKNMNALVDENLIASGDQKNLLQNSLVAIVPADGTNTVASET
DLTSDSIKTVAIGIPESVPAGTYAKEALTNAKLWDELESKLVQGKDVRQVLQYVETGN
ADAGFVYKTDALTSQVKIAFEVDKNSYTPANYPIGIIEGTKHRTEAEQFYAYLQTPE
VLDIFAKYGFTIPK"

CDS 285890..286576

/gene="modB"

/locus_tag="EFAGFIKM_00256"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AF01"

/codon_start=1

/transl_table=11

/product="Molybdenum transport system permease protein
ModB"

/db_xref="COG:COG4149"

/translation="MNVNAIDWSVFWSPVRLSLQVALLSSVVATVLGIAIAWKMSRSS
FRGKILLETAFMLPLVLPPTVVGFLLLVILGRKSLFGQWIETIFSAPVIFTWWAAVIA
SVVVAFLVYQTMKSGFSGVDRDLEDAGRSIGANEWQVFRYISLPLAGRALMTAFILG
FARALGEFGATLMIAGNIPGKTQTVPTAIYVAVDSGNQTMAWAWTVSIIISFLMLLM
TRQQRDGKND"

CDS 286850..287182

/locus_tag="EFAGFIKM_00257"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNTKSDCGVSLQIDYLDLLHFAIQIQDQEWQQSLIRQLKIFQT
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KIKWASRR"

CDS 287481..288320

/gene="tcyK"
/locus_tag="EFAGFIKM_00258"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34852"
/codon_start=1
/transl_table=11
/product="L-cystine-binding protein TcyK"
/db_xref="COG:COG0834"
/translation="MVKKRGIQKFR TALLFITMLAVLAGCSTGTASNDSESASAAGDT
KVKKIIVGTGTQFPNVCFIDENGKLTGYDVELIREIDKRLPEYEFEFSTMDFKNLLLS
LETKKIDLIAHQMEVNDERQAKFLFNDEAYNIFPNKIVVSQKNEEVKSIEDLKGGKLI
VGATSNAAVLAEKWNAANGTGIDIVYSGAGEDTITQIKTGRVDATISTQFAIDYQNKA
VDAQLKTVGDALSNSKVYFILNKDEQELKTKVDEALKAIKEDGTLGKLSTEWLGADYT
VEE"

CDS 288344..289087

/gene="tcyL"
/locus_tag="EFAGFIKM_00259"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34315"
/codon_start=1
/transl_table=11
/product="L-cystine transport system permease protein
TcyL"

/db_xref="COG:COG0765"
/translation="MGKSFDLSLVLDIFIPELLRYLHITLIVLGGIVLGLVGGVLLAV
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TYALSDAASFAEIFRGAVRSVDKGQTEAAYAAGMTTFQSFRRIVVPQALIVAFPNMAN
TLIGSLKDTSLAFSIGVMDMVGRGQTLISATSHALEVYISLSV VYYVIVIVLEKGF AF
AERRLQRHERKRVVHKPAIRAKRLKRIAG"

CDS 289084..289803

/gene="tcyM"
/locus_tag="EFAGFIKM_00260"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34931"
/codon_start=1
/transl_table=11
/product="L-cystine transport system permease protein
TcyM"

/db_xref="COG:COG0765"
/translation="MSNMSIDLQFIYTSFFQILKALPLTLVITIVPLIAGFGIGLATA
LIRIYRVRWIHRIADFYVSFLRGTPMLMHLFLIYYGIPMIIDKLAERYGWAFQSSSIP
ILVFVLIASFSLTAGAYMSEIIRSGILAVDIGQMEAAHAVGMSTFQALRRIIPQAIGA
VLPNLCSMFVGFHLHGSTLAFTVSQMDILGKADVVASVSLKFLEAFIAAAFIYWGLTII
AERITALLERRVAVYSKGGVS"

CDS 289800..290552

/gene="tcyN"
/locus_tag="EFAGFIKM_00261"
/EC_number="3.6.3.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34900"
/codon_start=1
/transl_table=11
/product="L-cystine import ATP-binding protein TcyN"
/db_xref="COG:COG1126"
/translation="MITLTNIHKTFGKQEV LKGIDLTVEQGDVVAILGPSGSGKTLL

RCVNFLERADEGEVQISGLTVDCCKHARKHDIVQLRRKTAMVFQHYNLFKHKTVLDNVT
EGLIIAQKMSKADARTRALGVLEQVGLSAKINEYPSMLSGGQQQQRVGIARALALNPEV
ILFDEPTSALDPELVGEVLSVIRSI AQEGITMIVVTHEMGFAREVANRVVFM DGGSVV
EEGTPEEVFVRPKQERTRQFLSRYS SDWSYVI"

CDS 290674..290961

/locus_tag="EFAGFIKM_00262"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQSKIDEIITHIAHSHQQIARVLDAKRQVAVRMSEIINHLPDIE

PELDGVDGLLDSSGQINKSIISYLGGLADLEEAVAETLTQVMREIAVQEEE"

CDS 290985..291326

/locus_tag="EFAGFIKM_00263"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSREQSLILMLDAAAKMQWNIALILEAKAIEAEKVRNWTNLNHLN

GDTFLTHGDQVGEPLKMHDQLVELLEGLTRMETGLCNNLKAVMVQN DSEDGGGMDGGM

FGGMDLGDMGK"

CDS 291323..291622

/locus_tag="EFAGFIKM_00264"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSLMRREQEAKLALIESIAHSQQALARILDSVASVTAHSEVSAR

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CDS 291624..291965

/locus_tag="EFAGFIKM_00265"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLKKKKIRLRTKRALLIRGARLRKIRKLRALRAKRVLHKRPLKG
RSAWLKKKKRAVRRHRSPKPVQPVVPATPTDPNPDGAYSQGYNEAYNEGFNAGFAKGF
EDGHQLAYKAQ"

CDS 292219..293313

/locus_tag="EFAGFIKM_00266"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKNVAKRKHRLTEAETAYRGGYAEGRRFGGCQAMMERVQMFEP
TLRDMKVLYIPQGFDAIDEGVTLALQQSVRECVVGSPAAMLQEASQHRPDVVLVMNGL
HVFPADHVEQVNGIRALGIRTAVWVDDPYFTEDTSLCQHYDVVFTHEEAAVPFYLG
HGANQVIYMLAVNPGMFQPRRAAPQHQHDICFIGTGFWNRIALFDELAPFLADKKVF
IAGSQWNRLARFDVLGRFIHEGWIAPEGTVDYNGAKIVINIHRTCENGEDNRNTHHL
EGHSINPRYEISACGTMQITDARADLPRYYKPGYDIETFTNAAELQRKIHYYLKHEE
ERQAMAWRGLLTMTNQHTFTRRIGQLLEHL"

CDS 293374..294513

/locus_tag="EFAGFIKM_00267"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSLKHRKTKKIHAPVLSLADQARKNGQHAGYDAGKEEGYLRGRA
NYIVNCAQEPLPFRQLHVLYVSSGKGFYSPLDEAIMATLQGMVAQVTLSDPRQPISE
IALQTRPDLVLVLDGMDIEHIDAIRQAGIQTAIWLTDDPYTDMTLEIVTHFDHVF
TLELNCIDLRYQIGCASVHYLPFAAFTNHYPITTPSPLKRDVSFIGSAYWNRVYFFN
PIMPQLMSHNTVFNGIWWDRLPDYTAYGEKIELGRWMSPPETNDVYNGTKIVINLHRS
HEDDSVNNNHLKIPPASPNPRTFEIAASTTLQLTDARDDIARFYKPGVEIETYSSPQE
LLDKVEYYLTHEKERREIALRGLERTLKDHTYGKRINEMLTIIIFP"

CDS 294532..296205

/gene="mshA_1"

/locus_tag="EFAGFIKM_00268"

/EC_number="2.4.1.250"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01695"

/codon_start=1

/transl_table=11

/product="D-inositol-3-phosphate glycosyltransferase"

/translation="MHSTLYRIIVYRVRAAMATKPKMMLFSHVCNTRSITGAEKLLH
FMREIGTIFECVLVAPQEGKLAGLARRFGIQVKICTLPMLHGVYTPYLGIADDAEHLR
HTPAYQEAVSLIRETAPDIVLTNTCVNVMPAAKSLQIPIWKITEIIHTNEHTTEA
IQMIGRYADWIIIGISETAVAPFQEAGMGDKVTIISPTWEPALPAPDRWVHLRERKRKE
LGFKSSQTCIGYISSFIYDAKGLKPFVDMALRICETHSRCRFWIIGAPSDKKYYDECV
SRVKKSGYSRRFTFTTFEENVSLAYTAMDILVIPSMVKEGFGMTALEGLYFAKPVI AF
AQGGLKELMESVGS DAFLAPPGDTEALVTLATSL LNDAELASNTGWRNRTEAERLYGV
ETYRTKLHTMVTQWLLRFPGWFAYIQPPNGPVYTHGEGGLRTVLVLEPTTVRALLFPL
TVIQALPHSSLPPIALGHDAPVASGTVP AVKPIQQRGKTRKRRRKPLAPHSRRDREGL
KRTSGTGRRKGRTRTTKGPRPHMGKSASRRRKSAKAGRSRAGRKGSNTR"

CDS 296202..297311

/gene="wbpl"

/locus_tag="EFAGFIKM_00269"

/EC_number="5.1.3.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:G3XD61"

/codon_start=1

/transl_table=11

/product="UDP-2,3-diacetamido-2,3-dideoxy-D-glucuronate
2-epimerase"

/db_xref="COG:COG0381"

/translation="MKAGITMKIMTVLGTRPEIIRLSLIISKLDQYASKHILVHTGQN
FTESLSGLFFKEMGLRAPDYVLQDEAATLGRQLSSMFTQMEDLILQEKPKL LLLGDT

NSALCAILAERMGVPVIHMEAGNRCFDLDVPEEKNRKVIDAISTVNMPYTEQSKKHLV
SEGVPSRRIVLTGNPIYEVQMQUHYDAQVSSSKILKKLKLKSGQYFLVTAHRAENVDHAP
HLLIEMKGLNQVAEEHGLRVICSIHPRTAIRIAEHLHLEMNPLVEFHEPFGFFDFVML
ERHARCALTDSGTVQEECCIMGVPTVTMRRTTERPETVDCGSNVVSGLDAARIADCVK
VMTKMSSDWDCPQGYKATDVSSKVVKFLLGGKMHV"

CDS 297304..298290

/gene="pseB_1"

/locus_tag="EFAGFIKM_00270"

/EC_number="4.2.1.115"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O25511"

/codon_start=1

/transl_table=11

/product="UDP-N-acetylglucosamine 4,6-dehydratase

(inverting)"

/db_xref="COG:COG1086"

/translation="MFENKRILVTGGTGSWGYELVAQLLPQQPSEIIVYSRNESSQVA
MSREFEDPRLHFRIGDIRDKDALTAACQHVDYVFHLAALKHVPVCEDQPYEALKTNVI
GTQNVIEAAIENKVEKVIYISTDKAANPSNFYGMTKAIGEKLIVYANLLHSDTKFVTV
RGGNVLTNGSVVHLFKNQIRQKGQVSITDMSMTRFFLTLDAILLKFASVESVGGE
IFVMTMPTCKIVDLAEVLIEDSGVENVSIVERGIRPGEKIHEILMSEFESMTTVVYDE
QYLVILPTLGIPGLREHYTNCPPVSFNSFSSEHQLMTKEEIREILKRGGFLS"

CDS 298287..299114

/locus_tag="EFAGFIKM_00271"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLLILGGNGMAGHILVDYFRRQGVHSVFYTSRDVTPNGLLLD
VNDSFMVDRLEAVHPDVIINAVGVLNNFADEDKITAYHINGFLPHRLRRVADTIGAR
LIHISTDCVFSGERGAYREDDVTDGTSAYAITKALGEVQDEGHILTIRTSIIGPEIRQG
GIGLMQWFMSSTGEVGGYTRVFWNGVTTLELAKWIDHYLASSVSGLIHLAHPAPVSKH

DLLVLFKQTDWKQDVTIMRDDSVVQDRTLVSREDVKTDLPDYSTMLKELALWMEQS"

CDS 299096..300037

/gene="rmd"

/locus_tag="EFAGFIKM_00272"

/EC_number="1.1.1.281"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q6T1X6"

/codon_start=1

/transl_table=11

/product="GDP-6-deoxy-D-mannose reductase"

/translation="MDGAELRGKKVLITGASGFTGRHAVSYFREAGAVVAAVRRPDV

YSFGKGAQVHVCDLNDKQQVRHLIGEVQPDYVLHLAGKNSVPDSWSDPLLVLETNVMA

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QQIMLAEPGNLIGAGPSTGICSLVRHVACEQAGKTEAFRLSGRDNTRDFLDVRDAV

RAYATLLIHGSSGTYPVVSVERSLEIADLLSMTEAEVVRWDGASSGPDGSGKQ

EELSLLRKLGWQPLIPFATSLQDILSDVRVQQGRTTS"

CDS 300034..300750

/locus_tag="EFAGFIKM_00273"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNPRVSIVIPFYNCYPVPQAIQSALNQTYPDVEIVVVNDGSTRH

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SGVGLFDELLPYTHDLDLWMRIVLNGHRFPYLNEPLTAYRWHGAMGSRHADVIGREA

SMVWSRYREPLLQRIATLGG"

CDS 300847..301563

/gene="wfgD"

/locus_tag="EFAGFIKM_00274"

/EC_number="2.4.1.305"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:B5L3F2"

/codon_start=1

/transl_table=11

/product="UDP-Glc:alpha-D-GlcNAc-diphosphoundecaprenol

beta-1,3-glucosyltransferase WfgD"

/translation="MEPKVSIVIPFYNCAYIEQAVHSALHQTYPHIEVIVVDDGSTEH

VEKLQPFMDSICYIHKENGGTATALNEGKIHATGDYFVWLSSDDVMLLDRVEKQLKFM

REVKASFCHGAYHYVNEKSEWLDTVHPEVGSRLMLQVLLEGCPINGCTVMLEMEAFE

RFGLFDTDTRYTHDYEMWMRLFPMYELFYNEPLMCYRLHESMGTKRHFKAALVAEMEQ

VQAKHRPILFNLLQIGGYWK"

CDS 301623..301760

/locus_tag="EFAGFIKM_00275"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKHFLSVISGSSFFALWTAMINLLNDLSQENKAIRFSILAQRNV

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CDS complement(302131..302301)

/locus_tag="EFAGFIKM_00276"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTLLVPSDLYNRWFSTPVSTPHIDVDYAVMNELMKKLPGYVFP

DPASMAIMNSKD"

CDS complement(302298..303536)

/locus_tag="EFAGFIKM_00277"

/EC_number="2.4.1.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WMY9"

/codon_start=1

/transl_table=11
/product="Glycogen synthase"
/db_xref="COG:COG0438"
/translation="MKVLLVTYWELTHMGGIWTVKQLADRLIALGVEVDIMGTNGAH
NEVYVRNLNRAFSKDKVWPMQLAKLNPTDLPQFTADPLLAYYELNRYAFEMAAAYLGV
DHYDVIHAQDPVAAVAIKRILNRNIPLVTSYHGALAREAFYDAQNSNPQLTLP SYLQS
KRGRYFLSLEERSAAQSELILVSSHVIKSTLTAVPESKFRQIPYAVDLPAYRASAA
VKFRQRPPAGKKVIAFTGRLEYIKGVHVLKALASLKNKRSDWVCWIAGEGNLTDEL
SQAASTGIGADVFWGKLDNIPSFLRHADIYVQPSLQDTQPFSVTEAQLAGVPVIVSG
TAGMPEMVDPGRTGWVPPQDVDSLRELLDALLEDNVTRKTVGAAAKAWAEQHRSL
EVMGFRTFQVYQEAIYRGGLTT"

CDS 303723..304082

/locus_tag="EFAGFIKM_00278"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAVYLLEIHENLLQTFAPVKYMDVELAYVGGEEGTDV FVGGASM
HGELYRHLFHLTSNSGGAGGNQVIHNLDTSEPYELRVISNSSSPNHLVIRIYCRSIH
GQTLGILSEYQMMKLAD"

CDS 304301..305830

/gene="hsrA"
/locus_tag="EFAGFIKM_00279"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P31474"
/codon_start=1
/transl_table=11
/product="putative transport protein HsrA"
/translation="MDKPAIYWLEKSVENVKEQTAVPQEPAEFSLKAIILPLLAIIVG
MIMVILDSTVVNVAIPNLVQYFETDLKTIQWTVTGYTLALSAVIPLAGWLDRFGAKR
VFLFTIAMFTLGSVLCSIAQSPEQLIYRIIQGLGGGMVAPIGMAMVFRLAPPERRGS
IMGMLGIPMLLAPALGPVLSGWFIESLSWHWIFLINLPIGIAAFILCIKFLPDTRGR"

TPALDLLGMILAPIAFSMLAYGVSEGGTSWTSATTLTGVIVGGVALILFIIVELRHQN
PLLELRVFKSSDFSRGII LAWVSQVALFGAMILIPLYLQQIKGYTALETGLILLPQAL
ASGVGMPLGGRLFDKIGARPLAFVGLGIISGALFILSSITAETGLGLIITALVMMGLG
MGLSMMPLNTHVLNAAPRKL VGRVTPLTAAAQV VVSFAVAGLTGFLT SRIADNTTST
EPTAIVHGLVAGFNDTFFLAACIALFGCLLSLILRKPKPMPEEELQNGDKPDPAMMMG
H"

CDS complement(305895..306968)

/locus_tag="EFAGFIKM_00280"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKVLFTFYVPSGGVDTLNRLRTAVLKRHGIEAHL LYSTG SGLQ

NNSDTPIFTASDEDIHHIIH THHYDAIIATSDIAMPGR LRGLGYTGRIIFE AQGLGT

RDQALETIQMGVPYLQAHCDAAVIPPTDHLLDMFIHICPWLHRFVIPNMLD TDTFAPI

LVDTPPYPVLA WVGRL EHNKNWREYLIISSELVKKNP KARLWLFHDPTLANPEDEV MF

RHMLAEYGLEDKIGIFINVP HFQMPTYYSMIAASGGIMLSTSLLEGFGYAVAE AISCG

CPVLSTDSDGVR SFITHNKTGKFYPIGDVKA AVAEAKDLMKNKKLREYIRIQGRQHMS

LSFSPDRYAISFREMM TALRIFH"

CDS 307214..308347

/gene="btuD_1"

/locus_tag="EFAGFIKM_00281"

/EC_number="7.6.2.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01005"

/codon_start=1

/transl_table=11

/product="Vitamin B12 import ATP-binding protein BtuD"

/translation="MLEVKQVSKVYEGQRGVHQLDFTMERGEIVGFLGPNGAGKTTM

RMITGYVHPTAGSIMVDGVS VHEQGQRVRSKIGYLPETPPLYPDMTVQSYLK FVANLR

DVPAREVKLRVSEMVSRLGLQGRERQMVRGLSKGYKQRLGLAGAIHKPDLLVLDEPT

SGLDPNQIIEIRDLIRELGENHTVLLSTHILPEVSMLCNRM LIINQGQLVLDGSPQHF

GSAMGDQFKVSIEVKATAEQLHNVLTPWEKVRSEVIQASDANTAKDTSLNDSANTVK
MLLTGENSEDFREELFYLLSGAGLPILEMKKENLSLEQIFLKLTTEATD TDANSADV
DKVAGAEMDQDVTSDIDSSSTSGTSVSTAADALSQARKGEDSK"

CDS 308344..309060

/locus_tag="EFAGFIKM_00282"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRRMMAVCNKLQAYFLSPTS YFAFAVYVLM TSLLFYSSFVYYQ

PSIVDYRLVLGDTLSMLLFVPLLTMRLVAEEFRQGTDELLTSPARVTEIIFGKYLA

SLAILVVLILCSLVYPFIMSFYGTLDMTTVWMSALGLFFLGGSMM AIGLFASTLSQHQ

MVSAVAGFIILLVLWMLDSFAGNTGSALQQWLDPFALTNRFD SFMKGVLSGPDILYYV

TLSSVFLLLSIQIVERKRWR"

CDS 309065..310459

/locus_tag="EFAGFIKM_00283"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKWLSHTNSTVLSVAVIGIFILLTLFLNSLGGFQLDLTSNKQY

TLSDQSLTAIKNLKDDVNILVLTVENANNTVLNREVTDMVEEYTKRNSKLIKQYNLT

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MSSTEMHKMVF LTGHEELSLAQMTTLQSSLEQNNVQTEELQLNQAGKVPEDADVLAI

GPQRDLSDTEMKAIRTYLSNGGKLLLSLGFVEDMKSSWKNIDALMADYGVVDEHAVMV

DNQQASTMGPLWVVP EYGTHAITDKLAASQLYPMLSLSIALTSKEQDKYTLSPLIHSS

NDSYGETNIGLLQNETTND AEEDIQGPVELGYAADTTDGKPKAVILGSSIFMQDSEI

ANGGNRDFILNTVNYLSEKENGLTIRPRVQAGYEMAYLNGEQARTIFFVAIVAFPLIF

VIIGVLLWWRRRRV"

CDS 310456..311472

/locus_tag="EFAGFIKM_00284"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRKWVPTILVVIVLIVGWAYAASQNYFREEEAVQAKLLGIQSGD
IQSITIHDTEATSDAAATSTLTLENGVWQMIEPKAYPLNGYSVSSWLDALSGANQEL
VVEEAPTDLDKYGLGTDATRMDIKLKDNREIKLTIGGQLPADDARYVRVDSGPVVAVQ
TEAITSIALSRRDLLDTPFNMNETNVGSLEWEGEAATWMLTSTSENGVAEQTWTLNG
KTIEATDAVSLIGIKINLSTADDVRKASELKGTVPRTLSVEQTVSGQQVRDVYRGLT
VPSEPDQIWWITPDGQWAYGMDATSLTETEKFPDTIKASATSSEESSSSANDETTSSS
TDGK"

CDS 311746..312735

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/inference="ab initio prediction:Prodigal:002006"
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SPYSTSGIAPGLNTNSATDRSHMGNDRSIYGTMTGAVGMMRGLTNSGKARGTDDGHY
GMKSEGQRVDSTDDNTSAEIKGKISAKIKQFAPNIENVYVSANPDFVEHVENYATDIR
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CDS 313196..313804

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/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MNEKIVVAAMRVFEEQHGFARTKDFIEAGVSPYYIKKLESAGEI
ERVKQGIYRQSGQFNEPPNEMVEVSKLVPKGVICLLSALSFYELTTYNPWEYQIAIHR
GGKKPKLPDYPIKVIYLADVQYKIGIDEVCIDGSAVKIYDREKTICDMVRYREKIGI
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CDS 313804..314202

/locus_tag="EFAGFIKM_00287"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS 314221..314724

/locus_tag="EFAGFIKM_00288"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MQFDIGFGDVVVPKPQLIEYPVLLDMAAPQVQAYSKESEVISEKF
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FAGNEGRTKQWQAFLLRRLGVVEEQLAFQDVMDALVSFLEPVYHSIIDEKEFFRCWSYTE
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CDS 314897..315121

/gene="gerE"

/locus_tag="EFAGFIKM_00289"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P11470"

/codon_start=1

/transl_table=11

/product="Spore germination protein GerE"

/db_xref="COG:COG2771"

/translation="MKGIDHKSFKLLTHREREVFELLVQDKTTRDIAGQLFISEKTVR
NHISNVMQKLNKGRSQAVVELIKLGELKI"

CDS 315590..316129

/locus_tag="EFAGFIKM_00290"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDRFLNEFENQFRAAFLTVLEQTMVKVEHEKVYACAFGTDSDWV

TLFMAVNTEESLSKHITNMKEQGLCDSEQDEIYYRWGCSEYQYGEDTHFNHISRLLYA

TEEVQEYKEEIIRIIIAKVNETADDVFARYGQAKADITFFVSLTDDDLAEEIENQSVN

QMTVLSLASKFLKRYDGIN"

CDS complement(316270..316617)

/locus_tag="EFAGFIKM_00291"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNRRQRKKFIPFTWIIATKQTEAHAYYALYIDWKRGGRLSWEG

WNQLEDLLQFHIPIKRKAGGRKSFSQPAAKIAKRALHLHLNEVQFEQLEQLFYQSLSK

KRWRMFIQTNRNL"

CDS 316841..317704

/gene="ybbH_1"

/locus_tag="EFAGFIKM_00292"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q45581"

/codon_start=1

/transl_table=11

/product="putative HTH-type transcriptional regulator

YbbH"

/db_xref="COG:COG1737"

/translation="MAAILRALQQELNNLPSQERRIAEVIMQSPSDIPGWTISHLAEQ

SGTSAATVTRFCKSFHFKGFPDFKMKLAAELSRASDETAYQDIVAGNPLSKIVEAIEA

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QSYRVQHNGGA"

CDS 317708..318442

/gene="nagB"

/locus_tag="EFAGFIKM_00293"

/EC_number="3.5.99.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O35000"

/codon_start=1

/transl_table=11

/product="Glucosamine-6-phosphate deaminase 1"

/db_xref="COG:COG0363"

/translation="MKMNIRIFENEEDLNATGAGLIASLLQTKPRAVLGLATGSSPVG

IYKQLITLYQKGLVSFSQASSFNLDEYVGLPTEHRESYRSFMNEQLFNHIDVDIARTQ

VPDGQAADLEQECNSYEQRLDDRGPVDLQLLGIGHNGHIGFNEPGTELTGRTHVVDLK

EETRKANARFFDSIDEVPAQAITMGVGTILKAKQILLIARGEKAEIIREAFMGPIIT

ACPASLLQCHPNVVLLDRAAGRLVR"

CDS 318439..319659

/gene="agaA_1"

/locus_tag="EFAGFIKM_00294"

/EC_number="3.5.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8XAC3"

/codon_start=1

/transl_table=11

/product="N-acetylgalactosamine-6-phosphate deacetylase"

/db_xref="COG:COG1820"

/translation="MTGVNSHEPGGQRDENISLLRGKLLLADEILEDGVIWRDGGKIH

YAGIPEGLPEQIRREALPLSVPERGLIVPGFIDIVHGGNGEDFMDASPEVLDKITSF

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QNPEHIILPDVSWLEAWKQYPGLIRQVTLAPEREGALEVISWLREQRITAALGHTDA

TYEEVERAVEAGLHHAVHTFNAMTPLHHRLPGAAGAVLSDPRISAEVIADGIHVHPAA

ISILAQLKQHNDQLVLITDAMSAAGLDDGEYKIGDLPVIVKHGEARLKDGGALAGSTL

TMIRGFRYLIQEVGLSLNAASRAASLTPARLLGIDHRTGSLTQGKQADIVLLNAELDI

EGVWVKGRRIGESY"

CDS 319824..320195

/locus_tag="EFAGFIKM_00295"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MERNAMLEHDPFITVLAEKLIHGYAFYGEHYNETDMELYRRH

LFTSFSNIVWVELDARKKYMIVDHRGRNTVMKLIEGMLNTRRTLRLANQAMAGTDTAGV

QQEIAHLSKLVHMLKFTTFRT"

CDS complement(320815..322170)

/gene="dapE"

/locus_tag="EFAGFIKM_00296"

/EC_number="3.5.1.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01690"

/codon_start=1

/transl_table=11

/product="Succinyl-diaminopimelate desuccinylase"

/translation="MKEQTYFEQNREKHLAELNEWLSIPSISAISEHKEDINRAAQWA

ADALTRAGMENVEVIQTAGHPIVYADHLHAPGKPTALIYGHYDVQPDPLNLWETPPF

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GVPNALHALVSLLASLHDEQGRVSVDFYDGILPLSPEMREEFVKQGFNEEQLRQDLG

LEQLYGEEGYSFVERVGARPTLELNGVWGGFQGEKSTVIPKEAHAKITCRLVADQDP

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CDS 322386..324791

/gene="yesS_2"

/locus_tag="EFAGFIKM_00297"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31522"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator YesS"
/db_xref="COG:COG2207"
/translation="MEPTRSDRIFGRFKRLSDLKAGRHKGRFYRNSLMLILLIASIPG
LITGIVMYQQVVGRMETEFNQMHQNQIENRARNVDDQLAYLEMNLSHWAPEPRFGNAL
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AYDRYLSMGNHVYWTDWVSSSNRDTEPSTNDSPLHTDAGNALVLVHKIPGESINPFGA
LIITLDNEKVASLLKTLTPYDEGLTFLMDQEGNTLVGTGNPGTAGETSAFEQQLKEEVA
LHVGSRSFLFRYEDQTYSVSYGSLSRIDSDWTYVSAAPLTSVTSPVKLVSKIIVIASA
GSLILGLLLSWFASRRISPVARMHLHLLTPGRNETTPTDAKLDEFELLEQQWNEELTSR
SVTAHRQLQEQLPHLRDSFVLQLVQGHLAYNEQDLQQRMRNLGFELEGQQFLLVQMY
FTGYEQLQGRFGSKDTGLVTFAAVNITQEVAKNYFRQISVMNFHDLSSAMLVIAPQDE
PVKSQALLWGQELVEVIGRTLKMKVTLMVSRPAASLQELPGRFVEMEQA VAYRSVEEG
SQILDLEDEACFHKNEAASYPLGLERELLQAVRLGKQTEAERVLEQFMSEITRTGSTE
FQVQQMMLQLLGSIQHMMLQTGVTPYKLFGGYNMYEQLSGIREPVQMRQWMMNEVFIP
YIQEVEVRSQEPLKLVVERTMLYIDTHYRSDISLENCADEEQMTPYALSKAFKQVSGI
NFIDYLTRVRMDAAKQLLRETTMKINDVAVAVGYQHSYFNRIKKQEGVTPSQYRDQW
FGQ"

CDS 325070..326053

/gene="yteP_2"
/locus_tag="EFAGFIKM_00298"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:C0SPB3"
/codon_start=1
/transl_table=11
/product="putative multiple-sugar transport system
permease YteP"
/db_xref="COG:COG4209"
/translation="MNGKTDWNTNGTATAQADMATRPLKQESNWK RQIKRNKWLYVLV

LPGFLYFVIFKYLPMWGIIAFQDYQPFLGIRESNWVGLENFTNFFSNPDFFRLLRNT
LVLALYDLIFFFPAPIIIALLLNEIRVAFFKRTIQLVYVPHFVSMVIIASITYVFLT
PQGGVLYDLIAWITGKPIDVLSSPGSFRPLIIVQMMWKEMGWGTIIFLAALAGVDTEQ
YEASIVDGAGRLRRMWHITLPAIRTTIVILLILRLGNFLDTGFEEQIYLMTNSLNRDVA
DVFDYVYTVGITQGAFSYSTAVGLFKSVVGIIILVLSNKLAKKFGHPGIY"

CDS 326066..326953

/gene="araQ_2"

/locus_tag="EFAGFIKM_00299"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MNSRLYNPAGKVFDIFNYVMLGILGILTVLPFLYIIGNSFATE

AEITERSFFLIPKVSFSAYEYIFSSSTIFRSIGVSIFITVAGTLVNLFFTLTMAYPL

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KNFFQQMPPGLEEAARIDGCSDLGVLWRIVLPLSKPVIATFALFYAVGHWNNFFSALL

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YPFLQKHFAKGVMLGSIKG"

CDS 326972..328477

/gene="lipO_1"

/locus_tag="EFAGFIKM_00300"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37966"

/codon_start=1

/transl_table=11

/product="Lipoprotein LipO"

/db_xref="COG:COG1653"

/translation="MGQKTGFKKGALLLSASLVLSTILGACSTDKAGSGTAAGGTDEI

TIMLPNFEAENPPENSPVIQKLEELTKVDVNLQWVPSSSYEDKFNITLASGKLPQIMV

VLGKSPSFINAARTGAFWELGPYLDYPNLSQMNEIITNNASIDGKTYGIYRARALGR
NGVTIRKDWLENLGLLEPKTIDEFYNLLKAFTNDDPDGNGKDDTYGLVASKFTGPWDN
MQVWFGAPNKWGDDGSGGLIPAHETPEYMEALKFFRQIYSEGLVNKDFAVMDATKLPD
PFVNGQAGVMVDVADNAQRMDQKILDKDPNATGRVDVLQAMEGPKGLRDMPTSGYSGL
IAISKSSVKTEEDLKKVLSFLDQLNEPELQALLYNGLEGKQYEKKEDYIVPSTDKLAL
RDLQGLNQILMFVPEDRTLRLVQQTPVREKVAQVQKANEIIVIANPGEPLISDVYAQKG
PQLDNIINDARIKIYVGQIDEKGFEDAVALWKNNGGDDYVKEVNELYAALK"

CDS 328610..332002

/locus_tag="EFAGFIKM_00301"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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PEAKQRQLVHHQLVVQGGEAVDLELPWGRVLVAKAIPKDEQGKRLWQESIDLRSKIGN
IQTHQVYQETGLTSYNRKRFFTYRTAFRLWVDPAGDWELIIFQEKEIDDFKYGNFV
DPCHKEAMSRFIGLTHERYKSAVGDRFESVIKGMFSDEIAPLGRIPWSPQLPRYFSER
CGYSLIDSLPALLYSDVPDAHRIRYDYYQSLHLLLRESYHKQVHDWCEEAGIQYAAEA
PGVRMTTQLFSHMPGGDSAHEKIGRSLSWILERYGQKMRDNPKMVSSLARQLGRSRNL
IECFHSVGWSMTLQDAKWMIDRMAAMGTNFYNFHAFYITIGGLAKHDAPPSQFLQNPY
WKHFRQLGDYTGRLSYLMSTGAADIRIAVLDPSTTFWWSLMGNPLHGFEYSGEDESERV
QLERLT KDWMRITTHLLENRRDYDHLDPPELLAEADLTGIIQIGVARYDVLILPPMLN
LEAAAWEQVKRFVQQGGTVISVGMPPHIAIQGSPEGDEAAQFFGAGEQPQEVYWGRS
VTTDHDNRET MWHQGE GNAYFLPAGTGQDDFSLELISLLLDQVLPEPICWIMEEESA
SLLMHTRELSAGEHMFVLTNQEGQDLKGQLKLVARQLWDGEELAEGACIVAERLDLET
GRLQILPYTSSGGEWCISLTLAPYEAHAVRLTLQPAKEEALTTKVDVADKTGSTFGAD
VSAGV NQACKIMVPSEGPWRLET VQSNILRMGQFHLEASNANGIILESQHVAVKPFID
QAAELSEQQHLPVQFNQVFGTPKKASVAYPIECRYTTTFELRTALPACLLFMDRAAIS
GTWSMEINGQPLGKEQFDPIETDHNNIACDITELLHSGLNEMTVIVQVTKDEDGIVD
PLYLQGRFGVEFH YEGMASLVREPDTALCIGPEPQPLYPHFAGEMSYKCTFWLDELGE
DVASFELEFSDWRVQDVTEVRVNGHSLGVRCWSPYRWKGDASWLRPGENDIEVRITNT

LIGLLEGTYFDSEHHRLQDAGHVLLKNSDKGVEAGDGTSYSV"

CDS 331980..332801

/locus_tag="EFAGFIKM_00302"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGHRIRFD RYPGGVMKALT SYDDGVVH DRRLEICNRYGLRGT

FNLNSGTLGNPGRIEAGEVAELYTGHEVAVHTVTHPTLPYVPNELLTEEIIEDRKALE

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HDLAGHAKRFIQHSGKTGTPLLLYVWGHSYEFNDNDNWEIIEQFGEQIGGRDDIWYATN

IEVIAYWKAVQRLECSADRSIIHNPSAIPVWFTADQQVVEVQGGETLRLSERIKV"

CDS 332859..335036

/locus_tag="EFAGFIKM_00303"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYDSIPDILTVAQRYIGDHPKHSFLFRAHNQGGFRRLGDYRYD

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WLYSEPVDPEVLSLPRDGMMEETGLTWYPRRGWTDDEEQGAGSFARIFGTEQLAVAYA

WSRLDVTLPGSTPVILNGRHDGALTLYVDGTEVYSAGSSGNFRIELPRRYGSSDVVVK

GEVQAVGGSWGFTLEDAERSGSAGWRLKPSHPVAGCSDPWLYTG VFAPGAEP THVDVV

RTD TVFDDGAQGVYWRVDLPDTHVRPYLENTHYGKWNYP LGVTLLG LLQTGQELGRDD

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TELLSILPHDHVKRSELLTFYRDL SQGYLALQGENGLWHQVLNRPDSYEETSCTSMFI

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CDS complement(335227..336102)

/locus_tag="EFAGFIKM_00304"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MIHIGLTGWGDQEDLYPNRTKAKDKLSLYGQYFSTVEVDSSFYA
VQPRDRMARWAAETPESFAFIKAYQGMTGHLRGKPYFTSTSEMYKAFQESLEPVIEA
GKMQAALFQYPPWFECNKDNVKELREVKLMEGIPCALEFRHRSWYEGDMRERTLSFL
KEQGWIHSVCDPQAGLGSIPVPQATDSEMTLVRLHGRNVSGWHQNGAPNWRETRYL
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SEPEKEEGPEQLELF"

CDS 336335..337078

/gene="cypM"
/locus_tag="EFAGFIKM_00305"
/EC_number="2.1.1.301"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:E5KIC0"
/codon_start=1
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/translation="MTEWYEKSFGEYLLVYKHRDVQGAHQEVHKMINWLKLEPNAEV
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DEGQRIEEYRKIEEGFVQKEIRITDTSGHEPRVYQERVKLYTREQLSQMLSAAGLRV
DQVHGGYDEEKYDEQTSRPMIFVGRRPVE"

CDS 337106..338089

/gene="gloB_1"
/locus_tag="EFAGFIKM_00306"
/EC_number="3.1.2.6"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01374"
/codon_start=1

/transl_table=11

/product="Hydroxyacylglutathione hydrolase"

/translation="MKRTEEISMTEGIHRVKISMSFPLRWVNSYVLSEPDGKITIIDP

GPRNSETEQEWSEALEDLGLTFSDIRQIVLTHQHDPHLGLSGWMQQMTGAPVRMSTRS

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EWLNMGGKRWWAVETGGHAPGHLSFYAPESMEILCGDAVLPQISPNISLQPGSDPQPL

LSYMEGLQRLGELNVKQAYPGHRNPFAQFTERTVQLLAHHEERLQKMTERIQESSANA

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CDS 338288..338704

/locus_tag="EFAGFIKM_00307"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTRRKRNQWRKWQASAAATLTVAALFQYVRTSDAFDVAYAAAANG

TDTSVTASSQVDTHDDVMDEWINSTTDSNNWNTQDNDNNDSSQYNGTSDSTQAARPDQS

TSNEGNYSDSQRIGQNNQGTDSGYSSGNYQSRTGAS"

CDS 338701..339744

/locus_tag="EFAGFIKM_00308"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSRTEQVARPLRFQFRAMNTDVEVQLSAGREEAEHAATVVKNWF

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LDPGAELDLGGIVKGWAVERIADWLQRTLHIPAGLINAGGDIQVWGSPDHSQWTLQVA

DPLHDQENVSGVVRLQRGAVATSGVSRRQWQNTDGS LAHHLIDPRTMEPADTDVLQCT

VMGQHASQCEITAKTVCILGSAEAVGWLNRHYDRHDVLWMTRDGSYIFRGNTDTLAEH

WPGFDPDHRFSLI"

CDS 339777..340430

/locus_tag="EFAGFIKM_00309"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MAQWIVDFLPTWNIIRISGIAAYVLLFAGVFLGIAQGMPMAKGK
PKAAMFKWHTRTTWLAFLGLVHALTYIDHYSPFTWGELLIPFTASVHPIGSGGLTL
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CDS complement(340592..341158)

/gene="ypjQ_1"
/locus_tag="EFAGFIKM_00310"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54173"
/codon_start=1
/transl_table=11
/product="putative protein YpjQ"
/db_xref="COG:COG1267"
/translation="MEHPEQEKIPYSLNSRKVAEATREWLHKRGVTIPEIAELVMLLQ
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YGVDEILAFSIVNVYGSIGFTNYGYVDKLPVLERLNDKSLGPVHTFFDDIVGAIAS
AASSRIAHRKQSELEEALGEKPVSDDAV"

CDS 341431..342486

/gene="gerM"
/locus_tag="EFAGFIKM_00311"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39072"
/codon_start=1
/transl_table=11
/product="Spore germination protein GerM"
/db_xref="COG:COG5401"
/translation="MRKIHSLRTVSAAALLSIPMVLSGCGMFGAQSSEAVDPPPIQE
AAMIQAAEGNGALAMLPLTTVYLQDQQGLLAPVSLTLPSTGDASSPKTALDTLVTGGA"

YAGMLPEGFQGVLPQGTVVQNVTIHADDKLAVVEFSGNFAKYDAKEERKMLEAVTWTL
TGTPDVENVQIWVDGKKLTQMPVNSTPLPEPLNRAVGINLDLGDTFVTNSSPVTVYFS
AASPAGIQYYVPVTRLVTPGEDRVQAALNELIKGPDKGGELEEVMTGGTELQSVKTAE
DGTVTVALKDDMFAEGDIVPSELLQSVLTTVENTASKDAKVQIEWNGQKTMGDDNR
DYSAPVSKPEYINEIPI"

CDS 342814..343569

/gene="rph"

/locus_tag="EFAGFIKM_00312"

/EC_number="2.7.7.56"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81LA9"

/codon_start=1

/transl_table=11

/product="Ribonuclease PH"

/db_xref="COG:COG0689"

/translation="MRSNGRTSEQLRPLNLTVNTNKYAEGSVLIEVGDTKVICTATVE
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NLQALGERTITLDCDVIQADGGTRTTSITGAFVALALAVNKISQQHKLQVFPITDFIA
AVSVGVVGEQPVLDLNYDEDSKAKVDMNLVMTGGGKYVELQGTGEEAPFDRRELNAML
ELGEQGILEMIERQKEVLGPIALKIGARGLGEA"

CDS 343571..344194

/gene="rdgB"

/locus_tag="EFAGFIKM_00313"

/EC_number="3.6.1.66"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P52061"

/codon_start=1

/transl_table=11

/product="dITP/XTP pyrophosphatase"

/db_xref="COG:COG0127"

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VEDGVTFAENAWKKAKAVGDALGLPVLADDSGLCVDLLDGEPGVYSARYAGEGATDAQ

NNAKLLETLESLKSGEDTEQPLSPARFVCALVLYDPTTGDKYESEGTAEGWITAQAA

GAGGFGYDPLFYVPEYEMTMAELTLEQKQAISHRGHALRALVSRLEG"

CDS 344545..345387

/locus_tag="EFAGFIKM_00314"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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SFSVMGSSGLSLESLQHAKLEELIIICGGLPKEVLSSITHAELPELRKLELYLGVDNY

GFNGSLEDVLPLEKGLFPKLVYLGLKDSEIQDEIAKAASEAPILDQLEVLDLSQGT

SDEGAEALLASDKIKKLKHLDSLHYMTNEMIIRWNQSGISVDVSDQQQSDDEDDWRYP

SLTE"

CDS 345391..346656

/locus_tag="EFAGFIKM_00315"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSGVKEMNESLHQPIDVPDLTQDQPFLIGNPDNRRTQGLQEAR

HRLGLKPAVVLPAQQLQNWRHGRTIADTVDSNLPVPLIRIDAPGEDWEVECELLFLG

AMNDTLALTDGIGAEAFSAEQALALEQDWGRIYAPAQWFRGWKACLDRIQHEAREVWP

EVRFMNDPADIQLMFDKRTCQQHLSSHGVDVPPALQTSQPIRNYMELRSSMKVDEMHR

VFVKLACGSGASGVVAYQVNPRTGDEIAVTMGMEQRQGKTIFNEGRRLRKYTRSEEI

ATLMNWLCAEGAQIERWMPKATLDQRAYDIRQLVAGGQAGHAIMRLSRTPIITNLHLRN

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CDS 346649..347434

/locus_tag="EFAGFIKM_00316"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPDMENTIVGSHDLLMITLDTLRYDVAKLEEENCPNLCGSGPWEEK
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GFAAEGYRTICIGGVIFFTKKNPLAKVLPGYFQHSYWRMNFVGTNPKSTEHQVQHALK
LLEQTAPDEKIFMFLNVSAIHGPNRYFVQGAKEDSVETQRAALRYVDEALGPLFEAMR
KRARPAYCLAFSDHGTAYGEDGYQGHRLAHDVWVWTVPYREFLV"

CDS 347482..348870

/locus_tag="EFAGFIKM_00317"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEKHIQHHTTGHSTQSGSNIATSLSEVLAFPYRSYLYSYPHKTA
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ERQAKQWAPITSRRPYSRFAIGGGTPTLLNEVQLNRLFDIAEHVMGLDPAQASISVET
SPDTVTEAKLAIMKERSVDRVSMGIQSFIEAEASAIYRPQKPQEVERALEKLTRYDFP
LLNLDLIYGLPGQTVESWIYSLERVLAYEPGEIFIYPLYTRENTIVKPDDIRRGQPD
RMELYKAARETLKSKGYVQYSMRRFAKEQSSSKALLPYSCQEEGMVGLGCGARSYTSE
VHYASKYGVSYKATQSIADYVATERYDVADYGIVLSREEQRRRFILKALLHREGLTL
SDYQQRFGTDVMSDYVWLAELLTEGMAELESDEDKQVLRLTEEGLGYSDAIGDWLISA
EIREQMEGFVFS"

CDS 348867..349730

/locus_tag="EFAGFIKM_00318"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRATLYYRGKLSSCNYPYCPFSKTVDSKETLEVDEQQLRQFV
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RELDASKAAFWATYHPRETKEASFVKKCLTLRQMGLAFSVGTVGLRSAFPAIESMRQA
LPDDVYMWVNAFKDRPKYYTPEEIQFLRGLDPLFEGNLQDYESLGKRCAAGSEVFYVQ

GSGHVKRCYKDRRIIGHLYRDGLQALSADRPCRMKKKCGCYIGYIHMEDSPFQETFGSG

LLERNPVLIDR"

CDS 349862..350179

/locus_tag="EFAGFIKM_00319"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAIKGQKYKTYSEKIKKEAIRLHTVEGWTYRKINEHLGIHDPGR

MKRWMRKHREQGEFGLMDQGRRRKEYLDQERYVQKLKRENELLKKCLVIWKEEANKKD

FRS"

CDS 350128..351012

/locus_tag="EFAGFIKM_00320"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISBth8"

/codon_start=1

/transl_table=11

/product="IS3 family transposase ISBth8"

/translation="MLGNLEGGSKQERFQIIKVAAYGDIQKLCDVFGVSRSGFYAYV

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LFNNEIVAYEIGERNDNELVLRTFSKAFKQTDVTGLVHSDQGFQYTS HAYHDMLPK

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QRKLKKLTPVEYRRQFAA"

CDS 351336..353030

/locus_tag="EFAGFIKM_00321"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRVSISRKLLLGFGSVLLLLVAVVVISYTQFISVEKTFTDLIR

ERTAKLLTIKNMIIDVKSQQVALRNFVTEENDQSEQQFKSFYEDYRKTSEELRSGIQT

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EQHQQNSLDTGIVNANQLIQKVLRLIMIIGIISIVLGVVIALIMGRIISKPV AHVARA
ASRIADGDLTGEAIVVRNRDEIGELAESFNKMMDNLRHLIHQVGQNADRVAASSEELT
ASTEQTATATEQVATTMEEIATGMDTQVSMVGDGFHTINELSTGFQQMTVNTQNMSDE
ATNASAKTISGNDAVQSAVGQMNSIHQTVRVLAKVIEELGNHSDEIGSMVESISEISA
QTNLLSLNAAIEAARAGEHGRGFEEV VATEVRKLSDQSAKSAEQISVLVAAIRNGMNNA
SQSMGEVNAEVQEGIELVRKAGGT FEEIREAVSNVAGQTQEVSASIEQMAAGVEQINV
SMKTIMEVTENAAAGTEEVSATSEEQLSAMQEIASAANDLSSMAEELQESVSRFKV"

CDS complement(353173..355017)

/gene="asnO"

/locus_tag="EFAGFIKM_00322"

/EC_number="6.3.5.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O05272"

/codon_start=1

/transl_table=11

/product="Asparagine synthetase [glutamine-hydrolyzing] 3"

/db_xref="COG:COG0367"

/translation="MCGITGFIQWNRDLTQESELLVRMTDSL SNRGPDASGTWISNPC

AFGHRRLSVMDPENGAQPMHALQGDSYTVVYNGELYNAPELKKELLQRGHQFRTQCD

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GSEPKALLIHPDVEAAVGPEGLAEVFIVGPARTPGHGVYSSLSELKPAHALIYNRNGI

RTYAYWKLESQNHEHNLEETA AEVRSLLQDTLERQLASDVPVCSLLSGGLDSSALSAL

AVDYKRTGQGQVSTYSVDYVDNAKHFAQHSFQPGADGPWIKRMVDELKTDHHWIEIE

NGELVHALTQAMLVRDLPGMADV DSSLYLFCKEIKKGATVAISGEAADEVFGGYPWFH

REDMLNSGTFPWSVAPDMRAALLSPDIREWIRPLDYLADRYSDAVA EVPLLDGETGKA

AQMRVMSYLNITRFMPTLLDRKDRMSMGAGLEVRVPYCDHRLIQYVFNIPWEMKITGG

REKGILRKALEGVLPDDVLYRK KSPYPKTHNPQYLA AVKQQVLDILDDPTSPILPLID

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CDS 355210..355509

/locus_tag="EFAGFIKM_00323"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDSMKYYVSV MGRSVIPDPSVTSYEWIIQATPQAEQLLGLLSL
MQEKEEEAFPGMVFPWPDTP EESVN RAYETVLQQVYREIYRLGTPETRYQIEQST"

CDS 355541..355897

/locus_tag="EFAGFIKM_00324"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MYAIQDAKIRRLTEVDGLSCAEVEVQPGNAGDP SLLVYVASTQP
GNSLEVVRIVRNHSDSAIDWYNNNMHTAFEEATDNAFENSEGMTVEEDKASFQSELF S
FLLGPTLQRYLIGQA"

CDS complement(356073..356366)

/locus_tag="EFAGFIKM_00325"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRQLLSALS YFSIFFAPFLFPIIWIVAKDDYIEGHAKRALFSH
VFPFLAAIPLFYFFVTAHSLGSAVG FVILFFVIYGLSFVYNVVKGIQVLREYA"

tRNA 356656..356731

/locus_tag="EFAGFIKM_00326"
/product="tRNA-Arg"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Arg(tct)"

CDS 357023..357793

/gene="tam_1"
/locus_tag="EFAGFIKM_00327"
/EC_number="2.1.1.144"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P76145"

/codon_start=1

/transl_table=11

/product="Trans-aconitate 2-methyltransferase"

/db_xref="COG:COG4106"

/translation="MKSLNQWQADEYDDKLAFVSGYGKNLISWLQPQKGEYILDLGCG
TGDLTHEISLAEAEVIGMDASPDIMIRRAREKFPELEFVEGDGHQFETNRLYDAVFSNA
ALHWMRSPRLVVDISIWKSLKPGGRFVAEFGGKGNVQTIVNALEQVMERNTGIRASERN
PWYFPSIGEYSHILEQVGFVVRHAYHYDRPTRLEDGEQGIVGWLTHFGGDYFEGLSHE
EIQQICHETSQIVMSHLWKDDAMYADYKRLRIEAVKPE"

CDS 358176..362135

/locus_tag="EFAGFIKM_00328"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKRLISTLLSVLMVFSIILPAAGAAPADSVIQLDNLPSTAEAK
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SMETKAVTQVEQQQSFVHSLTQKKIKHEVLEEYAYALNGVAIELKGNQVGQLLQIPG
VVSVPDLEVTIAPETDEVNPYMKDTAPFIGAPEVWDLGYKGNIGKVGVIDTGIDYEH
PNLQEAYKGGWDFVGNNDNPYEATYQEWKASGEPEFNATGSAYYTSHGTHVAGTVAAR
EAGDYGIVGVAPEADIYAYRVLGPYGSQTSWWLGGIDRSVEDGMDVINLSLGNAAND
PSYITSVALNNAMLSGVTAVVASGNNGPNRYTLGSPGASAMAITVGNSTGPSQLITAD
THFWIGEEGEEAQPEQQPVPEVEQSPELGTAPGTEEPEGSEQDVPATADEESATAVED
TVSNEAEVNPVGEATTEENTPSASPSAPIEASPEAAPVEEESVIAPTEAPLAITESVY
RLDLMGWLSLADPETVLTGKYELEYAALGKPTDFEGKDFTGKVALIQRGEIAFVEKIA
NAKAAGAVAVIVYNNIPGPIGVSLGDNFELIPTLSMSKEDGDVIKAEKDAGQAVEVSF
SDFERSQTPGDEMSSSSSRGPAKVTLDIKPDIVAPGTSILSTIPAYGKDEPDADYAQA
YDRKSGTSMATPHVAGLIALIEKHPEWTPFDIKVALMNNSKVLDTTKFDVFDQGAGR
IQAVNTIDPAAFVKVLDVTQYTESGSVVEKENITGSINYGNFLSTDEKTITKTIKVEA
LNGSGGDYTVNVNPNTRNVAGVSVAVDKNSFTLNGLLAVTITVPRGVTATTEAQGYI
EVSNGTNTFTVPYVAHFNVTLSGVKYIETVKGTEKNPFHYPLKADGTLDLNVAMEFY

NPMTFALIEIYDGLNPEGGYQDGYIGSIFGNYNFNANARYNLAWDGSYADYTTDEV
TEIPDGLYTVDITTIGTDGKTYKEDTSPFLVKKTAPAVTAPEALEFKEDSAVLNGSV
EDLYFRVAPALASGWDITFDPAASLEATYVVKKEDGSVYKEGVFEVQADGSFSLPLEG
IEAGEYAVELTVKDQQGLSGTANTALKLEAVETEPETPATKAPGTPVLSHNNWVGNGL
PEGAYIVTMNLWWGENATSYKLYEDGVLVDQKLTYNAPWAQFAQTKITGKANGTYTY
VAELTNDKGTTRSQTLTVQVTNATPGKAVLSQDNWDGDGHYKVTMNLWWGTNASEYRL
YENDKLIDTQELRSATPYAQS AVTTLSGKASGTYYRAELINAAGVTSTDTIKVKVK"

CDS 362290..362979

/locus_tag="EFAGFIKM_00329"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISSth1b"

/codon_start=1

/transl_table=11

/product="IS3 family transposase ISSth1b"

/translation="MSKRSPISYEIKIHVRRCLQHESNPNEAKQLGVHKNTVTDWI
RKYKVDGEDGLRESKRWKSYSKELKRSAIQDVLSGEYSVRVAKMYHISSKSVLESWI
SKYTEGVKMKPTRQRIESPHMKNKGRKTTYEERIEIVQFTIAHDLDYQKAIDKYGVSYQ
QVYAWVRKYQANGHEALKDLRGRKKLVEELNEQERLKLRIKELEARNEHLEMENALAK
KLAEIRRRNTR"

CDS 363108..363506

/locus_tag="EFAGFIKM_00330"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISSth1b"

/codon_start=1

/transl_table=11

/product="IS3 family transposase ISSth1b"

/translation="MPSNRELENFALAKEVKRRYNKRNGILGYRQMRTQLNRKLKKS
YNRKRYRIMRALELRAVIRKKRSKYLKVPALHIAENIMNRKFQAVAPNQKWCTDVTEL
KYGNGRKAYLSAIDGYDNSIVSWVLQPFQ"

CDS 363520..363855

/locus_tag="EFAGFIKM_00331"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISSt1b"

/codon_start=1

/transl_table=11

/product="IS3 family transposase ISSt1b"

/translation="MNTVKKAYKGNPNATPLLHSDRGFQYTSLEYNQLEKRYKFTKSM
SRVSRCLDNQPIERFWGTFKAESFYLEKYDTYDSLVRSVRTYIHYYNNFRYTERLNGL
SPNEYRRAA"

CDS complement(364003..365232)

/gene="yycB_1"

/locus_tag="EFAGFIKM_00332"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37482"

/codon_start=1

/transl_table=11

/product="putative transporter YycB"

/db_xref="COG:COG2807"

/translation="MSSSLQQHSSIHTEDEHSSTSKRFGLLLAGIIVIAATMRSPITA
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IGVALRLLPSVLSLYAGTAILGCGIALSNVLLPSLIKRDPLRVGIVTGLYSVSMNIF
GAIASGVSVPVAGATSMGWASLGMWALLSILALLLWLPQIAAGRQRMFIATQSEGT
PVRLRTSSLAWFITLFMGLQSLIFYTTITWLPEILAEQGFSPTSAGWMLSLMQMVSV
ATFIVPILAGRTRDQRVLTAITCSSLIVGYALLSGIASLVTIGVTLGIGAGASFGM
VTMFFVLRTKDARQAASLSGMAQSFGYMLAAVGPLLFGMLHDWTKGWTLPPLLIQVILA
IALLIAGIQASKNRMIG"

tRNA complement(365730..365805)

/locus_tag="EFAGFIKM_00333"

/product="tRNA-Arg"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Arg(tct)"

CDS 365994..366974

/locus_tag="EFAGFIKM_00334"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLIPTGDSGYRGGAPIKESTTPETEHHNNIVLFPKTLDDYYQIQL
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DDALTSWLSEKSLHPLLQFRVLQTLRRRGVQGMILFTRGEEQVEVEIDTVPLKPEEFP
LQIVQILERVADQTEVHEPTLFYFAQELWIQYVMAVYGTRDYVSMLEENDSMTDIWAA
ALHMTVADSLGGSHDEENTRSMYAVTGAMRFRLEQAYRSMKQFVSAGLDG"

CDS 367113..368453

/gene="tig"
/locus_tag="EFAGFIKM_00335"
/EC_number="5.2.1.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P80698"
/codon_start=1
/transl_table=11
/product="Trigger factor"
/db_xref="COG:COG0544"
/translation="MKATWEKIEKNLGVLEVEVDADRVTAALDKAFNKVVKQANVPGF
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ANGDVAVIDFDGSVDGVPFEGGQAERYSLELGSNTFIPGFEEQVVGLSTGDFKDVEVT
FPESYHAAELAGKQAVFKVKIHEIKRKQLPALDDEFAKDVSEFDTLEEKADLKTQLE
SRKADEAKAAQENAVVEKVAENAEVDIPAAMVDSEVQNMRRDFDNRLKNQGMNLEMFL
SFSGQTQADLRGQMVEDASKRVRNNLVLEAVGKAENIEVSDEEVNQELEKMAESYKRP
ADEIRGILEGNGSLDSLREVKLRKTIDVLVENSTVVEPVEAPAEVVAAEADK"

CDS 368833..369423

/gene="clpP_1"
/locus_tag="EFAGFIKM_00336"
/EC_number="3.4.21.92"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80244"

/codon_start=1

/transl_table=11

/product="ATP-dependent Clp protease proteolytic subunit"

/db_xref="COG:COG0740"

/translation="MSLVPMVIEQTNRGERSYDIYSRLLKDRIIFLTSAIDDDVANLV

IAQLFLAADDPEKDISLYINSPGGSVTAGMGIYDTMQFIKPDVSTICVGMASMGSL

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PLEKIERDTRDRFFMSAEEAKTYGIIDQVLSRPINS"

CDS 369436..370689

/gene="clpX"

/locus_tag="EFAGFIKM_00337"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P50866"

/codon_start=1

/transl_table=11

/product="ATP-dependent Clp protease ATP-binding subunit

ClpX"

/db_xref="COG:COG1219"

/translation="MFKFNDEKGQLKCSFCGKSQEQVRKLVAGPGVYICDECIELCTE

IVEEELGHDEEVDLKDIPKPKEIRNILDQYVIGQDQAKKSLSVAVYNHYKRINTQSKI

EDVELSKSNILLGPTGSGKTLLAQTMAKILNVPFAIADATSLTEAGYVGEDVENILL

KLIQAADYDVEKAERGIIYIDEIDKVARKSENPSITRDVSGEGVQQALLKILEGTVAS

VPPQGGRKHPHQEFIQIDTTNIFICGGAFDGLEQMIKRRIGKKVIGFNTVSEQKDLK

PGEYLGMLVPEDLLKFGLIPEFVGRLPVISTLEPLDEDTLVRILSEPKNALTKQYQKL

LELDNVNLVFEPAAALLAIAKEAIKRNTGARGLRRAIEGIMLEIMYEVPSREDVTNCVI

TEEVVEKRVPPELSQSKDDKQEESA"

CDS 370789..371907

/gene="ispG"

/locus_tag="EFAGFIKM_00338"

/EC_number="1.17.7.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81LV7"

/codon_start=1

/transl_table=11

/product="4-hydroxy-3-methylbut-2-en-1-yl diphosphate
synthase (flavodoxin)"

/db_xref="COG:COG0821"

/translation="MWGEKSLMYLRQDTRPVKVGNTIGGSNEVIIQSMCTTKTADVE
ATVAEILRLEEAGCQVVRVTVNNEEAAAAIKEIKKRINIPLVADIHFNYKLALLAIEN
GIDKIRINPGNIGKRAKVEEVVKACKDRGIPIRIGVNAGSLENHLLKEYGYPTADAMV
ESALYHIGILEELDFHDIIVSLKASDVPMIAEAYTKAAQIIPYPLHLGITEAGTLFSG
TIKSSAGMGALLSMGIGSTMRISSADPVEEIKVARDLLKTFGLITNAATLISCPTCG
RLDIDLFSIANEVEEYISKLVPIKVSVLGCAVNGPGEAKEADIGIAGARGEGLLFRH
GKMIRKVPPEIMVEELKKEIDKIVEAYEETGVIPGRSH"

CDS 372075..373829

/gene="lon2"

/locus_tag="EFAGFIKM_00339"

/EC_number="3.4.21.53"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42425"

/codon_start=1

/transl_table=11

/product="Lon protease 2"

/db_xref="COG:COG1067"

/translation="MEFGMVIMLIQLFFGVVIGLYFWNLLRGQKTNRSAVERESRKEL
EKLRKLRSISLTKPLSEKTRPATINDIVGQKDGLRALKAALCSANPQHVIYGGPPGVG
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AMGVAGIPQPKPGAVTKAHGGMLFIDEIGELHSIQMNKLLKVLEDRKVFLESAYYNSE
DTHTPAYIHDIFQNGLPADFRLVGATTRSPHELPPALRSRCMEVYFRPLLPEEIGRIA
EDAVQKIGFSPCPDAVDVVKRYATNGREAVNIIQLAAGLALTEKRETLQASDVEWVAG
SSQIQPRPDRKVPTQPQVGVNGLAVYGPNMGTILEIEVSAVPALKDQGRINITGVVD
EEEIGGGSRTLRRKSMAGKSVENVLTVLKAMGIRPNDYDLHVNFPGGTPIDGPSAGIA
MATAITSAIQRPPVDHETAMTGEISIHGRVKPIGGVLAKVEAAFQAGAKTVIIPAENW

QSIFENLDGLRVIPVDTVQDVFREVFAPWPESQQMEQTKLAEETVAPAPEIFPPASAS

YLRADVPRPGQVTDGSGC"

CDS 373916..376255

/gene="lon1"

/locus_tag="EFAGFIKM_00340"

/EC_number="3.4.21.53"

/inference="ab initio prediction:Prodigal:002006"

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KQMEKTQKEYYLREQMKAIQKELGEKEGRAGEVEELRTQMEELGLPDKVKEKVEKEID

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CDS 376412..377068

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/db_xref="COG:COG0218"
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REELKLVQMVMVDMRHEPSKEDKMMNEWLRHNGLPVWVATKMDKIPKTRRAKYIKVIK
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CDS 377336..377923

/locus_tag="EFAGFIKM_00342"
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KGFTMTYVYAQGTVRKIVEKTGENTRVIYEYKNTLLELQHLFQARDVEREINRVYAEI
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CDS 378593..379978

/gene="hemA"
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/inference="ab initio prediction:Prodigal:002006"
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CDS 379993..380820

/locus_tag="EFAGFIKM_00344"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/translation="MTLAEQVYEALIYMYALSLLFYFSDCIRRNAGAKRTGTGFLVVV

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LKKKKWNDTMRRLPSLEVIGKYMDGATLIGTPLLGVSVMLAVLSIVAERRWILLDLK

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CDS 380826..381476

/gene="cysG_1"

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/EC_number="4.99.1.4"

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/codon_start=1

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/product="Siroheme synthase"

/translation="MDRYTPIFVNTSGKKCCVGGGRVAERKIKGLLHAEAQITVISP

ELTPVLKQLHHESRIQWIDRSYRNGDLRGAF LVYAATDCSEVNSTVVRDAEAAGILVN

NAMSSEHSSFITPSVVRGRLSIAISTAGAGPAAAAEIRATLERQFGDEYETYLEFLH

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CDS 381479..382435

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/locus_tag="EFAGFIKM_00346"

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/codon_start=1
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/translation="MRTIKVGSRQSALALTQTGHVIQDLRDICEREGLAFD FEVHKIV
TKGDLILDVTL SKVGGKGLFVKEIEQAMLDRTIDMAVHSMKDMPS ELPEGLINGAIPR
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LETEGFDAILAAAGLYRMGWEDRITEYLTETACLPVGGQ GALGIECREDDEELLHLL
QLYNDPETAFPVQAERRFLSVLNGGCQVPIGAHAVVWPQQDADSLNGENTLQLTGMVG
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CDS 382440..384002

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/locus_tag="EFAGFIKM_00347"
/EC_number="4.99.1.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01646"
/codon_start=1
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VTNATGTLVFMMGVAKIGYISEQLIRHGRPAQTPVALIRWGTRAEQDTLTGTLEDIEA
KVIAANFQPPAVIVGDVVNQREQLKWAEALPLFGKRILVTRARSQASELVNRIEELG
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RSIHQARIAAVGPSTADALRKHGIVA EVVKGPFQAEGMLEAFESELKEGQRVLLPHGD
LARTWLRDQLRERGLQVTEAITYDTILAGEDDDELLKLEEGGIHAVTFTSSSTVTNF
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KRTGTKEGALRN"

CDS 384105..385106

/gene="hemB"
/locus_tag="EFAGFIKM_00348"
/EC_number="4.2.1.24"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P64334"
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TRLIKSWYPELLVADTCLCEFTDHGHCGMVHTVEIDGHICGDVLNDESLDLLVKTAV
SQAKAGADIIAPSNMMDGFVQAIRAGLDENGFSHIPIMSYSVKYASAFYGPFREAAADS
TPQFGDRKSYQMDPANAREALREAETDVLEGADMLMVKPSLSYLDVMRTIKDQFDLPL
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CDS 385135..386439

/gene="hemL_1"
/locus_tag="EFAGFIKM_00349"
/EC_number="5.4.3.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P30949"
/codon_start=1
/transl_table=11
/product="Glutamate-1-semialdehyde 2,1-aminomutase"
/db_xref="COG:COG0001"
/translation="MTAQLGNRRNDERSRSAIEEAKQYIPGGVNSPVRAFKSVGLTPI
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TEMAKLCERVPSIDIVRMVNSGTEATMSAIRLARGVTGRSKILKFEGSYHGHADSL
IKAGSGVATLGLPDSPGVPEGVAVNTITVPYNDLESVTLAFERYGEELAAVIVEPVAG
NMGVPPASGFLEGLRSLTTQYGSLLIFDEVMTGFRVGLNCAQGGRYGVTPDLTCLGKV
IGGGLPVGAYGGRRDLMEQIAPTGPYQAGTLSGNPLAMAAGYTTLKLLTPEVYDRLE
TLSARLQAGFEKNAAETGIAITINRVGSMVCPFFSAVPVTNYDIAKESNLDQFRRYFA
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CDS 386436..387341

/gene="rluD_1"

/locus_tag="EFAGFIKM_00350"

/EC_number="5.4.99.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P33643"

/codon_start=1

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/db_xref="COG:COG0564"

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PDGSRADQAITLDHVVASYEMNGIQASVRHVRHRLDEDTTGPVLYAKNAFALAKLDEA
MRRKEIGRHYVAIAGGQIPLRLKIDAPIGKDRHHKQRRRVSEGGQEAVTHVEIVEVW
ERATLVRLKLDTGRTHQIRVHLSYAGHPLIGDALYGGRADVIGRQALHGEMIKFGHPL
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CDS 387714..389297

/locus_tag="EFAGFIKM_00351"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

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EEQSAEYANENRQPDANEDPASLTANGDELASHEQYSEPSPISSFMAETADRLASYPE
SEPLPLEDESSGWSEPSVDALPANSRSADQAVSEPTAHSSNELAAPDVPDAPEVWHF
ESVRSVPQQENQAVADVVPVESQAENWQGVFASSEPGNAEEDRPPFEATGIDEFVQNEA
FVPEPVAETEDKPELKVAFGSKKESAPRQEEGVGISSLLSSGRAARDAEVERGDEVPA
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CDS 389484..389687

/locus_tag="EFAGFIKM_00352"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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WAGSSRYLLEVSRHVQRVKSILL"

CDS 389796..392462

/gene="valS"

/locus_tag="EFAGFIKM_00353"

/EC_number="6.1.1.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P11931"

/codon_start=1

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SGAVKITPAHDPNDFEVGLRHDLpQITVMDESGTMNAEAGKYQGLDRSDCRKQIVADL

KEQGVLINIEDHthQVGHSERTGAVVEPYLSTQWFVEMKPLAERAiKKQqSGEGVNFV

PDRFEKTYLNWiENVRDWCISRQLWWGHRIPAWYDEETGEiIVSAEDPTTLPEYAGRK

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GQDLRFRWERVEQARNFANKiWNASRFALMNLEGfTYEERDISGELGTADYWiLHRLN

ETSRDITRLIEAYEfGETGRVLYNfiWDDLCDWYIEfAKLSfYGEDPVAKKKtQSVLA

YVLDQTMRLiHPfMPYISeiIWQHLPHEGETITLASWPVYDPALenPEAVAEMNLLMD

TIRAVRNIRAEVNVPMsKKiELMVKANSAETSSiIARNShYIKRfCNTSEFDsGLDLN

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CDS 392490..393917

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/locus_tag="EFAGFIKM_00354"

/EC_number="6.3.2.17"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P15925"

/codon_start=1

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/product="Folylpolyglutamate synthase"

/translation="MPSGRFFHSNSGPKVNQMTELDGTDAAPLLTYNEAVDWINGLI

PFGIRPGLERIESLMSMLGNPHQRLKFIHVAGTNGKGSTCAFLTSVLLQAGYDVGTF

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YAEECYPDVVVWETGLGGRMDVTNIVAPVSVITNIGMDHTDVLGDTIEQIAGEKAGI

IKPGVPVVTCAQPEAVKVIQEKAQQLQSSVYLAGDQFSYHRLDSNENGQSFHFTGPF

RDLDVRIRMQGS HQCDNAAAALMVLELLRQYMAFMLDDNDIALGLENAFWAGRFEKVV

DEPRIVLDGAHNPEGAESLAKSIMDVYPHNKLILMMGMLANKHHEAYLQHILPLVDTL

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VSGTLYLIADVRAALLHQTDSEKGW"

CDS 393974..395293

/gene="murC"

/locus_tag="EFAGFIKM_00355"

/EC_number="6.3.2.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9HW02"

/codon_start=1

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/product="UDP-N-acetylmuramate--L-alanine ligase"

/db_xref="COG:COG0773"

/translation="MSAIARVMLEMGYTVTGSDVASQELTEKLAAGAKIYIGHTAEH

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VTNIEADHLENYNDSFEELKRAYVQFLSQIRPEGTAIVCSDDENVQAILPELKSRIIT
YGIDRAADYTATDIVLGDRRISFTMNHQGAAMGTVELSVPGKHNVYNAMATVITCLEA
GIPFEKIVAAIIQFHGAKRRFQVLGEARDMLIIDDYAHHPTIEATISAAKATGKRII
AVFQPQRYTRTFFLLDAFSRAFAEADVLITDIYSPAGEKQIEGVTSARLVELIVQNS
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CDS 395410..396639

/locus_tag="EFAGFIKM_00356"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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KEIVNPEINPAIFGVKQEDVQFFFTNSSALVEQLSTLSIQQLGQSAPAAVSTETMTAI

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CDS 396785..397027

/locus_tag="EFAGFIKM_00357"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MKKNFGMLLLFLLLGWMAGAWIAKALQPVKAVAFITKATTIRWS

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CDS 397122..397733

/gene="maf"

/locus_tag="EFAGFIKM_00358"

/EC_number="3.6.1.9"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q02169"
/codon_start=1
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/db_xref="COG:COG0424"
/translation="MDNTQQRPIILASTSPRRKELIASLHLAFDVIPSHANEDTPPEW
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CDS 397771..398460

/locus_tag="EFAGFIKM_00359"
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/inference="similar to AA sequence:UniProtKB:Q02170"
/note="UPF0758 protein YsxA"
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CDS 398644..399678

/gene="mreB"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q01465"
/codon_start=1
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MPLEQVETMEIRGRDLVTGLPKTITITSDEISEALADTVNAIVEAVKVTLEKCPPELA
ADIMDRGIVLTGGGALLRNLDKLLAGETGMPVIVAENPLDCVAIGTGKALENIHLFKS
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CDS 399865..400737

/gene="mreC"

/locus_tag="EFAGFIKM_00361"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8Y6Y4"

/codon_start=1

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/product="Cell shape-determining protein MreC"

/db_xref="COG:COG1792"

/translation="MFELFKLLGNKRLFVLLVGLVTFIALMGFTLSPRTTLLSWPEKFL
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EGLVGIVISHVSSYTSTVNLLTSMDANDPTSNAIAATAVGKEKVFGMIESYDPKTGMLK
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CDS 400737..401270

/locus_tag="EFAGFIKM_00362"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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VMVSVVILGSLLNDTMLFFLYKLFQLNHVTFDWALIEYMIPNLFIHFVFALIIYVPLR
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CDS 401346..402008

/gene="minC"

/locus_tag="EFAGFIKM_00363"

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/inference="similar to AA sequence:UniProtKB:Q01463"

/codon_start=1

/transl_table=11

/product="Septum site-determining protein MinC"

/db_xref="COG:COG0850"

/translation="MTVKSNHVTIKGIRDGLVFLDDQCEFEELLYELRYKLEHSHQN
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 MCGMVRSGQVLHHEGNLLFLGDINPGGTVTCTGDIYVLGSLRGMAGIGGDEEAIIA
 ASVFAPTQLRIADIISRPPEWESRETGMEFAYLQDNQMQIDKMSNIVRLRRDFNVFK
 GV"

CDS 402012..402806

/gene="minD"

/locus_tag="EFAGFIKM_00364"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q01464"

/codon_start=1

/transl_table=11

/product="Septum site-determining protein MinD"

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/translation="MGEAIVITSGKGGVGKTTTSANIGTALALLGKKVCLVDTDIGLR
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 SSHIQSPKLVNRIIRNNMVKSGDMLDIDGILQVLNIDLIGIVPDDELVIKAANSGEPT
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CDS 402956..403804

/locus_tag="EFAGFIKM_00365"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/translation="MNTKLRIKQRREERIRRLMEGATVEVLQEQLGSLLDKNEIIHP
KPFTPSEGIQERDPEWLWKKENGHFVPGGHSRFNLFKSLFKRTVISALIFGGVWGLFQ
LDTSWTTSPKTVIADALHRDMDFASAAAWYERHFGGTPSFLPVLGHTTDAVNGLKVRQ
LLGKPISGTVVQPFALSMKGIEIVPDAAGAELIQVASSDAGRVM EVIGDAASGFTVVI
QHTGNVTAIYGRLNESEVSVNDWVEAGNPVGSLKATGGEQPATLYFAVKEGEEYVDPA
EVVALD"

CDS 403791..404657

/gene="spoIVFB"
/locus_tag="EFAGFIKM_00366"
/EC_number="3.4.24.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P26937"
/codon_start=1
/transl_table=11

/product="Stage IV sporulation protein FB"
/db_xref="COG:COG1994"
/translation="MPLIRVWGV RITFHPFFVIIMMASLLTGHFIELITLFAIVFIHE
CGHAAAAALLGYRVLSIQMLPFGGVAVIEDGGTITAYREIIIALAGPLQNILMVGVM
LLQYGNLGDVPFLNYIIQGNLLIALFNLLPVLPLDGGKIVQALVSLWAPYYTTLMWTY
RISILCSVG VILY AISRWFTGDYGLPLNILLIGLFLFYSNVTDYRNV PYRFIRFLMNR
EGVFARHAATGSLAQPIISFPAKPLDTILRLLKRERYH MVYVMNRQGRIMAVLPEQRI
IGSYFQQNGDKL"

CDS 404764..406014

/gene="rng"
/locus_tag="EFAGFIKM_00367"
/EC_number="3.1.26.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A9J0"
/codon_start=1
/transl_table=11

/product="Ribonuclease G"
/db_xref="COG:COG1530"
/translation="MKQMIVHNEHNLMQMALLEEGKAVEFTAERTRDRGLLGSFFKGR
VVNVLPGMQAAFVDIGQKKNAFLYVDDVLHPHLEKQPKVKPSISELLRPGQEVIVQVL
KEPVGGKGARVTTHYSLPGRWLVMYPVADYVAVSKKIAREGDRSRLKALGEQLRRDEE
GLIIRTVSGEEQHEAIKSDLET LRAQWYLIREKADSLPSPSLLHRDHSMVQRIIRDVY
TPGSDEVITDSEGQAREVKALLEEISPGHQPKVQVYRGTESIFAAYGVQEQLNKDFAR
KWWLPGGGYIVIDHTEALTVDVNTGKYTGAGGDSLEETVTETNIQAAVEIARLMRLR
DIGGMIIVDFIDMEEASNRHEVAATLEGELKKDRTKAFVMGWTKLGLLELTRKKVREE
STLPYEPCSSCHGTGKRYISPLH"

CDS 406170..406481

/gene="rplU"
/locus_tag="EFAGFIKM_00368"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P26908"
/codon_start=1
/transl_table=11
/product="50S ribosomal protein L21"
/db_xref="COG:COG0261"
/translation="MYAIETGGKQYKVQEGDVLFIKLTANDGESVTFDRVLAVSND
QGLTAGTPLISGATVTAKVEKHGKGQKVIVYKYPKKNYHVKQGHRQPYTKVTIETIK
A"

CDS 406496..406825

/locus_tag="EFAGFIKM_00369"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIIVQIFRDEDGNIERFSIEGHANFAKRGEDIVCAGVSAVTVGT
VNSIETLTGVEMDAKMKNGLSGSLPLLERGETWSQVQLLLESMVVMLSNIAESYGKY
IKIQQFK"

CDS 406849..407160

/gene="rpmA"
/locus_tag="EFAGFIKM_00370"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P05657"
/codon_start=1
/transl_table=11
/product="50S ribosomal protein L27"
/db_xref="COG:COG0211"
/translation="MLKLNQLFASKKGVGSTKNGRDSNAQRLGVKRADGQTVTGGS
LVRQRGTKIHPGTNVGIGKDDTLFAKIDGVVKFERWGRDRKKVSIYPVNVAPVAAAVE
A"

CDS 407311..408048

/locus_tag="EFAGFIKM_00371"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKSWKRVPWIAACSLLIPLVFVMLYPAMISSVVCALWSVAVLLI
SVNAMKKQAEAERRAIQSMEKTAIASLNHHRHDWMNDLQVLYGYLRLGKLDKSLQCV
ERIKERVTEESRISRLGIPSLVFYLQSFASGIALDLHVEIEDELQLSALVSPEDGES
LTGAIADAIRAYQYGGGRSSWGEVRKLTNFGQDHGDVVRLDGDQTPDPETLRQLTA
VLKGKKVRTEQIPSEDTFIQFRMPCGI"

CDS 408066..409376

/gene="obg"
/locus_tag="EFAGFIKM_00372"
/EC_number="3.6.5.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P20964"
/codon_start=1
/transl_table=11
/product="GTPase Obg"
/db_xref="COG:COG0536"

/translation="MFVDKAKIYVKAGDGGDGIISFRREKYVPNGGPAGGDGGRGADI
IFRVDEGLRTLMDFRYQRHFKAPRGEKGRNKSQHGANAENMIVRIPPGTIILDEDSGE
VLADMTRHGQQVVIARGGRGGRGNIRFATPNNPAPELAENGEEGQERYIVLELKVMAD
VGLVGFPVSGKSTLLSVSSAKPKIGAYHFTTITPNLGVVGVGEGRSFVMADLPGLIE
GAHEGVGLGHEFLRHVERTRIIVHVVDMSGSEGRDPFEDWQKINDELKLYNPLLAERT
QIVAANKMDMPDSEANLEQFLQQVREAQPDIEVMPISLTRKGIQELLYRAADLLDQV
PDERVVEEVADVSEKRVYSLDKKEDDGFKIVRENEMFVVESAKIDRMMKRMQLNSHEA
ILKLARTLRVMGVDAELRKRGAVEGTIVRIGDFEFEFVEGSSYY"

CDS 409605..410042

/locus_tag="EFAGFIKM_00373"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNERYYLVREDILPEAVVKTMQVKELLASGDVKTVHEAVEKVGL
SRSAFYKYKDGIHLINQLERERIVTISIDLEHQSGILSRVLGHVAGYGANVLTINQSI
PLQGRANVVISVETTHLHGEIGEMLDRMQDMPGVRRTRIVGQG"

CDS 410101..411387

/gene="hom"

/locus_tag="EFAGFIKM_00374"

/EC_number="1.1.1.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P19582"

/codon_start=1

/transl_table=11

/product="Homoserine dehydrogenase"

/db_xref="COG:COG0460"

/translation="MKPVKVGLLGLGTGTVGVVRIVEGNQEDLSSQVGSPIVIEKIAV
KNTEKERVIAVDRAKLTEDPWEVIRHPDIDVIVEVMGGIDQTKEYILEALERGKHIVT
ANKDLMALHGTEILAKAQEKQCDVFYEASVAGGIPIIRTLIEGFSSDRITRIMGIVNG
TTNFILTKMSQEGASYEEVLAEAQALGYAESDPTSDVEGLDAARKMAILSTLGFRTNV
ELKDVTVKGISSVTREDIMYAKRLGYEMKLLGIADRIGDEITISVQPTMVRQNHPIAS

VNGVFNAVYVHGEAVGETMFYGAGAGELPTATSVVADIVAVTKNLKLGVNGLKAIVPY
KIKRLQSDEQIVSKNFILLHVDDKAGVLAQITQIFAEDVSLASVVQQPNEHNPD AEI
IIVTHNASKASMDKVLKHFESLSVIRRIKSVYRVEG"

CDS 411503..412573

/gene="thrC"

/locus_tag="EFAGFIKM_00375"

/EC_number="4.2.3.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0R220"

/codon_start=1

/transl_table=11

/product="Threonine synthase"

/db_xref="COG:COG0498"

/translation="MRYQGLLQTYREHLPVNENTPLLTLQEGNTPLIHAENLSEELGL
NVYFKYEGLNPTGSFKDRGMVMAVAKALEEGSRTIMCASTGNTSAAAAAYAARGGLNC
IVLIPNNNIALGKLAQAMIYGAKVIAINGNFDRALEIVREITAKHPITLVNSVNPFR I
EGQKTAAFEVIEQLGEAPDVLAIIPVGNAGNISAYWKGFKYKEAGKSSTLPRMVGFEA
EGAMAIVKGEPILEPETVATAIRIGNPASWKTAVAAAEESSGGQINYVTDEQILTAYRT
LASREGIFAEPASAASLAGVYKLKSEGYFKGGETVVCVLTGNGLKDPNIAIKTVATEP
LVVEDTEEAVMAAIAQLEQQSV"

CDS 412570..413538

/gene="thrB_1"

/locus_tag="EFAGFIKM_00376"

/EC_number="2.7.1.39"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8Y4A6"

/codon_start=1

/transl_table=11

/product="Homoserine kinase"

/db_xref="COG:COG0083"

/translation="MSLREKVTVKIPASTANLGPFGDTLGMALSLYAWLEMKP AEQTT
FHLHGNHLLTGLPTDKSNLIYEVAQMVFN EAGVSLPELEISMYSDIPLTRGLGSSASAI

VGALAAANVLIGAPLSDAKLLDMATSLEKHPDNVGASLYGGIITAAWNGQQVDHIRIE
PHQDLQALVIVPEFQLSTSKARNVPEQFGMSDVVHNISRSSLVAALASGRLDMIQK
AMSDRIHQPYRASLVPGMAEILEHAVDHGALGAALSGAGPTVLTLDVDRHDTRKEGLEQ
YLLDTMEREGISASALWLDPDLGDGVTLPDQDERPFLDRIKGEVNA"

CDS 413535..414407

/gene="pheA"

/locus_tag="EFAGFIKM_00377"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P27603"

/codon_start=1

/transl_table=11

/product="Bifunctional chorismate mutase/prephenate
dehydratase"

/translation="MKRIAVLPEGSVSHEAIDFLFNGEPLNLLHSLISDVFRATDSG
NAEYSVIPIENTIEGSVSLHMDWLVNEVDIPMQAEWVYPSIQNVIGHGSEFKTESGEY
DFGRITKIMSHPAIPQCQNFIRLHSPGAEEGVNSTAEAVEIVKKNPBGKGVVAIGTK
LAAQKHGLDIMAERVTDHDNNYTRFVLIGHEPVNIPREPDHVKTSLVTLTPEDAPGAL
HQVLSAFAWRKLNLTRESRPTKKRLGSYYFYIDVVETVDSVLLTAAMAEIEALNCQV
RVLGSYPCYTYP SR"

CDS 414556..415440

/gene="ilvE_1"

/locus_tag="EFAGFIKM_00378"

/EC_number="2.6.1.42"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O86428"

/codon_start=1

/transl_table=11

/product="Branched-chain-amino-acid aminotransferase"

/db_xref="COG:COG0115"

/translation="MAEQWIYLDGQYVTKENATVSVYDHGFLYGDGIFEGIRIYNGNI
FRCKAHLDRLYDSAKSISLNIPLSIDEMLEVMAETVRRNDMRNGYIRLIVSRGPGNLG
LDPLRCPKASVIIIVEQLAIYPEEAYLTGLKAVSVSQRRNIPDALNPKIKSLNYLNNI

LVKIQSNYSGAGEAIMLNSQGYVTEGSSDNIFIKNGVVYTPPCYLGALEGITRQAI
DLCGELELELKEVPFTLHDVYIADEVFFTGTAAEVIAAYEVDGRTIGTGVAGPVTCLK
LEAFRQIVDKDGYKVWES"

CDS 415636..417258

/locus_tag="EFAGFIKM_00379"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKIHMVKKGDTLYLLSQKYNVALDKLIAANPQITNPKLDIGMK

VKIPAEPVTPKPEGVLHSHKVQQGDSLWKLAAQAWGVPLKDMVNANPQLKNPNALLVGE

TVYIPSIHAQGNSTNSNGASNIAAHEKLSPEGKEYTGVKEPEPPAPVTPTPPAPVAEV

PVPVPAPPPANTEKPNVKPELEVLPQLPELPEVKPEKETHKKEEVKPEVYVKPVAESK

KYTMPNLSPEIMPLPVMPTKSPTEVAPATKKPCGCGNKLHHAPAEHPYAQIQVPVQE

VYGAQQDMYTAGASNNASFPGIPEVSPYSGSDLPNPWTGAEQGYNHNNVMPNLSADM

QNNSFPIAPAGEVNSPFPTYAAPSHMNHQPPFISPYSMPLPYPPCGCGSHTHMPQYTYP

SHGYQDPAWNMYGPSYGMPPMSTSTMPNQPIEYAYQNPYPTQNMVPPSPLGAFGEMY

PPQGQGKGKGGKGGREDANLSQVAIEEVGSDSEGKSKQAGSKPAAAKRRTSKAPLKNKS

KVSVSGKTSREGAAASNQRKSDKKRRNPWIQN"

rRNA 417809..419359

/locus_tag="EFAGFIKM_00380"

/product="16S ribosomal RNA"

rRNA 419670..422590

/locus_tag="EFAGFIKM_00381"

/product="23S ribosomal RNA"

rRNA 422670..422781

/locus_tag="EFAGFIKM_00382"

/product="5S ribosomal RNA"

tRNA 422868..422943

/locus_tag="EFAGFIKM_00383"

/product="tRNA-Asn"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Asn(gtt)"

tRNA 422948..423019

/locus_tag="EFAGFIKM_00384"

/product="tRNA-Glu"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Glu(ttc)"

tRNA 423026..423101

/locus_tag="EFAGFIKM_00385"

/product="tRNA-Val"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Val(tac)"

tRNA 423119..423192

/locus_tag="EFAGFIKM_00386"

/product="tRNA-Met"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Met(cat)"

tRNA 423220..423297

/locus_tag="EFAGFIKM_00387"

/product="tRNA-Asp"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Asp(gtc)"

tRNA 423321..423395

/locus_tag="EFAGFIKM_00388"

/product="tRNA-Gly"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Gly(gcc)"

tRNA 423402..423478

/locus_tag="EFAGFIKM_00389"

/product="tRNA-Arg"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Arg(acg)"

tRNA 423494..423574

/locus_tag="EFAGFIKM_00390"
/product="tRNA-Leu"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Leu(caa)"

tRNA 423581..423654

/locus_tag="EFAGFIKM_00391"
/product="tRNA-Pro"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Pro(tgg)"

CDS 423856..424548

/locus_tag="EFAGFIKM_00392"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNTFNFRKQFKRRWRRWKRTVWMTAALLAVTILAYSGLSISAI
ERLLTTFSEATSVMPVTQETRSEQEIQALVEQLDSDPDHLTSVVLETQYICGVETE
QLGKMARPQLKMLLAQHPEWDATVGTSDELHLKQRVDDLSPCKQQAYISIDAVGNLN
LYEGKPAEEKVIRTFQLDVGTLESSLPEGVLEQLQQGIRIQDKDEYDSVISTFSDYA
VDEDHHLIRNGG"

CDS 424851..425360

/gene="ruvC"
/locus_tag="EFAGFIKM_00393"
/EC_number="3.1.22.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A814"
/codon_start=1
/transl_table=11
/product="Crossover junction endodeoxyribonuclease RuvC"
/db_xref="COG:COG0817"
/translation="MVLRLFLGIDPGIAIVGFGFVDKIGSKVVPVQYGCITAEHTPEE
ERLLHVYEGMVQLIDKYKPDVALEKLFFNRNVTTAMSVSQARGVMVLAAAQKGLPIA

EYTPMIKQAVVGYGKAEKKQVQEMVKMFLRLQVVPKPDDVADALAVAVCHAHSYTLN

SKLNEVLRK"

CDS 425357..425971

/gene="ruvA"

/locus_tag="EFAGFIKM_00394"

/EC_number="3.6.4.12"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A809"

/codon_start=1

/transl_table=11

/product="Holliday junction ATP-dependent DNA helicase

RuvA"

/db_xref="COG:COG0632"

/translation="MIDFLRGQFIHVENDYIVLDVHGVGYRVFCPNPFAFAKQEGEIT

VYTHHHVREDAMLLFGFVTRDEQRLFRKLIEVSGIGPKVALGILAGGTPEHVVTAIYQ

ENLTFLTKLPGIGKKTQRMILDLKDKLDSFGAAAYATGLFAPPSEESGSGSAWDEAR

EGLKALGYTDSELDKVLKLLKDVTTADSVDVLMKKALQMLFTG"

CDS 426027..427037

/gene="ruvB"

/locus_tag="EFAGFIKM_00395"

/EC_number="3.6.4.12"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32055"

/codon_start=1

/transl_table=11

/product="Holliday junction ATP-dependent DNA helicase

RuvB"

/db_xref="COG:COG2255"

/translation="MDDRIISANLMMEDQNVELSLRPRYLNEYIGQNQVKENLKIYIE

AAKFRNEALDHVLLYGPPGLGKTTLANIIANELGVNLRRTSGPAIERPGDLAALLTNL

QEGDVLFIIDEIHRHLHRTVEEVMPAMEDSALDIMIGKGPSARSVRLDLPSTLIGATT

RAGLLSAPLRDRFGVISRLEFYTVDELAYIVSRSTEILGVEIVGDAAEEIALRSRGTP

RIANRLLKVRDFAQVRGDGIITQTLAEEALQRLQIDPRGLDDIDHKMLKSMINSFRG
GPVGLDTIAATIGEEESQTIEDVYEPYLLQIGMIQRTPRGRIVTDLAYHHLGLPVPPRD
GK"

CDS 427143..429230

/locus_tag="EFAGFIKM_00396"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGKAIRTKKWSRRLKVLAAALLTVGCLQVPAYAAGNDGQTIRVA

MFANLGSTYKSTTPLITLESTGQWSIQSESGANVSLPAGQVRFSADGFRVKVLETADF

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AGQKPAVTGSKRLSAGTYGSIQEAEEAAQANLLSAGVSSAYPVLQLSGGSQAYAVWVGE

ASTDAELTALKNSVEAKAPGVSLSPVNTNAGLIIRQDAGLSTDALKTAPHYTIAGTES

KALVQGNNGNIKVVERSQRTYRGDMEISIVSGDLALNVVPLEQYLYSVVGADEVYSSW

PAEALKVQAVAARSYALQQGERFKIANVVDTTLSQAYNGIGSENDKVTSAVDATAGEV

VKSGGKIIEAVFSSNAGGQTAHPSEVWNGGAGVFTNVVSSGDTSAQAGLHTWYHVLLG

TGVSGYIREDNIKELTTKTNAGLAKVTVTAQNTNVRVPLIQSTVEPVAKMNPNGNEAV

VLAKVAQSNDYAWVRGPFTSAQLVKSLQGKTTASVPASISTLEVTKRGPSGRALEVTA

NGQAMTVKYADTYRSALGGLPSTLFDIAGTGSYTVLGADGKTASKTGSNGASVLSSSG

AGTSSGNALVMSGDGQARAVTQGQTFMFIGQGNGHGLGLSQWGAKGMADEGYDYQAI

LKHYYQNATIVKE"

CDS 429237..430265

/gene="queA"

/locus_tag="EFAGFIKM_00397"

/EC_number="2.4.99.17"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32054"

/codon_start=1

/transl_table=11

/product="S-adenosylmethionine:tRNA

ribosyltransferase-isomerase"

/db_xref="COG:COG0809"

/translation="MNVNLYDFELPEQLIAQTPLLDRTASRLTLNKDSGEINHQTFF

DIIDFLNPGDTLILNDTRVLPARLFGTKEDTGAKAEVLLLKNVEGDKWEALVKPGKKL

KAGSVIVFGEELKAIIEEGEMGARTLTFTYDGIFQEILDRLGEMPLPPYIKETLDDR

ERYQTVYAKHEGSAAAPTAGLHFTDELDDQIRAKGVNNAFITLHVGLGTFRPMMSVDVW

EDHVMHEEYYSLSQETADLINQTKANGHRVFAVGTTSCRTLETVGSKFENGILQASSG

WTSIFIYPGYSFKVIDGMLTNFHLPKSTLVMLVSALAGREHIMQAYEEAIQEKYRFFS

FGDAMLIY"

CDS 430309..431445

/gene="tgt"

/locus_tag="EFAGFIKM_00398"

/EC_number="2.4.2.29"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P66905"

/codon_start=1

/transl_table=11

/product="Queuine tRNA-ribosyltransferase"

/translation="MAAITYEHIKTCKQSGARLGRVHTPHGIIETPTFMPVGTQATVK

TMSPEELKEMDAQIILSNYHLFLRPGHEIIREAGGLHKFMNWDRPILTDSGGFQVFS

LSEMRKITEEGVNFRSHLNGDKKFLSPEVAMEIQNALGSDIMMAFDECPPYPAEYEV

KKSLERTSRWAERCLESHDRPHDQGLFAIVQGGMHEDLRRQSAADLTSMDFPGYAIGG

LSVGEPKHLMYGVLDYTLPLPSNKPRYLMGVGSPDALIEGSIRGVDMFDCVLPTRIA

RNGTTMTSQGRLVIRNAKFATDFGPLDPECDCYTCRNYSRAYLRHLIKADETFGLRLT

TIHNLHFLQNLMRNVRKAIMEDRLLDFRDEFFDQYGLHDNDKGF"

CDS 431513..431824

/gene="yajC"

/locus_tag="EFAGFIKM_00399"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ADZ7"

/codon_start=1

/transl_table=11

/product="Sec translocon accessory complex subunit YajC"

/db_xref="COG:COG1862"

/translation="MFQGMTLAGAQGGGIVSLIVPLVLMVAIFYFLMIRPQNKQKQR
NSMLSQKKGDKIVTIGGLHGTIAEITDDVVVLRVNDVTKLTFDRNAISTAVARDTAV
E"

CDS complement(431948..432340)

/locus_tag="EFAGFIKM_00400"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQLIRRLVSFRVSNPILSGLCQAFVWMFIGAFILSLFLWMSGMR
EQDLSLYTYVVHGLSLLVGGFVAGKRSGEKGWYYGGITGIVYGLLVLLIGFLALDASF
NWKDSLQLLSAFFISALGGMFGVNTHR"

CDS 432524..433282

/locus_tag="EFAGFIKM_00401"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31533"

/note="UPF0702 transmembrane protein YetF"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNFPDVGSHIFRTILMYFLVYCAMRVMGKREIGKLSMFDLVVSI
MLAEMAAFVIEDIDKPLSYGIAPMLTLIIVQIGMAFIGLKSRRLRLIIDGKPTVLISK
GVLHRDEMQRQRYNLDDLQQLREQNVDSIGEVDFAIETTGLTVFPKDKNTSNDNSN
SSGSDSEDSSSSSKTGKNQIDGFPNIKYEGLPLPLIMDGKVQDQNLEIIQKTRFWLK
NQIQHNGILDVKDFICSIDHNGKIYVSPKDDK"

CDS complement(433290..434993)

/gene="spoVB"

/locus_tag="EFAGFIKM_00402"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q00758"

/codon_start=1

/transl_table=11
/product="Stage V sporulation protein B"
/db_xref="COG:COG2244"
/translation="MKNNGFVPFMIACTFNRRGVVLKKQTFIQGAMILLAAGIINR
ILGFIPRIALPRIIGAEGVGIIYQLSYPPFFIVLVTITGGIPLAVAKLVAEADTGANRY
SPQRILQVSLSTLTGTVFMFLCILFAPWVTKYVLTDERVYHTFVSMSPMIAIIAVS
AVYRGYFQGKQNMMPPTAISSIVETIIRIVCVIWFALLPHGIAQAAAGAMLGALVGE
FGGMLVLLWKYNRQKKELPLAMQQNMSDLTTKPSAKPLNPIPSVLKETGTPQPGIIRR
LLAISIPVTAGRLVGSLSYLAETIVTAQSLALAGISKGLATAQYGALQGMIIPLLLP
GALTSSLATSLVPSLSEASAQGDRAIHKRMHQALRLALVTGAPFSVFMVLAEPMCL
VLYNDASIGSMLKLMAFPALFIYIQAPLQAAALQALDRPGKALLNTFIGAVIKITLILT
LASRPEYGIFGAVIAICVNSTVVTLLHAQSVRSLLQFRFKMMDWVKTGAGMFIMGAAT
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CDS 435143..435391

/locus_tag="EFAGFIKM_00403"
/inference="ab initio prediction:Prodigal:002006"
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CDS 435483..436733

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/locus_tag="EFAGFIKM_00404"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32047"
/codon_start=1
/transl_table=11
/product="Protein translocase subunit SecDF"
/db_xref="COG:COG0341"
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AEPLAQVTKASLVQTAKSLESANALGTSEPEVTTEGSNRIRLKLAVTDEAEVR
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KFSEITKRLIGQPLAIYLDDELLSAPTVRQQQLTDGSAQISGAYTRDEANQLRDTINLG
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HTWLVLAI FYLGEFVLTLPGIAAFILGIGMAVDANIITYERIKEEMRSGKSILSSVKA
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CDS 436723..437631

/gene="secDF_2"

/locus_tag="EFAGFIKM_00405"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32047"

/codon_start=1

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/db_xref="COG:COG0341"

/translation="MRFNWNFDYVKGSKIAYIFSILTVTGIIISILALGLNYAVDFRA
GSNVDISVSKAITAEQIKPIVKDIGVDEGDVTITPGADRVNVRFSNELDETQESKFKQ
EFTKLDASASYEVNTVDPEMAKELERNAIYAVLIASIGIMIYVAIRFEWRFGLA AVIA
LFHDAFVVISVFSIFRLEVDLTFITAVLTIVGFSINDTIVIFDRIRENLRFAKKTTKA
DLREVVNRSLAQTMTSLNTTFTVFAASICLFIFGGESIRMFSLAMVIGTLFGAYSSI
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CDS 437705..438664

/gene="mneP"

/locus_tag="EFAGFIKM_00406"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SP78"

/codon_start=1

/transl_table=11

/product="Manganese efflux system protein MneP"

/db_xref="COG:COG0053"

/translation="MTREHIPSAQAATWSGIAGNMGLAVIKAGVGYMANSKSLADGL

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LYCSLAVLIGIIGSMAGEETGLSMLLYLDPTAALIASCFVLHKGYRMIVDTVYGSLVQ
ELEQEEASDFKETVQRVYGIITIEHLVAREQEHDVTIELVISVNPRISILEAQEIANR
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CDS 438705..441113

/locus_tag="EFAGFIKM_00407"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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GIEVIVTDHHEPPEILPEAFTLINPKLPGCPYPFKGLAGAGVALKLAQALIGEVPGEW
MEIAAIGTVADLMPLEGENRVIVSYGIESMRGSRLPGVSALLEISGVDQSQVTSINIA
FAMAPRINASGRLDHAGRAVSLTTENLDEAHTLAGQLDLLNRERQQVVEGILQEATA
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DFVPQRLADDECRISDVPLKVIQEIDRLQPFMSNPSPRFVLRSVTVKETRTMGREKR
HLKLVLEQDGQQLQETVAFGKGALAEFLPGSVIDVMGELSINEWNGMRKPQLMLQDIH
VPQVQVFDLRGNAEPLNAMKHFLNSLEVHLRYKSGSVGAIVRKETDVSEGNLSLYEPCL
WVYDRKVGLFPCNAAAQHYGQEQRVTLFVFDTPETPEQLNAMLALFSGAENIILLHGS
GNRRDRLQMPSRDLFKRIYMQVLKWKAEPVVEEQEITPVLSRQCGCSPRMITMMLDVFE
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CDS 441151..441663

/gene="apt"

/locus_tag="EFAGFIKM_00408"

/EC_number="2.4.2.7"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P68779"

/codon_start=1
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/product="Adenine phosphoribosyltransferase"
/translation="MDFKDYIRVIPDFPQPGISFKDITLLKDGEMYRNAINELKVMV
SDLKIDVIAGPEARGFVVGAPLAYALGVGFAPIRKSGKLPGETIEVGVDLEYGKDTLA
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EIDVFTLMNY"

CDS complement(441817..443133)

/gene="uraA"
/locus_tag="EFAGFIKM_00409"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AGM7"
/codon_start=1
/transl_table=11
/product="Uracil permease"
/db_xref="COG:COG2233"
/translation="MQREIQVNQKMPLGSGSLLSLQHLMFGSTVLPNLFVDPSPM
ILLMNGIGTLLYILMCKGKIPAYLGSSFAFIAPVTMVLKQHPENGYSMALGAFIITGL
VFCFVALIIFAGTGWINVVFPPAVMGAIVALIGLELVPVAAGMAGLINSDPVANPNW
VPQAKPIILSMATLGITVIGAVTFRGFPIIHILIGIVVGYILGYSMGLVDKQAIANA
DFISLPTVTTPTFDWSVIFTILPVALVIVEHIGHLLVTSSIVGKDLSKDPGLHRSLL
GNGVSTILSGFVGSTPNTTYGENIGVMALTRVYSTYVIGGAAVIAIVLSFSGTFSALV
ANIPVPVMGGVSLLLFGVIAASGLRILVEQKVDFAKPTNLLLTLVLVIGLSGTEVTF
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CDS 443507..445684

/gene="relA"
/locus_tag="EFAGFIKM_00410"
/EC_number="2.7.6.5"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O54408"
/codon_start=1
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/product="GTP pyrophosphokinase"

/db_xref="COG:COG0317"

/translation="MGIEQLLEKAGAYIKEPDLVRIEAYEFADQAHHGQTRKSGEPY
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ERIQFRSKEEQQENENYRKMFIAQAQDIRVIVIKLADRLHNMRTLKFQSEESQRRISYE
TLEIFCPIANRLGISAIKWEMEDIALRYLNPQQYYRIANLMHKKRAEREQYIDTVMDG
ITNKLDEMGIQADLSGRP KHIYSVFKKMTTKNKQFNEIYDLLAIRIIVDNIKDCYATL
GIIHTLWKPMPPGRFKDYIAMPKANMYQSLHTTVVGPNGEPTEVQIRTWDMHRTAEFGI
AAHWAYKEGAANGNH FEDKITFFREILELQNEAQDASEFVESLKMDFFSDLVFVFTPK
GEVIELPIGSVPLDFAYRIHTEVGNRTIGAKVNGRIVPLDYHLKTGDIIEILTSKHSY
GPSQDWMKIAKSSSHARAKIKQWFKKERREENVEKGRES CERELKRMGLDPSAWMTDDK
LMEAAKKYAFNDIDDM LAAVGFGGITAAQIVTKATEKLRKEQEESLLELNSEMRELK
PAPERNRPTNGIRVKGIDNLLVRFARCCNPVPGDDIIGYVTRGRGVSVHRSDCPNIP
TSADGEEAARVIEVEWEENIEASYSVDIEITGHDRNGLLNEVLQAVSESKTNISAVTG
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CDS 445697..446158

/gene="dtd"

/locus_tag="EFAGFIKM_00411"

/EC_number="3.1.1.96"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0A023W421"

/codon_start=1

/transl_table=11

/product="D-aminoacyl-tRNA deacylase"

/db_xref="COG:COG1490"

/translation="MRVLVQRCKEAQVTVGDELTKIESGLMLLVGITHEDTAKDAQY
LADKVSGLRIFEDDQEKMNLSLLDVGGAVLSVSQFTLYGDCRK GKRPSFAAAARPEAA
ELLYETFNQLLRDKGIQVETGRFGAMMDVTFTNWGPVTLMLESPVRQEPSA"

CDS 446235..446402

/locus_tag="EFAGFIKM_00412"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MRQSAKETRTRTEPLLLPGNLYESLHLARSAAEYVATIWALQDS
DKGKQSHLPRS"

CDS 446670..447176

/gene="yhbO"
/locus_tag="EFAGFIKM_00413"
/EC_number="3.1.2.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P45470"
/codon_start=1
/transl_table=11
/product="Protein/nucleic acid deglycase 2"
/db_xref="COG:COG0693"
/translation="MSKVAFLANDFEDSEMQVPYDEVKKAGHEVEIIGLKAGETLKG
KGGKASYTTDKAIGDASASYDAVVIPGGSSPENLRSDAHILKFVTEINSAKKPIAAI
CHGPQILASAGLLKGRITISYPPLKDDMVNAGAEFKDHEAVVDGNYITSRTPEDEPAF
VRELLKVI"

CDS 447281..447727

/locus_tag="EFAGFIKM_00414"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTKHIQAYFRTEDEAEGARTSLQTFRTEHLEVGQLDSAVGRDTR
VMVPLVPYNTAGGVGTNGAMGVGAAPGVPASENVIPVVANVDRDAERDTRDRVNEDGD
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CDS 448319..449626

/locus_tag="EFAGFIKM_00415"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MRMARDRFKGEVLVLSKVGRNDLCPCGSGKKYKKCCLNKESSAVE
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EPEVILEALVLWNGYSRQTRPTVKKTGFSFSAIEYLLSEEYGFNVSKAELADKYEVT
GTISRKVKEMNSYIEEYGMGGTDELLMLNGPGTSKDKAQALLSKAREASSSKRRVHL
AETALEMYPDSSDAYLILAEESDNENDARSYLKEGIAAGKRELGELFFEENKGDFWGL
HETRPYIRICKSYAESCWFGGDTKEAAQILEHMLELNTEDNTGARYLLAAVYLYSNQL
DQAEQLLEKYGKGDAATAFAYDQIILEYKKNGITSQKMLYRVARGVNVKHVPDYLLGL
KRLPHNLPDFVGLGDSDEAIEYVIMHSRLWASAPDLLKWMLKQ"

CDS complement(449656..450780)

/gene="cheB_1"
/locus_tag="EFAGFIKM_00416"
/EC_number="3.5.1.44"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00099"
/codon_start=1
/transl_table=11
/product="Protein-glutamate
methylesterase/protein-glutamine glutaminase"
/translation="MLNLARRSLKEVRGYLHQIESPQEILPIIQLQLVEDFQAQAR
VNVHFRTFGEEYPLPKLAKMAFYRCLQESLTNAVRHGESTEITATLKFEQRQARLEIQ
DNGKGMEEWQDGFGLNAMKERTMNLQGQVSVYSEPGEGTLVTCTLPRQVELSDEVIRL
LIVDDQPFIRESLRTILEGHNDLQVVGMSDGLQAIERCEQDQPQVLLDLMPNMDG
ISAAKVIKQKWPHIRILVLTTFQDTEQALEVLRSGADGYLLKSIEPRELAETIRLVYR
GGTLIDQEMSHKLFKLEMDKTGNKMLEPNTSENFGLTSREMEILQLVCKGLRYKTIA
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CDS complement(450834..451466)

/locus_tag="EFAGFIKM_00417"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MRNLFETVKQWFWYDWIMFIFRLIFSISLMFTTVQLHEQIPLPL
WALIFWQVFAFSVPWLCLQLSYKYLLTEIIFSGGLCLYLSSLFPEAYLAFLTYAFLI
AVNSARQSYRWTGPITILLPILINVLSHQSNYWVMMIQIGLAYAIGFAFHLLVNNHR
QSEIIREQNTVLQQYFSQIERITLAEERDRLSKDLHDTIGHSYLPLSSWG"

CDS complement(451575..452162)

/locus_tag="EFAGFIKM_00418"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKTIRCFFQNGYFLLLTATGLFYFCFYLTITLGLGLSFTVA
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VAIYWLMMKLWIGLLCLLCAALLCLMPLLLMLTPLFFPIFDIQFFGIQIDTFMKSLFI
MAMGVIFAFISSWILKVLVLLIGGYTRQMTKSLNR"

CDS 452367..454319

/gene="dap_1"

/locus_tag="EFAGFIKM_00419"

/EC_number="3.4.11.19"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01960"

/codon_start=1

/transl_table=11

/product="D-aminopeptidase"

/translation="MRKAIRNTSLAVLLISASIVTGCTATNGAVASDQKSTEKVSLEG
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VFQIGSVTKSFTALAAMQLVDQGKIDLKHDIQEYLGEMKVPNKTGKPLTMFDLLTYTS
GVDLPDIVTDFSVEYLNKDIPMKGYLNQNIPTVVRPPGEAYTYDNYGFMLAGYAVENV
SGMPYSQYMEKNVFKPLGMNKTSVRLTPEVLSNVAAHYGPSGELQPTMGFAPSEKPEG
GMTSTGGDMAKYLMHLNKGFEFEGKEIVSPKSIDLMHTYQVYADPTIPITTVGFEGYF
NNVMNGQHVLKGGNVPGHSSLIAILPEKNTAIYLSYNNDMMMSLDVYEAFMNHYPK
TVKTQPSTYSNVSKQAAQAYVGLYKNTRLHSIRTKISYANGNLLMETGTTGKHTLKMV
HPLLEFEAGNKMAFKKDKSGDITYFYTNPKGMDFVAHAQVKMKTAFSDDVPNNSVY

KSYIDNLNGLDIMGAQSGNRFDPKGKMTQGEFSDVLLRAHGMHTFPDEFRENKKRMIE
GIPNFQPKSLITRQMAAVMIQNLKHAAPGTNVKLIGKTDSWAVDAITALVSQGIVDPD
TKINSNQTVDFRSKQTLRQEARCPA"

CDS 455055..456308

/gene="hisS"

/locus_tag="EFAGFIKM_00420"

/EC_number="6.1.1.21"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P60911"

/codon_start=1

/transl_table=11

/product="Histidine--tRNA ligase"

/db_xref="COG:COG0124"

/translation="MAFQKPTGTQDLLPGVVEKWQYVEEKARDLCRRFNYREIRTIPIF

EQTSLFVRGVGETTDIVEKEMYTFDDKGNRSMTLRPEGTAGVVRAYVENKIYGEPDVS

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VEINSVGNSTSRAEYRETLGFLRPMKDSLCKDCQSRMERNPLRVLDCKVDQDKFVGA

PSILDSLDEESLNHFQAYLDDFGVDYAVNNRLVRGLDYTLTAFELKAQGIGAID

TVGGGGRYNGLVGDIGGPDQPGIGFGIGLERIQLILEHQNIEVTTLAPLDVYFVALGE

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LKSMDTGEQQTVKLDDLVAAREGK"

CDS 456523..458301

/gene="aspS"

/locus_tag="EFAGFIKM_00421"

/EC_number="6.1.1.12"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P67015"

/codon_start=1

/transl_table=11

/product="Aspartate--tRNA ligase"

/translation="MKRSHHCGALTPAHIGETVTLNGWVQTRRDLGGVLFIDLRDRSG

IVQVVFNPAYSGEALQIADRVRSYVIAVTGKVVKRDAETVNKNLPTGEIEVQITEIE

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FVEVETPILTKSSPEGARDYLVPSRVHEGEFFALPQSPQIYQLLMVGGVERYYYQIAR
CFRDEDLRADRQPEFTQVDIETSFLQQDDLLPMMEELMAKLLRETKGIELELPFQRIT
YADAMGKYGSDKPDLRFGMELVEMNDIVANSVGVFASVIEKGGEVKVLNAKGCWTWS
RKEIDDLGPFAARYGAKGLAWIQVKDGEFKGPIVKFFTPEEIEAVKERTGAEDGDLLL
FSADTKKVADV LGALRLKIGRQLGLIDDSKFKFAWVVD FPLLGYDEDAKRYVAEHHP
FTRPKDEDVHLFDTPGAIRAQAYDLVLNGYEVGGGSMRIYKRDVQEKMFALGLSTE
VANEKFGYLLEAFEYGTPPHGGIAFGLDRLVMLLAGRTNLRETIAFPKTASATDLLMN
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CDS 458320..459078

/gene="tcdA"

/locus_tag="EFAGFIKM_00422"

/EC_number="6.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q46927"

/codon_start=1

/transl_table=11

/product="tRNA threonylcarbamoyladenosine dehydratase"

/db_xref="COG:COG1179"

/translation="MLHQFSRTELAIGPEGLDTLKNSTVAVLGIGGVGGIAVEALARS
GVGRIILIDKDVVDITNINRQIHALTTTVGQKKADLMVERVKLINPECDAIALNMFYT
EETYEELFKYELDYLVDASDTIYKIHLIKECLKRKIPMISSMGAANKMDPTKFQVAD
ISKTTMDPIARVVRTTLRKDGIKKGVKVVFSTEKPMKPREDVTQKIVPENAPEIRKAK
QPPASNSFVPPVAGLIMVSVAIKDLLEIAENKQQ"

CDS 459554..460852

/locus_tag="EFAGFIKM_00423"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0A2A5K485"

/codon_start=1

/transl_table=11

/product="Nucleobase transporter PlAzg2"

/translation="MKHGWMTRRLGMEPGDQWKKEVVAGAI SYFAVVYIVMVNATILS

DAGMPLQAAMVGTLTISIAGCLLMAFGGKSPIIVPGMGINAFFTYTLVHSMKLSWQE
ALAVVTVTGILFAIVAFTSLYKMISEAIPKNLQHGITVGIGLFLTFIGLQKSGIVIAH
QTTFVAIGHFNDPNVITACVTLVLALILFIRNVQGGLLISILVGTGLAYVLGAVNPGE
SVSAMDALRQYGGFLGELSLMKLADVAFWIAVFLLLLIVVFENIGLITAQTQMIGRPE
RFKGSRLALSISTVLGIFGSSPPVAAAETTAGIAAGGRTGLTPLVTAVLFGATFFFI
PLLGYPDSAIAPILIIIGGLMVQGVKDMDFGDFTEAFPAFLIMVMIPFTYSIVDGMA
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CDS 460926..462725

/gene="bmrA"

/locus_tag="EFAGFIKM_00424"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O06967"

/codon_start=1

/transl_table=11

/product="Multidrug resistance ABC transporter

ATP-binding/permease protein BmrA"

/db_xref="COG:COG1132"

/translation="MEEQQQAGQNEPKVGKKGFKDFVKLIASNPPKLILALILTL

IQTAGLIVPLMTKGLIDGLTTSALNKSIVLLLLGAFVIQAIASGISIYMLNYAGQRV

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GGVALLFYLDWVMSLIILSLVPLTLLILLPVGKKMYKISKKQQDEMAGLTSVLSQVIG

EIRLVKAYGTEKQEVEAGDSRIRKMFAFGLQEARILALIGPLFTFVMTAVLVVILGVG

GMRVASGLLSPGELVAFILLFQVIMPMGQFTTLYSRLQKVVGATERIQAILADEEPP

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CDS 462872..463537

/locus_tag="EFAGFIKM_00425"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MARNKYPEQTLDLILAVSTQMFTEKGYEKTSIQDIIDELGMSKG
AIYHHFKSKEDILSAVMEKELGRAEDMFMELIQNTHAPNARQKLISILENIIVDPGIQ
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MLLVNIWINPLLFRDRAQTLERLKFLQHMMKLLGADIVSEQLIQRITNRHASTGGYA
EAE"

CDS 463574..464365

/locus_tag="EFAGFIKM_00426"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLKSSELAICKSIDIDQPIQDIQLNWLSGDIRVLPVDELHVI
QYADTWFSKLRLMQVNIQGGTFSIADGRKRRGLVGINIGRTALEIQLPDRVFDRIILLN
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SAKIDISGEFRHLQIITTGRKLNMDCLKMPEKFHSVSTGAKAVVSIPDNEGFRILLKR
RSGALKSEFDLTPLHGDSNCLIHKSGKSEFQVDIRGGAFHLKSRK"

CDS 464411..464581

/locus_tag="EFAGFIKM_00427"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAGWIVGISFSTIVLLIGIYGALNSRSRQARNKWAWWFILFGCC
ALVSAIINYQFR"

CDS 464718..466898

/gene="helD_1"
/locus_tag="EFAGFIKM_00428"
/EC_number="3.6.4.12"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32215"
/codon_start=1
/transl_table=11
/product="DNA helicase IV"
/db_xref="COG:COG3973"
/translation="MSDSFQSAYQEEYRLERTMEEVDSQLERLQNIPVYTGHDFTEQ
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PAVSDEFLVYRLGENKDNKLRDIVSTIQAEQDLIIRAARNTALIIQGVAGSGKTTVAL
HRLAFLLYQYKEQVSAEKMVIFAPNHMFLDYISDVLPELGVGDIQQRTFPDWAMNLLG
LEMLANTSDTLNTWFEKPDARPELNDDVPGRYKGSIRFMELIREWLSGMEADSVPDM
DFSPWDGTVLSKTEIESWFGEEYKHYPLAKRKERV MARVHRWIEMELKKPMPEAVRKE
RKKKASTREKAYAKKWPQYEPLTYKQLFKAAGGSPASLSGLIPKLV MKQTAADLK
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LGDLSQGIHEYRGVHAWEE MSSLFP EEQNAYFALTRS YRSTMEIIDYANTIL ERGVKS
GITAIPVFRSGDPVRTLAYGGEGRTASLEQALKVLT VKDYRTVSILRTLHEAEEIHR
ELQAAGWDLNLIDGGKKQYTGGHSVLPVYLSKGLEFD AVIVADV DQKHYPNAGDAKL
LYVGCTRALHELWLFHDGVLPIYAAATHNPDGEPVTIQGWPELG"

CDS complement(467021..467923)

/gene="yijE"
/locus_tag="EFAGFIKM_00429"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0ABT8"
/codon_start=1
/transl_table=11
/product="putative cystine transporter YijE"
/translation="MSSSHDKDTRIIKPLKYTLIIILTTIMGTSFPVGKIGMLYAPP
FLLMGIRYILAGGLMALFLRKRPLPTGWQSWLKIILIGLFQSAGVMGCAYYSMNWITS
GESAIITFTNPLLVIILSALLYRVTYRFSQWIGVILGFIGIMLTFGWQMSFSPGTWIG
FGGAISFAVSTLLIKRWGNGYDTFVL TAYQMLAGGAALLLSVWTEQPHFMVNTTSVM
ALLWLTLVCSIIQFSLWFYLLQNSDPAQTSSYLFLAPFFGV LSSWILLGEHVQWFALA
GGLFIGIGIFLVNRRSSRM RNSVT"

CDS complement(467920..468663)
/gene="fabG_2"
/locus_tag="EFAGFIKM_00430"
/EC_number="1.1.1.100"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P99093"
/codon_start=1
/transl_table=11
/product="3-oxoacyl-[acyl-carrier-protein] reductase FabG"
/translation="MTYWKNRVALITGGGTGIGRAVSEMLAERGALVAVNYSRSQDAA
RETVQHILDTGGHAFVQANVANDLDVRRMVTVTETYGPITALVNNAGITRHIPMHD
LESVTDDVWNELVDVNVKGMFHCARAVTEGMRQAGAGSIVNLGSIAGSTGSGSSLPYA
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EDIAHMICAALEQQSMTGQLITVDSGQTL"

CDS 468800..469690
/gene="yofA_1"
/locus_tag="EFAGFIKM_00431"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34685"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator YofA"
/db_xref="COG:COG0583"
/translation="MESGDLRIFQCVAQEGNLTKAASKLGYVQSNVTARIRHLEAEVG
TTLFIRHNRMGTLSPAGEMLLTADKIIIGLLNDASKALRATSTPSGPMRIGSTQTAAA
VRLPELFVRYKQYPDVSLSLVTGNSQILMDQVIGYELEGAFIGPCDHPDIISIPVF
DEELFVVYSGMGPTDEDLKSIPVYSMGCSYRQILEEWLEVGGVTHPVIMEFGTLEA
IISGVTSGMGISLLPEIVIRHQIENGLLRTHLPVGMNRMTHFITRKDAFVSSALHA
FMAMLPREYDMIESGEPSEV"

CDS 469733..471040
/gene="rarA"
/locus_tag="EFAGFIKM_00432"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AAZ4"

/codon_start=1

/transl_table=11

/product="Replication-associated recombination protein A"

/db_xref="COG:COG2256"

/translation="MDLFSFQQDSKPQARLLADRLRPEHLDEYIGQEHIIGPGKLLRR
AIEADQISSILLYGPPGCGKTTLAHIISQQTQGQFVRLNAVEASVKDVREVIEQAQTN
KQLYGTKTILFLDEVHRFNSSRQDALLPAVEKSTIIFIGATTENPFHYVNGALMSRST
LFQLESLNKDHSLIAMRRALSDADKGLGFMELQADDEALEHIATMANGDIRRALNALE
LAALTTPPEKDGSIHITLGVAEESIRRPVKADESTQYDVLSAFHKSIRGSSDAALFW
FLYAVEKLGMDPMTFIRRLIAASSEDIGLANPQAMTQAIGALDAYRNNGWPEAKLNIA
QAILFAVESPKSNAVYTAISKAMNAIDEVKSAEVPLHLRDTHYSGAVKLGHEGYQYPH
NYPGHYVKQEYLPKQLSRRVFYEATEQGNESKIRLNQQRREL"

CDS 471073..471474

/gene="crcB_1"

/locus_tag="EFAGFIKM_00433"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00454"

/codon_start=1

/transl_table=11

/product="Putative fluoride ion transporter CrcB"

/translation="MKELLYIGAGGFLGTLTRYAIQLAIPTVHGGFPWAVLLINAMGS
LFLGWFFTIAPGKITPQLRLAIGTGFTGAFTTFSTFTLDIVRLSEGSEWISAAIYMI
VSLLAGLLLCALGMSLGQRMLGAQRQEGDAS"

CDS 471471..471830

/gene="crcB_2"

/locus_tag="EFAGFIKM_00434"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00454"

/codon_start=1

/transl_table=11

/product="Putative fluoride ion transporter CrcB"
/translation="MILWIGFAGVLGAVLRYSLGKVVSGLLGTAFPWGTWIINISGSL
LLGLLYGWHQSAMISDGIWVIWGTGFCGAYTTFSTFGYETLGLMSRQRYASGALYVIS
SVVVGVLACLAGVWLTA"

CDS complement(471935..472630)
/locus_tag="EFAGFIKM_00435"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:ISfinder:ISBth8"
/codon_start=1
/transl_table=11
/product="IS3 family transposase ISBth8"
/translation="MMAIHFENREFGYPRMTTALWEAGLNVNHKKVWRIMRELSIQSV
IRKKRKKSSYTPSVIYPNRLKRKIHATAPQQKMVTDITYISDGNSFVYLSVIQDLFNN
EIVAWQLSKRNDVQLVLDTVEQWTQKRDVSEAVLHSDQGFQYTSQAYNTRLEAFGVKG
SHSRKATCLDNACIESFFSHLKTEKLYLNQCNSEAEIRQAVEDYMYNYNYRRFQAKLK
QRAPIEYRCALAA"

CDS complement(472795..473139)
/locus_tag="EFAGFIKM_00436"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MILGGDIFMAKKGQTFQTYTEEFKLNAVRSYVEGSSSYKVAER
EGIRNCSQLKVWVKWKNGEAFDERKNSVPNPLKGRPRTAFGSVEEERDYLQAQVDYL
KKRYPNLVKEKR"

CDS complement(473267..474556)
/gene="mnmA"
/locus_tag="EFAGFIKM_00437"
/EC_number="2.8.1.13"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q99TM8"
/codon_start=1

/transl_table=11
/product="tRNA-specific 2-thiouridylase MnmA"
/translation="MLTYLHALWKRKIDDIPKCAPVVDTIQNWPGVSYLESGYARIRN
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FGHCTAEEDSEDVRRVCEQIGIPYYTVNFEKEYFDKVFTYFLDEYKSGRTPNPDVMCN
REIKFGEFLNKALDLGADYVATGHYARLIEEDGTLKLLRGVDNNKDQTYFLNALNQNQ
LSKAMFPIGHLPKPEVRKIAEAAGLYTAKKKDSTGVCFIGERNFKEFLSNYLPKGGD
MVDIATGEVKGRHDGLMYITLGQRQGLGIGGSGNGEPWFVADKNLEKNQLLVQGDH
ASLYSTGLTATGVNWIAGAEHMPNVPYRCTAKFRYRQPDQGVTLTWQVDGSVDVQFDQ
QQKAITPGQAVVFYDGEVCLGGGTIDQVQKVPVPAMQ"

CDS 474713..475132

/gene="cymR"
/locus_tag="EFAGFIKM_00438"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34527"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator CymR"
/translation="MKISTKGRYGLTIMMELAARTGEGPTSLKSIAERNQLSEHYLEQ
LIAPLRNAGLVKSIRGAYGGYILAGDPATVTAGDVIRVLEGPISPVDFTTEEDDPAKRD
LWLRIRDGIAEVL DSTTLKDLITFQDQDKKDSYMFYI"

CDS 475307..476458

/gene="iscS_1"
/locus_tag="EFAGFIKM_00439"
/EC_number="2.8.1.7"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A6B7"
/codon_start=1
/transl_table=11
/product="Cysteine desulfurase IscS"
/db_xref="COG:COG1104"
/translation="MKRIYLDHAAS TPMHPQVAEAMMNVMTGQFGNASSIHAFGREAK"

RTVSGARDVIAASLGCFDELVFTGGGTESDNLAIFGAVVSRQEKGKHVITTAIEHHA
VLHTCQELERQGYEVTYLSVDRHGRINLDELQEAIRPDTVLITMMYANNEVGTIQPIR
EVGELARQHNILFHTDAVQALGSQNISCKELPVDLISFSAHKINGPQGVGALYVRRGI
VLEARAHGGLQERQRRAGTENIAGITGFAEALKIASAQTEVHRQHDLELRKLLLEQLE
IHVGTEHFHVNGHLEHTLPNILNISFPEVSTETMLMNLDMEGIAVASGSACTSGSLEV
SHVLKSMKLPETFLHSAIRFSWGLGNTTEEIMITAEKIGTILGRLRNRP"

CDS 476623..477144

/locus_tag="EFAGFIKM_00440"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLQEMIGLAVFDVEDGKQVGKIQDFIVNDDWEIEGIELENKGL

FTNHVKIVQWQDIVAYGEDAVMIRNQQAVRKTGADDIKYTYLLGRSKLKEMSVLTEEG

LLLGRVSDVYFDQELGNTIIGIEITDGFVSDLIEGRKWLPCTSDMSIGESAIMVPSLS

EQRLENAIHSVNG"

CDS 477149..477364

/locus_tag="EFAGFIKM_00441"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNMKCPNCSSKDIGKIGSHQFYCWGCFIELTVNGEKMSVYQVEE

DGTLSSLDDLFFGDELPQDFPHLHASS"

CDS 477661..478728

/locus_tag="EFAGFIKM_00442"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WFM5"

/codon_start=1

/transl_table=11

/product="Putative transport protein"

/db_xref="COG:COG0628"

/translation="MEQLTKNKLFRYAIWLLLGLIILYFIWLLRPLLLHIYAFLKTVL
APFIVALIISYVLNPIVSM LGGRKVPRTIAVLLIYAFFLTCLGVILMNVIPVLIEQLG
ELNEHMPELSMRAQSLMNNMDHKLMPPSVRTGMNSWFFQMEDRLTQGITVLM DNIGAT
INVLFNVFIVPFLIFYMLKDFEVFERTIVAYLPRSRKAIVSVMKEIDTALGNYIRGQ
FIVCVIVGIFAYIGYIVIDMPYALLLASIVAVFNIVPYLGPFLGAAPAVVMAS TVSFK
MVLLVVIVNTLCQVLESNVISPQVVGRTLHLHPLSIIFALLVGGELAGIVGLILAVPV
FAVLKVIVQHFFAYYIKRRTV"

CDS 479164..481794

/gene="alaS_1"

/locus_tag="EFAGFIKM_00443"

/EC_number="6.1.1.7"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P67011"

/codon_start=1

/transl_table=11

/product="Alanine--tRNA ligase"

/translation="MKASEIRSKWIEFFASKGHKIEPSASLVPHNDPSLLWINAGMAP
LKPYFDGREKPENPRLANSQKCIRTNDIENVGKTRRHHTFFEM LGNFSIGDYFKEETV
TWAWEF LTSKEWIGFDPERLSVTVYPEDEEAFKLWNEKVGLPAERIIKLDENFWDIGE
GPCGPCTEIFYDRGEAYGNDMSDPEMYPGGENERYLEVWNLVFSQFNHNKDGSYTPLP
NKNIDTGAGLERFASILQNVDSNFD TDLFQPMIQR TAALAGVKYND SVEIDVALKVIA
DHIRTVAFAVG DGVLP SNEGRGYVIRRLRRAVRYGKVLGLDRPFLYELTTTVGEVMG
MYYPEVVDKQEFI AKVIKTEEERFHETLTDGLAILADISGTAKSEGRTVISGPEAFKL
YDTYGFPFDLTEDYAAEHGLTV DREGFDASMQKQRELGRAGRQENESMKVQGGPLADL
EVKSEFVG YTDLLTEAKVVAIVAGDALVESVGEGQTCQVLDKTPFYAESGGQVSDQG
LLRGAGVTAKVQGLFKAPLGQH VHLVTVESGELRVGDVINA EVDSAKRGDI IKNHTAT
HLLHKALKDVLGTHVNQAGSLVEPQRLRFDFSHFGSITPEELTEIERQVNEQIWNRLN
VNIELKAIDEAKEMGAMALFGEKYGDIVRVVQVGDYSLELCGGCHVNNTSEIGIFKL V
SESGIGSGVRRIEAVTGRGAYLYVESQLELLKQSAALLKANVADV PKRIEGLNQQ LKE
AARETESLQSKLSAMEAGQLTDQVVQAGNTQLLAARVDAPNMDALRTVADELKVKLPN
AVLVLGAPADGKVN FVAVPAEQVKQGLHAGKIVKEVAAICGGGGGGRPDMAQAGGKD
ATKLDEALKLAVSLVSGHNA"

CDS 482037..482297

/locus_tag="EFAGFIKM_00444"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q836B3"

/note="UPF0297 protein EF_1202"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDSMDKTVKFNVKGDEQEASSKEILLTVYDALVDKEYNPINQIV

GYLISGDPAYIPRHNNARSLVRKKERDELIEELVRSYLANHR"

CDS 482426..482842

/gene="yrrK"

/locus_tag="EFAGFIKM_00445"

/EC_number="3.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34634"

/codon_start=1

/transl_table=11

/product="Putative pre-16S rRNA nuclease"

/db_xref="COG:COG0816"

/translation="MKILGLDYGDRRIGVAASDAFGWTAQGLEVLRERRRDEGEFTRIA

DLVREHEISEIVGLPKNMNGTVGPRGEICIAFADRLRDELNLPVHLWDERLTMAAE

RTLIEADVSRKKRKQVVDKMAASLILQNYLDANSRR"

CDS 482855..483154

/locus_tag="EFAGFIKM_00446"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q97SX0"

/note="UPF0473 protein SP_0194"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAEDQLGMEEAEIIYIADDEGNEEEFEVIMKFEVDGSEAKYMM

VAPVEPEDGETDVYAFRYEEEGDDIKLFVIQDDAEWDIVEETFNTFLAEDEEEAN"

CDS 483155..483469

/locus_tag="EFAGFIKM_00447"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTEYSRKDLKWTDSLRLAFGAHVLEEEENGKSQPYDLLAEFEVN

GQQYAVLRSSLRPYDEVELLRVSPGSEDQIMPELVTIDDDDEWENISELYDECTLPID

ED"

CDS 483546..484586

/gene="mltG_1"

/locus_tag="EFAGFIKM_00448"

/EC_number="4.2.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0A0H2ZLQ1"

/codon_start=1

/transl_table=11

/product="Endolytic murein transglycosylase"

/translation="MKGKAIVVILLIIVLAGGAGGYVWSMIRPVEASTEPVVFEIKS

GSGTSKIADQLQEEGLIRSGLTFKGYLKWKKLGSNFMAGTYSMNPGVTYDEIVSKLSS

GEVVPEEMVKFTIPEGYNVLQMAGKLSYEHVDRDEFIKLANDPSAFDVDIIKDIPVD

EELRYVLEGYLPETYELKKGSSTHDVMQRMLEEFQTKINSIPDLEAKLQEKNLSLHE

LLTIASLVEKEVVVDEERALVAGVIYNRINQDMKLEIDATVQYLLDRPKERLFFKDLK

VKSPYNTYLNKGLPPGPIASPSLPSIEAALNPEASEYLFYVTKKDGSSGHLFAKTYKE

HQQNIAKSKAAQ"

CDS 484601..485530

/gene="rlhA"

/locus_tag="EFAGFIKM_00449"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P76104"

/codon_start=1

/transl_table=11

/product="23S rRNA 5-hydroxycytidine synthase"

/db_xref="COG:COG0826"

/translation="MSKKHELLVTAANVKEAEVLLQAGADALVIGDDRFGMRLPGSFS

VEETAEVVAIAAKHQARVYVSMTNLMSNELLKELPEYVQALGRIGIDGVEFNDPSVLA

TMKEYAPHVKLHWNAEMTSTNYATANYWGTKGASRVVLARELNMDDELTEMVPFLKVEA

QVQVHGMTNIYHRSRLVQSYMAHQGRPVEGHLGKERGLFLIEAERRDEKFPIYEDIN

GTHIMSSERICILEDLHLLMEAGVHSFKIEGMLKSLTYNEAVVRAYRTAIDSYVADAD

AYAFYEEWLAEVRKLQDPERELSFGFFYKEQVY"

CDS 485548..486876

/locus_tag="EFAGFIKM_00450"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="METVAVQRKFSGKRNRLDKPELLAPAGNLEKLKFAIHYGADAVY

IGGQAYGLRSNADNFSFEEMREGVEFAKKYGAKVFVATNIYAHNEDVEGIETYLQNL

NAGISAIIVADPAIEVALRAVPGLEVHLSTQQSTLNWQAVKFWKDEGLPRVVLGRET

SFEEIEEIKANVDIEIEAFIHGAMCSSYSGRCVLSNHFTDRDSNRGGCCQSCRWKYDL

FEDAREDTVWVSEEDMQMKAPAPFKLGENQLPLFQEQDNSFSMSGDKDLCMIGHIPELI

DVGVDSEFKIEGRMKSIHYVATVNVYRQAIDAYMADPENYVLKPEWVEEMNKAANRPL

NTGFFYDTPDHEDHIYEPEEKAVPFDAGLVMGYDAETGMATIQQRNHFKPGQEIEFF

GPGGHFFKQVVGIEIQDEEGNVLDVARHPLQLIKMKVDQPVSYFDMMRKKK"

CDS 487117..489399

/locus_tag="EFAGFIKM_00451"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVQKKQKDSGEQVIKSEQVNPEQVQKVKKEKVGKSKITGNGKKL

LKFDRSKLKLGWIKTDWVKKQFKNRDWKNLGGSSFQQIKKANPVKSVGKFLFIFFAG

IMIFVVSGLLSYSKAKGTIEKNASRANQETIDQTKQKMDIILERFVDTSTQIFFDPE

MQSLLQKMSDQNLTA YDTFINSSSINKQLSNVAFTNKSMEAIYLVPTDDTKSVMGTGS
NSSSMGNIRQEA WYSELIEAGGYRWLPTEVKEDGSTPTFKIARSMKNLQGTTQSYVLV
IELKLEVLEEQLKSLDLGPGAVLQLIAPDNKVVASSISDRTGQDTELA FVKELTEPAG
STNTEY MVDGKSTEMLAVYSTMDTSNWKLVGMIPTSVLVQDAKGILTTLWMLIDAG
IAVLIGIWMVRMIARPLGKLKDLMQEGAKGNLKV RTPYSSQDEIGQLSSAFNLMMEQI
TKLVEQTNRSAQEVLDTASELSSASKKTAVSASEIAVATEEIAGGAGSLATEAERGNE
LTDNISRQM QS VIAANEQMGDSARHVEKSSQTGTQHNLNQLMTKTQKTEEMIGALVNKV
DSLKESTSSVLKVLEVLQNITKQTNILSLNATIEAARAGAAGRGMVVADEV RQLAAQ
SRQSIEMVGEITDKIMTEMNETVDALSAAYPLFKEQMDAVKDTNVIFASVQEQMGAFV
ERLGMVTGSIGDLNKSQGT LSEAMSNVSAVAEESSATSQEVASLSSEQQNISNQLVNL
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CDS 489415..491334

/gene="pbpl"

/locus_tag="EFAGFIKM_00452"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32032"

/codon_start=1

/transl_table=11

/product="Penicillin-binding protein 4B"

/db_xref="COG:COG0768"

/translation="MRKTCPAHGTGFLFVYRIIPSHISNNMVKTTKGEIGMHLLAKRR

IYITCILLTLVFGLLILRLGWVQIVQVNQTMPGSHRTVREMSVLQRERGVMLDPGRGQ

FTDYKGEALTGKLQWGLVLPQASPLEKLRKQGALEGSEMIQLAAILHTDPDQLKKEW

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EQPESSKVLTRHQDEVKQPFAMKSGAAGLERTLEPLL RGIGPTLVSRMVSGGGEIIPD

IQPHVIAPTNSHYPLRVETTDAELQRGLEELTQESGLQEGAIVVLDAANADV RAMIS

RPFYQPQHVDPKQSAWGNRAIQGAVPGSIFKIVTAAA ALEYHAVSNGEEFHCGGEYGR

YGLSCWKEHGHGDLNLEQGFAESCNIVFAETARRLSMEQLENTADRLGLARPIGWEGK

QMAGMPVLRHFDHEDHGRVRTEAVSSADEGAKIQTAIGQRDVLVTP LQAANLIVTLLH

DGKVSSPRLVKRIRYADGGTMLELPLHDSPSASGQIAPATAHKLLSWMNKVVREGTGK

SLQRARWHVAGKSGTAQVQKHGEKRNNQWFIGYGPVEQPQYAVAVLVQNVSPDSQHQA

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CDS complement(491313..492509)

/locus_tag="EFAGFIKM_00453"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0A1W5X0D5"

/codon_start=1

/transl_table=11

/product="Sodium-lithium/proton antiporter"

/translation="MLPLYKKYGRTVFDIALLVLTVYVIMYGFSQLYHVAAPVFLSFI

VYWMIEPLAKFLHRKGLPKTLGAAISVLLFLALIVAAFFGVGLIISQISNLQDNFPV

YIEMIQREFTNLVLFIQDKSDALPDGVM EKANDYFATLTGFLSKWVTSGAQFVVGFLS

SFSSFITNFGIAIILAFFLSIEIESWRKFARAKTPKTLKSAIEFMRNHVFKTIRSYLK

AQMIMMLITFVLIYAGLLILGTSNAFTIAAVCAVFDLVPLLGVPPVVFIPWIVYLFIIIG

NSSLAIGLIVILAVTMLTRQLLEPKISGNSIGVSSAYLMLSFMLISLSIFGLAGVVLS

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HEDSAK"

CDS 492684..494087

/locus_tag="EFAGFIKM_00454"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTTILHSILLWLLYLSSFYAFIPSLISRFFGFRVFRRGRSDTQF

ALTFDGDPDPHYTPRLDLLRQHQAKATFFVVG EHAASHPELIQRIHEEGHLIGIHNY

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SSMFEDWRSRVGAQRLTERMLKELRGGEV MLLHDRGTTLGADAHAEQMLQALEVVLQ

EAERLGLQSVRVDTLMGGITVSESQNKMQ LQTPLKLWKRIVVALWLGWEKLFHWVYHL

RTASPEDPMLHFRSRVYHGARVEMNDGHV IQNGDPVIELHFDNQKLFELGVTSSSMH

LAIRMIRTMEQQLPDLARMVALEPELRS AKAIVGVSMINRGPEKFGFTIQELPPGPFS

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CDS complement(494173..495858)

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/EC_number="4.2.1.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P51785"

/codon_start=1

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/db_xref="COG:COG0129"

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LSLTSVFEGVGAYQAGKIDDKSLLELEQFGCPTCGSCSGMFTANSMNCLAEAMGLAMP
GNGTILAVAPERREFVKQSATQLMELIKMDLKPRDIVTVEAIDNAFALDMAMGGSTNT
VLHTLALAHEAGIEYPIERINEVANRVPHLAKLAPASDLHIEDVHNAGGVSAVLNELL
KKPGAIHGDCITVTGKTIRENVEGKEIQDTNVIHHLDNPHSEKGGGLAVLFGNLAPQGA
IIKVGAVDASVGGYHKGPAICFDSQEQALEGIANGKVKEGHVVVIRYEGPKGGPGMPE
MLAPTSQIVGMGLGAKVGLITDGRFSGASRGISIGHISPEAAEGGPIAFVEEGDIIEI
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CDS complement(496167..496418)

/gene="gsiB_2"

/locus_tag="EFAGFIKM_00456"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P26907"

/codon_start=1

/transl_table=11

/product="Glucose starvation-inducible protein B"

/db_xref="COG:COG3729"

/translation="MARQPTSEHKMSREEAGRLGGKATSKNHDRSFYQMIGKKGGEAT
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CDS complement(496542..497582)

/locus_tag="EFAGFIKM_00457"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
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PHMRLSFFAPYLLLWFLASHFCWRLRLTISWKPIYRLIGSIALGVIAGYLPIDGFW
LSFSRTFVFLPFFVIGYDYGATIRSRLLSGWGRKTAAILSALLWIGYGGLNISSGW
LLGSMTYAELGHHEWYAGIFRLGVYLLEIASAALFLAWVPSLTSRLTDLGRRTLYVFL
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SFNRHEVFKRSA"

CDS 497805..498770

/gene="kdgK_1"
/locus_tag="EFAGFIKM_00458"
/EC_number="2.7.1.45"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P50845"
/codon_start=1
/transl_table=11
/product="2-dehydro-3-deoxygluconokinase"
/db_xref="COG:COG0524"
/translation="MSTSPYPSPEIITFGESMGLLTAKDTRGLEYAATLDKSFGGAES
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KQAGVKVSFDPNLRKLWSADEARPVILRLAELADYFLPGLDEMKNLYNEENDQKVLE
RLSAMKAVCIVKGGPDLTYVLANGTLTEVPYFKADNVLDTVGAGDGFCAGFLSGLLKG
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CDS 498859..499524

/gene="kdgA_1"
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/inference="similar to AA sequence:UniProtKB:P50846"
/codon_start=1

/transl_table=11
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/db_xref="COG:COG0800"
/translation="MKKLQLLQKITDNGVVAVLRADSADQVIAMAEQAIAGGIKVIEI
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KAE"

CDS 499619..500383

/locus_tag="EFAGFIKM_00460"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
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FLASYPDEKGSVKSLGIPALSILGTKDEVVNATKYQSGRMYLPEDTVYYTIEGGNHAQ
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CDS 500448..501215

/gene="gph_1"
/locus_tag="EFAGFIKM_00461"
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/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00495"
/codon_start=1
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/translation="MTMLQVNGVQIPCKGILFDKDGTLLEFLQLWGPWAETLLSQLQA
RMNELGASFTVEREHLVGTIHNAEGHIVGYDPQGPLAIATVDECTGLLAGQLYAAGIP
WNEAITTIRQFSSVAMRSVRERKSAEPMSGLLDLQKCRADIPLAVTSDSTAAAE
HLDWMGIRSFFTSIVGCDRVTQGKPDREAALLACRELHIDPAEAVVIGDSNGDMQMGR"

HAEVSYTLGYCPHLDQGSHLVDAHAIRHYNEISIL"

CDS 501488..502228

/gene="cobB"

/locus_tag="EFAGFIKM_00462"

/EC_number="2.3.1.286"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P66815"

/codon_start=1

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/product="NAD-dependent protein deacetylase"

/db_xref="COG:COG0846"

/translation="MNATEQLAAWIQESSRIVFFGGAGTSTESGIPDFRSAAGLYQTE
QHSPYPPEELLSRHFFDQHADIFYGFYRGKMLHPDAEPNGCHQLLARLEQEGKLQAVI
TQNIDGLHQKAGSSNVFELHGSIHNRNACMDCKQFYTLNDIIQSQDTVPRCTTCGGVIK
PDVVLVEEELDQTTLYRSIDALSSADLLLVGGS�TVYPAAQLITYFQGKHTVLLNAT
PTAYDRRADLLITEPIGEVMNNVDQLLG"

CDS 502307..503314

/gene="gpr_1"

/locus_tag="EFAGFIKM_00463"

/EC_number="1.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q46851"

/codon_start=1

/transl_table=11

/product="L-glyceraldehyde 3-phosphate reductase"

/db_xref="COG:COG0667"

/translation="MVYVASDTRYETMKYNRVGRSGLKLPAILSLGLWHNFGGINNAEN
GRNMITRSFDLGITHFDLANNYGPPAGSAEQLFGQVLAQDLKPYRDELVISTKAGYYM
WPGPYGEWGSRKNLVSSLNQSLKRMGLDYVDIFYSHRYDPETPLEETMMALDHIVRSG
KALYVGISNYPAEQTRQAAEILKGLGTPLLIHQPKYSLLDRWIEDGLQDVLDEYGTGS
IAFCPLAQGVLTNKYLNIGIPEDSRAKGPSVFLNENNISPETLRKVRALNQIAAARGQS
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CDS complement(503395..504369)

/gene="rhaS_1"

/locus_tag="EFAGFIKM_00464"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MSDQSNPKKESLASSNEKIQESPSGKSGALSYSVASNPVYYEQG

ALHVLFAGASQTLPGHALGPKLFDYYLLHYVEKGAGTFRTELHTYELSAGDCFLIHPG

QLVSYQSHARNPWQYRWIAFTGSQAAQHTEEAGFRPEKSVFHAGPSCGISDWLSVMQD

AFAERKESSHFTSLGTYMILAEAQNHLSQGQTLIPGESSIRRTVKQMIQYMSTQYAY

PVSIEQMSASLGYNRAYLSRIFKQETGLSPVTYLLKLRIKSRQLLRERPDLSIEQVS

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CDS 504523..505704

/gene="galK_1"

/locus_tag="EFAGFIKM_00465"

/EC_number="2.7.1.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9R7D7"

/codon_start=1

/transl_table=11

/product="Galactokinase"

/db_xref="COG:COG0153"

/translation="MNVTELKQKFIEKYGESGADIRVFHAPGRVNLIGEHDYNGGYV

LPAALEFGTTLIRERQDNKLQLASTNMSYEGVLDTSSIGKEKTGEWADYPVGVMVEL

QGKGVNVKKGYDFLYHGEIPNGAGLSSSASLEVLTGFAIQSLEGVADIDTVQLALLSQ

KAENEFVGVNCGIMDQFAVANGAQDHAILLMCDTLEYEKVPFRTGAYKLVIGNTNKRR

GLVDSAYNERRSQCEQALAILKEQLPALNYLAQLTPEQFVTLQDQIKDEKVRQRAQHV

VEENARVLASVEALQGNDLETFGKLMNASHESLRDLYEVSCDELDVMVEEAQRIPGTL

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CDS 505706..506695

/gene="galE"

/locus_tag="EFAGFIKM_00466"

/EC_number="5.1.3.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7WTB1"

/codon_start=1

/transl_table=11

/product="UDP-glucose 4-epimerase"

/db_xref="COG:COG1087"

/translation="MAILVTGGAGYIGSHTVAALLERGEEVVLDNLQTGHEREALLGG

KLYEGDLRDKEILAKLFAENSIDAVIHFAANSLVGESMKDPVKYYDNNVFGTLCLEA

MNAANVRRIVFSSTAATYGEPEKVPIEESDRTEPTNVYGETKLMMERMMSWFDKVQDI

KYVSLRYFNAAGAHDSGKIGEDHQPESHLIPLVLQTALKQRPHIAVFGDDYATEDGTC

IRDYIHVSDLADAHLRVDYLRKGENSENVFNLGNGTGFSVKQVIETAKKVTGLDIPVV

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CDS 506710..508308

/gene="galT"

/locus_tag="EFAGFIKM_00467"

/EC_number="2.7.7.12"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:E8MF11"

/codon_start=1

/transl_table=11

/product="Galactose-1-phosphate uridylyltransferase"

/translation="MSQTHIAAGATERTPEQQEALHAIERLVAFALQKQLIEADWDY

SRNLLLEQFGFSEPYAGELDTNVPDGPQAMLDTLIDYGFSIGLIPENSDFRDLDAK

IMGHLMARPSEVVRAFRHTEQTEGIEAATSQFYDLSINSNYIRMDRISKNVYWTQDTA

YGDMEITINLSKPEKSPKEIAMAKLLPPPVYPKCQLCRENVGYAGRVNHPARQNLRFI

PLELNNEPWLFQYSPYVYYNEHCIIFFHHDHVPKLTKDTLRLLAFVGEYPHYFIGSN

ADLPVGGSSILTHDHFQGGRRHTFAIQNAQPEAVFRHADAPGLTSLVKWPMSVMRLAS

HDPAELLEAGNAVYEAWKVYSDSTVDIEAFSEVDGEQVPHNTVTPIVRRSADGGYEMD
LVLRRNNRTNDVHPEGIFHPHREMHHLKKENIGLIEVMGLAILPGRLEELDSIADILA
GDAKLAEAAKASDHVLNKHHLGWAEELIERFGPKLDKEQAVAIVQQEVGLKFAEILEHA
GVYKYDEAGRQAFRRFVSSMGYTE"

CDS 508464..509036

/locus_tag="EFAGFIKM_00468"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNIPLITDAEELQGMVGEPHEHVRNKAISFVDSHVQNFISMSP

FFLSTSDRDGKSDVSPRGDGAGFVKVYDYLRLVYPERPGNRRIDSLNMLSNPGIGML

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LWASETWVDAEDLPSTSEMFRHLEINGLL"

CDS 509130..510293

/gene="adh2_1"

/locus_tag="EFAGFIKM_00469"

/EC_number="1.1.1.192"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A4ISB9"

/codon_start=1

/transl_table=11

/product="Long-chain-alcohol dehydrogenase 2"

/db_xref="COG:COG1979"

/translation="MRSFQFYNPTRLIFGKGQLEALKTEVPKYGKRVLLVYGGGSIKR

SGLYNQVIGLLKETGAEVTELAGVEPNPRLSTVHKGVLDLCKTNNIDLILAVGGGSVLD

CSKAIAVGAKYDGMWDFQAQRKAVAQDALPLGTVLTMAATGSEMNSGSVITNQDTQEK

LGWGSAYSFPFSILDVNTYTVPLDQTVYGMVDMMSHVLEHYFHLDPVQLGFCE

TILRTVMEAAPRLVEDLENYELREILYCGTMALNGVLNMGLAGDWATHNIEHAVSAV

YDIPHGGGLAILFPHWMKHNLVDVNVDRFKRLAINVFEVSPEGKSDRQIAEEGIDALSK

FWTSIGAPNRLADYDIDDSQIDVMADKAMLFPGFGNFKKLQREDVVSIIKASL"

CDS 510573..511088

/gene="yuaF"
/locus_tag="EFAGFIKM_00470"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32077"
/codon_start=1
/transl_table=11
/product="putative membrane protein YuaF"
/translation="METIYWGCLIGGAIFAVVSLVLGDLIDGLLDGAFELPGLDFFKP
VVLGASITTFGGAGIMLTRYSSLSAMSGLILSLLIGIAAAMLVFFAYIKPMRNSDVSI
AFSMKELSGKIGEITIPVPEKGFGEVMIRFASGSTIQTASSFEHLPIAAGARVVVDV
VDGVLRVSEWD"

CDS 511188..512738

/gene="yqiK"
/locus_tag="EFAGFIKM_00471"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P77306"
/codon_start=1
/transl_table=11
/product="Inner membrane protein YqiK"
/db_xref="COG:COG2268"
/translation="MENLDWDVLLIPIVVGVILILGLAFWARYKTVGPDEAMIVTGS
FLGSKNISDDDDSGRKIKIVRGGGAFILPIFQQSEFISLLSHKLDVSTPEVYTEQGVPV
IADGVAIKVGGAVEDVATAAEQFIGKPVEALRSEAQEVLEGHLRAILGTMTVEEVYR
NRDRFAQEVQGVAARDLKKMGLQIVSFTIKDVRDKQGYLDALGKPRIAAVKRDAEIAE
AEAMRDARIQKANAEEQGQKAELLRDTNIAEAAKEKELKVATFKRDQDTAKAEADQAY
HIHEARARQTVVEEEMKVELVRKEREIDLQEKEIVVREKQYDAEVKKKAEADRYAVEQ
AAEADKAKRMREADAVQYSIETHAKATAEQKRLEGQAMADAELAKGTADAEVIRLRGL
AEAEAKEKLAEAFQKFGEAAVLDIIVKMLPELAGKIAEPIASIDKLTVVDTGKGEGAA
RVSNYVTELMATAPEMLKSVSGIDVEQLIKGLTKSKTPAPVAIQQSEAATTPSIIDKI
VERAGVDE"

CDS 512904..513758

/gene="glcT"

/locus_tag="EFAGFIKM_00472"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31691"
/codon_start=1
/transl_table=11
/product="PtsGHI operon antiterminator"
/db_xref="COG:COG3711"
/translation="MSSLHVDKALNNNVIIAQHPEHGEVVIGKGIGFNRKPSDHIPL
MAVEKMFILKNQEQEQYKQLLPQVDEALIEIINEVITYIAERTDVPLNEHIHIALTD
HISFALKRKEQGIIQNPFLYETREIYPPEYRMGEYAVRLIKEKMGVDLGMDEIGFVA
LHIYSAMTNQNISQVREHSQILITDLVNLVSDQLDYSFETESLDYSRLLTHLRFALERV
RRGDKVEELHKLDSLLKLEYPEMYSLAWKLTVMKRLKLPVYPAEVGYLTIHLQRLN
QRKEEENK"

CDS 514046..516097

/gene="ptsG"
/locus_tag="EFAGFIKM_00473"
/EC_number="2.7.1.199"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P20166"
/codon_start=1
/transl_table=11
/product="PTS system glucose-specific EIICBA component"
/db_xref="COG:COG1263"
/translation="MFKKLFGVLQRVGKALMLPVAILPAAGLLLIGNMLVNPDLQY
VTALDTPWVNSIATIMMAGQIVFDNLALLFAVGVAVGLAGGEGVAGLAAIIGYLMN
VTLGTAVGVTPAMIGEVPGYASILGIPTLSTGVFGGIIIGIAAALCYNRFFKIELPSY
LGFFAGKRFVPIITSVVSLLIGLLLVIWPPIQNGLNTVSHFMVDTSPTLSAFIFGVV
ERSLIPFGLHHIFYSPFWFEFGEYVKNAGDVIRGDQQIFFNQLRDGVNLTAGTFQVGK
FPFMMFGLPAAALAMYHEARPEHKKYVAGIMGSAALTSFLTGITEPLEFSFLFVAPIL
FAVHCIFAGLSFMTMQILGVKIGMTFSGGFIDFLIFGIIPNRTPWWDVIIIVGLILAVI
YYFGFRFIIRKFNKTPGREDATPETESGGGSGSTDDLPHNILEAFGGKENIKHLDAC
ITRLRIEVNEKSNVKKDRLKQLGASGVLEVGNNVQAIFGTRSDTIKSQMQDIAGRTP"

APTPAAAKPTPEEEKAQGEQGERIVAEDIVMPVNGELLDITNVPDPVFAEKMTGDGFA
ILPHDGTITSPVYGKVFNVFPSKHAVGIMSDGGKEVLVHIGVNTVKLKGQGFFNVLVQE
GDLVSAGQPIMEVDLEYVKANAPSIISPVIFTNLPEGSTVTLKKSGVLKVGEQPIIEI
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CDS 516112..516450

/locus_tag="EFAGFIKM_00474"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MASKCKYMQCLNQTTSEMIVMQQTFRITDEDGIHARPATALVN

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VNEGLGEINA"

CDS 516443..518155

/gene="ptsI_1"

/locus_tag="EFAGFIKM_00475"

/EC_number="2.7.3.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P08838"

/codon_start=1

/transl_table=11

/product="Phosphoenolpyruvate-protein phosphotransferase"

/db_xref="COG:COG1080"

/translation="MLNVSGIAASAGIAIAKAFIEHPDYSVEKRQINDVDAEIAKLD

SALGKSQAELEAIKERTLQELGEKKAEIFASHLLILNDPELIDPVKARIADDMINAEF

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EDLTPSDTAQLNRQFVKGFATNIGGRTSHSAIMARSLEIPAVVGTKDILAQAKQGDMI

IVDGLDGHVLVNPTDEVIAEYRAKQEYDAQRAEWRKLRDEPTVTVDNVHVELAANIG

TPNDVTGVLENGGEAVGLYRTEFLYMGRDKLPSEDIQYNAYKAVLEKMEGKPVVVRTL

DIGGDKELPYLDLPKEMNPFLGFRAVRLCLDRLDIFRTQLRALLRASVHGNLRVMFPM

IATLGEFREAKAVLLEEKEKLVAEGIAVSDSIQLGIMVEIPSTAVLADQFAKEVDFFS

IGTNDLIQYTMAADRMNERVAYLYQYPNPAILRLVKMVIDAAHREGKWVGMCGEMAGD

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CDS complement(518398..519978)

/gene="gcvPB"

/locus_tag="EFAGFIKM_00476"

/EC_number="1.4.4.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P99168"

/codon_start=1

/transl_table=11

/product="putative glycine dehydrogenase (decarboxylating)

subunit 2"

/translation="MTQDTTTTTTSVQQQSVTGTSVSTSVQPETDTTFSQTLSPAP

EQSLIFELSSPGRVAYSLPECDVPRQSADTLIPREMLRSEAAALPEVFEVDVIRHYTA

LSRRNFGVDNGFYPLGSCTMKYNPKINEDVARYNGFAKHPYQHESIQGALELLYTL

QNDLAGLTGMDAVTLQPAAGAHGEWTGLMMIRAYHEGRGEKRTKVIVPDSSHGTNPAS

ATVAGFETVTIPSRADGLVDLDALRAAVGSDTAALMLTNPNTLGLFEKDIQEIASIVH

QAGGLLYYDGANSNAIMGITRPGDMGFDVVHLNLHKTMTSTPHGGGGPGAGPVGVKNRL

IPFLPKPMVIKNDDGMYAFDREGDQSIGRVKAYYGNFGILVRAYAYIRTYGPEGLRRV

SECAVLNANYMMARLAPYYEIPYPGVCKHEFVMSGRGLKQYGVRTLDAKRLLDFGYH

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RLDETTAARKPVLNCACS"

CDS complement(519975..521330)

/gene="gcvPA"

/locus_tag="EFAGFIKM_00477"

/EC_number="1.4.4.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P64218"

/codon_start=1

/transl_table=11

/product="putative glycine dehydrogenase (decarboxylating)

subunit 1"

/translation="MSKHRYIPMTEQDQSAMLATIGVDTLEDLFQDIPKEIRYQGELP
VSSKLDEYALTRHMSKQAGANANFETHASFLGAGIYDHHVPSVINHVISRSEFYTAYT
PYQPEISQGELQAIFFQSYICELTGMAVANASMYDGATAFAEAGNLAAAATRRKQLI
VSRTVHPEARQVLQAYAHGLSLEIVEIGYKDGVTDWALQAAISDDTAAVMIQSPNFF
GAVENVKQAADLVHAHKGLLVVSANPLSLGLEAPGKLGADIVVGDAQPLGIAASLGG
PTCGYFAVSQPHMRRIPGRIVGQTTDRNGKRGFVLTQAREQHIRREKATSNICSNQA
LLALSASVYMSIMGKQGMIDVADLNLQKSHYTLNLTAI PGVSLTFNAPTFNEFVIKL
PEGTDVDTLQLKLLDAGFIGGYELGRDYPELAGQMLIAVTERRTKEEIDEFARALEGS
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CDS complement(521327..522463)

/gene="gcvT"

/locus_tag="EFAGFIKM_00478"

/EC_number="2.1.2.10"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54378"

/codon_start=1

/transl_table=11

/product="Aminomethyltransferase"

/db_xref="COG:COG0404"

/translation="MSDLLRTPLFPLYQQYEGVRCIDFGGWELPVQFSGIQKEHEAVR
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VYKLEDQHYMLVNVNASNIDKDWAWLQEHLPVGSMTNDSEQTALLALQGPLAVDIIRK
VTDTDVSSIEPFRFVQDAEVCVGLLLSRTGYTGEDGFELYVPADQAAVWVWGLMQAG
DGHGLVPTGLGARDTLRFEAKLPLYGQELSATISPLEAGVGMFVKLNAGPFIGHEALL
QQKTDGLARKLVGIEVLERGIPRPHYPYIAEGVQIGEVTTGTQSPTLKRNLGLALIDS
KYAALGTPLEIEIRGKKLKAEEVVKTPFHKRTRTSKTPTQGADQA"

CDS 523251..523643

/gene="gcvH"

/locus_tag="EFAGFIKM_00479"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0QYG3"

/codon_start=1

/transl_table=11
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/db_xref="COG:COG0509"
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CDS 524063..525517

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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P50852"
/codon_start=1
/transl_table=11
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/translation="MSNLDQSSNSKGGLRVGVQRFGRFLSGMVMMPNMGAFIAWGLITA
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GQSVLYMLESNPGPGLGILLAYCFFGRGMAKSSAPGAVIIHFFGGIHEIYFPYILMRP
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SFLVAHVLLKTGKQKDEDLESASSRMKDMKSQGTVPNAGITANQHEADRAPDMASSTV
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CDS 525556..527658

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/codon_start=1
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/translation="MSITKRQREIVEFLLEHPHEVTAGEIAVEVKVSTRTVHRELQMI"

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CDS 527655..528089

/gene="mtlF"

/locus_tag="EFAGFIKM_00482"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0H3V2"

/codon_start=1

/transl_table=11

/product="Mannitol-specific phosphotransferase enzyme IIA
component"

/db_xref="COG:COG2213"

/translation="MSMLTTDKVIMNATAQDKYEAIRMAGQILKDAGHITADYIEKMI
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CDS 528086..529231

/gene="mtlD_1"

/locus_tag="EFAGFIKM_00483"

/EC_number="1.1.1.17"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P09424"

/codon_start=1

/transl_table=11
/product="Mannitol-1-phosphate 5-dehydrogenase"
/db_xref="COG:COG0246"
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RIVPIQHHEDPLHVQVEPFYEWVDRSQMAPAFKPVEGIVYVDDLEPYIERKLFTVNT
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CDS 529374..529691

/locus_tag="EFAGFIKM_00484"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
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CDS 529640..530524

/locus_tag="EFAGFIKM_00485"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:ISfinder:ISBth8"
/codon_start=1
/transl_table=11
/product="IS3 family transposase ISBth8"
/translation="MLGNLEGGSKQERFQIIKVAAYGDIQKLCDVFGVSRSGFYAYV
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SRIRRKRRSNSSYAPAQRVAENRLKRDFSQEPNQKVVTDITQYRVGERWIYLSAID
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CDS complement(530565..530816)

/locus_tag="EFAGFIKM_00486"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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CDS complement(530955..532958)

/gene="mutS2_1"

/locus_tag="EFAGFIKM_00487"

/EC_number="3.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00092"

/codon_start=1

/transl_table=11

/product="Endonuclease MutS2"

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IGILEQADTSTLVLIDEMASGTDPEGVGLSIAMLEELHSRGATVVATTHFGEIKHFA
AATPGFENARMEFDTVSLQPLYRLRIGEAGESYAYSIALKLGMPQRIERSKSLSDQS
ISRDRTLGFTSPPLETPVLT PDRSVAEADGPAELSKRNQSKQSKYSIGLHKNTTPRES
APPAPAKNFRKGDRVYVAYLNQSGIVCDVEDSRGNIGVMLRGRKVKIHKRRLTLHISA
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CDS 533487..535823

/gene="yesS_3"

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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31522"
/codon_start=1
/transl_table=11
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AVSYRQSPLNGWLYVSVVSLGQITAQSQKIALVTGIATLVMLCVTGLFAIYGSRRMYS
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VSGISRSYACIGDTPRAVQESREALQGRVSLGSRIILHYEDIQPRGQMEAALYTQLR
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CDS 536106..537059

/gene="yteP_3"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:C0SPB3"
/codon_start=1
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permease YteP"
/db_xref="COG:COG4209"
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FFPLPIVLALMMNEVRRERFKRFVQTLVYVPHFVSWVVVGVFYMLFTTEGGAINELL
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RWRQTWHTLPAIRSTIVILLILRLGNFLDTGFQIFLMLTPTNRDVGEVFDYVYTK
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CDS 537105..537977

/gene="araQ_3"

/locus_tag="EFAGFIKM_00490"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

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KHFAKGVMLGSVKG"

CDS 538040..539539

/gene="lipO_2"

/locus_tag="EFAGFIKM_00491"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37966"

/codon_start=1

/transl_table=11

/product="Lipoprotein LipO"

/db_xref="COG:COG1653"

/translation="MKATKKKAVAVLSTLALVTGLLAGCGSDEGQAAEGGVQNVSAI

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KDWFEKLNKVPATPNEWYETIKLATSDPDGDGQDNTFGLMLFKKYNEQYSFTTRL
GVSGFAPNKWKVEDDGSFTPEFMTPEYMQVLDLLKRLYDEKLLNQDFAVFDSTAEKK
YDSGVVGIRVGVAQNGKSQQRLSKNNPDGVVDIAGLLGANGDRVAGQTGNSGILAFP
KSTVKSEEELKNLLSFLDKLMDPEMATLLMRGMEDKHYTEKVGEDQVEMSDFAFQREV
KPYRDNLPHYVEGYNVPKLDTELGEKGTALAKELAEHAVPNPALTLYSPTYGDRGADL
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CDS 539564..540667

/gene="yteR_1"

/locus_tag="EFAGFIKM_00492"

/EC_number="3.2.1.172"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34559"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG4225"

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AALQLLLVEQRTDPRSGLLYHAWDESKEQRWSSGETGCSPHVWSRAMGWYVMAVVD
LDYLPVDHPQRGQIVGIFERVANALVHVQDQQTGLWPHLLDQPGRERNYLEASGTSMF
VYALAKGVRKGYLSGKFAVAEKGYQGLVQHLLQTDREGVLSLTQCNGGAGLGGSPYR
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CDS 540776..542287

/gene="lipO_3"

/locus_tag="EFAGFIKM_00493"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37966"

/codon_start=1

/transl_table=11

/product="Lipoprotein LipO"

/db_xref="COG:COG1653"

/translation="MSPKGPMSRLGGIVVIGAMSAGLLAGCGGEKAPAAGEGKLPISI
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YRKDWFDTLKLDIPKTLDDWYEVMSIRKDDPDGNGKEDTYGALLFKKYNEGVSSPLT
RIAVSIGGVNKGWVDDAGKLTPEFLTTEYVDTMKLFRKFSEGLINSDFPALDPSDAD
KKMDSGLVGMKLNQVAQNGKSSQRLTPNAPDGEIDVAPFQGTGIRIAGEPGNYGML
VIPKASVTDEEQLKQVLTFLDQLMDEELSALQLRGLLDVHYTKTADGKTELKDFDAYQ
REVKPYRDNLLSIEGYNVPELVDVPIGMKGTKMARENEQYAIANPALTSSAIYTERG
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CDS 542635..543903

/locus_tag="EFAGFIKM_00494"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKPIKGHEKKEKRNWVWVGLLTAVLAGTLLPVGPVHLTSTAN
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RATGLEKVEGQNPFFADLKGHWSEAAVSQLVGQGFINAGDYAKGFNPNAELTRYEMMKW
IANGLIKSGASFQDAFNDTKNTLLPTPEVNRGTIRAEQIPYLALVRGTGIVGGFQDGT
LKPADSTTRAEVSAILLRYMDVEGTDAGKYSDLNEMREVGTTGTNLTTVSNYKYIKGN
FGDIVNTEYTLKNNVGVRVYHRFIVDTRGTPKPKGLYATLFVDQNNLTRAQKGRFSTY
AEITFTSKLDKSNLLTIARANDNIAIPIQRLFNVSYLKEKGFITLPDDSNAMLKQGV
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CDS 543912..547595

/locus_tag="EFAGFIKM_00495"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS 547767..549815

/gene="pula"

/locus_tag="EFAGFIKM_00496"

/EC_number="3.2.1.41"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O33840"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG1523"

/translation="MIEEDKQELLISEDYKGRDLGVTLEAQTCHFVWSPLAVQMEL

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NAVDPYARAVTMNGEMGVIVRLEQTHPNGWSEDIRPELTSPVDAVLYELHVRDFSIQP

SSGITNKGKYMFAFTETGLRDSEGNLTGIDHLVELGITHVHLMVPVDFATVDESKVDGD
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HTFDTAGSSFEKLVPGYYRQNADGTYSNGSGTGNEVATERTMVRKFIIESVRYWAE
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ILENETVRRSLLANGIVLTSQGVPLIAAGDELLRSKYGDANSHQSGDVVNAIHWEQKK
LFKPIFDYYRGLIRLRREHPAFRLRTREEIENHVCLIEKGNGLLAYELNGTAASDWE
RIVVIYNAAKENRDISVPTGTWNVIVEKGQAGIDTIRTIQDGQVHVNAISLTMYSNS
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CDS 549969..550187

/locus_tag="EFAGFIKM_00497"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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NFFCQDRYKCCQSMALVFISYILKAIAN"

CDS 550303..553179

/gene="glgX"

/locus_tag="EFAGFIKM_00498"

/EC_number="3.2.1.196"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01248"

/codon_start=1

/transl_table=11

/product="Glycogen debranching enzyme"

/translation="MPEWTSFCYEGNDLGLTYTRAASTFKLWAPTAQQVYILIFDDEG

HYND SGKVQE HENGQEHTLKC DADGIWSLKLSGDWTGHYYMYRIIHDDQRIE VVDPY

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RGEASITVHCGDITASCM LQVDYRHAERIEIVGEPV MYMTRISRFRALVLDQFGQPLQ
DSNIRWSSSHPELA AVSAAGIVRAMTPGVTHIIAEAGGIRATLGVTIHKQISRTVTLR
YEREDQHYEGWDV VVWGTGMEDGAVRLEQVGNAAEARFRVAPGLHHLGLIIRLNEWEA
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CDS 553460..554089

/gene="rplY"

/locus_tag="EFAGFIKM_00499"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A7B3"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L25"

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CDS complement(554545..556317)

/locus_tag="EFAGFIKM_00500"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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GIWTESREVPRYNLNNEEIEYSDVITMYRNFKVSDDTRGVIVLNIKREYIERRLNDLAT
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LGAAEQGKPLPLHRTKGNSVYSQIIRSLQNFIEHNYMRVQLSESQYKTQAAQFAALQ
SQLNPHFLYNTLETIHWKAAGYTEGPNELTSIVEHLSDILRYSLDGQNGLVPLNVEIA
NTKSYIAIQKTRYGERFDIWWWEYDAELEKYQVLKLIFQPLIENSLQHGLSRSDQKLAV
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CDS complement(556321..557061)

/locus_tag="EFAGFIKM_00501"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5HJF7"

/codon_start=1

/transl_table=11

/product="putative response regulatory protein"

/db_xref="COG:COG4753"

/translation="MYNLLITDDESEIRNGLSNYFPWHEFGFQVVGQACDGEGALAFI

QEQPVDVLLCDIRMPSLSGIDVAERLYRQGSEVKVLLSGFKEFEYAQLAVQYGVKRY

LTKPTKYTEIAEVFGHLRSEMDNARMPPHSASTAESSLADQTIEKVKAYLQDNLSA

ATLENAAKHVFLNPFYLSKYFKTKGENFSDYVTKLRMHRAAELLKTTYCKTYEISEI

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CDS 557444..558442

/gene="oppD_1"

/locus_tag="EFAGFIKM_00502"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P24136"

/codon_start=1

/transl_table=11

/product="Oligopeptide transport ATP-binding protein OppD"

/db_xref="COG:COG0444"

/translation="MLLELKDVRTVFKTEKGEVTSVDRVSLKLEKGETIGIVGESGCG

KSVTSLSIMRLLGKNGSIREGEIWFMDKDLAKLPESELRLIRGGDIAMIFQEPMTSLN
PVFTIGNQLTEAIRLHTDLRGKAAEGYAVEMLEKVGIPRPEAIMKSYPHSLSGGMQR
VMIAMALSCKPKLLIADEPTTALDVTIQAQILNLMKELREEMGASIMLITHDLGVVAE
MADKVVVMYAGQVVEETDVFTLFKPLHPYTKGLMRSIPHIETDAEEMLASIPGAVPP
LTNMPKGCRFHTRCEFAEGKCLSEAPTLLPVQEGHQVRCWMAQDPDAWKTRREEAI"

CDS 558439..559437

/gene="btuD_2"

/locus_tag="EFAGFIKM_00503"

/EC_number="7.6.2.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01005"

/codon_start=1

/transl_table=11

/product="Vitamin B12 import ATP-binding protein BtuD"

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LELYQGETLGLVGESGCGKSTIGRSIIRLENPTDGRWIFEGQEITTSTMSDLRGERTK

MQMIFQDPYSSLNPRMRVQELLAEPMRVHGLAGGAELARIDNLLDTVGIPRSYKQRF

PHEFSGGQRQRIGIARALSLNPKLIVCDEPVSAIDVSIQAQILNLLKELQRELGLTYL

FIAHGLGAVKYISTRIAVMYLGKVVEIGTKERIFASPRHPYTQALLNAYPVPDPRKRG

QERIVLQGDVPSPASPPSGCRFHTRCPFVQAKCKEEEPQLQGGEHAAACHYPLTTG"

CDS 559460..560410

/gene="gsiC_2"

/locus_tag="EFAGFIKM_00504"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P75798"

/codon_start=1

/transl_table=11

/product="Glutathione transport system permease protein

GsiC"

/db_xref="COG:COG0601"

/translation="MFTYVIRRILIAIPVLFGITIINFFIINLAPGNPIDMYMTPDTP

PELLELRKEQLGLNDPTIIQYFKWLGQLLSGNLGYFSFSTSESVSLIGERLGQTVLLG

ICALIIGLLIALPIGIMSAVRQNSKFDYLMTGLSFVGT SIPQFFLGLLCIYIFAVQLG
WLPVGGTEDLGGGGGFGDRISHLVLP SIAMAVGIAGRKVRYIRASMLDV LKQDYLR TA
RAKGLKEFFVTNKHALRNALIPIITVVGMEIPMLFGGAVIVEQLFQWPGIGQLTIQSI
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CDS 560463..561362

/gene="gsiD_2"

/locus_tag="EFAGFIKM_00505"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P75799"

/codon_start=1

/transl_table=11

/product="Glutathione transport system permease protein

GsiD"

/db_xref="COG:COG1173"

/translation="MSAVQTPVAGGVILPIQQEEPEGVFRQMARRFLKHLAVAGLVV

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WTLVLVLALFSWPSIARLVRGSVLTLKQMDYIKAGVALGLSTPRIVFRHILPNALAPI

IVNATFGVAAAIMAESGLSFLGMGVQPPTASWGNMLTDAQSISVMTDQPWLWLPPGIM

ILVTVLAINFVG DGLRDALDPKQ"

CDS 561421..563070

/gene="appA_1"

/locus_tag="EFAGFIKM_00506"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42061"

/codon_start=1

/transl_table=11

/product="Oligopeptide-binding protein AppA"

/translation="MKRMRKAWICGVL TLLMVLVTACGSNSDSNTTSSPGSDGESASA

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EGQTELAFFEKVDDYTFVIKTKNPMETNQFKSQFGTYFRFLPEHVLKDVAPVDLNKNE

FMMNPTVTNGAYKFVKFAKDQYVQLTASEQYYEGAPKIKDIYIKMMPATNLAAQLQTG
DIQLTSPGVGLIPVQDFDKVANMANVTTGYGDANNPNLMFINTKKFPDPKVRQAIAYA
MNRQLIVDQLLKGGQGELVDGMLGQNHPPYNNKDIPLYGYDPEKAKALLEGAGWDFNQTI
EFVVPTGNKIREQASDIIAENLKAVGLKVQVTKLDFPTTYQRALKHDYDLTIINLGF
LDPNSVLGLFKTGVSFNIADYSSTEVEDELLVQGAEELEPSKRFEIYKQVQQMLHDDVP
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CDS 563110..564093

/gene="oppF_1"

/locus_tag="EFAGFIKM_00507"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P24137"

/codon_start=1

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/db_xref="COG:COG4608"

/translation="MRGLKKERPPLLSVESLKTYPIRQGIFSQVTEYVKAVDGVSFS
IREGETLGLVGESGCGKSSVGRLLQLETPYEGRILYAGRELAELGKRELRRTRASLG
LIFQDPYSSLNPRMRIGDILAEPLLAHRLESRSSVWNRVDMLETVGISIEDKSRYPY
EFSGGQRQRIGIARALSLNPKLIVCDEPVSAIDVSIQAQILNLLKKLQKENGLAYLFI
GHGLGAVRYISDRIAVMYLGKIVEIASREKLFRAPKHPYTNALLSANPVTDPKLRSQK
RIIIQGDVPNPVRPPGGCRFHTRCPIAKAICREFEPALKGHDHAVACFAFD"

CDS 564180..565658

/gene="abgB_1"

/locus_tag="EFAGFIKM_00508"

/EC_number="3.5.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P76052"

/codon_start=1

/transl_table=11

/product="p-aminobenzoyl-glutamate hydrolase subunit B"

/db_xref="COG:COG1473"

/translation="MNEKIIIEVTTYIEGKRDLFIDVSDSIWGFATRFEEFESADLL

CKALEQEGFSVERGVAGLATGFIGSFGDGSPVAILGEFDALASLSQQAGAAVFDPVV
PGANGHGCCHNLLGAGSLAAFAVKDYLQEHGISGTVRYYGCPAEESGSGKAFMARAG
LFKDVDIAFCWHPATMNVVMHMSSLANLHVHFKFAGRSAHAAAAPHLGRSALDAVELM
NVGVNYLREHMISDARIHYAVTNTGGFAPNVVQAEAEVNYLVRAPKSSQVAELFERVL
DVARGAALMTGTKMSYHYEGGASNLPNATLEGKMHEFLSGLELPVYTEDELAFAQEI
FDVIPEEDKTSASRQNGKGVHDMLSAHPLAGFVAPLMETMRVMPASTDVGDVSWNVPT
AQCGTATWAYATPVHAWQTVAQGKSGYAHKGMMLLAGKAMACTAIAALLDPALIEKAKE
ELAERLEGESYVSPFPDEVMPNLSFSQSTGGAANEQTPVNM"

CDS 566301..566819

/locus_tag="EFAGFIKM_00509"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFDPTVYDNLKVGFEFENLYDMDNLDERIQITGRKDRLEMAVMSR

EFMLQFCLRDLPEVTGEVVLSSSLEELAAEILETPGASPGCRLELRFSMVVKDPEKQC

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ANVMNQLLQLHN"

CDS 567095..568066

/locus_tag="EFAGFIKM_00510"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTEKLIRLLRILQAIQANPGISAKELALKCGTTVRTIYRDLRIL

DRVAPIMNEGYGKGYRFIGEFAMYPLDFTEQEAMVFSLLPSVVDTSKLPAEFDSAFDK

VMSAHTKLKSRNSDIVENIAGIIRMGTPAYREEGKDPNLLIPIIEAILSQQTIRTQYH

TLTRNEITVRDIDPYLIPRDQRFYLIGYCHLLQKVRLFRISRFLDVTRTNAGFDKGD

FNITQYMKNTWSIDRGDENIHFVRFSEKVAPYIKEEEMFVRPRMTNMSDGGLLFEVT

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CDS 568109..568471

/locus_tag="EFAGFIKM_00511"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSTKLFAAMYGMDHYHGVQALHVGDTVYLVKDPDNRLDHQAIKV
VIPPIGAVGYIVNDPLVVP HGCWTGTAFYDV FHLTC AKVRFMMRDMVIMELIEMSHI
PVPQMDSL IKGWQFREKA"

CDS complement(568493..569596)

/gene="cotSA"
/locus_tag="EFAGFIKM_00512"
/EC_number="2.4.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P46915"
/codon_start=1
/transl_table=11
/product="Spore coat protein SA"
/db_xref="COG:COG0438"
/translation="MKIAMVAPEKLPLPGNGSVEICILG IARELAQRHQVTIISRQMQ
GLPATEQIDGITIQRPASSPV MYTKAVIRLLSQQPYDVIQVDNRPRSMATIKRAFPR
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DLSRFRPVESSEEQIHLRTQFGVTKPFSILYVGR LIPGKGVDVLIRATALLQQQVPVQ
LVVAGKGPPYYMRKLRELAQKQKVHVSFRGQINHEHIDQLYRAVDCLVCPSQEHEAFG
LVNVEAMASGLPVIASDNGGIREIIESGINGYLV TAYKRPQRFTSYLYKLASNSTFAE
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CDS 569812..570123

/locus_tag="EFAGFIKM_00513"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLHSTLGRFRLMLWLQGISYVLLL FVAFPLRDAGVMPQAVTWFG
NLYGFLFLMYLLFMVTMYTSQKWRLRRPIALFFV SFIPLGNMIYDVV VFRKLYRQLNK"

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CDS 570398..571219

/locus_tag="EFAGFIKM_00514"

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/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLDVSLLEYGWVLAVLVVLEGLLAADNALVLAIMVKHLPEDKR
KKALFYGLMGAFVFRLGSLFLISFLVDVWQVQAIGALYLLYISINHIVKKILGSRNKT
DEAADSTPKPKKQSSFWMTVFKVEVADIAFAVDSILA AVALAVALPPSGLPPIGGLD
GGQFIVIFLGGFIGLVIMRFAASYFVKLLHSRPGLEVA AFVIVGWVGKLA VITLAHP
SLGVLDEHFPENKIWKFGFYIVLITIAVCGWFLSSKVPEKEDENPV EEEKQAGL"

CDS 571402..571497

/locus_tag="EFAGFIKM_00515"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMLGYDLIQ TGRNVDTIAYPAHRFIGLIRST"

CDS 571722..573185

/gene="rtcB_1"

/locus_tag="EFAGFIKM_00516"

/EC_number="6.5.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WGW4"

/codon_start=1

/transl_table=11

/product="RNA-splicing ligase RtcB"

/translation="MNTEFNLFTNPNELTGAYRHEVKLPAGDLTVYAAQQLFSSLDYK
VFEMANNNLQIPGISYMSYTPDVHVGVGTCIGTTAVWDAQSGYVSPSIVGSDIGCGMR
VHMTNLHKDELKDIKLRRLVKAIEKVLPMEANQRGHYLDIRLEHIVRKGLHGLPKKY
IPDSYTPKKSTALTHVESSKFSYDEDVLNHVPDMTWHRSHRQLGTLGGGNHFAEIQAI

EIAEENREIAEAWGLYDGQVVVMIHSGSRAWGGYVSQTSSSAIAKVMQRLNLGTSDPR
LVFAPLEHAEGRHVNMYSALNYAVVNRHLIAYAIREAFRDVFGSKCEFRTLYDLMH
NYAWEESHADQGSFFVHRKGATRALPAGHPDNPYPYQATGHPALIPGSMGTASYVMVG
QPQGADNYYSICHGAGRIRSRTATKRLISVEDFAAALGVGTEDEIVVNQRSLESIIDE
SPQAYKNVDEIIDSVTGAGLAQVVAKCKPLVAVKGAK"

CDS 573185..574489

/gene="yjoB"

/locus_tag="EFAGFIKM_00517"

/EC_number="3.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34703"

/codon_start=1

/transl_table=11

/product="putative ATPase YjoB"

/db_xref="COG:COG0465"

/translation="MTINEKQTDPTQAIYTYDEQHDTRIRVEGYAIYSRLIRGISEAL
HQRYGVEYKLYASSDPNNEYWELLREDLQNGSDEVELVARIFEDLELQTLHYDDGDV
PTYGVHYSIRNNVFAYPKWGVLRVPFFRENGIYSEDFVFAIGDEEMKQFLGVRER
ERQQNMKKVTVYTDARNGSDRHVESITRSVGREDVLSAQIKQDIFRSLDQFFEADRS
FYRDYDIPYKRGILLYGHPGNGKTTLVKSIAGSIPGPAAYWQITEYTNSSESVREVFEA
AKRLAPMVLIIEDIDSMPDEVRSFFLNTLDGATSKEGIFLIGTTNYPEKIDPGLMNRA
GRFDRAYEIPLDEALRLQYLRQRGFTIFAGEEGTVEAARLTDTFSLAQLGELYVSAA
LEWHQNGQTDIVKVIQSMRGELDKSHKHTWLAQPGKGRAGFY"

CDS 574798..575055

/locus_tag="EFAGFIKM_00518"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGWLWSLIIGGIIGWLAGLIVGRDIPGGVIGNIIAGFIGGWLGG
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CDS 575234..575749

/gene="msrA_1"
/locus_tag="EFAGFIKM_00519"
/EC_number="1.8.4.11"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54154"
/codon_start=1
/transl_table=11
/product="Peptide methionine sulfoxide reductase MsrA"
/db_xref="COG:COG0225"
/translation="MEKATFAGGCFWCMVTPFEEQPGIHGIISGYAGGHVENPTYEQV
KTGETGHVEVVEITFDPDVFPYERLLELYWPQIDPTDDGGQFQDRGTQYRTAIFVHNE
RQRELAEHSKQELAASGRFTQPIVTEIRDAAIFYPADYHQDYHKKNEKHYKEDRALS
GRDEFIDENWK"

CDS complement(575832..577103)

/locus_tag="EFAGFIKM_00520"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MHTLTKHKSKTWAALILSGMLLFTMNTTGAAAESTESMPKPAWT
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TVNSPISISLLDNDTLMVASSQGVQSNGSVRSAISLYDKKGLITEKTINGNVLKADH
GRIVVDASKQTKVGNFWQQAANPKVEIYDRTLNRLSFYQFPANANTLGDGGGESLAIL
DDGSIIMRANFENTGNRLMGFGIDGKLAWGRAITGDAYIQTAGNGYTVFTGQKLELYT
MKGKVTERTFKDAQPALMRVDQTQDGQYQLDFAKTGYILDPQTLEDVHIYTTASVPS
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CDS 577366..577962

/locus_tag="EFAGFIKM_00521"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MNWSENATVWVIGCIIILLLLAWIIRRVIGRGQRIRSEANPRKI
TIKDIDKMEDGSEFELYLYHLFEELGYDEVHKTTSRDFGADLVFVDRLGRRSVIQAK
RYGANHPVGLSAVQEIYTSMYEADRSLVTSARYTEACRTLAAVNGVKLLDREDLM
ELILLFKARRVEEALELIEEDDHEPIETWQSRRKRQSR"

CDS 578082..578309

/locus_tag="EFAGFIKM_00522"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MARTQTQKALRKAERSGQWCSEQSRRVNGDYGALSQHVRMLMPTK
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CDS 578359..579606

/locus_tag="EFAGFIKM_00523"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTTALHMNKKIVRRFLLQTQALLGRWPAVSLPSGPDQVLSLIRS
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LFEPVRARLRERLAPSLQGLEKTQHVLRQLKEEGPLPSRAFRAVERVSGYWDSADVP
KTKDITLALNLLLSAVIRVVARQGNERYFHITESLQQQGLTMKEDIDVLAQRQALL
DKYIYAYRVVDARDPRLGWLKSTAAERRADIAARVSDGRMIPLKVEDVATPYIRAED
EDLLHMEREEPHYDPSGPVRFLPPLDNLLWRRERIVDLDFHFKWEIYTPVKRTYG
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HGARSITIEKTVPKELKKLLKLI"

CDS complement(579812..581005)

/gene="fabV"
/locus_tag="EFAGFIKM_00524"
/EC_number="1.3.1.9"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9HZP8"

/codon_start=1

/transl_table=11

/product="Enoyl-[acyl-carrier-protein] reductase [NADH]"

/db_xref="COG:COG3007"

/translation="MIIKPRTRGFICTTSHPVGCAAQVQEIDYVKSQPELKGPRNVL
VIGASTGYGLASRVVSAFGAGANTVGIYRPPSSSTEKRTASAGWYNSAAFEKAAEEAGL
KSYSVTGDAFANETRDKAVELIRSELGQVDLVVYSVASARRTDPNTGEVFNSVLKPIG
QSYTNKTVNFHTGEISSVTLEPANEEEEIRQTVTVMGGDDWELWMDALQQGGVLADDAT
TIAFSYIGPELTHAIYRDGSIGQAKNHLEATAHKLNDRLSAKGGRAYLTVAKALVTQS
SSAIPVPLYISALYKVMKEKGLHEGCIEQLQRLFADRLYAGGEVPTDAEGRIRIDDW
EMRADVQEEVAKLWNELTENIYDLSLEGYRREFFQLFGFETDGVVDYEADVDPNVEM
PHLVN"

CDS 581209..582489

/locus_tag="EFAGFIKM_00525"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLKERIELLSKRKQIFRKDLVEGLVTQAHFANILADRYPLPEDL
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IQYYRSKMAFVDVLTHATRLSELALPGSEFWLSVQNIKMEAYIQVKQYEEAKQVFELT
MRHVYDQRMFHRLSGLYVAYSGYCFAMGLVQEALSALTMAEANLVYAGNQGDLVTAIA
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LAQSV DQLLKCATTQDQQMSATFYQSHLALAHGDREVFMERALACLPYFESAQHVMRL
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CDS 582767..583183

/locus_tag="EFAGFIKM_00526"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MGWFGKKNKQEDAIKADKIMNKGLTGMMMKG FVSKEHREAINQ
SLDSAKQAQLAASGSLPLTATATVVTITDTGKLINFDP IVVLVDVTETNGNQYQRTL
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CDS 583295..584089

/locus_tag="EFAGFIKM_00527"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MVGFLRFIVGLTVFGVGFFPFLAEQWWNDSFKFVQAWWYAPAIF
AGFALIFVPAILSNIFGVGRVKTGLPAVGVIKTIQQTGTYINEQPEVRLGLTVSRKGR
EKYDTEMKAVIPLTSMAQFQTGSFIPLVSVKDERKVGIDMQGQLSQEDMQQLLDEKM
VQQGVSPPEMMDIARTGEKAMAKILDVTPLGSGGSNKIKLQLKLSITKTNGETFNVTQ
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CDS complement(584188..585003)

/gene="COQ5_1"
/locus_tag="EFAGFIKM_00528"
/EC_number="2.1.1.163"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01813"
/codon_start=1
/transl_table=11
/product="2-methoxy-6-polyprenyl-1,4-benzoquinol
methylase, mitochondrial"
/translation="MQDIRRNNVERFKGFGTLYDQNRPAAPTEVVDILT TYLGSTPRM
VADIGCGTGLSSWIWLNEAERIIGFEPSSDDMRSAESKWESAGKPDNLR FVSGLSHDL
GLPDGSVDVLTCSQS FHWMEPQPTLREFARVLRTGGVFAAYDCDWPPMLDWQLEQAYL
QLNKEADQRAASLAPQDSQAHKWSKDGHLLQQIQSGLFRYVREIVFHHHETFTADRYV
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CDS complement(585077..585994)

/locus_tag="EFAGFIKM_00529"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLLLLLLEKKKATAPELARMFEISVRTVYRDIDRLSAAGIPVYTT
TGKHGGIHLMDNYVMDKSLLSEEDQNEILMGLYSISAIPLHNSAHMLQRLTALFDHKL
DWIEFNFPWGSIPLQERELFNQVKQAILTNQLITFHYVNSDGEKSIPTVEPQKLIFK
NSTWYFKGYIHDDPDRKEFETFKMKRITQLTFLARKHDHHSVTAGSNDPESEAAPVLTS
LTLSFSSNIAYRVYDFFEPSLIKKEHDGRLRVSLELNVGEWLYSFLLSFGSELTVIEP
VHVGQELLRRHIKAVEHLQNVNMNKLPNNE"

CDS 586107..587540

/gene="bglH_1"
/locus_tag="EFAGFIKM_00530"
/EC_number="3.2.1.86"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P40740"
/codon_start=1
/transl_table=11
/product="Aryl-phospho-beta-D-glucosidase BglH"
/db_xref="COG:COG2723"
/translation="MTMKEGFYWGGATAANQFEGGWNQGGKGPSTSDMMTGTH TIPR
RITPVLEEGTYPSHEAVDFYGHYKEDIAMMAEMGFKMFRMSINWSRIYPNGYDLEPN
EEGLQFYDNVFAELKKYNIEPLVTISHYETPFGLTQKYNGWASREVIDCYIRYCTTLF
NRYKDQVKYWLTNEINCLTMPMGAYMAAGILFEGKETLVDGVDDPQTRFQALHHQFV
ASAKAVKLGHEINPEFKIGCMVAFMTYPNTCNPNDMLLAQKKDQLSNMICGDVQVRG
AYPGFAKRFFAEEGIQIEMQPGDEQTLREGCVDFYSFSYYMSLVESADESLERAEGNL
LGGIKNPYLEASDWGWQIDPKGLRYTLNHLVDYQIPLMVVENGLGAVDVVEEDGSIQ
DDYRIDYLGKHIEQMKEAVADGVDLIAYTMWGCIDLVSASTGEMKKRYGFIHVNKDND
GNGDLSRTPKKSFWYKKVIESNGEEL"

CDS complement(587708..588376)

/locus_tag="EFAGFIKM_00531"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIHNWKKNISFPLLVAALCMIAFISIALSISDNQIHRFDDTLIG
WIQGLESPGMTQFMHLFTWIGSEMPVVFITIAMIVLYVCLRHKRELLFLACVLAGST
LLNALLKLVFQRRARPTINRIIEVSGYSFSPGHSMAAFSLYGGLAFLIWKHVPTVTGRV
LMIVASAVFILTIGISRIYLGVHYPSDIVGGYFLSGCWLSTCIWFYRRHLERMSQLQS
RRLA"

CDS 588546..589118

/locus_tag="EFAGFIKM_00532"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKRSWVMCMLILLVTSGLALFPGDKVFACSCVESDVQKRLETY
TTVFTGKVVKKERSQQSKHDGLLREYTFDIDTAWKGVNAKKMKILASDGGSESCGIQF
EKNQSYLIYAYQYEVDHKLHTNLCSRNPVPIEQAGDDLKLLGAGKVVSKEDFGETTDGR
SEYFQLILYGGVILLAALAIVWIWKRKKRI"

CDS complement(589247..590023)

/locus_tag="EFAGFIKM_00533"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MERFNYKKSQDVLALSASFDFAYKKHCHEEYAVGVTLRGIQQY
NLDGQYQASHQNGVMLFNREQSHDGSSYDKAGIDYVMLYLKPELVEEIIGKKELRFGS
PIVYDPELARNILMLNDAVQLRQNEAECSESVFDLVHLLAQKEMDTKLWLPQDNLVRK
AKEIMFCSTEDVLKLDNLSSEFGMSKFQFIREFKAHAGISPYQFFLNCKVERARQSIE
KQKDVTAVADCGFVDLTHLNRHFKRVFGVTAYEYMLQLN"

CDS complement(590043..590624)

/gene="eamB_1"
/locus_tag="EFAGFIKM_00534"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P38101"

/codon_start=1

/transl_table=11

/product="Cysteine/O-acetylserine efflux protein"

/db_xref="COG:COG1280"

/translation="MNLASFLIYCIVVTFTPGPSNIVLSSVQQVGARQTMHYVWGAT
LAFGLLLTASAFNLQLLAGVLPGLKVMQIVGGLYMVYLAYKIYKMGTTEDAPKQVTG
FWNGFIMQFVNPKVVLFTFTVIPSIVLPFYQSSSFSLFVLLITFIGFLAYSSWVVF
KVFKTLLNRHQKLLSILMALFLYSIIVSGLI"

CDS 590831..591838

/locus_tag="EFAGFIKM_00535"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKMLLVYILLISAFALYVLRFEYTSQVNSSWEDRGLRGDIGET
YIMITFQSGLEYWKSPLKGFEDAADALGVTVEYRGATRYDAKEQTMVIEQAIARKPAG
IAISAIDPQSLVPAINKAIDADIPVVLFDADAPGSQAYSFLGTDNYKSGVMAADKMAE
LLGREGEVAVLTLPGQQNHEERTKGFRDTIKERYPSMQIVEVADGHGDAMVSRDETQR
MMKEHPELAGIFVTEATGGAGAGEAVQTAGDRHPLQIISFDTNKATLDMIKNGTISAT
IAQGTWNMGYWSLQYLFHLHHQLTVPAPSSSGENAPLPVMVDTGISVTRSDVDDYYA
K"

CDS 591828..593798

/locus_tag="EFAGFIKM_00536"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPNNKEDFKSPGHWSRRAILSTFRNGIRRLRLRNMPRLRYQLMLL
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FDPDIDAFMNDKMPQNDDAGIEPMNMDTNAETEQRNRLYGIKQTLQGFTTLYPEIAGIV

LVNANGDYISNEMYPRAEQSLIQENWYQKASANPGIFMVLGQPKERNLTTHVRYKDDE
IVSVARSITDEASGRVRGVIMIDLKLRSVSQAARNVTLGKSGYVMVTD AEGQSVYKPE
HPLIEHIPTDWFP SGESGTF TADTEGGTLLFMYQSSTFTGWRTVGVFPTRDSISEVRQ
IQFYVVSFV FV VCLFGLSASLWFSRSIAQPIFRLMSYMRRAETGNLRPGRWSDRADEI
GMLGNSYNRMLAQIRQLISL NELRERQKRDAEMRSLQEHIKPHFLYNTLDTIHW MARK
EGAEDVSGMVGALSRLFRIGLSKGQDYIPLHSEIEHMTSYMQIQQTRYRDR LQYTLNI
PEELRDLFVLKLLLQPLIENAIYHG IKGRRGPGHIRVEARLEHNRLLLTIHDNGAGMS
NERLAEMQQLLEAPLASLEASSPGMTGKSYGMLNVQARLRLSFGDEYGIVLESQE GEG
TSVTIIHPLMREL PPTKQINNEERQESEWENS"

CDS 593783..595105

/gene="rssB_2"

/locus_tag="EFAGFIKM_00537"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00958"

/codon_start=1

/transl_table=11

/product="Regulator of RpoS"

/translation="MGKFMKSTVTTSTETDETSALTTVMEITPD SHVAKKYRVLIADD

EPIIREGIRDAIDWTTLGMEVVGEAEDGEEALERAADLGVDIVLVDMNMPFLNGIELI

RALQQKCPGCRYLIISGHDEFAYAQEAVRLGVEDYILKPVQAEQLYAALERLHQRLTE

EHQRTAYVQQA AHQIERNIPLLRQRFMLEWLEGQAEGRDLTEQLVFLRLPAVSPVQIG

VVRWPAAEARQTILREND RQLFLYAVENIISELLGDLPHVLFRDVSGLIGMCLWQEAP

EEIESLLEQQISSCLNIAIHAHVETHAGTLEETPD TYRHCRERVYGEVQLSPLVRRAR

QLIHEEYAERELTLESLASRLQVSAVYLSRVLKKELNDSFVTLVTHARIRKAIQLLDS

TTLPIHTIAERVGYDTQH YFSTAFKKTMGISP VQYRKNGGTAYQPSAN"

CDS 595358..596509

/gene="chvE"

/locus_tag="EFAGFIKM_00538"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P25548"

/codon_start=1

/transl_table=11

/product="Multiple sugar-binding periplasmic receptor

ChvE"

/db_xref="COG:COG4213"

/translation="MYCKRYLITHSEPYDVRKGELHMKKGAMLIWLLVMTLMLSACNL

AESGPGSKEKGYVGISMPTKSSERWVG DGENMVRLFQEQGYKTDLQYAEDVVENQISQ

IENMITKGVDVMVIASVDGNTLTDVIKKAHDEGIQVISYDRLIRNTPYLTYATFDNF

KVGV LQASYIEQKLGLKDGKGPYNIELFGGSPDDNNAYFFFDGAMSVLKPYIDSGKLV

VRSKQMTMAQIATLRWDGALAQSRMDNLLSAYYSGDHLDV LSPYDGISIGISSLKG

IGYGTSNKPLPVITGQDAELASIKSIVAGEQTQTVFKDTRKLAECTVEMANSILQGKQ

AEVNDKTSYNNGIEVVPAYLLDPISVDRTNVEQDIVGTQYYTKEEIGLK"

CDS 596531..598096

/gene="xylG"

/locus_tag="EFAGFIKM_00539"

/EC_number="7.5.2.10"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37388"

/codon_start=1

/transl_table=11

/product="Xylose import ATP-binding protein XylG"

/db_xref="COG:COG1129"

/translation="MAGIILEMKNMTKTFPGVKALENVNLKVREGEIHSICGENGAGK

STLMKVLSGVYPHGTYESDILFQGKNCEFKDIKQSEDLGIVIIHQELALIPYLSIAEN

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KVRL LILDEPTAALNEDDSENLLQLMLEFKKQGIACILISHKLNEVSKVSDSVTILRD

GKTIEM LDMKKEKV TEDRIISGMVGRDLTSRYPERHATIGEVILEVKDWT VYHEHHAE

RKVLDQIH MNIRRG EIVGIAGLMGAGRTELAMSIFGKSYGRNISGQLIKNGKPIHNNT

VTEAIQNGFAYVTEDRKEYGLILMDDIKRNISLTGLSKLTRNAV VNEREEVLVAEKMK

KSMNIKAPSILQKTGNLSGGNQQKVVL SKWIFAGPDILILDEPTRGIDVGAKFEIYTI

IHRLAAEGKGV LVISSELPEVLGLCDRIYVMNAGRITGEVSREQASQETLMRYMTKSG

GGKHGNDNKAFQK"

CDS 598065..599228

/gene="xylH"

/locus_tag="EFAGFIKM_00540"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AGI4"
/codon_start=1
/transl_table=11
/product="Xylose transport system permease protein XylH"
/db_xref="COG:COG4214"
/translation="MEMITKLFKNNIRQYGMIIALVIMLLFEVLTGGLLLKPINITN
LILQNSYILVLAIGMVLVIITGHIDLSVGSIAAFVGAVAAIMMVDWQLPAWLAVIASL
LVGALIGAWQGFWIAYVRIPAFIVTLAGMLLFRGLTMIVLEGQSISFPFGGFQKISSG
FLADIQFSGFGLVSIIVGLVLTWYIVNELRERRSQRKYGFEVVSQGLFLLKLIVVAV
VTNLFTFVLASYAGIPNILLVLLFVLIVVVSFVMNRTVMGRHVYALGGNEKAAGLSGVK
TKKVTFWVFNMGTLAAVSGLIFAARLNAATPRAGTNFELDAIAACFIGGASASGGIG
TVFGAIIIGGLVMGVLNNGMSLIGLGIDWQQGIKGLVLLLAVAFDIYNKNKRMA"

CDS complement(599353..600723)

/gene="mgtE"
/locus_tag="EFAGFIKM_00541"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q830V1"
/codon_start=1
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/product="Magnesium transporter MgtE"
/db_xref="COG:COG2239"
/translation="MNGPHTKKDFSVEEITEQLVQHVSRLNPDFYKLVKELHPYDLS
LVYKKFPPEETNRLLLLFKPDALADLAETLKLHEQIQLFERLGPRTLQVMMQMDKSD
LIRFMHDLPAKRREELLSNMNLDHSAIIRSVLNYPPELAGRIMTDQYRTLLAHETAKE
ALRQSQGTMHISPSSYLYVTDNEGKLVGVVSYRSLALADDKTQVEELMTRRVIHATVD
MDQEEAAQLLQRYEFIALPVVDENHRLCGIIQMDDVIDIIMDEASEDLAKMGGGSKDI
DFDTKPLVAVRRRLPWLILLFIGLISGSIVDFEDTLNQVVALAFFMPMIAGMTGNT
GTQSLAVVVRGLIGRKLDKATVLALIGREIKVGTMIGLVCGLLITVIAYFWQGDWLLG
AIIGVSLFTLVIGTLTGTCIPLLLSRFKVDPVASGPLITLNDILSLFIYFGIATR
FLDALM"

CDS 600914..601618

/locus_tag="EFAGFIKM_00542"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEVDIRTQLLSMVEPEYQKFSAALIPNITNVLGVRLPALRKIAK
QLAAGDWRTYLETAEDEYFEEVMLQAMVIGHVQADLDELLKAIETFVPKIDNWSVCDS
FCAGLKYTKVHSEPMWAFLQPYLRSDQEYEIRFGVVMLLNFYLNERYIDQVLSALDQI
RHEAYYVKMAVAWAISMAVVKQPEVTMRYLNRNTLDDFTYNKALQKITESYRVDPEK
QMIRSMKRKVKKQITS"

CDS 601661..602215

/gene="ogt"

/locus_tag="EFAGFIKM_00543"

/EC_number="2.1.1.63"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00772"

/codon_start=1

/transl_table=11

/product="Methylated-DNA--protein-cysteine
methyltransferase"

/translation="MRKKLMYTTMQLDGRPWVLLATEQGLCRVVMNPNETLEDWNGWIQ
KVAPGVELEENEDALKQTGMMDWLQSYFAGELIAYTDAIPLDLIGTNFQQEWWRELGR
VPYGEIRTYGDIAAAIGRPSAVRAVGAANGANPIPVLLPCHRIIGANRKLTGFRGGLE
MKRTLLEDIEQIEGVTGGHARFHF"

CDS 602453..602758

/locus_tag="EFAGFIKM_00544"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSYAPQKRHSNRAKRWIITIGIFIVVQIIFIAIDGTFLEPSIND

SDNVLAKTVRGVLESKLLTERIAPYSFPFFNFLFLIVHVVAILIQALGDSILAIFAKR"

CDS 603257..604531

/locus_tag="EFAGFIKM_00545"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEDIHISSEELNGVHLHLYNTNKFKTVSIMLTMKSPLQESLITA
RALIPHILNGGSINYPNRKLIQQLDKLYGATLLLDVQKKGEDHSIVFRMEIPADKFL
DNSASLLKSSLELLHEIVYNPLIENGGFHSIIVEQEKRSLKQRIDSIHNEKMLYANVR
LLEEMYKGEPYQIPAFGRKEDINSLDAISIQAYENMLQTDRFDLFIVGAFNEDQVKL
MVQNIKFCEQHNNNEFMKGFSSASVTVNDIKVIQDKMDVKQGILLGYRISSTIQDEDEYE
AARVANAIFGRFPSSKLFRNIREKESLAYFSHSQMESNKGLLIAMAGIDFIHYERVVE
MIREQERAMKQGKFTEAEVEQGKGMLINLLEAHDSPVGIMDIFIQSVDSGLSIDIHD
QIQRISKISKADVICAARKWELDTIYFLNREE"

CDS 604537..605820

/locus_tag="EFAGFIKM_00546"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHPIIYEGLEETIYYEKLPNGLLEVYIHPKKDFHKT VATFTTKYG
SIDNKFSPGKDYSVQFPDGAHFLHFKMFECEKWDAFHKFAEQGAFVNAFTSFTRTA
YTLSATSRIKENLTLLDFVQEPYFTDETVEKEKGII EQEIKMYDDNPDWRARFGVLD
NLYKSHPVKIDLAGTISSIQITKEDLYTCYNTFYHPSNMLLFVIGPVVPEEILRLVR
SNQEQKEFPETKKIRRRFFPEEGA AVNKSSSVIKLLVPIPKVFIGYKESFPIKQGQEIL
KYELSLNVLLELMFGIGSEAYEKMYENGYVDNSFNFEYTHEKNFGFSIIGGN SHSPED
VIKIISETIEKFKKDSINKDDAERVINKEIGAFLSAINSPQFIANQFTRYRFNDL DLF
DVLPIESLTASDLEDVLHVHFSSDSRTTLIVKDK"

CDS 605847..606698

/gene="lnrL_1"

/locus_tag="EFAGFIKM_00547"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94440"

/codon_start=1

/transl_table=11

/product="Linearmycin resistance ATP-binding protein LnrL"

/db_xref="COG:COG1131"

/translation="MSNLEIKNVRKSYGNKVVLKGISFNVPYGSIVGFIGDNGAGKS
TTFKIVLGLISNDDGMVNIFGEENINKNPKIKEKIGVVFDAANLPAHLTIKQLNKVFG
KLFDSDWDQDNFHRVLSSFSPLVDKKVNEFSRGMMSMKLSVAVALSHNAQLLLLDEATGG
LDSSSREEVLNELKSFASKENGGILLSSHIMSDIEKIATHLVIIEGEGEILLNAEKDEV
FEKYTIVDMDMEKLNLSLNQDIVVAKRNFDTYYSVLVSDKKQLPHDLVTKPISMDDISL
LLTRSNE"

CDS 606699..607340

/locus_tag="EFAGFIKM_00548"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNGLLTSYYLVYRSSFLYTGLAILLSVIILTFADASMHRVAL
LNILLMVMSALDVIKFEGKSGYDKYVLTLPVSRSTIVQSHYLFYFLVVIYGVILSYSI
FYVYDLVSGTPINEMSNSIFFGIFAVLLTGAINFPLYIFGPEKSDSITLGSVGGAIL
VTIVSQSLVGIVASFFNPINPDLLAPIIYLIFGVIVYIVSLWAAILIYRRKEF"

CDS 607464..610076

/gene="ramC_1"

/locus_tag="EFAGFIKM_00549"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O88037"

/codon_start=1

/transl_table=11

/product="putative SapB synthase"

/db_xref="COG:COG0515"

/translation="MEGNMLYNLYLKPNSEYYGKLENDEKKQNRyelGDIPDTYAVIS
DRESVWKHYHVKGSRLPDQGWKIHTALFEESQNLLDRVSKLCIDERIEFKHLKDRQS
FIKTNSKNANRASSGKFITIYPVNNNVFVKLLDMLCLATQGFKKGAYILSDKRWKNSN
VFYRYGGFRSIYNEYGEHCKIDGQGNLVKDERTPFYQVPDFVKDFDDYLNSLNYSDDL
ETKGDGNLERYEIESALSYSNAGGVYRATRKKDNLNVIIKEARNAGLDGSAHDSLSR
QIKEYDALAKLKDVTGVVSLIEYFQEWHEYFLVEEFIEGGDLRQWLAQHFPFRDDE
MRNHAANVKKVLLQLFTLIDQMHHKGIAMGDFQPANIMVADDLTVRLIDFETAMHVTS
KDKPTMMTIGFASQEMKISGARDWFGKKLTkYLALPVLSSSEVLDEYLQYNHFRWIK
EYEDSFYQFIVDLQEKCDQKIRNYQEYFPKEMVLYDKTSDFNISSITKKLIEGMQDNL
TNDERFVHGDIRQFEMNGGKFNFLTGGTGAAFTLIKNNTNSLEVDKWIQDFLLGNLNT
IESNGMFDGKTGILALLYETGYEAVVLNELKNIRANMNESNISLRSGLSGIGLFVISL
YIETENDEYLQFAKEIEESIERNRNDARFSTNDWMAVGIGVIDGLSGVSLFYsAMYS
ITDDKQYLERARQLIKEDLEKTIFDEVTGSLQTLNRRNRQLPYLSGGSIGIGIAIwFL
NHVSGEDAYQEEINAITKLSQICSTISGGLFDGAGSFLIPSLMKNIGGREViiKEVL
SLLNLFLIDKNGYYVYPGQFSYRLADDVYTGsAGIILALMGIVKDNPLYWLPLVNLDE
FLTRTKAHDVSVTS"

CDS 610142..610270

/locus_tag="EFAGFIKM_00550"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNAVLELQKLAKDKEGKGQAVDGTITTTWTVTTLSTISNSC"

CDS 610307..610435

/locus_tag="EFAGFIKM_00551"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKAVLELQKLAKDKEGKGQAVDGTITTTWTVTTLSTISNSC"

CDS 610581..611414

/gene="COQ3_1"
/locus_tag="EFAGFIKM_00552"
/EC_number="2.1.1.222"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00472"
/codon_start=1
/transl_table=11
/product="Ubiquinone biosynthesis O-methyltransferase,
mitochondrial"
/translation="MEKLLDIAKIPEPFEEGSVQIWLDNADRVFLKAHFDENIPGGS
KGNFYFIDETVNFISEIAPLTYYKKIIDLGCGPGLYSQNLAARGYDVVGVDNFNEKSIEY
AVHEAQKKGLIIDYRIEDMTNIEIEQEFDLALLIYEIYSVFNPNRKKILSNIHRGLK
SGGLVLLDVLSSENSYEKFEQNFMWGLTRKDNPFSDKKHLSLFASIKYPDHVTLKSNVL
VFGDGELVNYHYWNQHFTIESLEKEVNDAGFTLEKIYADVNGGEYQAEGESFAAVLKK
K"

CDS 612033..613259

/gene="atzC"
/locus_tag="EFAGFIKM_00553"
/EC_number="3.5.4.42"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O52063"
/codon_start=1
/transl_table=11
/product="N-isopropylammelide isopropyl amidohydrolase"
/translation="MEKVYWLNTNVTLELDYVREGKQVTGTRTSPAHLRIEDGVIAEIV
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LLPKLLPDAKRQAESILTIQGYGSTHVRSHCNIEPVSGLKRLEATWQALESFSGKIS
SEIVAFPQHGLLRSHSVELMGQAMKEGATHVGGDPHTVDEQIEKSLNAMVELAVQHQ
AGIDIHLHDGGQAGKQTLLELANLTEAAGLQGKVTVSHAFWFASAEQQEAEDMAQRMA
SLGMSIASTVPIGRTMMPLPMLHRMGVNVKLATDSLTDHWSFGNGDLLEKAGRFAEL
YGYSDELSLSQSLAFVTGGITPLDSQGEQVWPVKVGTASFVLVHASCSAEAVARRSAR
QAVWYKGQLVSGSTAD"

CDS 613387..613797
/locus_tag="EFAGFIKM_00554"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKIEYATEADYDYIIERDRHIHQPLVTKISEKEIFILWDEDEG
SRVGWMRYGYFWDNLPFMNMIWIDEPYRNGGYGKKVVHYWENLMKQQGFDTVMTSTQS
DEHAQHfYRKLGYVDAGALLDTQPLEIILIKKI"

CDS 613830..614279
/gene="bltD_1"
/locus_tag="EFAGFIKM_00555"
/EC_number="2.3.1.57"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39909"
/codon_start=1
/transl_table=11
/product="Spermine/spermidine acetyltransferase"
/db_xref="COG:COG0454"
/translation="MEQVTLQPITKENELECIHLKPREDQLDLVASNADSLIHATKEI
TSKPYGILAEDQMVGFIKFDNEIYNDGYYWILRFMIDEKYQGRGYGKLAIQEVHMLQ
ERSDCQQIRVSHVPHNIAANALYKRCGFQETGEFEDNGDIILSYQVR"

CDS 614297..614725
/locus_tag="EFAGFIKM_00556"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIREAEARDAAVIERLYKELLPNNLNTKVLAERIEEVRNNPNSF
LFVYEMDDQVIGTAHLHICLDALVENRPFVGVVERVIITEHVQSKGYGSELMKHIEHVC
VQKNCVKVFLTSGSSRNEAHHFYTKLGYDGESSKAFKKYL"

CDS 614767..615495

/locus_tag="EFAGFIKM_00557"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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YFDAQGEVRFWVNIDFWYGLTLTFAVAIIGLLLSTCSIIQIHGMLNKL VNKYISMIVV
GVILLSSIGVYIGRFNRWNSWDVLSRPGKIFVDLVNDFNAANSIMVEFVAIVFTVQL
FGYVILSLLTARSSSSSSSLERIRV"

CDS 615618..616562

/locus_tag="EFAGFIKM_00558"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSLTEWSTDILQYDLSDEYSIRKADFAEWGLYCTVYYDMRYVGF
FREEEFSSSKISAYWIYKGESKIGGVRMEPNRMYHLFFIPPFQQCFEVLKLLKHKLLQ
WSDRTRKILTFEILPDQVDLYARAGFWPVEFRCRMQRPTDHFEIEWDSRVTVRSPKI
IESETGTRKYVNEDEIAQC DLESFAGSLEATRRKHTTLADFIPSDDPNYTNEILTQAS
TFVYDKETGQLIANCRLCLQDNQAAVYSIGVRPAYRGKGLATLMLQRALNELKGKYPV
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CDS 616559..617299

/locus_tag="EFAGFIKM_00559"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKIAILTDIHGNVPALQAVLADIDLRGDVEHTFCLGDMIGIGPY
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RIQALPKFVEKEVEGHRFLLTHYHMSNDKLDVIDKEPSGTKLDAKYHGTGHDLVCFGH
YHILHYYKTDQRIYLN LGALGCNDLAIARYGIVDLQEGKVDVKFIGVPYDNREYLKSY

ERLNVPDRAFILQAFHGNQLEREDSERS"

CDS 617334..617483

/locus_tag="EFAGFIKM_00560"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGMIIMLVVYLFLGIYVVKVGIDNSKNSQHTKEILSELREIKEL
LKERG"

CDS 617501..617959

/locus_tag="EFAGFIKM_00561"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSRAPFQILVFPYIRLKDSNDYAYAIFRRSREGYWQGIAGGGED
EEKPLEAAMREAFEEAGIPLNSKYRSLNSRSTHSVVDVVGYFMWGPDTFVIPEYCFGV
ELDEMDLSLSNEHSEYKWLAYEEAREILKWDSNRVAIWELNQRLIRESSK"

CDS 617987..618514

/locus_tag="EFAGFIKM_00562"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIYDLQGEANMEPIVGMLFSAVRENSERLKSITEGTSQEEVDYK
GEKNQFNSTAQLIRHIMFVDMNWVYRIKGVVLPQSLIEQYGPMTDENNRLPLVQDVSR
DTLISQYEGVLTLLKETCTQVADADLDRVVTFGHQNEKQATVRWRLWHMADHNRYHQA
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CDS complement(618581..619486)

/locus_tag="EFAGFIKM_00563"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIKANGKPPQLPLYEALASEVRWRIMDMIADREMNVKDIAAVLE
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IAVGHYTAFDIHPTCGLGTLEKEIGVWDDPRYFLDPERVHAAILWFGKGYVEYKTPNF
VLPDQTTDAIEISMELASEAPGLRDHWPSDIRFTFNGVSLGTWTSPADFGRAARGKYT
PEWWHRNVNQYGLLKTIRIDASGTYMDGERMSDITLADIKLSEPFWTLRFTVDEESPN
VGGLTIYGAGFGNHDQDIVIRVLQI"

CDS 619667..621157

/locus_tag="EFAGFIKM_00564"

/EC_number="3.2.1.55"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A7LXT8"

/codon_start=1

/transl_table=11

/product="Non-reducing end alpha-L-arabinofuranosidase
BoGH43A"

/db_xref="COG:COG3507"

/translation="MKYNNPVVKGFYPDPSVIKVHDTYYMVCSSFQYFPCVPLFESED
LLNWKQIGHCLTRKSQIQLETVNSSGGVFAPTIRHNDGRFYMVTTNDTTHQNFYVWTD
DIYGEWSEPIYVDQGGIDPDLYFEDGKTLFMSNGVDDEGVGGIVQCELEIENGRKLTP
SRSIWNGTGGRYLESPLYKMNGYYYLLAAEGGTEYGHMVTYARGTSSSGPFAYAHN
PVLNTRNLGGYELQGVGHGDLVQDDLGNWWLFFHLGFRQIGRWATYHHLGREVFLTPIT
FDEDGWFTAGHEGTTLSFETNRIPDTVIQQDKKHYYTFENTDWNLDWCYLRHPNTEHY
QLELDKLTGTGTEVTLDPASPTFIGLRQKDFNATISVDVSLRSGEAGITIYMDENHH
YEVAIRGQQDGYKVIERLNIGDIKSREHEVDLGNKQHATLVIRSSQERYSFQADGE
EILLGTAQTRYLSSEVAGGFTGVLIGLYASGQDTSAEFTNFKCDYH"

CDS 621256..621828

/locus_tag="EFAGFIKM_00565"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MEVHYKMPESLEGIVRIDKELRKEHDATLHDYVGFYISFNDED
RYYCTPDDAIIFGRTGADGDHFAFFTFNRSISDLEEAPVIFIQPTAFGNQVTLVARNL
KDFVALFINLKEVYVLERFRFYKNKLDFMNDYNDNYMEDIRMRESYHLIIELLKENI
KGIAEIDDVYEYIIIESRKQIELGINNDDFG"

CDS 621929..622474

/gene="coaE_1"
/locus_tag="EFAGFIKM_00566"
/EC_number="2.7.1.24"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P9WPA3"
/codon_start=1
/transl_table=11
/product="Dephospho-CoA kinase"
/db_xref="COG:COG0237"
/translation="MEDQWRIAKYDPAWRDLFLETGSKLREALGEKAVRIDHVGSTSI
VGIDAKPIIDIQISVDNYENLSDYKREIETVGVFRAENPDKTKRYFREEPGNRRIHI
HVRQAGSFSEQMTLLFRDYLRHPEDCLKYAEKHLMSLYKDQRPKYVEGKGPTVWS
ILQRAHRWSQEIGWQPAKSDA"

CDS 622515..622937

/locus_tag="EFAGFIKM_00567"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNMGRKLMTTVLTIICTLAASIISMNESYSFDFYILIYLVYAT
PLILLIGLPLSILLDYLLSRIQFPNHVLYLSTRILGYACAGVLGMYIYYLVMGAGEAI
LDFKETLVLTFLGVLAAILFVLIDMGLEVLLKKQRRKS"

CDS 622968..623489

/gene="sttH"
/locus_tag="EFAGFIKM_00568"
/EC_number="3.5.2.19"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q1MW86"

/codon_start=1

/transl_table=11

/product="Streptothricin hydrolase"

/translation="MTTHCALLIIDVQVAMFDEADPVYQGERLLQKIQVLIARAREAG

HSIIYIQHSEGAGSPLERGTPGWDIHPSIAPIAGDLVIEKETPDSFHKTNLHLKLQED

GVTELILAGMQTEVCVDTTCRRAFSLGYTVNLVQDAHSTWNSKTLQAEQIIAHHNTVL

RLFANVMDTENAL"

CDS 623489..623971

/locus_tag="EFAGFIKM_00569"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLGKRRRFWFFIGAAIMFLYFLITSNPDPNKPISRNVISTEMS

VVVYTRTGDGGAHVSIIDNVTLSEKEDTSRIVGWLNAAPESAKIPVDDVTGSIAGIALK

LKHNAKVTIQYNRKQIIVSTKSRFNRDSKYILDQKDLRDFLDQKLEGTYFGEDTVSVE

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CDS 623984..624262

/locus_tag="EFAGFIKM_00570"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTINKRIMNLSAWLAVLAIICIPGTLHTEDGPLRTEYGFPLRFF

TDYHYANSEGTIWFISGIYLNVLVLLYLFNVLFYAGIHVILYIKKKLTK"

CDS 624499..624978

/gene="yizA"

/locus_tag="EFAGFIKM_00571"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7WY73"

/codon_start=1
/transl_table=11
/product="putative protein YizA"
/db_xref="COG:COG2318"
/translation="METFFRYNWMVREQWYVWCEDVPLELLRPRTGGVGNILQTLFH
IIDVEWSWLQLLQGKPDDAENFANYQNLEAVRRHDKLRPDVEAFVTAWESRMEKRAY
IDHRSAGKASTDSWGEVMRHVIVHEIHHMGQLSVWARELGKQPVSANVIGKGLIIPD"

CDS 625021..625449

/locus_tag="EFAGFIKM_00572"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIHCRRATIQDGEVMSQLSHQLGYVSTTEEIKERLTLLSSLPDH
YVCVAEIDSRVVGWGHVQGRHSIESPSFAEIGGLVVDGIHQGMGIGKIIMSECEEWAR
VNGFDKIRVRCNGKRESAHRFYIAIGYEEKKWQKVF DKRL"

CDS 625483..626355

/locus_tag="EFAGFIKM_00573"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTIQLSQMNWVELDERIQQVMEQEYQIIPPPGLEASVMRIEME
DQRYVLKVWDKDSKPDIKQYRLLSKLYQSGIRVSKPYGWGLDEQENQVLLTSYNGKP
VTQLTPTKMTHLAERLMEVHRYPVNEVSTGEDEEYIFRYDFVQYFFHQIELHDDINDL
LANLIQVQVIRQDRLIHGDYYLGNILEMDDHYTIVDWTNGQYGDPRYDMAWSVFLITV
YNGESYGEMYRAQFARSASYTYTLEEEQVFEAVACLRWILLKRVGDVPMGPNVMERVH
SMAIHNPYLNEHLL"

CDS 626492..626839

/locus_tag="EFAGFIKM_00574"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEQKVQTYFELKQQQKDIEQQLSVLRDEIVAYCAEQGVYETQVG
GYTVKTVLQNRKEYDDQKLYASLPDPDIWRLLSKVDSHKLKSLIKLNILSEEQINPAC
TVKQVTLLQVDKL"

CDS 627079..627894

/gene="xynB_1"

/locus_tag="EFAGFIKM_00575"

/EC_number="3.2.1.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O69231"

/codon_start=1

/transl_table=11

/product="Endo-1,4-beta-xylanase B"

/translation="MPTEIPSLHAAYANTFKIGAAVHTRMLQSEADFIAKHFNSITAE
NQMKFEEIHPEENRYDFAADKIVDFAVAQGIGVRGHTLVWHNQTSKWVFEDTSGAPA
SRELLLSRLKQHIDAVVGRYKGQIYAWDVVNEAVEDKTDLFMRDTKWLELVGEDYLLQ
AFSMAHEADPNALLFYNDYNETDPVKREKIYNLVRSLLDKGAPVHGIGLQGHWNHGP
SIEEIRMAIERYASLDVQLHVTELDMSVFRHEDRRTDFTAPTSEMAELQERRY"

CDS 628284..628454

/locus_tag="EFAGFIKM_00576"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MERTRNYLLIFAGNLVAAYYIFEEGTFAKPLMFATLMLLIMTI
DYMKSARNKYTLE"

CDS 628620..629438

/gene="punA_1"

/locus_tag="EFAGFIKM_00577"

/EC_number="2.4.2.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77834"

/codon_start=1

/transl_table=11

/product="Purine nucleoside phosphorylase 1"

/translation="MHQSAHIQEARDYILNRIHTKPAVGMILGSGLGALADEIENATV

IPYTDIPYFAQSEAIGHANELVIGELMGKTVVAMKGR LHYYEGFTLDEVTFPVRIMKA

LGVEQLLITNACGAINTSFEPGQLMLITDHINLVGNNPLMGPNN AELGVRFPDVSQVY

NRELRSIALKVAEEQNVGLQQGVYAWWSGPAYETPAEIRMIRTMGADAVGMSTVPEAI

VAIHGGMKVLGISCLTNMACGILDQPLSHDEVIEVAAQVKTTFIGLVKGILKEI"

CDS complement(629556..630632)

/gene="degA_1"

/locus_tag="EFAGFIKM_00578"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37947"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator DegA"

/db_xref="COG:COG1609"

/translation="MAKEKVTIQDIADALGISRNTASKALNDSGNIPDETRNRVIKKA

IELKYKQFAYMDNEHVLTKAPGNIALLTENLPNTSHFGSLLISGLEKRISAEGYNLSI

HIVREDDQDTLTPNNFDIAKVDGIICIELFDLEYTQLITDLGIPTIFIDCASNICYP

EFKADLLLMENEHSIYQLTTKLIESGYTSIGFVG DYNHCKSFNERWVG YQ RAMLEAGL

QVDLSHCIVDNDRLCFSGKPGWLNQRVAELASLP SAYVCANDFI AVDLIRALKDRNVAV

PQDIAICGFDNAPQSRIIEPALTTVHIYSNEMGIKTAEMLLSRINSPTQPYQVSHIVT

KPIIRESTPAIMADHSQMVHSSAK"

CDS 631068..632033

/gene="yteP_4"

/locus_tag="EFAGFIKM_00579"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system
permease YteP"
/db_xref="COG:COG4209"
/translation="MDNIADSKKGEGRVLKVRTTSGHRLQQLKKNYFLYMLLAPALIL
TLIFKYIPMYGAIIFKDFSPIKGIMGSDWVGLKHFEKFIASPNFDIILMNTLKL SFL
GLIFSFPVPILLALMLNQVRKAGIKKNIQLFLYAPNFISVVVVVGMFLFISPTGPVN
QLATWITGQPIMFMSEPEYFRWIYILSDIWTGAGWASIIYVAALANVDPELHNAANLD
GANLLQRI RHIDLPTIRPIMAIVFILAAGGIMSIGFEKAYLMQTS MNLPSS EIIATYV
YKVG LQSGDYAYSAAVGLFNSVINVILLVTN LIVKKLNEGEGLY"

CDS 632050..632931

/gene="araQ_4"
/locus_tag="EFAGFIKM_00580"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94530"
/codon_start=1
/transl_table=11
/product="L-arabinose transport system permease protein
AraQ"
/db_xref="COG:COG0395"
/translation="MVVKHTGMDRLILTNAIFLTCAVLVVVVPLIYIVIASFMDPTV
LLNRGLSFNVSDWSLDGYQMILSNPAMIRGFANAVLYSVSFALITVTVSIFAGYALSD
DRLAGRGFFMIIFIITMFFGGGLIPTYLLIRNLGMLDTVWAIIPGAVNVWNILSRT
FFKGVPRELKEAANVDGASEMKIFFQIVIPLSKPIIFVLALYAFVGQWNSYFDAMIYL
DNP NLHPLQLVLR SILIQNAAPGMISDQLAMAELKRLSEMIKYS AIVISS LPLIIMY
PFFQKYFEKGMVGS LK"

CDS 632987..634594

/locus_tag="EFAGFIKM_00581"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKVNKSRKAVTTASISMLSAMIFLTACGGGGGGAASEAQSPDG"

KVTLNFIQTSSPLAPADPNDKLINKRLEEKTNVHINWKNYTSDFAEKRNLAVASGDL
PDAIFDAGYGDYDLLKLAKDGAIPLEDMIEQHMPNLKKVLEEAPYKSMITAPDGH
YSFPWIEELGSGKQRIQSVDNLPWINVEWLNKLGLKMPTTTEELKEVLIAFKTQDPNG
NGKADEIPLSFINKPGGEDLTFLFAAFGLGENWDHTVVTNDGKVVFTAADGYKEAVK
YIHELVKEGLVDVESYQQDWNTYLAKGKDNKYGMYFTWDMANITGMNDTYDVLPPVAG
PNGEVNVTRTNGIGLDRGRMVITSSNKNLESTAKWVDQLYDPLQSVQNNWGTYGDESQ
QNIFEFDKAGMLKHLPLEGSAPVELRQKTSIAGPLAILDSYDKYTTKPEDAAWRME
LLDKVMVPHMKAENVYPSVFFSIDELDLSTIETDLFAYVLRRLRTEWYQNGKIDQEWD
AYLKELDRLGLQEWLQIKQAGYDRNNK"

CDS 634620..636092

/gene="sacC_1"

/locus_tag="EFAGFIKM_00582"

/EC_number="3.2.1.80"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P05656"

/codon_start=1

/transl_table=11

/product="Levanase"

/db_xref="COG:COG1621"

/translation="MSTILKQDYRNEYHFSPKEKWMNDPNGMVFFNGEYHLFYQYHPF

GTTWGPMPHWHGHAUTRDLVTWEELPVALAPDEHGMIFSGSAVVDWNNTSGFFEDEPGLV

AIFTHHLEVPNEHPHQRLQSLAYSKDNGRTWTKYEGNPVLTHESFVDFRDPKVFWEHT

KEWIMIIACGQTVCLYRSPNLKDWTGSEFGGEGIGSHDGVWECPDLFPLAVDGDGSGQV

KWVMLVSGADPAFKEGSRTQYFTGDFDGSTFVPDEASHTIRWIDHGRDNYAGVSWSD

IPAEDGRRLFMGWMSNWMYANQTPTNDYRGAMTIARELSLETRSSEVILIQRPAELE

QARTPVLSLQDASIQVSEQLNALQLVNYEIHAEWTPNQSFHFALRSGADNETLVGVD

ANRGEVYIDRSGSGIGDFHEHFLSRHAAELKDVNANQSLRIFVDQSSVEVFANDGQAV

ITDLIYPDVDSKGISAHSENTDLVFSSSLHIYEISPTKAKG"

CDS 636121..637008

/gene="gmuE_1"

/locus_tag="EFAGFIKM_00583"

/EC_number="2.7.1.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O05510"

/codon_start=1

/transl_table=11

/product="Putative fructokinase"

/db_xref="COG:COG1940"

/translation="MRIGAIEAGGTKFVCGVGNEHGQIEDQISFPTEHPETTLAKVIE
YFRDKDVEALGIGSFGPIDLQPDSTYGYITTPKPGWENCNVVGTLKHEFPVPFGWD
TDVNAAALGEVTWGAAQGLDNCVYYTIGTGVGVGLVAGGQRVHGLLHPEGGHIRTRRH
PDDHFAGLCPYHGDCLEGMAAGPAIEARWQIPGSELPADHPAWEIESFYIAESITTAI
LLHSPQKII LGGGVMQQDHLFPMIREQVVRNLNGYVNAAPITQHIDQYIVQPGLGQHA
GLCGALALGLEALQHAAQA"

CDS 637263..637700

/locus_tag="EFAGFIKM_00584"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISPaen4"

/codon_start=1

/transl_table=11

/product="IS1595 family transposase ISPaen4"

/translation="MNPITMRQAVQADQEQLADLRALVLYDDLTRLGRYDDVKVRERF
RNTFNPAQTQIIEVEGSMVGCVALPKPKSEAYLLEHFYIHPDYQGQRIGTQVLNMLLEQ
DEVQGKRIILNVLQGSPARRLYERFGFILDSEDEVDVFM SKHL"

CDS 637976..638257

/locus_tag="EFAGFIKM_00585"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQEYPVAYDQFDVHFYQVWEMFSEQKLDVSALDEDLRVLGLNSI
SFIKLIIALENEFNIMDDEYLELENFTTLQHLKDSLRLKCINYEIPNES"

CDS 638350..639546

/gene="acrC"

/locus_tag="EFAGFIKM_00586"

/EC_number="1.3.1.95"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:G3KIM8"

/codon_start=1

/transl_table=11

/product="Acryloyl-CoA reductase (NADH)"

/translation="MKVELNAEQLMWQEQFKDFVDSEIIPYASLNDSEERIHPELLAK
ITEAGYLGSMPLKEYGGMELDNITIGILNEEVGRGCSSVRSLLTVQGMVGLAILRWGT
EQQRQYWLPALATGTTLGSFGLTEPSVGSDAKSIETTAVLDGDEYILNGHKKWITMGQ
LADVFLILAQCENKPTAFIVERDSIGFSVEPMSGLLGARASMIAELKMDSCRIPKENL
LGQVGTGLSHVALPCLDYGRYTIACGCVGLAKACLDASVHYANSRIQFGRAIRENQMI
QKMITEMSVNMKAARMLCYRAGYLRDVGDPESIMETWTAKYFASTMVNKNVASDAVQIH
GANGCHRDYPVERYRDARINEIIEGTTQMHEILIATQEVVTHRREMRRSNKAEKVKD
SANRNV"

CDS 639690..640496

/locus_tag="EFAGFIKM_00587"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRIGQGQTAEIFRHGETSILKLFREDFSAEAIQHEFDNTRIVL
ELGVKCPQTIDMVTINNRRKGIIFELASGRTLLEEMIIKPWSIERRARQMAALHHQIHQ
QSGERIQKHKTVLEKNISNASDLSDEKQIMDYVHSLPEGGSCHGDFHPNNVITG
KESWIIDWMTGASGCPAADVARTLVLLKYGNLPGAPLMMKVLLKIIKSRMSKAYIEY
YLSLSGMDIREIHRWVLPAAAAARLTWIPPEEKKDLLDYIRNQLKKFNTT"

CDS 640571..641377

/gene="rhaR_3"

/locus_tag="EFAGFIKM_00588"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11
/product="HTH-type transcriptional activator RhaR"
/translation="MDFQLRSVVSYDMVVREKKHLFDLSLRQIAIFEVMDALEISVF
SKTVQVKAGAVLLANKIRLQNYDKPVLKMRGIIFGSDLLERLP SCHILSENGSKHYDL
AVSLLNRTVESREDIEIAERDFLEVYSSYYQTNLTNLMRPETDREDSVKRNLVMICKY
IQNNYEKPITLQFLADMVGYNPVYLCNLFSKVFNV SPLKYLQQIRVDKAQEYVTKTDL
PISEITTKLGYSSSTQFSAMYKKKVGKSPTEHRNQFRSNKGDLP LSIQST"

CDS 641466..642173

/gene="lgrE"
/locus_tag="EFAGFIKM_00589"
/EC_number="1.1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q70LM8"
/codon_start=1
/transl_table=11
/product="Linear gramicidin dehydrogenase LgrE"
/translation="MKKIQLFCLPHAGGSAMIFHRWKSSLSPFIDVIPIELKGRGARV
GEPFYESFEEAIEDIYPTVSSLIHGYPYAIFGHSMGSWMALELYYRLAQSTKQLPEHMM
LSGNRAPHIFKDENIHALPDEEFRETIQNMGGTSDEVFTNKELFSLFAPVLRADFRIV
ELYRFQPKPFKVQSDITVLTGRSDTRVKSSDLIGWKKYAGSQCDIVKLDGGHFYIQEN
IQETTRIINEKLQPYVI"

CDS 642197..644761

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TSINIGANTVAFVDDQMFELEEVQFEHAEVR CIDAAQYLDIPDMMMNPRFITEDSKL
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CDS 679642..680916

/gene="fenF_1"

/locus_tag="EFAGFIKM_00598"

/EC_number="2.3.1.39"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9R9J2"

/codon_start=1

/transl_table=11

/product="Malonyl CoA-acyl carrier protein transacylase"

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CDS 681004..681984

/gene="lnrL_2"

/locus_tag="EFAGFIKM_00599"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94440"

/codon_start=1

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/product="Linearmycin resistance ATP-binding protein LnrL"

/db_xref="COG:COG1131"

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DEPTKGLDPVISRRVREFIKSYVRDEGKSIILTSHILTEVEDMTDRVSLMRKGTLLKT
GTIAELKSNLGAVEFIDIPRADLPPSIQERITALPEVTSTIIEEEEDTVSFGITNLYD
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CDS 681981..682853

/locus_tag="EFAGFIKM_00600"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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AESMMILVTCLVVIVALMALGVMIALLGILYRQVSSIVGILFIMFEFVAGAYFPVDQF
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KVEKMAKKKGLNLI"

CDS 682891..686577

/gene="dltA_2"

/locus_tag="EFAGFIKM_00601"

/EC_number="6.2.1.54"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00593"

/codon_start=1
/transl_table=11
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WEDQHISLPVVSSEQLAYLIYTSGSTGRPKGVMIEHRALRNFEVGVRSIPFEAGKRI
LALTTFSDIFVLETGLANGLTLIMAVEEDQLSPSRI AHLIVTHNIELIQITPSRL
RMLQIGLTVDSPVWSVIQTLMIGGEALPYALYEEIAGMTSARIYNMYGPTETTIWSSI
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SLFPVLNFYSIGVLPVMINDRMHYRFDEHQGILRLEYQAVLSDDQLIERMGLTYETKT
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LGELRDMFIDHVRVTPGEINQELSHLLSFIQKTYQFN EEEEDSPDTAYAEVLQSIVDI
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CDS 686570..687595

/locus_tag="EFAGFIKM_00602"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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EWSTDYLNGIWAIKTDKEYKEPSEYYYETVLQFSKENLMNILKEYVGETNQVRSILRK
DHRYLGSEIYDKMIDMLGMQKEGMQNQPFAIHPFHLLYEHKQLLAQAILDFLPDPSLK
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YQSQLGQ"

CDS 687750..688979

/gene="sbnD_1"

/locus_tag="EFAGFIKM_00603"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2G1N0"

/codon_start=1

/transl_table=11

/product="Staphyloferrin B transporter"

/translation="MPQWKRNLYILWFGLFFNHMAYSLSVPPFFIFLQNDLGIQSGLE

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EKTLFIGLIGGGIGSLLQMTATNLIYFGSLRFVYGLFFAAVYPALNALIIKYADHDFR

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KTELрмаVDSGSTNMKK"

CDS 689010..690332

/gene="moxC_2"

/locus_tag="EFAGFIKM_00604"

/EC_number="1.14.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34974"

/codon_start=1

/transl_table=11

/product="Putative monooxygenase MoxC"

/db_xref="COG:COG2141"

/translation="MSQRQLKLGANLNGVGNISIFWRHTDIPINASVSLEFYKKQVRI
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FTVARQFASLDQLSGGRAGWNVVTSPLEGSALNFGKGEHPNHALRYEIAEEHLNVVKG
LWDSWEDDAFVGDKQGVFFDPAKLHTLNHKGTHFSVQGPLNVGRSKQGYPVIFQAGS
SESGKDLAARSADAVYTGHE TLKEAREFYRDVKARAVAYGRKAEDILIFPGIGPIVGR
TAEAEQKYQEIAELVNIDQALNYLGRYFDHYDFSQFPLDEPFPEIGEIGSNSFRSTT
DKIKQQAREQGLTLRQVALLASTPRTSFIGTPDQIADQIQEWFEGEAADGFNVRTVVP
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CDS complement(690496..693645)

/locus_tag="EFAGFIKM_00605"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

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CWLDEAVDDLVTGTAILTVNILD AHAPERTKLLHALQQSFRLIDWSQPKSDIFYSS
VHDARDDLSVRLNAMDKASDVTVTCIGH THIDVAWLWRLKHTREKCARSFSTVMRLME
MFPEYVFLQTQPQLYEYVKEDYPELYESIKERVAEGRWEAGGGMWLEADCNL TSGESL
VRQLLIGTRFLKEEFRTDCRYLWLPDVFGYSW SLPQILKKSGIHTFMTTKISWNQYNR
MPFDTFHWRGIDGSEVLTHFITTP EPWSEPGSWFYTYNGKIIPKTVKGIWDAYRDKEM
NQDLLLSYGYGDGGGGVNREMLEMRRRLDQLPGLPKVKTGRADDYFEKLQETVEKTDS
YIHTWDGELYLEYHRGTYTSQAYNKR MNRKLELAYREAEWLNALQSIVHNDWNLYQAK
SLTAGWKIILRNQFHDIIPGSSITEVYEDSR IEYAEAEQIGSHVDTQARLAIAGSGES
PYTYTIWNSSPWVVT EIVSISVASDELETGTWLSDSGEILNAQYQDARWAVEVKDIPS
LGYTTIHFQSSTVNAISEQSPFIHTANGIETPY LLEWNESGQLNRLYDIELHREVL A
KGARGNVLQVFEDKPLAHEAWDIDIFYQEDMREITKCTSIEVVETGPLQAVIRFAWEY
LGSTITQNMVTYTGHRRIDYATEVDWHEQQQLLKVAFPVGIRSTEATYDIQFGNVKRP
THWNTSWDWARFESVGHQWADLSDRGYGV SLLNDSKYGYDIKDNVMRLTLIKSATHPD
PHADQGLHSFTYALLPHQGDWLVG GTVQQAWLLNAPARYTQGVSEQPSCSMFSLSGST
AMISAVKKAEDSKRVIVRIHDYSGSMNTLELTSDLRIHAWREC NLME LPEGELLYDTP

ITFALEPYEIKTFEIDLRV"

CDS 693895..695709

/locus_tag="EFAGFIKM_00606"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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YAYSyrTERGNFDYQLRLLKDEASIANVVLYSTDQEFFYVLNRETQHFYYHPKLSAG
HQQWFQRLRNAPWQYMGSEPLFEGKMADEPTPSYANVLKDSVTLKQYGAIMFELNTD
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KVQLLNIGNTGMVVASIIPESHKQSLQAIRFSLIGIVILCIMVSIAVTFTIIRRYSK
KIHRVLVYMRRWQEGDLKRIEMEGEDELQQISQRFNHMCDRLESYIETVYVSEIKQK
NAQLVALQAQINPHFLYNTLESIRMKAISLGARDVGQMIYILATMFRHLIKKQTHVTL
VEEIELCGMYLALVQYRYEDKLHVETHIENAAAGSMVVKLLVQPIIENYIVHGFRTYD
DDNRISITAEENGIVIRIVKDNGKGISAERLLELQQGLHKGDEAAETSDRSLGLKNI
HDRIRLNYGSDYGLHLNSVEGEGCEVTISIPVTREEMG"

CDS 695706..697265

/gene="rssB_3"

/locus_tag="EFAGFIKM_00607"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00958"

/codon_start=1

/transl_table=11

/product="Regulator of RpoS"

/translation="MRSVMLVDDEPLIVKGMQAIIDWDQNNMQIAGTACNGLEALAIM
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RAQLLEIPMNKSTYCAASLRIVGDDKGDDPQMYLPGIAEQCEQIGNKGLPDGCGIICF
PDQDGDIMLLFVSAGTEGNDEWQLQALTRMKQAVTEDTDARVWGIIGQSESTYLGFPK
SCKSVKLWLQNHLFKDCNTFIMQVENQEATNQHQEKPGPVMEQFHKLLRDGEGTEVDR

FIDFFNVEGKEVCLPRTPFSNSAIQLMLAAKELEKTPDYGDIFGPLSRIHTLNKLKQ
LVRKVVHRTLDRYHTVEKTYSPHIMAVLEVVKNHYPDELSKTLTSQRLELHPNYLGHL
FQQEVGTTFSQYVNVQYRIERATHLLLYSDKKTAIEIAGEVGYWDSTYFYRQFKKYAGVS
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CDS 697527..698456

/gene="yteP_5"

/locus_tag="EFAGFIKM_00608"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system
permease YteP"

/db_xref="COG:COG4209"

/translation="MQDIFKSLMKNKAFLLLVLPGAAWFIIFAYLPMFGTIIAFKDFR
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MNELLNKRLAKIYQTAMFMPYFLSWVVIISYFVFSFLSVEKGVFNQIITYFGGDPVSWY
SETGYWPYFLILLGLWKGAGYGSVVYLAAGIDRSYYEAAMIDGATKWKQIRYITLP
LLRPLMIILTILAIGGIFRSDFGLFYQVPRDSGALYPVTNVIDTFVYRGLTIMGDTGM
STATGLYQSVVGLILVLLANYAVRKIEKDYAVF"

CDS 698479..699435

/gene="araQ_5"

/locus_tag="EFAGFIKM_00609"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein
AraQ"

/db_xref="COG:COG0395"

/translation="MSNLSQPVKRASAHAKRTGKKSRDLNAISPLSNVIFNIAIGLFA
LSCIFPFLFIVIISFTDEKTLAINGFKLFPEVWTLDAYRFLMESGQQMAQSFGVTLTV

AVVGTALTLYLVTTYAYAISRKNFAQRRFFSFLAFFTMLFSGGLVPSYIVVTQVLHLR
DSIWALILPSIMNAFYIIVMRTFFTTTVPDAVIESAKIDGATEFGIYTRIVLPISLPG
IATIGLFSTLGFWNDWFNALLYIDNANLIPLQTLIRIQNNMDFVVQNSSRVVSYDIA
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CDS 699494..700993

/locus_tag="EFAGFIKM_00610"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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ENYDIAFTSSWAYDYLPNATRGAFPLINDLLDKYGQGIKEQLDPRFLTGSQIDGQNYA
VPVNKELASQWVWRFNKQYVDKYNMDITKIRTLEDLEPYLQQIKDNEPADITPLAVPK
GFKPYLAFLDFLLGDEFVGINMNGDTGKYVNMLESEELNSSLKTIRKYYQAGYLRKDV
ATLEGIDNIKTGKWFVDREQTQPYAELGWSRSAGYDIVTTPMQDPVIFTGSATGAMHA
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GFALGNLFLTYMHKEDPADKWEAFKEFNNSAKVAPSFNFNPNPDPVKTEVASISAIVK
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CDS 701092..703749

/locus_tag="EFAGFIKM_00611"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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AGMEIIWYDSMTKEGNISWQNALTDNRNTMFLQDNGSKVSDSMFLNFWWNLDLGSSAAKA
RSLGRSPFELFAGIDVEAKGYDTS LKWNLLFP EEPKPAVTS LGIYRPDWSFN SAESVTD
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GTQVRETGWNNRSLQDVLPTWRWLTESKGKALTPSLDWSDAYYGGSSLKVAGTLSSAN
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TDILNLTPYKGKRIVALSLYFDSKEIISDYDIHIGQISIQNNANPVKPLEAVQALNVI
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VTEGWSWTFDNGSPAVSTEQNPVVTYDKEGTYNVTLTATNSSGQDTVTKESLITVSKA
ASGIQNALGKKATADHACGSAEGAEGAIDGKVTGNSKWALGNQPHWLQVDLGKEHQ
ISGFVIKHAESGGEWSGFNTSDYSIQVSADGVNWSDVVHIQGNTAAETSDAIALVKAR
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CDS 704364..705191

/locus_tag="EFAGFIKM_00612"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIRGLTSAGLGNIENEQYITNAAKYGFQSVDLNPLSFIEEVGK

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CDS complement(705262..706140)

/locus_tag="EFAGFIKM_00613"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRTKHPIIVITGATSGLGQLAAMELAKRGAHLILTARSKERADA

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PFTARGSSPIYGKTKLLNIMFTGELARQWCGTGICVNALNPGFNVTGLGRELWFASVL

EHILTFLHIGDPRRGADIITRLAVESKYGEVSGGYFNVGTGASIVPMHPGGDEAMQNR

LWIFTTQLMKDHGVLD"

CDS 706277..706750

/locus_tag="EFAGFIKM_00614"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSENPVTKDRAALELALGEQIHALISASHALNVRSAERFDANL
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LLSLTELGGQSTVAALKEKESAFYNRISRWDDKELERFTAMLRQFNGLDDETVEA"

CDS 706754..707701

/locus_tag="EFAGFIKM_00615"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKTERQLAITLELQRRKMLRAEDLAAQFETSVRTIYRDIQALS
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KKMPGTDGNRYNMREVSPYGLSLVQENWMLIARCDMRQDIRHFRLSRMTELSVLEDQF
LLPPDFDLNSYRPPDDRNEQVLIRAKPEIADKVMEALHFYMDAFEEQEEGVIFHFRVR
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CDS 707769..708305

/locus_tag="EFAGFIKM_00616"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKSTTEVLKSFETAVERYLAELNKLDMGSLHKKQSEEEWSIGQM
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HYRHHFLQLDRLKSNLEM"

CDS 708332..708808

/locus_tag="EFAGFIKM_00617"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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CDS complement(708851..709357)

/gene="yidD_1"
/locus_tag="EFAGFIKM_00618"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00386"
/codon_start=1
/transl_table=11
/product="Putative membrane protein insertion efficiency
factor"
/translation="MRNSESEELIFNNMPSEEEELIRLLHTHHEENDPRSSFYIRTHVI
PEIDWLKSLNVTALFAGLIISMICFYLLNPFIPVYALLSAQIVFIASMLFIVLRRV
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NGGGYDYP"

CDS complement(709374..709595)

/locus_tag="EFAGFIKM_00619"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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CDS 709861..710454

/locus_tag="EFAGFIKM_00620"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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/product="hypothetical protein"
/translation="MTDTSGNRKVDGYLKKLKTWKEESTKLREIIRDFELTEDMKWMH
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CDS 710576..710833

/locus_tag="EFAGFIKM_00621"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
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ALEFLDGEPPVEDIPPPQRIMPELLNSRDKAYLEANITYY"

CDS complement(710989..711735)

/locus_tag="EFAGFIKM_00622"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MLVSGFFLSVTGGHGAPFLALVGDSPWEARKNVRINVKHGVDLI
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SRLVYDSMLKGVKQAIENDITIGIGTDAAMPYVTHYDMWREMDHYMRQANLNNKQVID
MVTRTNAKILGVDDVTGTVDIGKHADLIII"

CDS complement(711729..712184)

/locus_tag="EFAGFIKM_00623"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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NIPSHYTTIDLSGKYVMPGLINAHVHLFADGKPFSLSVSEGLLQFAYDRILNTKFGRN
VLKKRMKRNALTALHAGVTTMRSVGEFFYTDVQSYGMRLTTVTLSPIC"

CDS complement(712529..713140)

/locus_tag="EFAGFIKM_00624"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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ITYYFKNKKELFYAVPPDLVDYLKNVLVETIHFDNQTLFEETDSERKSALLQE QVDV
LRKYRNQIVIFEKNKG TIYTNAKNELVELMIETKKAYLKNQYKRYEIGTEENLILLN
ILAHNVIDMNLDLLKRDMSEDSRKQIFEALYVYRLYGMKSLNQ"

CDS complement(713560..714006)

/locus_tag="EFAGFIKM_00625"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFNYKEQHIYLETCSSKKKLQELRKNTSLLLKQID EKISIIP TK
SIPINCPQCRSSNTKKNGRLQKRSSCND CGQSFSNVYMPNIFQNTYYPEKKLKLICLI
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CDS 714174..714608

/locus_tag="EFAGFIKM_00626"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVKIFLGSADNPSALDDL RKIAALIEHVGHFVIPWNSPGVFPLG
KHMSDSL DNICKQVDAAILIFGEEHQVLF GNEFSLHPKPNLLY EYGLFKGYLGLERTI
ICRRGSSSIPSDLAGVIYCNLDKEFKAERELLAWLRLLSPKN"

CDS 714642..716177

/locus_tag="EFAGFIKM_00627"
/inference="ab initio prediction:Prodigal:002006"
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ALEYWKSLFGAFQTLHEASVDYIASLQTGMAEDLMATDSFLLYKDSITHYLQDFI
QALQRRSYKIEGNLSQITIGVRDLFLNEVLNDEWRIPKLEQLVTKSEYMDGLLEK
WSSLVRWFIGD DNSISDSFLLERATKEAIVKVRSASVRIQERKRSIVSRKKDL
DYLGKCFYRISDLDNA HKLSANVFGLFSARHLQGEDLRESDSKELSMWKEA
PIPRKIRSRSRKRSERQGILAAI NNSKLKEQFREAYVIRQKHELEFLIRMVN
SEEISISEFEPVKESTRLQMLGWISRCNA SSTYSFQNSEGIRIELGQPPDNKR
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CDS 716208..717437

/locus_tag="EFAGFIKM_00628"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MVKIKVGKLSARRQRMNRPDRNEILERKQICMNALLNRPWV
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FQEFREPLD YALFTYSLWYLESKIEGEQFLLTQLVIDIRQYMVEQEMNVDWGN
YYHRLSMARALKKL KNLNVIRAVDGEENWASNHEYHDVLYESTLYSRYILRN
FNAELSSYIHIDKFNDTKT TYSNETAGVDVRNRHELYRRILLEPILLNYQWSG
DPIYLKQELNLLIRNIGEMFGWQG SRYREGIFLFESNTITESEVFPTQLALS
DLAMLCGEVRKMKVINSESNEVDINGLLT LTKNEIERILIRLKSSFSEFWTNEH
KKKNSSELAEQICNHLAEWGFGYWEDHIFVNLN GAAGRWEVEYGLAEQDD"

CDS 717449..721558

/locus_tag="EFAGFIKM_00629"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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/product="hypothetical protein"
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GSGGQVVQEQTAYRDMVNKAVFGFRETESYKDLLKLLLELRSPKLSKDMKPSAIYEIL
NKSLPPLMEEDLSSLSDVLEDMDQITDRLDELQLHVAELTNLEKNYARYNEFLLYDAS
TDVIHRWKVHNQIISQLKQAEKHLEDLEESKTNIQKFLECKQRLGIVEADLEVLTQG
EAIGKQKELEIYEEQLREVRQQVQTLEEKVFSNQKKVTKLTDDISVLSETLHQLTKEQ
EQKIDEMEDMARIIEFHRHDIYHGVWDRSIPEENNWYRSWRGDLDShRKKLIFAQQIA
RKEGEASRVAKDVEIQLGEVLQQRHQVEEEQNICEQELEKIKENMRLDIVSWYRGLEF
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KKQLRLEEELEEWKVAKEPEPLKTEKRQSARRNRGPN SGAPLYAVCDFNDTLTQIQQA
QLEATLEQAGLLDAWILPGGKVELMEQQNTEEVWIIQISSNKKNGKTLCSVLHATPTE
KSGLSMEDINQALNSISWREQTELLINEYEKNRAYVTETGHFSLGPLSGTNISKSRSRSE
FIGEANRLLTQLEMARIEEEIKHLNEQIDDINQQLEELNINQKKMESEINSFPPDDH
LQIQLELFSKTTVRLDNLMEQEKNIEERYKLVSEWRALQMSLLEQTAEWSLLKNESQ
ISEAIEQCSVYNSYISELYSIWIQYRNSENKRSNEGLLADLLLDVEEDQMELVAKKN
LIIKRAEQVKLLNQIIEKGIDDIHRQISNFKKERELLGNEISRIQDLREDRSTQIGE
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GRVEKEYGKLFSNVNQDRIVSDLTKEFHTSKPNLIEYAIEMEYDTQNSSRIVILSKMD
RLHPVTPGLLLSELKQQIEEQQILLTARDRELYEEIIIGSVGKAIRKKIHRARAWVDQ
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FRVRILQAKQEAQREDGVL RNYIFSQLDYRSWFEFKLEHIKGDRTNYTELTPKFNVL
SGGEKAMAMYIPLFAATYSRYSEANLDAPKIISLDEAFAGVDDANMRDMFHLLTDMGF
DYIMTSQVLWGCYDTPVSLAIYEIYRPKDTEFVTLFHYRWDGESKVLIN"

CDS 721567..722976

/locus_tag="EFAGFIKM_00630"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MELLNRKTAKQYYSDPLFENLLNAVFNKYKGQNGVRGNILIIK
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VLKNVVEKGENPYSKLLVCMSALWHLLMRKEEMFVERGISTGKIRLPTFAAHVTKDPH
AFDKKKASGRLLWHALHDIDNHTSIINKIEKNERTVVQEYLLERQIYRNFDVLDDDL
SISHIFVPNLIRGTSPRTINLREVEEIQQLPKYKAVYIENPSIISYLADETIHFLNV
NKLSMEQLPENFPVLLCTTGQARAASKLFIEKCLASNPDCVIYYSGDLDPGVQMLYG
MKEQFTAKFKAWRMDSYIRKYVSPKSRPLSKEDLKFLIENEENLHRVMVQLGAKVYQ
ESFNKELGKDWIEVICEAI"

CDS 723084..723353

/locus_tag="EFAGFIKM_00631"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTSTNSEDFA SQYAQLVRQEHDYVNQLVTCNKLILDAMDIIAKQ
AGVLDMGTVKQAAYHLHAMEQDLNRKLFKVRLEKSILANQMSQST"

CDS 723550..724587

/locus_tag="EFAGFIKM_00632"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
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PELMYQPLGPRLKEQYEDVEVVIGNDMNLTVYGLYNQQQFEEKNFAVVTFPENHFPG
AGFIIDGRPLTGNTQFGGEVSFLPFGVSREEQLRMLKSTEGLQELVVQTLVSIIAII
PATIVVTGDTMDPAMRDGLTQGCLDRMIPLEHMPELIIQRDTRREYVTGLVAVTLESL
TYRIQVIEKQW"

CDS 724836..726092

/locus_tag="EFAGFIKM_00633"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNQQAGTQGNKRKFNKLYAMQLATIFLGFIVFGISENIKGPAIP
RIQDFDNLDEKQLGTLTSLNALGYLIACAFTAILVRKWGIKAVSIISFASMILSGVFI
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LLATGVMSLSVFGHELDWRGMYLVMLSLCLLPPIAALRSKFPGDDLPHEDRTSLKTLT
RDPALWLMVLILSFGVVSELAVGGWLVNFLEKAYTWDTVKASGLLSAFFLTFSLGRL
LGPLTDRIGFVLSLILFSAFSGVCTFVALAGGERLAIFFAISGAGIAMIIPTVMAFIA
RRYPNGSDTAITFTVTLMGVGVSIGNYVIGWVIEGVKNLYGSTTQLGLLRGLQAGYGF
IGLCAVICAASGVVLYVYLKRRQELI"

CDS 726197..726580

/locus_tag="EFAGFIKM_00634"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKRIGLLFLICLCPLIIVACNQKNNDDVVAEIEYHKEGNVIKIT
QRDTVNQILNILESAQKNKKVIDVGKTDEKIVVNYSSNDIKIFDLYIDFDKSVGMVVM
ESDSNYAYELSSQSIKDLKTILKGT"

CDS complement(726751..727356)

/locus_tag="EFAGFIKM_00635"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTEWITQFILFFKDLSYAGLVIALSFEFVPAELVLPMAGYWVYL
GDMKLWLAILAGTVGGTFGPLTYALGRYGGRPMVEKFGKYFLIRPHHLDASDKFFEK
YGSQVAFYGRFVPGIRTVISIPCGMAKMNVFKFSIFTFLAMLPTSLEYLGLGKLSQ
WEHVDEIVKPYIVPAAVVFLGAFGLYVLLKRWKRRTALNKS"

CDS 727645..727755

/locus_tag="EFAGFIKM_00636"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTVTSIIDQIHII EYAPSYAAVRKTVEAGWPTGVWF"

CDS 728193..728495

/locus_tag="EFAGFIKM_00637"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEHQPNERRGIAMTTATLSKWGNSSAIRIPNQLLKRLNLEEGSE
IEILVTEDNELLRLPKTKPVESNEELRNHLKTLLSKVKQDTRHEEIDFGTEGNELL"

CDS 728492..728827

/gene="mazF"

/locus_tag="EFAGFIKM_00638"

/EC_number="3.1.27.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AE70"

/codon_start=1

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/product="Endoribonuclease toxin MazF"

/db_xref="COG:COG2337"

/translation="MIIPKRGDLIWLD FDPQAGHEQAGRRPAIVLSELEFNEITGFAV
VCPITSQAKDYPFEVTLPEELPFSGVWLTDQLKSLDVRQRRIQIAGHAEPTSEFMKSV
LRNVRSILA"

CDS 729127..732294

/locus_tag="EFAGFIKM_00639"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
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TVRREMESSSNLYVFLAVHEKEVVGFC SFAHYRYDERALYVPLLNVRPDYHGYKVGRN
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EALTPYFEELD WYADSTREL VVEPDGRRERGFDFDYTWKKGDVSLRAEFEKSGRGLT
ALETPDYEISTEVDDHDLVFGSSYKVR YRIKNN SASELAVEIEGEDNKNIRFALDVAR
AVASGETIIVEGEFHVDPITEEQNNNKTHPVVASTWLIGGKKA EFR LGIAPKFPKIK
TILPVKELYPGIPDELVLNVENNVD AETEFSLDLPAGEFLEWAERSVRFTVPAKGKVS
VPVPFTLSYGLYSQEVEVTAIPAGNH AISFTSKLSVLMKGIEGKYGGQIEDQWVAVN
GAFSLHMNKQDNNMWIEYPGSRHSFWWTYPKLGKPF AEELSKKQAKEVNIYPEGERQV
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ILPYQDRFVDMGDSYAGDP SHWDSAQITENWLFCKEEYGASGIYWDLSLKLLRPEYTL
GFQHELGRIPAGAVVRTKATVYALNTFAKWQDFRA FARKQRNPV IPLLD SHLDLTLSE
GNPFAPDVLQATLTEHKL VPLAGKLELYVQQGGEPEVMANAKEFSPEQNLNSAKLTFS
PDEADRDQHVSGWKVRGLYRGEDRIQERTALWFPQSGTEVKQKIEEGSAGPLYTVDNG
VLSIAVAPVFGSVVHSLQYAGEEWLDSSYPEPAPRSWWNPWYGGLGVGVPGMNGFSRQ
LEQRAASWTEQKDQYGNVWKG IKLTTRIEKHEANRGITIHQH YLMLPSVPVLCTLLAV
TNESGLTLTDYSLAEERFLQPSSVFAEGWIEQPGKDRFPLGKVDVGLPLEDLLRVGSV
SRENMLHAVHRYPNQSAWGFANNQVTGLHVNHH LTLQHGETVWTEPTYLV LGQIPLSS
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CDS 732281..733159

/locus_tag="EFAGFIKM_00640"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MPIIDIHIIHLS DIDSFHQTAIDLSKVDYSAAGLKA EFDKNDVIL
GIGMGVTEQTKGAFPDSSSPNPMGLDLEEKVPSFLMECVGINPNALDGKNAQDELDRI
EARLQSPEVAGIKLYAGYYHHYVYDKIYTPVYELAAKYNLPVVIHTGDTYSMNGLLKY
SHPLTVDELALQQRGVNFMICHLGDPWVMDAAEVVAKNP NVYADLSGLVVGDRPHFER
FMNEPLFMDHFRRALVYSDHYEKM LFGTDWPLAPIDL YAEFVRRLLVPEQH HDKVFYEN

AFGLFPRIGQRIADLG"

CDS 733417..734580

/gene="adh2_2"

/locus_tag="EFAGFIKM_00641"

/EC_number="1.1.1.192"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A4ISB9"

/codon_start=1

/transl_table=11

/product="Long-chain-alcohol dehydrogenase 2"

/db_xref="COG:COG1979"

/translation="MRSFQFYNPTRLIFGKGQLQALQTEVPKYGKRILLVYGGGSIKR

SGLYDQVISQLNEIGAEVTELAGVEPNPRLSTVHKGVLCRTHNIDLVLAVGGGSVLD

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WAWFSEYSFPAFSILDPEYTYTVPLDQTVYGMVDMMSHVFEHYFHLDTNTPVQLGFCE

TILRTVIDTAPRLIKDPENYELRETILYCGTMALNDVLNMGLAGDWASHNIEHAVSAV

YDIPHGGGLAILFPHWMKHNLDVDVDRFKRMAVNVFDINPTGKSDKQVAEEGIEALRT

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CDS complement(734737..735162)

/locus_tag="EFAGFIKM_00642"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAKTALPTLLNVVRILLSVKLIYVIVSFIVFLIDFNQNMEAYLG

FLRKGDDLAYASGVILARMLFIIGPSLLAVIFITKRKFCLTVTFLSLALFVSIPNESN

LFTLIHLFALLIVLLHRPSKMYLKRKDTPVNEAVVEPKN"

CDS 735439..737496

/locus_tag="EFAGFIKM_00643"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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AIQGKNVISEGIVAKSSGQLGTAFAMPIYNENQEVQGVLSAASTSFFVNQLQNININ
DEGKVIILDRVGTVIYDSADEKLAGQKMESGEYQSLIDLPGAELQQGDISTDEKVAY
YSKIPRSDWTVVVEDKLSDVQKPLRAMAKQMYIVLFSIAVSVVAGILISLLVTRPIT
RLTVLFRQLAGGDLTVQAQGKYSGEFKQLVDSFNTMAAGNKQLISSMNHSIGILKTST
SELEQSTQQTSTTIAETTTAFEISRAMESQANDTGAIVDKFMNVGNKIANVNGMSQA
VKFKADEITDAFKNNHEVIDALIAVNGQNEIEVGNISKITVQLAESSSGIHQITGTIA
EIANQTKLLALNASIEAARAGDQGRGFAVVASEIRKLAEQTTAQSEDINRIVMQTIDH
VEQNNRSVQAIEAIAEQHKSSVSQTKETFNFTENMNEMMSQVQAIATEIESIERDKD
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KTK"

CDS complement(737597..737995)

/gene="yabJ"
/locus_tag="EFAGFIKM_00644"
/EC_number="3.5.99.10"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37552"
/codon_start=1
/transl_table=11
/product="2-iminobutanoate/2-iminopropanoate deaminase"
/db_xref="COG:COG0251"
/translation="MTATMSTIIHASTAPKFPLPFSHAVRAGDFLYVAGQVGVDPQTL
EPIGGIKEQTEQCIRNIEVILQEAGLTLDHIVKVTTHLARVEDQSEYNEVYARMIKQP
YPARITVFSGLGPLYIEMEVLAYAPSIRGE"

CDS complement(738003..739379)

/gene="gatA_1"
/locus_tag="EFAGFIKM_00645"
/EC_number="6.3.5.7"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9HVT8"

/codon_start=1

/transl_table=11

/product="Glutamyl-tRNA(Gln) amidotransferase subunit A"

/db_xref="COG:COG0154"

/translation="MITKPLNELTIAEAATLIKNKLISPVELTKSYLDRIEKVEPAVQ

AFVTVTAEQALQAARESEEKLMNGEYLGPLHGIPYGAKDIIHTAGIRTSAGSSTFPDF

VPGTNATVINKLQAAGAILLGKTTTTEYAFQGGEPTRNPWNLEHTPGGSSSGSAAAV

AAGMASFTLTGTQTFGSLLRPAAYNGLTCMKPTYGRVSRNGVITASWSLDHIGAFTRSA

QDNAIVLEAMAGQDELDPFTLPHGKPDLTNALEHPISEMVIGLPSNFFQTDEPAILLA

VESAIIVLEKLGMQWKKVDLPSYMGETIAAHRTVMRAEAAAFHQERFAEASDRYGHTM

REQLELGYQTSADVYLQAQRIRTFRSEMMMLFDEVDVLLTPSTPYVAPHGYKTGSP

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CDS complement(739573..740604)

/locus_tag="EFAGFIKM_00646"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRTFKKIAILTAMTVILTLLSACGSNATTPASGAGASNSGGQA

NTQVDKIMVSEVYHNLLYLPLYVANNQGFLEENRIELSSIRAAGSGPTALSSVISGES

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PTSSNSLLRKLAFADNNIDIDKDVITTEVQNGSELGAVLAGKADIAIVYEPQLDQGIAE

GLHIVHDFTKDYPDFAFATMNTTASFIEKNPDLTQRFVTSIEQALDYIQANPEGAKAV

AVKEFPNLDKNVVEQAVQRMIDSKVYPAEGLINESAFKTAIDMQRFIGNLKEDLAYED

IIDSSFTTK"

CDS complement(740639..741505)

/gene="ribX_1"

/locus_tag="EFAGFIKM_00647"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A9WGD1"

/codon_start=1
/transl_table=11
/product="Riboflavin transport system permease protein
RibX"
/translation="MKSTSPEITLAGKPARVVKSKRRQSTFSKEWLMTMLWRFIIVAV
ILVIWESAVRLKLVNGFLMGSPSAILDAAITMASSGQLLTDAFATVNATVIGFVAGSL
IGSLAGLLMWYSKSVARVLDPFIVAMNGIPKIALAPMIIIWFGSGIFSKIALASVATF
IVALLSAYQATHQIDESQINLMKSFGAKKSQIFRKIIVPSSLPWIISAFRINIGLALV
SVVGGEFISSDKGLGHMVFEVGNLFNLPAVWVGVMMLVAMLLYTCVGYIESRLLPW
NDNKTSSKSTSV"

CDS complement(741505..742401)

/gene="btuD_3"
/locus_tag="EFAGFIKM_00648"
/EC_number="7.6.2.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01005"
/codon_start=1
/transl_table=11
/product="Vitamin B12 import ATP-binding protein BtuD"
/translation="MTIMQTVYMIRNIFINVMLINIKLHQETKKHQAVGKGLPIMAIQ
IQGVSKSFVSATGEDIQVLAEVSMQIKKQEFFSIVGPSGCGKSTIFNIIAGLLKPTNG
KVIVCGEEIDQTTGHVGYMMQKDLLLPWRSILDNVTLGLEVKGMSKKDRGDIAMDYLD
RYGLASFAEAYPSTLSGGMRQRVALIRTLVTQPDILLDEPFSALDYQTRLILEDEIL
SILKSEGKTGVLITHDIEEAIAISDRIAVMSKRPTTVKQVYDIGLASQYGSALKARSD
QKFKQYFESIWSELDIQMGRIS"

CDS complement(742513..744192)

/gene="pucR_1"
/locus_tag="EFAGFIKM_00649"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32138"
/codon_start=1
/transl_table=11

/product="Purine catabolism regulatory protein"
/db_xref="COG:COG2508"
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SPLLSSPVLLLGSKKQITASSNYVQQLDDQSLAAPILTFIDENPSFHTAISICLLTAD
KYRHAELHPIFTDRHEGYLIALYDSSAISKLSTLALQAVNVIGLELTKKQAVKERSR
RYKNEYFSDLIQGFIRSEQEALHRGKKYGLQAKGSSVLIIAKKDESLAGIPKQNSTSS
GEERFISERDANYELIKQEFARLDLSFVMFTKNDQFGILVFLAESSWDEHTVVQQLER
MASNLYSESQSLSFSGIGNPYTNVLDIGLSYKEAVKALQSGYQMRKTRFAHSYQTMDI
SRLLRMIPHDEMLQFHQETFKPFNDRDPNERSELMKTLSSFYENHCQIVDTAKELFVH
RNTVIYRLEKCEKLTGRNIKDPMESLRFRLAFALESLLNVNPAPSEANHTS"

CDS 744411..744887

/locus_tag="EFAGFIKM_00650"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKGKGLVSLLLASVVAGSILVASTTAAERVVAQTPMEAATEYFQ
AYIARDVEGMMFYSKDTNYLDEKSREEGYVKDFKTNPPTGYEIVETRQINTDEVQLYV
VQKYAGQGYEQSPPLPYKIFKSENGWKVLVEPLEINTVTGKVTGTPihalQYTDH"

CDS 745044..745688

/locus_tag="EFAGFIKM_00651"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKISDRLLRQYLDHVVWICGGPCGGKSTMTKLLSSKWDNMNYSS
DDHTFDYQKKANPQDHPAILRHFIDWEWFFLGRGNDRSHWLNSVFDESVEFIILDLLQ
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DPQRAREETLNTVVRASNHYLQQAQYQLKWFMRTSQSNKDQMLLEVEKHFGFR"

CDS 745930..746442

/locus_tag="EFAGFIKM_00652"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKKRLFATVISLALATATVTACDSTSQTQENMSNPKTGVLSSSE

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DPDDTVQLTY"

CDS 746528..747061

/locus_tag="EFAGFIKM_00653"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHNMMNKRQFIEMTVKEQHSVVFKNRDEFFRGVAKGLKEGYL

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CDS 747135..747338

/locus_tag="EFAGFIKM_00654"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKEGIKNVLLGTVVVFVVGFSIILLTSSDIEAELTYAAIAYAL

LYLASVISVCTAVLLKKMTQLKK"

CDS complement(747479..748084)

/locus_tag="EFAGFIKM_00655"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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TYWRTGVNTECKFLLLNCFEQLALVRVQFSISGYNIRSQRAIERIGATKEGIFRKHR
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CDS 748355..748843

/locus_tag="EFAGFIKM_00656"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MTFPTHIVSAGGIVEDGTGNILLVKAHDDGWVYPGGITEVGENL
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SV"

CDS 749595..749792

/locus_tag="EFAGFIKM_00657"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAIMTDSRGNIFLEFIRIEYDKVITSTLDAPLTHALIVVKYQGK
YLFMHNKWRNNWELPGGIIEA"

CDS 749847..750065

/locus_tag="EFAGFIKM_00658"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDSAEFKGLMKFRLQPSFHGPERTEYGALFMGELCQLDDFVEND
EASSIILWDGTSEIGDIAEIDRKLIEFV"

CDS 750198..750605

/locus_tag="EFAGFIKM_00659"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLVLALSMIFAGCSPKEKNEDTITERIVTSDFVLEVTTPTVLGT
GETMKVKGTLKYRGMKPVEVSHGKPIIRFFFSGSDEQRNYGDVG YVTEFKSGQVVEVE
DEFIVTKKGKQNLIVDMTADISMTMNPIEIVVK"

CDS complement(750757..751119)

/locus_tag="EFAGFIKM_00660"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIIQVSPLAEARLTEKLGDRPGYFKLFYDTDGCGCDGIAVLLIL
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DLRDTADVAPQPTGWFVR"

CDS 751407..752435

/gene="degA_2"
/locus_tag="EFAGFIKM_00661"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37947"
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/db_xref="COG:COG1609"
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GFHRVYTDEGAGAAALAAEHLLELGHRDIAFVGGLKELSTTMVKVRVAVQKKLREHGLEI
PKERQLLGSFSIDDGKREMSKLLDRDNPTAVICVNDNTAIGA IKSTIEHGLSIPRDI
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QSTGPAAR"

CDS 752617..753888

/locus_tag="EFAGFIKM_00662"

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/codon_start=1

/transl_table=11

/product="hypothetical protein"

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QAYASKNQIIPDDMIQANNVNMSEYSDDIANLMKYDGKQFGLPDRAGAMVLFYNKD
LFDKAGVEYPTKDWTQDDLMAAAHKLTVKENGKTVQWGYPGSWWPQWMQLIYQNGGS
LFDESGKPTFNTDPVRKALQFMNDLTFTHGAGPTPTIADMGNIGADPLFAQGKIAME
TTGFWNIGSLAKVEGINWDISPWWGETNAFFNGLTITNASKHKEEAFKVIEALTTP
EAMQMPMVKAGQDAPATKAGLSSDEFLNAEYGGKKINMAAFSESTIYAEPFNPQWNEMMKL
INDKLGVYFNNKASLDDTVTEIQSGLERLYK"

CDS 753948..754877

/gene="lacF_1"

/locus_tag="EFAGFIKM_00663"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29823"

/codon_start=1

/transl_table=11

/product="Lactose transport system permease protein LacF"

/translation="MRVPSALCVMGGLNVIKKDGKWFYIFISPWLIGFLGLTLGPILF
SIYMSFTNWDLFQSPEFIGIDNYKTLTDDPIFWKSVGNTEFFYALISIPLGMSISLWI
AAYLNKKIKGITFFRILFYLPVVPVASSLLFIHLLAPTEGLINQALAIFGIQGP
AWLLDPNWVKPALILMSLWGVGGGVVLLLAGMKGIPQELYEAAAIDGAKSTQSFFHITFP
MLTPVIFFNLVTGMIGALQTFQVFIVTAGGPDNSSQMVPYLFQNAFQFYKMGYASA
IAWVLFIIIMVLTLLVFRSSALWVHYEEGKANE"

CDS 754870..755715

/gene="araQ_6"

/locus_tag="EFAGFIKM_00664"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MSNPSTVEKTISYIFLILVGVLLASPFLYMISIALASDATTVKS

AFTFVPMEFQWSNFYTIFTNNNLGTYLKNSVIITVFTIVGSVLSASIVSYGFARIKAK

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VMSIPKSLDEAAMIDGMGHPGIYWKIIMPLTYPILAAIAIFSFSYNWGNFMGPLIYIN

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SSGIK"

CDS 755806..757302

/locus_tag="EFAGFIKM_00665"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAHKEQRSRGKRSYILMGVALIALLAGGGIVINHAFANESSKTLE

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SNSPPYWMTISGSVTGAVDGSNNLRDDQYDAFADYLTEVVKHYRDEWGITFRTLNLPLN

EPSSDWWKKGNMQEGSHFTNEKQAEIHKVAASLKSGLDGTVISAADDNSIDETVFN

FNLYDQDTLDVIQQINTHSYNGSKMEELRTLAEQGGKLLWMSEYGTGGSEPHSHEDMT

SVQELAERIMFDLKIMQPSAWVYWQAVEDEGANNNWGFHANFNNGEEQYEMTKQYYGM

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CDS 757567..760608

/locus_tag="EFAGFIKM_00666"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
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LCAELGMWVIARPGPFICA EWDFGGFPYWLGTKEGVKFRENNETYLHYVNLYFDQLVP
IIRERQLSAGGTIVLVQVENEYGYLMDDAAASEHMNTLRDELLQRGIDATLITCVGGA
EGTIEGANFWSGADGHYEKLRVKQPDTPKMVTEFWTGW FENWGGPSAIQKTAPLLERR
IMEILRAGYTGISHYMFYGGTNFGGYGGRTMGSSDIFMITSYDYDAPLNEYGRVTPKY
AVTKNLSYFVHAFGALLMKTEGIPEEQIVVRHPEGISVRGRQADNQKIWFLESHKDER
ETMHITLEEGR TLQVSVNPGQIVPLLD RVQIAEHVYLTAGTMITGNEMINGDLTLFIV
AAAGQRSVIELEAEALNVT DSTVQVLVEHDSARNLHRFDLFHFQEPGMIQLEANGTPI
RFVILDQETMNRTWRLEATDQKGLRYVIGFDDVDVLP SGQVKGMITDPDRTIMLLGDW
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EDFSRYGQDFGYLLYECDFERPTEGVTNLILPDIQDTARIIVNGVQQALVRQVGAAGV
QLQVAQGQNTLQILVQHMGRLNFSPYLGESKGLAGAVYLG GKVQDIRRDWRMESGLVH
LDEVNSLQGSPLLSRSFTLDSMDRAILVGALSKGLRINGIEVPMEGYQDWFAFQTLDI
SLYIKPGETNTLEMPYSRSSLNRLELITYPSQGELKDWRMAGTDALLPQQQWESYEVG
QESIHLGAQGSIQRVGQPGIAAGGNCTANLVPD TTNESVNRATLSEKSHPVSNHTPV
GSYGQPVWYRWRFAKPTISEHHKVNLMRLTGMSKGTIHLNGHHLGRYWQIGPQEDYK
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CDS 761053..762402

/locus_tag="EFAGFIKM_00667"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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ATSVYTISAFTNTSES NMYIYESYNATHYGLLKGPAYTPPADLIRDPSIMKHTDGLY
VIYTTNWSGNTIGIASSPDKVNWTFVRNITLSTPTTIAHTWAPEWFKDSNGSLNIIVS
LSPGNYQNFKPYVLTASGSNLTSTSW SAPTELAGIAPNYIDTFIVKTGSTYHAFTKNE
TTKYIEYATSTSLTG PYTFKGTGDWAGWGSWVEGPALVQLDNGSWRIYFDGYATQKY
YSDSADNFQTWGVKQEIAGLTGLVRHMTVMKESGQPGDIRKLESFNVPGSFIRHYNQ

ARIDANVSPAEDAQFRIVPGLSNATGISFESMNYPGYFLRNNNGNITLVKNDGSTTFR
NDATFKRVNGLANASWTSYTSFSNPPLYLRHYNNMLKLEAVVTALDKSDATFREVAQ"

CDS 762640..764484

/locus_tag="EFAGFIKM_00668"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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RKAVPGYQPSPGVYDWNADANQRYMLQAARAQGVNVIEAFANSAPYWMTISGNVSGSA
NGGNNLKPDIYDDFADYLTEVVKHFRDNWGITFDSVTPLNEPISTWWKQGNDQEGMHF
DRADQNTILSQVQASLNAKGLSTKLSAPEEYSIDDTNVSFNSYSNAVKSAITQINTHT
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SAEGWGFFKNVLNNTQTTSYTVNQKYVVMGNYSKFIRPGYKIIGMSDANTLAAYDAAS
GKVVLVTTNSESTDITVNYDLSRFTNTGTSAQVYRTSSTEKLQQLTNISVQNKTFTAT
AKANSVTTYVISGATYNGGTGYESGAIYKLINRNSGLALDVNGASSTGGATIIQWNDN
GAANQQWKLESAGNGYYNIRNVGSGLLLDVNSGSTQGGAALIQWQDNGGNNQQWLPID
VGGYVVLGNRNSGLTVDINQGSITAGASTIQWADNGGANQQWSLVKVN"

CDS complement(764615..765706)

/gene="soxA"

/locus_tag="EFAGFIKM_00669"

/EC_number="1.5.3.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40859"

/codon_start=1

/transl_table=11

/product="Monomeric sarcosine oxidase"

/translation="MGMSAGYYLSRSGCKTLLIDAFDPPHTEGSHHGDSRLMRHVYSG
GPDYIAMALLAQKLWHELEETVGDQLFVPSGVINVVDPEIHSFHNRLSHADDAGIRYE
TLHAAEVMKRWPGITPEHYEGMYEPDAGYLYSEPCIRAFRKAETHGATLLTHTLVE
HIQYGPHSVAVQTSGGDYHANQIILSAGAWFQTLKPFVDLPIQAVRKTVGWFDPEA

LYGEAHFPGFTLAGKEGTYYGFPSIGGSGLKMGRHDTGQVWTPGSTMAPFGTEETDEG
DLRRLLELHMPQAAGALKRGSVCKYEFTSDEDFIIDRHPAHERVWLAGGFSGHGFKFA
SAIGQILSDLVQTGHTDRDISRFALSRFR"

CDS 765879..766436

/locus_tag="EFAGFIKM_00670"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISSpgl1"

/codon_start=1

/transl_table=11

/product="IS1595 family transposase ISSpgl1"

/translation="MSEQFRFDLFPLIQTERFILRSAEAGDSHDLLALYSDEAVVQYM

PFTPFESVEDAQGEMNWyTKIFKEHTGLRWMIEDRETRKVIGTCGFLNYEDVHNRAEI

GYDLRSSFWGRGVMTEVARAVLHFGFTSMQLNKIEAKVEPENEASIRLLHKLDFQQEG

VLRQHEFEKGRYIDLAVFSKLRSEI"

CDS 766546..767301

/gene="exoA"

/locus_tag="EFAGFIKM_00671"

/EC_number="3.1.11.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37454"

/codon_start=1

/transl_table=11

/product="Exodeoxyribonuclease"

/db_xref="COG:COG0708"

/translation="MKLVSWNVNGLRACVTKGFMDYYQESQADIFCLQETKLQAGQIE

MDLGEDVYQYWNyAIAKKGYSGTAVFSRIKPLSVRYGMEEVSEPEGRMITLEYDEFYLV

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LVSNQLAPKVADAHIDCHVMGSDHCPVGLTLQL"

CDS 767579..768517

/gene="rutD_1"

/locus_tag="EFAGFIKM_00672"

/EC_number="3.5.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00832"

/codon_start=1

/transl_table=11

/product="Putative aminoacrylate hydrolase RutD"

/translation="MLATGLLLL LAGTAYEAYQSTQDMKSYPPPGKYYEVSGRNMHLYT

AGKGEVTVVFASGWGTPNPYVDFSPLYDKLKSQVKIAVYDRFGYGYS DYTDDPRDVDT

ISEEIHQLLR TSGQRPPYIMVGHSLGALET LRFAQRY PDEVAGMVMIDGGSPEYYSRT

DLNTP EWMMDWSRFLVKTGIARTLLQSDRM MASLVIDPNLVTEPMKKAVTISTLRHAY

NDNVMEEVRNSRTNAACVLENKTKFGFPLTILTAGSEESDEDSHAWQDDQANFASWSR

HGTQLTVPQATHSIHNSQPDIVAAEIMKLVT PSSDL"

CDS 768514..768711

/locus_tag="EFAGFIKM_00673"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSNMIPQTHDEQE EEWGWMKKFKVITRFLSILVASCLLSVLSV

SVIWVKNNVHDVPVIQSFERD"

CDS 768734..768961

/locus_tag="EFAGFIKM_00674"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVTDGEEKELCIGLCGTGDDGVLAKKLT DAGQTIDDKNIIIQGT

DPETKDVWSLIGGTLAGQEGVIELTLTWTES"

CDS 769175..770152

/gene="ddh"

/locus_tag="EFAGFIKM_00675"

/EC_number="1.4.1.16"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:G1UII1"

/codon_start=1

/transl_table=11

/product="Meso-diaminopimelate D-dehydrogenase"

/translation="MIRVGIVGYGNLGKGVEKAISQNEDELIQVFTRRNPEQMVAES

TEVRFEHISAAEQYIGKVDVMILCGGSATDLPEQTPAIKLFNTVDSFDTHAKIPEFY

KEVNAAAEQGGHVSIVSTGWDPLFSMNRLLAQSILPEGKEYTFWGKGVSQGHSDAIR

RVPGVKAGVQYVTPVEEVINRIRAGETPELSTREKHLRQCYVVAEDGANQDEIRETIV

SMPNYFADYDTTVTFISEEELKSEHEGMPHGGFVIRSGVTGAGQKQIIEFGLKLDSP

EFTASVLVAYARAAQRLSVEGHKGAKTVFDIPLGHLSPKSAEDLRRDLL"

CDS complement(770311..771165)

/locus_tag="EFAGFIKM_00676"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSNQPFASPHLSADCEQCFGLCCVALPYGKSSDFAFDKASG

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YRSSVNQLLVQASEMVRANVPPTAHGQGKSKKSKKRTGSDFFGANLKGTDLRGASFRG

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LNIPSHWV"

CDS complement(771321..772706)

/gene="gdh"

/locus_tag="EFAGFIKM_00677"

/EC_number="1.4.1.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P31026"

/codon_start=1

/transl_table=11

/product="NADP-specific glutamate dehydrogenase"

/db_xref="COG:COG0334"

/translation="MSTITKETTESVQVTAAEYVHSVYESVVARNPHEDEFHQAVKEI

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QSFMTELYKYIGSDTDVPAGDIGVGAREIGYMFGQYKRIHGGHEAGVLTGKGLLYGGS

LARKEATGFGCVYFVKEMLQSKGLSFQDSTVVVSGSGNVSIYAIQKAQELGATVVACS

DSGGYIHDPQGINLDTVKRLKEVDRLRISEYIKEHPHATYTEGCEGIWSIPCDIALPC

ATQNEIDEEAAALLIKGGVKAIGEGANMPSTLAAIDVFHGAGVLFGPAKAANAGGVAV

SALEMSQNSMRLSWSFEEVDAKLHDIMKNIYTSCVEAAEEYGCEGNLVAGANIAGFLK

VADSMIAQGVV"

CDS 773095..773568

/gene="greA_1"

/locus_tag="EFAGFIKM_00678"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00105"

/codon_start=1

/transl_table=11

/product="Transcription elongation factor GreA"

/translation="MNHRTSRHNCREKLVSQLFTEGEEKRTFLDAYFDARDPERIQLE

KQLSAYTEYVEKLLLGPDEDLDSAVLIGSHIDFEYIDFHTSDSFMIVMPEDTNPDEGR

ISFLSPVGSQLLGSGVEIRSVHTPSGSMRIRITGIELRSETLNEPALGGADHAL"

CDS 773558..774064

/gene="khtT_1"

/locus_tag="EFAGFIKM_00679"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07535"

/codon_start=1

/transl_table=11

/product="K(+)/H(+) antiporter subunit KhtT"

/db_xref="COG:COG0490"

/translation="MHFKETDLPGIGRKYWLHTRSGEHLVIVIHNDERRDLFHMESGD

TPEEVGDMVSLVTLDDDEARAVAAIVGGMTYKPKFQDEREVMLEGLLIEWLRIEPHAA

SVGMTIGELDIRQATGAVILAVVTKDKEKHFNPGPDYAFTAGATIVVAGERNQIKHLK

QLLTDGRT"

CDS 774068..775273

/gene="khtU_1"

/locus_tag="EFAGFIKM_00680"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07536"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0475"

/translation="MDMLIFEVGI AVALITLTGLISSRLRFSVIPFYILIGMAVGPHA

PQIGIVDLRFIESSTFIEFMGRLGILFLLFYLGLEFSVSRLKSGKAILTGGMFYVGL

NFVSGLLLGWFM DLPLQETLVVCGIMTSSSTAIVAKVLVDLKR TANPETEIMGMIMF

DDLFAIHISILTGLVL SGATSFLSVLLVSL SALLFIVLFLIIGRKS IKYIDKALNIK

SSELFLLTVM TLLFLVAGFSETLHVAEAIGALMMGLVLGESRHVSRIEHQIMPFKDFE

GAIFFFSFGLTIEPASLG GAVGMTI IAVILT IASNYGAGMIAGRLAGMSPKASLNVGF

TLVSRGEFSIIMANIGKAGGLMASIQSFAVLYVLILAVLGPILT KESPRIYAQYARLR

KRMKRRETG"

CDS 775617..776333

/gene="yoaJ"

/locus_tag="EFAGFIKM_00681"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34918"

/codon_start=1

/transl_table=11

/product="Expansin-YoaJ"

/db_xref="COG:COG4305"

/translation="MNKKSRFQRLKWAGTGMLLSLVLFALPASAAWNDTYQGYATYTG

SGYSGGAVLLDPIPADMKITALNPFQLNYNGVKAALAGAYLEVQGPKGKTTVYVTDLY

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CDS 776443..777390

/locus_tag="EFAGFIKM_00682"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

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HLHIDRLPASESSIKILFIHGAGGNRLLAPYARMLQRHG YE VVSPDLPPYGLSYAMS

GTSINYELWIELLVSLIEREYKNDGKPIVVLGSSIGGMLAYHTSARSKRVKGLIATTF

VDTSNQEMRDQLAPNRLVSRAGKRMMDLFPGLLDHVRISVKQVSRMQLITNNKDLTRL

IMDDPQAAATRIPELLRTFLNKEPEVSPEQFSQCPVLLVHPELDPMTPIRFSQSFFD

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CDS complement(777456..778334)

/gene="yddE_1"

/locus_tag="EFAGFIKM_00683"

/EC_number="5.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37757"

/codon_start=1

/transl_table=11

/product="putative isomerase YddE"

/db_xref="COG:COG0384"

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SETAFVMPSDQANFKVRYFTPSDQVDLCGHATIALFYLMKTQH LVNVGIYTLETLAGI

LKVDIEVNGEVYLSQTLPEFGEIVDRQQIADSLRISMEDLHYELPVQIVSTGLPDIMI

AVKDVDVLT KIDPDFQRITEISKAHHAIGYHVFTLES DVM DVLAECRN FAPLYDIPEE

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VGGS AIHIENIQIHLP"

CDS 778531..779457

/gene="pikAll"

/locus_tag="EFAGFIKM_00684"

/EC_number="2.3.1.239"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9ZGI4"
/codon_start=1
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/product="Narbonolide/10-deoxymethynolide synthase PikA2,
modules 3 and 4"
/translation="MKAIVIEEFGGAEQLKEQEVAKPACGVNQVLIRTHATSVNPVDF
KIRQGYMKEAAENFPLILGGDVAGIVAEAGSNVTRFREGDRV FARPRQFGTYAEYVAV
DADIARIPEQLSFEEAAAIPLAAMTAWQALVDHGR LGKGQKVLIHAGAGGVGTYAIQ
IAKSLGAEVASTASESNEALLRSLGVDHFINYKKEDFSEILSGYDVVLDTMGGDIQRN
SFKVLKSGGHLVSLVEQPDEKLAKEAGVTANVFMMEPKGDQLDQLAELAAEGKLKSII
DGTYP LTQQGVREAHEKSETHHTRGKLVIQVQ"

CDS complement(779441..780079)

/gene="ydeA"
/locus_tag="EFAGFIKM_00685"
/EC_number="3.2.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P96658"
/codon_start=1
/transl_table=11
/product="putative protease YdeA"
/db_xref="COG:COG0693"
/translation="MMQTKNVYLYVFDTMADWEVGYLTAELNSGRYFRKEIKPLQVVT
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EGTVIAAICGATVALAKIGILDSRQHTSNDLEYLKMICPDYTGETYYVTEPAVTDGNL
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CDS 780277..781014

/locus_tag="EFAGFIKM_00686"
/EC_number="3.5.2.20"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A0ONLY7"

/codon_start=1
/transl_table=11
/product="Isatin hydrolase"
/db_xref="COG:COG1878"
/translation="MSNELIQAIQLLKEKKWVDLTHTFGPGSPHFSAFEAAQFDTLFD
HDQGFFAQSFKFPGQYGTHLDAPIHFVRDTRYLDELGLKELVLPLVIDQSAEVENNP
DFTLDVEHILEFEREHGVIEAGSFVALRTDWSKRWPKHETFDNKDDKGN SHAPGWSVR
ALMFLFEERKVQAIGHETFDTDSAVDYQKNGALLAEYYVLAQDTYQVELLTNLDQVPA
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CDS 781630..782088

/locus_tag="EFAGFIKM_00687"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MQIRAFQESDKDFIVSLALRFMDFELMSWRDPGKMEESQLSLAQ
ESVDSLSPGTEIFVAEDETGELLGFLEVQPHKDKLNDIEQGYIVAIAVSPQGEGKGVG
KGLMTKAEEWSRQKGYRQLILNVFNNNLRAVNFYKHLN YEIEVVKMVKEL"

CDS complement(782352..782552)

/locus_tag="EFAGFIKM_00688"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
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RRKKTEKKISQRFNQDPHSDQK"

CDS 782763..783215

/locus_tag="EFAGFIKM_00689"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MKQRMGRSWLLMLMHGILGIGAIVGGVILIIDPSGSMVNLPASL
LGNSPFASFLFPGIILLVLGVMPMTMIAISLIRYVHSGLGERLNLYPDRYWAWTFSLY
TGFALIIWIMAQVYWIQDVSIIHLVYFAWGVGIQVVTLLPGVQRIYSK"

CDS 783501..783617

/locus_tag="EFAGFIKM_00690"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVYVIMAVIIWAGTYASMALSKQPMEVKPKVKSMDLFE"

CDS 783762..784769

/locus_tag="EFAGFIKM_00691"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKANATMMKYINLNNVREVMQQIETATKPQLALLTNLSVVTIN
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LIHSHLIREIESEFQLNVLVENDVNAAISGYCTQHADMKEQSVAGIYFPNRYPPGMGM
MLNGQMIRGKNGMFGEIKYLPYSPDWHRDMSKDDFVNVVCHILQTINAVVAPHQIVY
QERVEREELDMAWKQYGKDHPMPSLPEIVHQDSFQHDAGLRGMVLQALKSGILSEA
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CDS 784831..785472

/gene="lacA_1"

/locus_tag="EFAGFIKM_00692"

/EC_number="2.3.1.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P07464"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0110"

/translation="MREEERIMKGVLFSPSPDELKIIKRRAHNLSQRYSTFEEQTEE

RDQILQQLLGQIGEGGFMQGPFFHYGVHTRIGEHHFGNYNLTIQDDAQVTIGDYTSI

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CDS complement(785535..787355)

/locus_tag="EFAGFIKM_00693"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKRTLISLLLLIVIVISGCSVKTKTESQAETTPADTTETAQKP

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YIAPLYISLKSQAVNQDILNVDTVRLSKSRAMAWEPIEFKDSSKNAKDPLILTQSASV

LTSLDPIKGNDGSINQLNTNMYVRLVNLTDQDQLTADGSLSHNFSIAEGNSDYFILR

DDINFAKIDNKKAVDTGERVGADDVIFSLDRAKNKDSVPDHRTYSLHEHIKEAEVTD

LSALQSIKQSSGNGTILEALEQGLGSKITELVTDKTKADNSAGKYQVVKLTTEPFPQ

VLNYLAHQSAQIVSKKQVESINTYDVASFVNKDIPYGDQNTVTEGAAYNNTLYTSGP

YILSYKNDYEGVFLKNPGYRKGTEDPKIAQVNVRFIADADSALSALRSSEIHLYYGV

PETKYDIIENDSKLKLQSLPSNAVSYLLFNTANREVAKSSDLRKAVLYSINQDEILSF

YKNNKLKAYSTVSPLVQTGNELKADPAKVKEFLSKYNASK"

CDS complement(787429..788940)

/locus_tag="EFAGFIKM_00694"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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NIFIVTAAFHILIRKARNVEYTFAYVMLLTQLFVIGVSALNVFKPYVADNFLPAMAVLI

FILVIDLVLIIVSRYNATSILPRWMIGVSVVILTSITGNVFALLLGISIIGRIRRQ

GKQKSNFWNDLWERLAPNMTAMSGLFFIIFLSISICSFFTFDYSMAVENNYSALLQP
PSLAYPLGTDDFGRCLFSRIVFGARISLIVGCMSTIIPVLIGGVLGAFSGFYGRHTDN
IIMRLLDILYAIPGILLAIIAAFGANTVNLILALSLGSIPTYARTMRASVLYVSTF
EFVEAARALGYNNRTIIFKHIIIPNSLAPMIIKSTLTIGGAVIATSSLSYLGLGVEPHI
PEWGNILKLGSTYLETHSYLAIYPGLAIILLVLSFNFLGDGLRDALDPKLEKA"

CDS complement(788977..790419)
/locus_tag="EFAGFIKM_00695"
/inference="ab initio prediction:Prodigal:002006"
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GILFLYGNPYLKYIFERILMTVFVILGVATLVFTILYMSPFNPAANILGETATQEIA
AFNQVYGLDQPYLTQLWNNIKGVALFDLGKSFAGNEDVTATIARKFPITLTLAVISLL
LALVIALPIGIISAIPNSWFDYTFMFIALIGLSIPNFWQGLIFILNFSIKLQWLPAT
FNPQNWLSIIMPTIVLGTGLTAAVARMTRSSTLEVIHEDYVMTARAKGLSERQVMLKH
AVRNALIPIVTVVGLQFGAMLGGAAVTEKVFNISGLGSYIVDKQFIPDIPSIMGGVIY
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CDS 790552..792321
/gene="gsiA_1"
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/db_xref="COG:COG1123"
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FQDPMSSLNPTIKVGKQISESLIKHQVSKREAKKQAIAMMERVGITRSEIRYNQYPH
EFSGGMRQRMIGIALACRPELLIADEPTTALDVTIQAQILNLMKDMQDQLGTSIILI
THDLGVVAGMCDRVVVMKEGQIVETGTTTEIFANPKHPYTIRLLNALPRLDQKKKPKP
VSLVPRDLEDDQPLLEVKSLRQHFNLGKGNTLKAVNDISFHIRQGETLGWVGESGSGK
STTGRAILRLHEPTGGDVLFGVPLNRLSASEMKTMRMHMQIIFQDPYASLNPKMRIM
DIIGEALDIHQLAGNAAQREKRVEELLEMVGLDPTHAQRYPHEFSGGQRQRIGIARAL
AVEPEFIVCDEPLSALDVSIQAQIVQLLEELQURLGLTYLFIAHDLSMVKHISDRVAV
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CDS complement(792436..793215)

/locus_tag="EFAGFIKM_00697"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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EKVSLLQGIRTGKDYLEATKKFMVDSQFPYDYKEMTTETIGGKEMDLMQITMDPGDGS

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CDS complement(793326..794087)

/locus_tag="EFAGFIKM_00698"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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ELIAIAKLIPAYMQNCYQSQQTAEVCDKPAVEFTERQLTILEMIAGGLTVKAIALKLK

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CDS complement(794114..795178)

/locus_tag="EFAGFIKM_00699"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTQEENTSGWDAIDQSMRELYGEQEPKHYGTALPYMLGGPDPLD

GISVYEVNTPMPHWHFVTYGFSELYEKEMQDASKSGYGFEFTFRLTRSEAETDPPAWA

LNLLQNVGRYVFNSGNIFQPGDYMDANGPICLESDDLTLTALSFIEDPDLPAISTPNGS

VQFIQMVGITGRELEMIQSWNARGFLSASSMFMPKYVTDLMRNSYADIPSVIQAVEDG

MEQDGSSTAFLFIQQLGWESPRKKLLQKSVPAKLQLGAKQAVLVGTILRSRISKGASL

SLIGPDTNILFEAGEQPAVLESDRQVTLTVNKQIVNELAENLRPVEGTFEITSLDHII

VQIVRTEIKDQEGHVIQTIG"

CDS 795386..795610

/locus_tag="EFAGFIKM_00700"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDGERYPGFRGPKSRCLPGNGGGSAGIKGSDYAYATLIFSMVRE

CERSYDPVKLILQNRYVTTLQEQTQQNLQ"

CDS 795789..797246

/gene="bglH_2"

/locus_tag="EFAGFIKM_00701"

/EC_number="3.2.1.86"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40740"

/codon_start=1

/transl_table=11

/product="Aryl-phospho-beta-D-glucosidase BglH"

/db_xref="COG:COG2723"

/translation="MTTAKKGFPENFLWGGATAANQLEGAFDKDGKGLSTADMIAHVP

KEKRTGGHAMEISSSRIEEILSGKIEERFPKRFGIDFYHHFREDIALFAEMGFKVFR

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AGREVIQHYVRYAETVFNRYKNKVKYWLTNEINVMLFSPYTG GILIDKVDNKLQTT
YQALHHQFVASALVTKLAHEIMPGSQVGCMLARMETYAATCNPVDVRLAQHENQINLF
FTDMHARGKYPNYMARYFEENDIVIQKEAGDDEILLNNTVDFISFSYYMSVTKSASAD
KEETSGNLTGGVKNPYLEASDWGWEIDPIGLRVTLNNFWDRYQKPLFIVENGLGAYDR
VEEDGSIHDSYRVDYLKKHIEQMKEAIKDGVDLIGFTAWGPIDLVSMTSEMSKRYGF
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CDS 797382..799070

/locus_tag="EFAGFIKM_00702"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRWSMNTKSMGWMLALTLSLSVIWPATVGAESTQVTRIQANTY

VGDPGEMVESFDITVANPEKYQNLKASDFEITGNYDGYPLNEAEEIIQNEYEDDGIKL

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GSNGEALSYRLKRSPSTNAQPLVWLHGGGEVGTDGRSHLTANRGAVVWTESGYDTSV

LAVQYPENYSFKIYDNPEQLAKMQAYFVAQYELIQKLVSEGEVDPDRIYLAGVSSGGG

GALRFMMQYPDLFAGAVVIAAKDTVADYTGSDGFKDALKDIVNVPIWLHHAAGDPTT

DSRTSILAYEALLELGSDPDIFVYDDDFMEGNNLYGGLKHWSWVPALASYQTPDFLFN

QDKGISDVDIYTRMDRRIKAHEIVDRTQLAVWIADFLKLPNPQYEESSDTERWSQK

AISQVTEAGVMQGTGNNKFSPLGDITRAQLAVILDKMKKNLGIQPDQSEAAMFDDVPP

THWAYEAI RNSSQYDIMGGKEAQLFAPNDVVDGEEFHDIMDRLYLTKANRHLED"

CDS 799092..800516

/gene="bglH_3"

/locus_tag="EFAGFIKM_00703"

/EC_number="3.2.1.86"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40740"

/codon_start=1

/transl_table=11

/product="Aryl-phospho-beta-D-glucosidase BglH"

/db_xref="COG:COG2723"

/translation="MTTPFPKDFLWGGAVAANQLEGAYNTDGKGLSVQDVMPHGITTP

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KGKVKYWLTFFNEINSILEEPFMSGGIYTPKAELSKQDLYQAIHHELVASALAVKLGHE

IMPEAKIGCMVLSMTPYPLTPNPDDVVAAMHAEQRNDIFADIHARGYYPKYINRYFKA

NNINIKFEDGD AEILKHTVDFISFSYYVSICETGDPEKRIEGKGNLFAGVQNPYLKAS

EWGWQIDPQGLRVTLNKYWDYRQKPLFIVENGLGAVDELITDENGKTVNDDYRIQYL

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KKKSFWHYKEVISTNGASLKNNNE"

CDS 800750..801601

/gene="licT_1"

/locus_tag="EFAGFIKM_00704"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39805"

/codon_start=1

/transl_table=11

/product="Transcription antiterminator LicT"

/db_xref="COG:COG3711"

/translation="MKIEKVLNNNVTVIDPGGNELVVMGRGIAFKKHTGESIDESLV

EKIFSLESKEVSQKLKTLSDIPVEYVECSDEIIRYAETVLGEKLHESIYISLTDHIH

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VNAQMNGEMRETISITNIVKDILNIVRRSFVIELDEDSLSYYRFLTHLKFFAQRVLQG

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RNEQTIE"

CDS 801730..803631

/gene="bglF_1"

/locus_tag="EFAGFIKM_00705"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P08722"

/codon_start=1

/transl_table=11

/product="PTS system beta-glucoside-specific EIIBC
component"
/db_xref="COG:COG1263"
/translation="MDKQQLSKDILKLVGGEENIDQVTHCMTRLRFNLNDNQKADKAT
LKNTPGVMGVMENGGQFQVIIGNDVPVVYNALVGNMSKSPTTDNASSGASTGEKKRN
PISALFDFISGVFTPILPAITGAGMIKGIVAILVALGWLSDTSSTYIILSAIGDGAFY
FLPIILAIISAARKLGSNMYIAAALAAGIMHPTITALLANGDTTFVGKIVIAATYSSTV
IPIILAIWIASYVEKAVIDRVTHASLKLLIVPTVTLIMVPLTLMTVGPLGTVLGNLS
GGISWLFDNMSIFASILIGGTMSLLIITGMHYALLPIIVGSM TLTGYDFIPLMFAAN
LAQGGAAGVGLRSRNSKTKSLAYSTGLTAIMGITEPAMYGINMKFKKPFIAALIGGA
IAGGFMGIVNVKAYVLTGLVGLPSIAAFISPAISTLLYALAGGLIAIVAAVLTYL
FQEEENATEPAPAAEPATPAATTSVVTEEAKAQDEQIFSPITGEVKPLSEVPDPAFSE
EIMGKGFAIQPSEGRVVSPINGTVFSLKSGHAIGLVSDTGAEMLIHIGIDTVKLKGQ
FFSPKVQAGAKVAVGDVLMFEFDREQIEKAGYTTITPVIITNMHQYESIESAGRTTIKE
KDLLFTAKA"

CDS complement(803698..804600)

/gene="benM"
/locus_tag="EFAGFIKM_00706"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O68014"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator BenM"
/translation="MDIKQCRYFIAIAEEKQITAAARRLHMAQPPLSQQKLMEEEELG
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QEPLFYISSTPLDCPTMGPGVEMGTIFEQLTGIPLLLPSTEGLGMFELIDKFREHQ
VTPSIMGECS DINMLLELVRLGFASSIVPHTVLQLYHEHPFHVYRIQDQHSTVGSALV
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CDS 804785..805372

/locus_tag="EFAGFIKM_00707"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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QYGADPKIADRDGITPLAHASRHRYAEMERLLTQV"

CDS 805423..806766

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/inference="ab initio prediction:Prodigal:002006"
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PGQHSGQPQNQAPAGLELFPWGAPRWEPGIVITAFFVGLVNMNTSITTLSTVEKLYRTE
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IGLTSPVTAFFAQIPPSVGSVAVLFVAYLQMFGTALRTLEGTTFNSKTIYRVALPVLTG
VAVMNIPAEAFQTLPMYLIISNGLVIGVLVSLVLEKTVNWSKMEQPATVSKAA"

CDS complement(806842..807219)

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CDS 807426..807875

/locus_tag="EFAGFIKM_00710"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS 807904..808584

/locus_tag="EFAGFIKM_00711"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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RGYAVEQT"

CDS 808614..809261

/locus_tag="EFAGFIKM_00712"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYTVQLERMREKLITLRLDPDLDFGAENHEYEMEPVWTQEDI

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FTEAWNWNWDWFEDSKEEEEWEALEHEYFDPKWSAGMLRISDFGCGISMNLIVKGASY

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CDS 809333..809734

/locus_tag="EFAGFIKM_00713"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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EPELRNFLNQFSTWVRNHLQLADGIEVTGNL"

CDS 809908..810456

/gene="sigV_1"
/locus_tag="EFAGFIKM_00714"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O05404"
/codon_start=1
/transl_table=11
/product="RNA polymerase sigma factor SigV"
/db_xref="COG:COG1595"
/translation="METKAEMNQRIYVQTEDETEFVQSIMEHQDTLISIAYSILNRQ
DALEAVQEMTCRAWIKRRTLNNKAFKSWIIRILYVCIDEQRRRKRAKPLAKEDMED
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CDS 810446..811588

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/inference="ab initio prediction:Prodigal:002006"
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VNTKMTDARTGYVLDNGNIGGMHSSNDKNTIHGRSTIDRNQNEPLPEQVNFQFQLSSV
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VEVSPLVTRVKFVHAPDQEIDYKTKLSLNEIVRPIEISTSRNGKQTKLSMVGGSGSE

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CDS complement(811712..813697)

/gene="bgaA_2"

/locus_tag="EFAGFIKM_00716"

/EC_number="3.2.1.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:D9SM34"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG1874"

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EGEVYYVGTWPEPSYFYQLFEGILKERDLAAKIQLPEGVELSIRTKGEQNFLFLINLT

NEQREITLDVPYRSLTSLRDLQKLTLPALGVDILTV"

CDS 813812..814654

/gene="rhaS_2"

/locus_tag="EFAGFIKM_00717"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

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/translation="MPHPNRNFPVLSSRDKLLPFYLLGIGLHHEQEHIRRDQGIEDYQ
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FETVGIVDTCVYTLAQPEYLLSRMRELLQAALTPQEQTLSTNYACSAVLYTLLTEIIQR
VSVEGSDTVGQQYERIKPVLIDYIEQHAAEITLPTLAGLICVTPEYFCHLFKKTGIR
PISYVNQVRVNKSKELLLDNVQRGMEDARQVGFESTSYGAIFKKLERITPGAFFRS
YQKS"

CDS 814945..815988

/gene="pelB_1"
/locus_tag="EFAGFIKM_00718"
/EC_number="4.2.2.10"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94449"
/codon_start=1
/transl_table=11
/product="Pectin lyase"
/db_xref="COG:COG3866"

/translation="MKKFSMLLLAVTLLLLTVSTAPSTYGAASYPNTGTNGLTGFAQS
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IDHVTFAHGSYSSGGSDLDKLLYIGDRADYITISNSKFANHKYGVILGHPNDGNSSYN
GVPHVTMSNNYFENLYVRGPGLLRGYFHLKNNYANNFNQAITIGEKARIYSENNYFG
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YAGSSNTTLVFGK"

CDS 816291..817769

/locus_tag="EFAGFIKM_00719"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MDRMDEIWKRNKLIGIILWIIAIGMGLAFTMPKLLVSNGVAL
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SEVRQNEVEHSKQRVETMLERVKESVEGLSRYTDQLKQKVNATGSITNEVTLGFSEVA
KGVEFQATSVAEISESLSVSDQHIKDVASYSQQMKELSASMATSTQTGSTQMDQLNIQ
MQDLYETIDTTANDMRKFNEESESMTLMLNSIADIASQTNLLALNAAIEAARAGEHGR
GFAVVSEEVRLAENSGQSASDIGTILSRKGGTQALTDRFERIRQSLQQGRDSVHTA
EEVFRITNSNSQHVLNQATDIETSSATMKASSTRVVNEVSEISSVTEQSSAATEEILA
SMEEQRNLTQKMVESFGELEQLIVNLNELVSDHQASSVANKL"

CDS 817968..819176

/locus_tag="EFAGFIKM_00720"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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KSRWLLKRDFELLAKHDYKFVSESDMTDADIPRIVELYKLLYLEKYSYHNPQFTERFI

AAAMASGTLRLYGLRKEGRDAVMGYFCRNGVMTTPLFGYDTTPQSVGLYRMLSACL

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CDS complement(819301..819666)

/locus_tag="EFAGFIKM_00721"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLIKLNWITLRVSNLEASLGFYHDMLGLPIQRRFESRGRQIAML

GIENEAKLELIEGSESILKPEAGVSIGYEVNSLDEAMERLAELNIPIVRGPIQPNPHL

RFIYITDPDGFQVQLAEHV"

CDS complement(819830..821482)

/gene="phoA"

/locus_tag="EFAGFIKM_00722"

/EC_number="3.1.3.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P19406"

/codon_start=1

/transl_table=11

/product="Alkaline phosphatase 4"

/db_xref="COG:COG1785"

/translation="MLNRFNVRAAKMMLAVTTIVTATLGGSSAAWAVEDTTSTTSASP
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TGYKSHTGFVGVLPDKATMPGQKAIAPGDERKPIASVLEASKLAGKATGIIATSEIMH
ATPADFSSHYPDRKKNYDALSKQQVYNGMDVVLGGGSKYLEPAGRKDGENLISSIKALG
YDYVTPAAMKASDSNKLWGMFAPAGMAYNMDRDPKQPSLAEMTSKAIEVLSKDKDG
FFLMVEGSKVDWAAHANDPIGIISDVLAFDDAVKVMDFAKADEETAVVAVTDHGNGG
LTIGNNATSGTYDKEPLSTFIGPLKKAKLTGEGVEAKLNAKRTNIKAVMKQYYGIIDL
TSEEIATIKAAEPGSLNYAIGPMISKRAGIGWTTGGHTGGDVVLYTYAPNNDRPFGVI
DNTDVAKYMARVLDLSDSVSKQLFVPAKQAFATAGATYKLDLTDKNPKILVTKGNT
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CDS 822205..824448

/locus_tag="EFAGFIKM_00723"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKTIKRSIAVATILGLCVSALPAYAAGNTASSSSAAMDKLIQSE
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VVGYLKQHPYVSEIVTGTEKFEPNAPLTAEGYAEMLLKVLGYEAGTDYEQGAASYAA
GKGIKALQGKGASQLTNRLMAEATAQALQIQLKNGSGTLEQSWLKHKEAGAFRPQTVQ
QTKYGAIDGKTYEQYGTLGWLGVYPYAAPPVGELRWKAPQEPDSWTGTRSAKEFAANSL
QISGKNTVGSSEDSLYLNIWRPDTTSSKLPMVFLHGGGNMTGSGKDFQGEQLARSTNS
IIISVNYRLGALGFFENAALKTGNALDDSGNYGLLDAFRALEWVQDNIEGFGGDTGNV
TLAQQSAGARDVLATLISPLSKGLYQKAVAFSGGLTTASPEEGEQKSEDLVKLLVQE
GKAANAEEAKAWIGKQSQAQLESYLRLPADKLVTAFGATAIRMDPFPFLFRDGTVIP"

KEGFDAINNGNYTKVPVLLGSLETEFSGFAFGDPNFSPSITDETLFTDKTKAEQYAAA
LKYGSEAYAGFNAERVAEQLTSEAGQPPVYAYRFAWGTQPGVISERLLTLLGAPHGAD
MDFYTGHADGIAAYFPDGYFSDTNKPGRDQLSAAMAAYLKQFLYTGNPGTGGSPDLAA
WTPWTKDAQAPIMRLDASNTTAEIGMSTQYNQ GKDAVMAKMKKELPEETYKLLTEKVF
AGRFFWE"

CDS 824596..824802

/locus_tag="EFAGFIKM_00724"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MISSIGIAGIITLLIFFIMIGLVLYLVFYLMKKSGVKKEVSAL

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CDS complement(824939..826525)

/locus_tag="EFAGFIKM_00725"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKRNQWLAVLSMTAILTAGATSYTSMIHAADATKPANDHVVLR

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IVDLTTYKTVKTYELGIGPDSIALSPDGLHAVIAIEDEELNKADEIDYANTKRPGSI

MVVSFAGGNVLEGEITNLPVSLDNVEGAIYPHDPQPEYVAISPDSKTAATLQENNVV

AIVDLETKKISSIFALGTTSHQADLKDDGIVQFKETLTARYEPDGIASFADGKYLLTA

NEGDLGKNEFEDGVKAGGRNIAVWDLQGQRMYSQNLIDEETTMVGLYPDDRSPNKGSG

EVENLTVATVEGKTYAVVASERADAILFFDLADPVNPDYLG LIPTAGESPEGIHRVNG

RNLFVSADESTGTLSFFAKK"

CDS 826847..827806

/gene="rhaR_4"

/locus_tag="EFAGFIKM_00726"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

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/translation="MRTDDALGVVYQHLYLTQEPYSQQDEHTYLLSPKAGSGNIKRVTT

YSGIEILYSQVEYHQPYPTYFASETPIVELQFALSGERNVDISGQDYSLSIGQGALIF

MHDFEAWFHPPARELYTSFSLGIPVSLFNAAAQLGGFKSIAFNQVLGRKVKPIVFQ

LDNRIRTMIDSLIVELNNSYRSSLMEATALEILNRFMQLFDLAPIAGFSREDIRK

LHKAREIMEACMVDPPSLLALSRQVGLNDFKLKKGFKTLFGSTVFEYLRQVRLDNAMK

LLRNQDNNVTEAAIAVGYSNVSAFSQQFYRKFGVKPSEMKKIY"

CDS 828120..829322

/gene="tetA_1"

/locus_tag="EFAGFIKM_00727"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P02980"

/codon_start=1

/transl_table=11

/product="Tetracycline resistance protein, class B"

/translation="MNRIRGSIFFSVFAAMLSLMLIAPIMPPLIRELGMKESHGLII

SLGSIMMACMAPVWGRWSDIRGRKPIILIGFIGMSVSCALFALALYGGLNAWIGGGVL

LTLIVTRSLIGMFIPAVLSSAQAYMGDVTEGEERGSGMAIIAANGLGLVFGPAIAG

AFTLIGLLWPLYFGIFIAIATFIALLLIPSAKPVIQAKPPKVNPFQRGLRMYLAAGL

VTMMGIMTLQVVGGFYFQDQLGLSSAATARMVSFGLMFGAAMLIMQVVQMKWLKWQP

RPMILLGSLFLIASMILFLVFNVLSMYYFSFFLFGMGSLMMPGFMAGASLAVSKEQQ

GGAAGLVAAIQGISAVITPLTTTLYQVDKHVPFMLVAVLVVLLAIMMLGMRKNQSN

VADSIHTL"

CDS 829514..829957

/locus_tag="EFAGFIKM_00728"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q03928"

/codon_start=1

/transl_table=11
/product="18 kDa heat shock protein"
/db_xref="COG:COG0071"
/translation="MFDLIPFRKRNEPFGHMLKSFNDMVENSFLSPFGTGSQPFRTD
IREEEKYSVEAQLPGIAKEDIDIQFQGNELIIRAKRNDIVEQKDDSNRIIRQERRSG
EFIRRFYVDHIDDEHIKALEEGVLKLEIPKRPGDDQSRRRIQID"

CDS complement(830093..830650)

/locus_tag="EFAGFIKM_00729"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIYVALLRGINVGGNNKINMKQLKETFEQAGMLDVVTYINSGNI
IFADHQUEHANANVEISHVLEQAIAADFGLQIRVMVRNMDEIQSVIQALPEEWVNDDTA
KSDVMFLWDEINDPSVLNQLPIKPEIGTLIYVPGAILYSVSREDASKSGMNKLVGSKV
YAYMTVRNVNTTRKIYALMQAAAEK"

CDS complement(830685..831335)

/locus_tag="EFAGFIKM_00730"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
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SALAILIEAARTYAGEVKDEETYETKPEYLEQVEPLLQDLLGEEYTAHLFEYLSFC"

CDS 831671..833305

/locus_tag="EFAGFIKM_00731"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"

/translation="MNKRKWLNGFAAGCLSIILVISGCASKAPQTASDTPNQATEQTE
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KETEGSEFLETFLDSDSRDLIVQTWGGTNTTARALKSIEEQYKDTAEWDAIRKKVSD
KLVLYIILDQDDSYNEYIAKNWPSIRILNDQSNFWHFAYAWKMHAEEVNLSKLHGDWMV
KNILNGH GKLM DMYASMGDGKMIEGELAE EQRGSAEYLKNNPQYDKYDFISEGDSPSF
FYLIDNGLRSMEDPSYGGWGGFRGVNDKLFRRNNVLDYDPYTKRYEAEYSLMRWFDDV
QDDFAARADWAVADTYEGANHNP SLTIKEGV DLSVSPGEEVTLHAEGEDPDGDQLTYT
WWRYFEADTYEDSKVTPNKVQPEMAGDLQLGLHRELAKDEQVDTIKLQGS DTEAVTFT
VPDDAKSGDTLHIVA EVQDDGEHQLKHYQRVILT VK"

CDS complement(833391..833954)

/locus_tag="EFAGFIKM_00732"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKKRIKEIAIQHFNRLGYEGTKMAQIAEEAGIRKQSLAYHYSS
KKALLLELYEEVQEEQQFVRQFFSDSVTQTLDQQLYAFLHEHKNRFLTNPNVSFMYI
LSFITPLEVHDFVLAQYRTYLGTLKEELAAVFTRHSDIRLSPEEATVAFVTVMDGLDV
QLVYETRQSYEQALAITWNVFWSGIQR"

CDS complement(833947..835161)

/gene="cntE_3"

/locus_tag="EFAGFIKM_00733"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0A0H3JTK0"

/codon_start=1

/transl_table=11

/product="Staphylopin export protein"

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GIWMILVFRVIHGFGLATTYFATIATENIPRDRRGEGMGYFGVGETVAISIGPLIG
TSLLFRYDYQSLFMGGMCILLALLMTVFVSRPKPTGGSSSMQTHVPSVKLIEKKVL

FPSLLIMLVGIAAGSIMSFVALFAAERGFENIAWFFFIVAIASFVRLFSGKMFDRWG
PGSVLLPSAVFAIAGLLVLIIAQSDVQFLIAGALYGFGFGAIFPAIQTWCVNLVEEHE
HESAMASFFNFFDLGIGGGSLILGVVASAFSYTVVYAISIGIFVYILLYLVYSQKQQ
RYTARQLEVDIE"

CDS 835313..835783

/locus_tag="EFAGFIKM_00734"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHTKTKLQELYQATQEANKELERLHEEYKIKEQALIKVNDQLET

LASTDLLTGLKNRRFFQEKMLESLMMFQEKQRYFSLLVVDIDHFKSINDTYGHPIGDL

VLGNLAGLLQSLSRSTDVVARYGGEEFVVILNALYASKTGGRNRVTHAAQMVKS"

CDS complement(835914..837401)

/locus_tag="EFAGFIKM_00735"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIRVVILMIPILMVLVSGCQNHTSAMKEPASVQKSDPQVIHYIS

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GEHIQLLGNTIHAIASYATPEGPDLRGRDAHGIAIYGTEHPQALRDIKDNELYDLT

LGSSESLAVNGNVDTFAIQDNIIHSDNIGIDLIGYEGTSEDDTYDQARNGIVRGNEV

YDITSNNNPSYGTDLPNDTNSAGGIYVDGGKDHIIDQNRVYRSDIGIEIASEHAGRST

SNITVRDNLIYSNRLTGIAMGGYDEERGATEDSKIMYNTLVGNDTLNAGNGQLFMQSR

TKNNTFIRNILVSGSSEVLIYNEYTSNTGNVFDHNVYSPGEQEDALVWVWKNKAYSGI

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CDS 837504..838160

/locus_tag="EFAGFIKM_00736"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
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CDS complement(838317..839657)

/gene="mdtD_1"
/locus_tag="EFAGFIKM_00737"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01577"
/codon_start=1
/transl_table=11
/product="Putative multidrug resistance protein MdtD"
/translation="MKDKIVMPLWTCCLFIVVMNTTMFNVSLPVIIHDLQITSDLGSW
VISSYSIGYALSTVIYSRLSDRIPVRKLLTVGLLILGLSSLLGLFAHNFAILLTRIL
QSAGAGVMAGLGLVIASRYIPVERRGAAIALISSGSAMAFGLGPIVGGLISEYWGWNW
LFAITVLVLLALPVLLYFLPRESVKTDQPFDVIGAILTVINATTLLVAITQQSWLWFA
IGVISLVVHLLYIRKASLPFVNPQVFRTPGYTRLILIGFCVLVNLGNLFLMPLVLAD
LYGRSSLAIGLLIAPGAIVAFAFCTRFVGRWIDRYGNMRFMIIGHILLA AVLALFMLGL
DQSALIITSGYLFFSPALSASMASLNNEASRVLPKAQIGSGMGMLQLIQFFGGSVSVA
VCGLLLHSIPGVSVEEAYHVYACLLIICVVS LGLTIWHSKASRPSIKPVTLDN"

CDS complement(839913..842564)

/locus_tag="EFAGFIKM_00738"
/EC_number="7.2.2.10"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q8Y8Q5"
/codon_start=1
/transl_table=11
/product="Calcium-transporting ATPase"
/db_xref="COG:COG0474"

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EGMLTGESEAAEKHAD TIPDEAPIGDRRNMAFSGSLVVYGRGMLVITGTALKTEIGKI
AELIENAEAKNTPLQRKLESFSKKLGFFILGLSILIFGIEAGRVWLTEGTENIGPSIV
NALMFAVAVAVAAIPEALSSIVTIVLSLGTNKM AKQHAIIRRLPAVEALGSASIICTD
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GDPTEVALIAFSNRVNKDYNEIRDQFPREAE LPFDS DRKLMSTVHTFEGQTALLTKGG
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DDEHDLTLVGLTAMIDPPREAVYGSIEESKKAGIRTIMITGDHKTTAQ AIGVDIGLAE
PDDLAITGAELDKMSDEELDQ QLEHISVYARVSPENKIRIVRAWQRKGKVAAMTGDGV
NDAPALKQADIGVAMGSGTDVAKDAAAMILTDDNFVSIVNAVSVGRMVFDNIKKAIAY
LFAGNLGAI IAILFALIVGWVNPFTALQLLFINLVNDSLPAIALGTEKPEPDVMRRKP
RDINEGIFAGGTLQAVITRGVLIGAAVIVSQYIGLGISEEISVAMAFTTLILARSLQT
FAARSNTQTIFQVGFMTNKFVLGSILVCLCLYAITLIPGVRGVFAIPDTFGWNEFLIA
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CDS 842874..844166

/gene="hcp"

/locus_tag="EFAGFIKM_00739"

/EC_number="1.7.99.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q01770"

/codon_start=1

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/db_xref="COG:COG1151"

/translation="MFCYQCEQTPSGGCTVVGVC GKNETIASLQDTMIFALKGIAAYA
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DRFGVPQPITVSQNQIEGQCIVVTGHNLYALEELLRQTEGKGINIYTHSEMLPAHGYP
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VAKITEDDFSPLIERALS LPAANVQSEQVLT TGYYHHETVIGLAPEIIQAVKDGHIRRF
FVIAGCDAPGKGGNYRELATSLPNDTVILT TSCGKFRFNDVDYGTVGDTGIPRYIDL

GQCNNSGSTVKIAMALADAFGCTVNELPVSIVLSWFEQKAVAILLGLFSLGIQDIRIG

PKPPEFISEGVLDVLVDMFGLKLITTAEEDMNAMLALS"

CDS 844464..845867

/gene="bglF_2"

/locus_tag="EFAGFIKM_00740"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P08722"

/codon_start=1

/transl_table=11

/product="PTS system beta-glucoside-specific EIIBC
component"

/db_xref="COG:COG1263"

/translation="MHNTQIENWLKLAGGKENIKLVEHDKGTTTLALKDSTRLNMSVL

ASTEYVVDIRVTSEQCHLVIRDESSLIYNALQGVGEEGTALQEAGHAKKNRFSILHF

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WVILTICAAAYLEKAVQRISPKFSKWMVAPFLTLILVPLVLMILGPIGTWIDEYLPE

ALDSL VANAPVLSV MLLGAIFSLMLIMGLHYWLI AIIINEMVMNGGSMVIAAMLVAIV

GQAGAALANGIRSKEPASRR LAFWATGTAILGVVEPALYAVNMRKRSSFYAALLGGAA

GGLYFGLLSVKAFAMVGNPSLVSLPLFIEEGSLNLLHTCIGVVIAFGVSGGLTYWMAG

MDRNGDRGHRNPALSNT"

CDS 846091..847716

/gene="rhaS_3"

/locus_tag="EFAGFIKM_00741"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MSDNMEWIAQWKSTNALSNAWITKGELHHFLSHTLIFIIDGKAI

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ELKPEHGILRSIDYMQQHYDQVITRTQLAQIAGISPDWHYSRKFSERYGKPPLDYLAHY
RIYRAQEELLTAATSQDIKKSGFEDAHYFSRRFKQLTGVSPKIYRQTMQQRKMVSL
SPICAEIMIH LGVIPHAVVTPILLSPHHHEQFIAHGVQMLEV TQYEVEIELVRQVQP
EMLIGNVLTEEVKRELRTIAPILTGLHQDVEPMLNQLAAWFYKEDEAYRLHQQMKHEV
SVAKRQLQPFIQSASTVMLLRVEAFGYRYLGGHSHGVSHLLYEQLGLTLPQALDSGTA
WFNPCSLELLTQANPDYLFVEKRIMQHFSAEENMRKLWESPQWNE LKAVKNNRVFYVD
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CDS 847819..848835

/gene="yclQ_1"

/locus_tag="EFAGFIKM_00742"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94421"

/codon_start=1

/transl_table=11

/product="Petrobactin-binding protein YclQ"

/db_xref="COG:COG4607"

/translation="MSRRFKGLGIMLLVISMMLAACSGGTKEENATAGTAGASTEGAA
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EAEYRPDYLKEHRVQIIEVEQYQYNYEQLLALSPDMILTAGEGMEQGVYDELSKIAPT
VALDANSEMKRAMPKLA AIFDKTEESAKVLA EFDEKASQAKEKIAAALGEKTVLVLRV
EHNRYRFMGPKGGSSSVFFYDILGLNSPEVIKDSTDWFSQFSLEFLPEMNPDIYFLED
RTLVG YDTKKSMEDLKASQVWSNLEAVKNDHVFPLKTSQFVSGVGPIGSVKLMDYVVE
KLVP"

CDS 848854..849861

/gene="ycgT_1"

/locus_tag="EFAGFIKM_00743"

/EC_number="1.18.1.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31475"

/codon_start=1

/transl_table=11

/product="Ferredoxin--NADP reductase 1"

/db_xref="COG:COG0492"

/translation="MDIYDITIVGGGPAGMYASFYSGMRAMRTKIIKQELGGFMRT

YPEKLIWDVGGIDPIRCEKLIESLERQARTFDPTIVFGQEIAELERREDGVFVLSMT

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SAVDWANEMGKIASEVTVAHRRHEFTGHESPVAQMKAQANVMTPFNISRLYGTGDKID

RVELAHVETGEITHVEVDEVVSHGYDRDFGNLVQWGLAREDYGVSDQRMRTNIPGI

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CDS 850114..850902

/locus_tag="EFAGFIKM_00744"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLNRHKGKRICRRKFKQSMHCRVKVKVVKVRPKVVVNAPQGAQGI

SGPVGPIGPKGATGAQGIPGPQGPGLKGATGAQGIPGPQGLQGIPGIQGPVGPAGAL

GAVGPVGPVGPVGPAGATGPAGPVGAGISDFLSVFRADPGTGTDTVPGNAPITLTGVL

ANVGGAFTFVPPSSTITINEIGSYLISFSIHNNQGNADFNLTVNGTPITVPVFTGNGGG

PISAEVIVTVTTVPTTIQLVNANATPAQLHNNLNTTVTILKLTP"

CDS 851216..851758

/locus_tag="EFAGFIKM_00745"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKQMWIIASVAVVIVIGTYLFASNTGEEEAGTANAPNIRKLVE

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ETQLSTYENDNTCITTMQLS"

CDS 851935..852936

/gene="fpuA_1"

/locus_tag="EFAGFIKM_00746"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81L65"

/codon_start=1

/transl_table=11

/product="Petrobactin-binding protein FpuA"

/db_xref="COG:COG0614"

/translation="MKKGLNGLLIMLAFVLVLACGCKTTTTTDTSQGSDSGSAPAEET
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DYDKMTEIFNNIATLKGEDKAKEVLSNLDQHYVEAKEKLAAAGKENFNFALTQAFTY
QNAVSLRMFTDNSVIGTLDKIGLVNDWQPDKVENYGFSTVGIESLTDVKDSNFIYIT
QPDDDVFGTAMKDNSVWNGLDFVKEKRTYQLDSTTWTFGGPISSKVLVDGVVEAITK"

CDS 852933..854981

/gene="fpuB"

/locus_tag="EFAGFIKM_00747"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81L64"

/codon_start=1

/transl_table=11

/product="Petrobactin import system permease protein FpuB"

/db_xref="COG:COG0609"

/translation="MSSVQGSKPAMNVRTISYGGGLTALIVLFFVSLCYGEASIPHL
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SGVRSNRLLLLPGVFIWGAALLVGADVLAKMVHNSSMELPTGAVMAIIGAPWLIWLVL
RMKAANGSGMSTSMSTGGAARRFAFGPMAVLFVITVVLILLSTMFGGMRIPLADWLP
SLFQSDGLFSALIQLRIPRTLVAAGAGAALAISGVLIQMAVRNPLADASIVGVSSGAG
LGAMMVIIWPGLPYLLPIAAIIGAAIAAVVVFSLAWKKGLNPSAVVLLGIAMSAIA
GAGIQILIVRGAVYGSSGYIWLGTSTYARTWEQVRVIGLFLVILVPVAWWLARRFELL
VFDDNSASGLGLGVRRTLLAMTVGVLLAAGAVACVGTGFIGLIAPHMVRLLTGNKL

RRSMFLSALAGAVMLVLADTIGRTVMAPTEIPSGILIAIGTPYFLYLMYRSNWRKSV

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CDS complement(855269..856441)

/gene="dapL_1"

/locus_tag="EFAGFIKM_00748"

/EC_number="2.6.1.83"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0LEA5"

/codon_start=1

/transl_table=11

/product="LL-diaminopimelate aminotransferase"

/db_xref="COG:COG0436"

/translation="MNFAKRMDFHNEGIFTRLLEIKRRRLENGQPVIDLSVGTPNIPP

AQHIIITALCEAAADPANYIYAVNDQSELLQATSDWYKQRYQVELDPATQICSLLGSQE

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IAHRAKFMVSYPPNNPTTAMAPDQFYLDLIAFAKKYDIIVLHDNAYSELVFDEKSCGS

FLAFPGAMGVGVFENSLSKTYGLAGARIGFCVGNATMVSMKKLKSNDYGMFLPIQK

AAIAAITGDQSEVERVRAIYEQRRDILCEGFSSLGWPIAKPEATMFVWSRIPAHYDSS

EQFAMDLVTHAGVIATPGSAFGPSGEGYVRFALVQDNEILQQAVQSVDDSGILKSS"

CDS complement(856536..858614)

/locus_tag="EFAGFIKM_00749"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSNMLNKWGKTGARTSSMANTLSIVLLVIIVVFAVLGTFMFAS

TRNILVKQQESMLQTKTEAIVSEFDALFKEKGALVKQMSTNTLFQQYIETTASAADAA

SSTYAAQTQATLAAIVKAEPSFADAWVAGLDGKGFVIQNDGVVSAPDFDIQSRPYYPK

VTDEDGLYFSDPYIDIAAGDVLMGIFYPIKDENTTIGFAAADIAFKDIPAIMESYSL

GSTGYSMLLSKSGEILYHPDQEKVLKENILNSTGDMGDIGKKMLAGENGVLQNMNDNGE

RRYIGYATSKDTGWSVGLTISEEEVLAEKTFWITLGGFAAATLLLVIICYITLRRRL

LRSIPQLLAKIKQIEQGDLTVKVDIKSNNEIGQIATGLNSMVQKIQAMLQMVGSSAQI

LNQSSNDLQAISRTAVTMNDTSTAIN EIANATNYQSIETENILRKTGSLSSQIDEIA
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VDTVKQIASQTNLLALNASIEAARAGEHGRGFAVVAEEVRKLAEQTAQATEEINKKVN
VIEEKTTL SVEHTMRGMKIAEENAKSVEDTKHVFFSINKDLKDLQQRMMQITTNTANV
HKHKDEIFQALEIISSTTEENSASTEEVSASTQDQLDSIEQVADLSKQLNQLSGKLQD
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CDS 858871..859899

/locus_tag="EFAGFIKM_00750"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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AMEQMQLRLN SPAKATRLDFIEHYRKLTFLELRGKFNGFDSIAACLQLHTLILNCTV
ESVDVLAELPMLQYLSLDQCELKGGLDVLTQSTISMLKLSSVRKLTSIQGLEQMRGLE
YLHLSLPKLEQLCDFSHMTSLRQLELDYMKSLRDTECLWTARALESELKEINTALK A
DSFARLTGLEHLRQIDFRFIDV NKGRIAAMRDHLDKAGKSHLLYENIPEHERMNSIGI
AHLSQVLM"

CDS complement(859976..860695)

/gene="rhlG"

/locus_tag="EFAGFIKM_00751"

/EC_number="1.1.1.100"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9RPT1"

/codon_start=1

/transl_table=11

/product="Rhamnolipids biosynthesis

3-oxoacyl-[acyl-carrier-protein] reductase"

/translation="MKNIIVFGASKGLGDAFVRGVPQSGDKVWVVSRSKPESLSVEDG
VERIWIQADLSELQAAEQVASQLQGETLDVLIYNVGIWEKEGFEEHYTFDKDEPADIS
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TEALREHTRNDRIAVTCINPGELAAEIPYEDGMERALAEYDGTRIPLQDMVAIVRCII

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CDS complement(860941..863004)

/locus_tag="EFAGFIKM_00752"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MWKKISALLLALPLLITSFPLTSPAASAATFSNPVIYADVPDSD

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RGSWASSLRYNNGIYYVAFGSLSTGKTYIYQTSNIETGPWTPYTLNSYYHDPSLLFDG

NRTFLVHGSDNISIVELTPDAKAVKSGGLNQVLIPNASSVAGSNMIVKAEGAHIQKIN

GMYVFLIAWPSGDGRIQLAYRANTLTGPYTGKVVLRDSGIAQGGIVDTASGAWYGLL

FRDSGAIGRIPLYLPVTWSDNWPVFGVNGKVPLNMNMPVEGQPAAKIYGSDEFNTTTS

GTPSVTQLLVNGGFEEISNIQPWTSNNTATINLTNAEAFSGTKSLLVSGRQQTAGGAKQ

MVTGKLVPGGTYSFSAKIKYTTGPASKTFNLSIQNGASYTGITIMGSATLTRGQWGTI

QGYTVPSNADLSQSFIQVETPYNSNPDPNTDLMAFYVDDVSLTSNSSSGTSSLATFW

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KDGDYAGLAAFQSKYGFVGKMTGSTKSIVMANASSGMTTEVATVPFNQNRILRVIC

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YFRVE"

CDS complement(863038..864972)

/gene="xynD_1"

/locus_tag="EFAGFIKM_00753"

/EC_number="3.2.1.55"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P45796"

/codon_start=1

/transl_table=11

/product="Arabinoxylan arabinofuranohydrolase"

/translation="MIRKPLVLLLSCLLIFVTLPESSHAANAATAVAKLPGNSNPLIDH

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SIPVAGANNANNGQGIKWATQSWAPAMAKKTIAGKEKFFLYFANSGGGIGVLTADSP
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KGEIGYMVSDSPMGPFTYKGFHFLKNPGTFFGVGGNNHHAVFQFNNEWYVAYHAQTVSK
AFLGDGKGYRSTHINKLTHNADGTIQEVQGNMTGVPQITNLNPYVRVEAETIGWQAGI
NTEPSQASGGPVANQNVTNIHNGDWIAVGNVDFGSAGASKFKANVASTGNGNIEVRDL
SPTGPLAGTLNVSSSTGGSQTWREMETNVTNATGVHRLYLVTGSGNGNLFKLDYWQFT
SGSGGNPNPNPNPNPNVTRYEAENMTLGGQYAGVVSSPFNGVALYGNNDYAAYNQYFA
FPTHQFSVRGASNNNNNTARVDLVIGGVTAGSFYFTGTEPTVQTLTGITHAIGNQEIKL
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CDS 865876..866235

/locus_tag="EFAGFIKM_00754"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MAIFSTGPIENNPVSGVRPTQQVTIRLASRAEVDSTVSIQGYV

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LVDAHRVVEHEKTVNNI"

CDS 866270..868054

/locus_tag="EFAGFIKM_00755"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSFLSTGPIENNAVSGVRPTQTVTVRIDNRSVDVSTSTIQIQQYY

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CDS complement(868121..868216)
/locus_tag="EFAGFIKM_00756"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MYEARSNPRLFMFLYSPYLSFEESLKTKAHT"

CDS complement(868235..870196)
/gene="rhaR_5"
/locus_tag="EFAGFIKM_00757"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01533"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaR"
/translation="MKATLNVQEHILIWNCASLKIMDVRHIVIQADECVRPYLPASA
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TGASLIDYLGIRMNKAVTLLQKTELSLQKVAVSVGYADVSYFIRMFKKHTGVTPKQF
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ELQPD LIVVWNDPETIEKLTKIAPTVAVEYGVPLRQQLMDFGKMTGREEQAKAWIAEW
DAKIAEYKPLVEQAVGDRTVSIFDTGSAKEFYAYGSFGRGGDIYGEFGLKAPPIQK
EAIDSGKGWAKLSLELLPQYAGDYIFISGWTGDESGDSVFEGPIWDNLPAVQNNHVYR
EESRGFVFSDPISLEAQLKFVVDSLTKTE"

CDS 870411..871340

/locus_tag="EFAGFIKM_00758"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGKRLLIALLSMIMLFGVVPAYGAGTSGNSLIWEGYNDNGRMVG

INYTTFTGKKSTTKSIYNKQASQQKIIGNWIYFLVEDEEDHYSIAKIKTDGSAFAYVS

QDDNFASFDVAGDTIYFVKSEYNGNLYDDLSYGSMKTDGTTKQIILPVSPFYNFINK

EYVYTERHTDLFYRMKKDGTATKLLSSKGVSVYKFYGNVLFSEIDGGYSSRGVFA

ELDGARKKTFASDGYIHPLAYLNNKFYYRKNTIDKVGNTRSIIYVYNRYTGKKNKFAS

IDYYDRFLGQVGNSLAFLTFPKGDVYKIGLDGK"

CDS complement(871568..871921)

/locus_tag="EFAGFIKM_00759"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNVTLWIVQLILALGFIYSGWMKTIRIESSKKTWAWVNDVPKSL

VIWIGIAELLGALGLVLPWALNITPVLTPIAAIALATVTLFGMLFHRRKEYRELGVN

IFFIVLALIIAFGRL"

CDS 872062..872454

/locus_tag="EFAGFIKM_00760"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTVYCKFGTALDILTGWKWSLILLRLLSNGTMRFSSELQKAIPDI

SKKMLTQQLKELEYHDIVHREVYAQIPPKVEYSITEYGQLMKPVLQTMSDWGAGHMQH

MEKLYSQEDEKGAHPSEPRKIDSLGGIG"

CDS 872471..873508

/gene="dadA"

/locus_tag="EFAGFIKM_00761"

/EC_number="1.4.99.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01202"

/codon_start=1

/transl_table=11

/product="D-amino acid dehydrogenase"

/translation="MNKQKIVIIGAGIVGACMAYHLAKRNQDVTVIERHSAAAREVTE
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KLNQEQLEALEPNLKEYPDEAMFVSEEGAVDPIAVTELLLSKAQEYGAKIQFDTNVTQ
LKQEGSRLVGVHTSKGFVESDVVLAAGTGPELCNPLGCHVPVTSSPSILIRMKTAN
KLIHTLISNAQFEARQLTDYTLLAAEDYIDESEANGPQAVGKRAYDTLRRSLKHGNQL
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NELDPCRLSRF"

CDS complement(873667..874461)

/locus_tag="EFAGFIKM_00762"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEFIHEDEKLAVSVIQAIHTGDIPTLEQLLAENPGLANIRILDR
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AASSNDVQVLDALLDAGADIETPGAVIAGGTPLDDAIAFAQWDAARRLVERGAIFALW
HAAALGDIHAIQE HFKGAQLPERYPWGTSTSPSPNSVTVAFWCACHGGQRETAEYLL
DQGAELNWIASWDGMTPLDTAKRNFSSSELIPWLESQGAKSASEIHR"

CDS complement(874495..875466)

/locus_tag="EFAGFIKM_00763"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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NNDRDQHSYDFALVEYVDGQKAEAYFQHKNHKDRDELFRIRDMLSNMHNIQRNVYGN
ANDNSKKAGPCYQVQRLDAETALSASKHMTDIRKNDERLLEKLYELEAAIQPRDLYS
FIHGELGPDHIWIDHAMQPCLIDIEGAGFFDLEHEHSFLEFRFGDFYHYLKNNDLDPE
RMTFYRFCHHLSLISGGLKLLHRQFPDQQFARGLSEYHARCAVQMLS"

CDS 875766..877652

/gene="rhaS_4"

/locus_tag="EFAGFIKM_00764"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MDIRHITMQRKEVLHSYRFPASCFLYMVRGNAVIRLDGKDHQVS

RFHVLHGGKGCCLNILPVEEFLEYMIYYKAIPLPERQDILALMEHRNPFKLQYGFA

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QMKYYMQEHYAEPITMDLLAELMDSSPRHLSRLFKRQTGYSPIDFVIQIRMNKAHELL

LATDATLQEIKAAGYDPDGYLLAKIFKKYMGAPIRYRKQHESPNVPSTVARLGIVQD

LTSLYIDNDYHNQHIFEEELLMYRSRKTPLAITLLLCLSLLSACSTGGAGSPSAKEG

SQKPTNQVAANNAHNTDTQSQMKTVTTLKGDIEVPVNPQRVVVLYLMGDLLALGVNPV

GISSVEEGAFAFASLEGATSLGAFNPDPEAVTALNPDLIIVTNEEIYGLKMIAPTVY

IPYDLPVEERMNLLGEILGKEGQAQEMLDNLHKKVEQSKEKLEQAGILDKVTIMESN

KGSMAMVTGLGYGRGSQIIYQYLGKMAPEVLQREIENARNDATSKDVSYEVLPEYVGD

YIFRSSFEGMVDLSDNSIWNNIPAVKEGRLIDMSFGLFFYNDIYSLDKQLDFIVDNLL

KTAE"

CDS 877720..878307

/locus_tag="EFAGFIKM_00765"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNYYFLESQYPRRGFISGGTTFTPQLDMNYLAIENTLPEGTTAE

VELLSTVRNLNVDFETITGRHVSDRFKKLLEETKTNTQFIPTTVCYHDGRAVEKTY

WTAHQLDRLDVFDERSEYGRKAVIAASVQQPPRKIVKVSQICLHEERIGKHEFFML
DYINIFKPIVSKDFYEVCRKHKLNLNVTEVGNVSN"

CDS 878764..880323

/locus_tag="EFAGFIKM_00766"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFINRTIRKFGVSVGIISMFTFALPAVGFSMPLQPTTIDKVEGD

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GVISNRHKGKALPNEFPENTGLQEGASATKPELYNNVSIFTPIEEINGNWWYGVLPKA

GKNVRFPINPFLGVMGVAPNTSEVVSSIPPIETGGNMDINELGVGATIYYPIQVKGGL

FYTGDPHFAQGDGEVALTALEASLRGTVRLTVLKKGDPSLPHSGEFTQPFAETEDYWI

PIGLDPLDEAMKESVRESIQFLSDKLMDRSVAYAYLSAATDYEVSQVVDRTKGVHG

LIRKTDLFLEHVDVAMNVGGTLIKPVVHNNEFYVPIRTISELLGGTVVWDNKTRTTQIK

LGTKNISAQIGSDVYSINDKLVFNSNVPKLLNGETVVPVSVINEILGAYVNWTTIDKT

LTANVSLSKKQ"

CDS complement(880535..881383)

/gene="sseB"

/locus_tag="EFAGFIKM_00767"

/EC_number="2.8.1.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WHF5"

/codon_start=1

/transl_table=11

/product="Putative thiosulfate sulfurtransferase SseB"

/db_xref="COG:COG2897"

/translation="MKNIVSMRWLLARMYEPDVVIADCRFLLGQPEAGRQAYEAGHIP

GAVYLDLEKDLSSPVSAHGGRHPLPDPAVLASRLSKAGIGSNSRIVAYDDQGGMNASR

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QASASGIAVLIDSRDARRYAGLEEPIDAKAGHIPGAVNYFWKDVLDWDGRWTDGTGVLE

ERFSKLDKDGAIIVYCGSGVSACPNVIALEEAGYTNVKLYSGSWSDWISYEENPVATG
EAHKDV"

CDS complement(881447..882391)
/locus_tag="EFAGFIKM_00768"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MTSLNRAGRSIYLLFFVGIIAISFSSIFVRWSTADVAVIAMYRL
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GTIAVAVHMLLGQFLRAGLSAFSYNFWVFFVAACTLAVYNLIMGHPFGGYAASEWGIF
LLLAIVPTIFGHYLFNWLLQYMNATTVSMGVLGEPVFSSLLAWMLLGESLSALQMSAG
VVIIFGVWIFIRYGKTKPQIASAEASVAGKGPIEPTTV"

CDS 882614..883522
/locus_tag="EFAGFIKM_00769"
/EC_number="3.5.1.104"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q81EJ6"
/codon_start=1
/transl_table=11
/product="Peptidoglycan-N-acetylglucosamine deacetylase"
/db_xref="COG:COG0726"
/translation="MTVRVQQERAGERGSIPPSTSRTKTHKRRKIRYGRVIALMLLV
LFVTGITYVFFGMTHWIKSVVAPPITVIEQPAKLGMIQVTPDAKEEPARFQGQVRKL
AYITFDDGPTEYTEQLLDILKQHEAKATFFMIGRQLNQHPKAVRLLKEGSYPGLHSM
THNYKKLYKSGNSANFVKEFKKEQKMQDLIGFTPHLIRAPYGSSPQIGEKFRGDIAA
AGFKMWDWTTDSL DWNLPQDPKIVARVSKSVHRDKEVILMHEREQTVQALPRILKLL
EDRGYEFVYDPDAHWWANFSGDTRL"

CDS 883560..884213
/locus_tag="EFAGFIKM_00770"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLTSKKVALAAVSVLLILLASGCGDPQEPAANQINQLVLSGQEI
DQSLKTLTSHEQEDMKLYKSILDKGKNKNSDLEALLDQAADHIHERRTLLKQAEEMK
QTNEKTVALRSSLKELSFKEETLAQAEKVLDDQYEARARALENFVVSQYLSLSADEQL
YDLMRESAEPNLVKIKRAIRVRNSEYAKLAEFRKQFNLQTKAFNGANAKLVQMDQAS"

CDS 884356..885246

/locus_tag="EFAGFIKM_00771"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRKGNTMKVSASLLVLLMGFSLVACGNSNPAAQPTVNNTEEQSP
APEQQPNESAAIEAEGILGWADPHTVEIRVNEKPMSFQVSEDLQKSLDDIDDEDSVR
FKYVEKTIDATTKQLVLTEIAKLESSDDNNGSNAGGTVTSRDKTSELEVTVEGMTEK
RPVTLAQAKGYSLYVFEPMAFDAEDHELTMNIDPDYEVEIEKLPANYNLDALKMDAKE
ELSETGEVKQLTAEQLSNGPMKDAKLYMMSQNDKKTEYFIVKELDGNGFIFHIQAPIG
EPSEGFLPMAYASLNSIMNE"

CDS complement(885289..885429)

/locus_tag="EFAGFIKM_00772"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MQQHRSFRLFVYARRGTARYIYLYCSNVNKTAYLLSQGNTLFRE
SF"

CDS complement(885501..886673)

/gene="mtlD_2"
/locus_tag="EFAGFIKM_00773"
/EC_number="1.1.1.17"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P09424"

/codon_start=1

/transl_table=11

/product="Mannitol-1-phosphate 5-dehydrogenase"

/db_xref="COG:COG0246"

/translation="MKAVHFGAGNIGRGFIGHMLSASDYKVCFVARNPCKISMLQERQ

EYPITLANRDQDTTIVNNVTAINVSEQNLVAEEIASADLITTAVGVSA LGDIAEPIAK

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IVPAQNHKDPLQVTVEPFYEWVVHRPALLDGFKKIDGVHYVDSLEPYIERKMFTVNTG

HCVAAYFGYLEGFKTIRQVMSNSTLRKVRHVMEETGQMLIQKHGFNAQKH NKYIDTI

LERFANPNLTDQVTRVGRSPLRKLSPHDRLVRPAMQASEFGIKIPHLTSAMAAAMLFN

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CDS complement(886721..887389)

/locus_tag="EFAGFIKM_00774"

/EC_number="3.1.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9X0Y1"

/codon_start=1

/transl_table=11

/product="Phosphorylated carbohydrates phosphatase"

/db_xref="COG:COG0637"

/translation="MIKALVFDFDGTIIDTETAWYIAFRDAYKEHGVDLTLEMYSQCI

GTSLKTFNPYEYLITDLNLPIDREAFRESVQLQHAALMNKEKVRPGIQEYLEQAREAG

LKLAVASSSKREWVEQHLEQLKLDYFEVIRTADDVANVKPDPELYTQALEALGVTAD

EAVAIEDSPNGARAAAAAGMHCVVISNTITGTLEFDMPHQRLSCLDTLTFNDLISKPL

VTTV"

CDS 887589..887732

/locus_tag="EFAGFIKM_00775"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIVYIENFNMYDLFSENDERCKPLTLLHVSGVLNKLFLQLKKIK

LFL"

CDS 887729..887944

/locus_tag="EFAGFIKM_00776"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKICYSDRSTAFDTFIIEMELNLLDFISFTPDQALWENGRKIL

KVYGVREEDKHVAKGPFQWLLHRACSG"

CDS 887892..888818

/gene="tri1"

/locus_tag="EFAGFIKM_00777"

/EC_number="3.2.2.19"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:B0KTG8"

/codon_start=1

/transl_table=11

/product="ADP-ribosylarginine hydrolase Tri1"

/db_xref="COG:COG1397"

/translation="MLQKDRFNGCFIGLAAGDALGTTVEFSSPGTFEPVTDIVGGGVF

GLEAGQWTD DTSMALCLAESLVRKADFPADQMRRYTNWYKVGYSSTGDCFDIGGAT

RSALERFEITGEAYSGSTDPMTAGNGSIMRLAPVVMAYANQPNEAVHYAGLSSRTTHA

ATESVEACEVLAAIIVAGLRGANKSVMLMPETCRQWREEPTFSPAIEEVVLGSYQRKE

PPEIKGSGYVVRSLAALWAFHKSSSFEEGALLAVNLGDDADTTGAVYGQIAGAYYGL

SGIPAHWRDKLAMRGTFEQLTDDLWLKATENR"

CDS 888844..890091

/gene="ydhP_1"

/locus_tag="EFAGFIKM_00778"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77389"

/codon_start=1

/transl_table=11
/product="Inner membrane transport protein YdhP"
/db_xref="COG:COG2814"
/translation="MSTTGHTIQPVSPSGKRGAFPLSLLCLTIGAFAIMTEFIIMG
LLPNVAIDLNVSIPQAGQLITGYALGVAVGAPILTVFTHKIPQKKLLVLLMCIFIIGN
ALSVIAPTYGLLISARILTAFSHGTF LGVGSIMATRLVAPERRAGAVSVVLAGLTIAN
IIGVPFGTFIGQQHGWRRSFGAITILGIISLMGIIRFIPVIPQGPPANLGQQFRNLVR
PQVLLVLLIGALGCGSLFTVFTYITPMLVDISGFAEQSVTWILVLF GFGVT LGNLVGG
RLADWKLMPSLIVNFGILAVLLAALTITLENPYLAVITIFFWGVAAFGIMPGLQIRIM
NMTREAPLLATTSSHSFNLGNAAGAYMGGYAITHHTGLISVPLYAAVIAGLGLLGLLF
SLFMERKHHGPEIAQVAEAASAS"

CDS 890493..891440

/gene="xynZ_1"
/locus_tag="EFAGFIKM_00779"
/EC_number="3.2.1.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P10478"
/codon_start=1
/transl_table=11
/product="Endo-1,4-beta-xylanase Z"
/db_xref="COG:COG2382"
/translation="MKKRLSKILSLSITAALLVPTMASATDMQETPAPAPIQSVIDQG
ATGTM DNTGQNALANTPVVPAPPGYDGYRNNIPHGNTNLISYYSTTVGNTRKATVYTP
PGYSPNKKYNVLYLLHGIGGDEYEWVNAMKPKNILDNLYSEGKLSQMIVVMPNGRAMK
DDRPVGDIFAPDKVAAFERFEQDLLKDLIPHIEANYPVYKDRNSRALAGLSMGGGQSL
NFG LKNLNTFAWVGAFSAAPNTQSVSQLVSNPGQVASQLKLLWISCGSSDGLLWVSQN
FKNGLSSMNIPHTFYLDVGGHEPSVWNSGLYQFSQRIFK"

CDS 891660..891839

/locus_tag="EFAGFIKM_00780"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MFYYKGAFRETDNVIYFKSEVPLTENDVWIFGEKTYFIESVEKE
FLLLQRVGSIVSVSL"

CDS 891970..892668

/gene="sigK_1"
/locus_tag="EFAGFIKM_00781"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P62181"
/codon_start=1
/transl_table=11
/product="RNA polymerase sigma-28 factor"
/translation="MPGLFTAIALFIKELTLLVSYVKNNAFPQPLAEGDEAKHLRLMA
EGNAHSRNLLIEHNLRLVAHIVKKFDNTGEDQEDLISIGTIGLIKAIESFQQGKGTKL
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QLKIEKSKIYRNLDILDDREKEVVIGRFGLEAGGEERTQREIAKELGISRSYVSRIEK
RALMKLYHEFYKQK"

CDS 892912..893103

/locus_tag="EFAGFIKM_00782"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIVFNSFQSYSSIINFIALLMISVANAIKRVWKTSLAIAFLVV
VALCLAYIFKYFYRYVLSA"

CDS 893423..894784

/gene="cycA"
/locus_tag="EFAGFIKM_00783"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AAE0"
/codon_start=1
/transl_table=11
/product="D-serine/D-alanine/glycine transporter"

/db_xref="COG:COG1113"
/translation="MQQETLTRGLKNRHVQLMAIGGAIGTGLFLGAGKTIQLTGPSIL
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ALIIVGLYMIFKGFTTDQGPASFTNLWSHGGWFPNGLHGFISFQMVVFAFVGMELVG
LTAGETENPEKVIPRAINQIPRVLLFYVGALLIIMSIYPWNAIVPTESPFVQVFAAV
GIAAAAGIVNFVVLTSAAACNSAIFSTSRMVFSMAKDHNAPESEFARLNKRKVPSNAL
FFSTIVILIAIVLNYIMPEGVFTLITSVSTVCFIFVWGMVICHRLRYRRTQPELASRS
RFKLPLYPFSNYLILAFVLVLAEDTRVALFVTPVWFILVAGIYLLKKKNLSN
NRQ"

CDS complement(894840..896024)

/gene="estB_1"
/locus_tag="EFAGFIKM_00784"
/EC_number="3.1.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9KX40"
/codon_start=1
/transl_table=11
/product="Esterase EstB"
/db_xref="COG:COG1680"
/translation="MRKKDMTTLHNYVDEAIDRALSEKRIVGTVVQVALRGELIYSRA
AGFADREQKRSMSENAFLASVTKPIVSTAALALISQGKLSVHDPVTRWLPAPFRPKL
ANGQDALISVHQLMHTAGLTYRFFQEDQGTIELAGVSDGMDWSEMSLEENLQRLASA
PLLYEPGNRWRYSIATDVLGAVIEKVTGMSLREAVQTLVTHPLHMTDTDFVAVDSERL
TAAYANGSEEPRLHQQELEQIPFIEGTAGFRLSPNRANRTSAYLSGGAGMVGSTGDFL
TLLEALRQGGQPLLTEAVAAEMSTNQIGDLVMPYWPGRGFGLGFTVLKDPVAAGTPES
AGTWRMGGTYGHSWFVDPKEELSVAaftNTALEGMSGQYTTDICDAIYAGIREGKEAV
RI"

CDS 896195..896647

/gene="lrpC_1"
/locus_tag="EFAGFIKM_00785"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P96582"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator LrpC"

/db_xref="COG:COG1522"

/translation="MDEIDQHILYHLENQARLSMTELGKLVGLSQPAVTERVKRMEEK
GIIEEYRTVISPTKLGKQSTAYVLFRTDCYPFLDFCRASPEVVECYSRISGEYNYLLK
ILTDTIQGLEEFENKCDPYGTMTLITMSSPIAHKNLVGGPNLLAQAE"

CDS complement(896742..897947)

/gene="nepI"

/locus_tag="EFAGFIKM_00786"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ADL1"

/codon_start=1

/transl_table=11

/product="Purine ribonucleoside efflux pump NepI"

/db_xref="COG:COG2814"

/translation="MTAHTPLPKQRELPSISSERLPWAGLLALAMAGFICILTESLPA
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LALGVPIGSFLSSYVGWRLIFGMVSLTTLIVVWLWRMPDFAGEPTGERLPLHKVFL
IPGVRPILFVVLAWMLAHNILYTYISPYLAQTVFANRVDLILLIFGFTSIVGIWLTGM
LIDRFLRKLVIISLASFALASVVMGIATHQPVIILGVMIWGLTFGGAATLLQTAIAQ
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YKYGFTAN"

CDS complement(898168..899232)

/locus_tag="EFAGFIKM_00787"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKFSSRTIGIAALSLLMLLAACSNSTSTSSPAEETTSTANTTET"

SAPAENTNKTTYPLTIENFTISGEGGEWKPKVQVFDKAPERVVANTQSAAEMLIKLGL
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GVGTVDGLNDMNIRTLQTTNHKGSLSLSYSDIAQLGQIFDVQENAATFTESLKTRVE
AIKASVADQPDHTFAYIVPATEDTITVSSMQNDTYQLDALGLLKLKNTFDGVQGEVSV
EQLITANPDYLLLSAYAGSPDIDKLIENLYANPALQSMNAIKNKQIYVTDIFSQFWGYG
YQILDGIEKMGQEMKANPIK"

CDS 899366..900475

/gene="btuC"

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/inference="ab initio prediction:Prodigal:002006"

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CDS 900478..901245

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CDS 902169..902822
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CDS 904324..905313

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CDS 905869..911595

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CDS 911778..913019

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CDS 913111..913551

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CDS 913583..914137

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CDS complement(914326..915183)

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CDS 916144..916620

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CDS 916684..933462

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CDS 933452..937651

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NFGFEWMVQKIPDSKLSTLDLSSLRMTLNGAEPISVIERFVKKFSSCGYRPNMMFP
AYGMAEATVGVCTSR LGEEPRIERISRTL VQEG LAVPVQLPSSDSHTSDVIEFVHEG
YPMTGIQIRIADEQGEVLDERVVGEIQIRGESVTSGYYSLPEINREMYVDGWLRTGDL
GYMADGSLVVSGRIKDIVFIRGQNHYAHDLEEILYQNSSIPRGNLTVVGHFNSLKQVE
ELLVFVKYKSGTPQFLDVRQDLIQRMRAGLGIEITHVLPIKVIPKTTSGKVQRFMLRN
EYERGVFTKDIEAIEELIRENTQQQGHETVSASSLEYTVRKAWADILQLPAGKIEMDT
SFLALGGNSILSYQLLDKLSAHMGRELGQELLVFCSTVREMVEYLQELPAETKDFEQA
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DDWIGELKQPDTFDHEFFEIPSEQA AFMDPQHRKLLEVAHEALEDAGMLVDHEDKRDV
GVYVGINPSTYFDLVIDYMNRS LGKAVHSHAMVGNMSNIAAASISHMYNFTGPALSID
TACSSFLVALTQAVAAIQDKRISGAVVGGANILATPHVHQLSRNAGICSSTQHTKVFD
READGSVLGEGTVVVYLEPLTEAIRNNKHVYGVIRGTAVNNDGYSLGIMAPNPQGQYE
VLRAAYRDANLNPSEISYIEAHGSGTRIGDPIEVNALLRLFREKGYPDSNSIGLGSVK
TNIGHLFAASSGASLAKVLLSMQH GELAPSLHMDNPNPALRLEQSPFHIVSEHKTWDV
PEGKTRKAGISSFGLGGTNAHIVLEEWKAPVRAAAPARGQLLTFSAKSEQALKKLIDN
TEQYVKKHADVAPEDLCFTRNRYRKHYRYRAAVVSSTGEWNIEEMEF GFKPRNRAAR
VNIVVGGHEIRGEDEA QARQVIRPDDFNEDKVSTLNYWVTLLTLVRLVPSIQEIRGI
AAGEELVSSLHLDGEEHHS AHASQSIPVNNRVTLDSLQDTPGKMANTDIVIMIAADQT
VQQLEYS GKESFIRLSAEPTLT MEDQLALLLGQLYVRGAALDWEQLHPNGSGQIVHLP
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CDS 937648..937905

/locus_tag="EFAGFIKM_00803"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MTKEEIELFIKSEIAAALNQEPEDIDEEMNFLKIGVSSVQALKI

INRARKHLQVDISPVALFEYKTIAEFAAYLNESLLQEGVAE"

CDS 937902..939053

/gene="mmgC"

/locus_tag="EFAGFIKM_00804"

/EC_number="1.3.99.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P45857"

/codon_start=1

/transl_table=11

/product="Acyl-CoA dehydrogenase"

/db_xref="COG:COG1960"

/translation="MIEVGVEQEIIHEAELFAAREIRPYAQQIQEQQAIPRTLIRAMA

EKGYLEASIPAIEYGGMGLGPKAYGLLTVFVGKALPAVRSLLTVHTSLVSETLVRFGTP

EQKSSWLPKLVKGEWIAAFGLTEPEVGSDAKSVKTEWREESDCYVLNGKKKWITFGHL

ADVFIHASNQGRSTAFWVERQFEGVQTKPIEGVMVAGETGIAEIDLHEVRVPKNHII

GRLNEGFYIVTGALDQGRYSIAWAGLAIAQEALDAMVTYSRKRKQFDQKLSHFQLIR

GMIGDAVTKVHAARALCLRAAELREAKDPQAAMETTIKYFTSKVAVEVASDALQVHG

ANGISNQYPVARLYKEAKILEIIEGSSQMQQEMISHYGLKAYYKRGGSV"

CDS 939050..940030

/gene="fabD_1"

/locus_tag="EFAGFIKM_00805"

/EC_number="2.3.1.39"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O85140"

/codon_start=1

/transl_table=11

/product="Malonyl CoA-acyl carrier protein transacylase"

/db_xref="COG:COG0331"

/translation="MTFCALFPGQGSQYMGMCSELLDSEPEANQIFAEASEVIGFDLK

ALVMEGTLDQLTVSEYAQPAVLTAASYVLFDSEVRRVTGMPDYAVGHSLGEISALVAAG

ALRFADGIRFTAQRGALMHRISIQEQKGRAGIVVDITQEALEELVENIRQNEYVTISGY

NSPGQFVVAGTAKGLQLLDDQVDGYGGEFIPFRMMPMKADAPYHSELMQFIQPELEEM
LAGISFSAPVFPICSTVHGEFISGAEDIPKLLSSQLLQPIRWNQALARVQNLGATVWI
DIGPGQSVRNMLAENKALPAAYSLDDPQDRSRLLDREAVNQTSGGGDKG"

CDS 940027..941346

/gene="hemL_2"

/locus_tag="EFAGFIKM_00806"

/EC_number="5.4.3.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00375"

/codon_start=1

/transl_table=11

/product="Glutamate-1-semialdehyde 2,1-aminomutase"

/translation="MITEMMQYNQRVKQWLPGGVHYNFHLPWEEETPLHFKHASRSRVT

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SAEMIRFGLSGTEIVQNALRLARAWTGKNRFVRFEGHYHGNADNIMGGKTARTGLPVP

SDYPGDMKGTKGRARDAMESQSYLLPWNDAPRLEELFRQYGDDIAAVIMEPVCVNGGG

VMPAPGYLQKVRQLCDQYQVVLIFDEITGFRMGLGGAQQLFGVTPDLTTLGKAIAGG

GVPVSALVGRADIMKLLVDKKVIHAGTFNGYPLGTAAVKATLEMLGRNGGQAMHSMNR

HAEMMHDILCQEAVKVGLPLIVQGPGSCASYHCCTEPLTDTADYTFELMSFDILLNSK

LAEHGVLVSTLSRMYPNILLDMQDVAWFGERVPAALAEMKEIYDELI"

CDS 941375..942226

/gene="mmgB_2"

/locus_tag="EFAGFIKM_00807"

/EC_number="1.1.1.157"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P45856"

/codon_start=1

/transl_table=11

/product="putative 3-hydroxybutyryl-CoA dehydrogenase"

/db_xref="COG:COG1250"

/translation="MHNRLIAIIGAGVMGCATALDVARAGYRVILQDISASVIEHAPD

VIRREYRSACFLKQGYGVPLDQIMERISFQTQDEGVVEASIIENVTENLELKKEVY

ARLYHKVRPDALFALNTSCISVTKLASFLPDPGRVIGVHLMNPVPVKSMVEVIKGHHT
TQGTEHEMVAFLETLDKSPVVEDLPGFVSNRLSHLLMNEAAYIVQDGIATPEQVDAI
MKKGFNYQMGPLETADLIGLDTVHSLKVLYDSYQDPKFRCCPMLQKMVDAGQWGRKT
GQGFYAY"

CDS 942246..943295

/locus_tag="EFAGFIKM_00808"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEKCLKDIKCIVWDL DHTIWDGVLLESADVQLKPGLKEVIEKLDQ

RGILHSVASKNDAELAWAKL NELGIAEYFLYPEIHWD AKSVSVQRIQQNINIGMDAIL

FVDDQPFELEEVQSVHADIQVLHADQYETMLDDPRLMPRFITADSACRRQMYQADTLR

KQAEQYEGPSEQFLATLGMKFSIYEATEDDLQRAEELTVRTNQLNATGITYSYEELH

QLMISQDHMLLVCELEDKYGTYGKIGLALIHMQQK VWRNLMLMSCRVMSRGAGSVLL

TYIMREAQKQKQMLADFKDTGRNRM MNISYRFAGFKQ QSADQEGRVLFYHDLQQAVE

FPDYIEVFVPEGQHQ"

CDS 943311..943574

/locus_tag="EFAGFIKM_00809"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDYRQEIREFIGNNLTMDHEDTQINDNDNYFEQRFVNSLFAMRL

VDFVERRFQIEIANEDLDLANFCTINRLHDLIERKLTEKEAAL"

CDS 943571..944455

/locus_tag="EFAGFIKM_00810"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MITANQASIRPVTSPATSPSNKYMYLFLGISFGTCYGIASLFMF

FADFIVPITGELTLMHPLAIVALYSPSIAGLITCYVMGGKEALKGMFMKLVPRRQDLF
WIPLIIGISIIFASTMHFGSLLFGIPVPELTYSVPEMIWLGIVNLIKETGLIGGLFGW
IGFLLPFLQGKLNKNNITSGELITGLLFGWLWLPGYLISSFGTSTTYIYYVQLMAFIVF
QSYIFNATKGTLLFYLLAFWLVTATGSQIDLYYFNPQVQIMQFFFFAISAIHVIFKR
KNVDTSLQTFPAYVLERK"

CDS 944481..945221

/gene="srfAD"

/locus_tag="EFAGFIKM_00811"

/EC_number="3.1.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q08788"

/codon_start=1

/transl_table=11

/product="Surfactin synthase thioesterase subunit"

/db_xref="COG:COG3208"

/translation="MEPIYLEQLQKGEGNRQMVCFPYLGGNSNSFQPLVPYLHDTEIW
AFTPPGHGLNTETPLEHMQQLVELYTSKLLDVIQPGSLLFGHSLGGITAYFVAQRLCQ
ERPDVAKTLRLVLSACNTPDECGMQNYDRMSDENLIDHLFSYEALPQELIHEKELLY
FLPVIRADFRMLESAATLEYEPLSLPVLYLWGERDRTVTLQSALRWGRYFGTSMKLQT
IKEGAHMFMMHQPSTVAHCLTSFMTPAK"

CDS 945257..947590

/locus_tag="EFAGFIKM_00812"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLLRMLRNDITRKKGITAALFIFVLLAALLVSSGSRMIMELTSS
IQYLFSESKTPHFVQMHAGELDQAKVNTWAEENAMVQQHQIVEMVNIDGSNLFLGAES
EKNSVMDIDFVTQNQGFYLLNLNSEIIQVNDGEIAPVYYMQQKLSVGDQVRIDNG
QFERSYTIVDFVRDAQMNPSVVHSKRFIVSAGNLQELKQSIGEMEYLIEFRLTDPGLT
SEFTQAYQNAGLPNAGPVVTYGLFQVLNAMTDGVIAAVIILVSLVLILIAMLCIRFTM
LATIEEDYREISVMKAIGIAEKDIKRLYLMKYVFMAGFASVLGYIASLGVNRLFVSNL

MLYMGKAPATLLHFAIPLLAAGIIFAMVVLF CRTVLR RFRSISAVDALRTGSLGDTQI
IRNRLSLSRNRWSSVPVFLGLKEVIQRIKMFRLLLFV FVSSFIMIVPVN FLNTLQAP
SFISYMGVGQSDIRIDL RHTDDVEQRYDNLVAQIQNDKDIKAYSPLVTSQFKIKNAEG
SYDNLSVETGDFSIFPLSYVSGNAPTTENEIALSDANSSELRLKTGEQLTLLVNGKDQ
MMTVSGIYQDVTNGGKTAKALLPYNKDSVLWYVVS LDLNNRGDMATKIAEYEA AFSPA
KVTDLQGYLDQTLGGTIEQLKLVTMLALVIGVFISILIT ALFLQMLVAKDNNDIAVLR
SLGFALSKIKFKYVVM SLVILILGVVTGTILSNTLG PLLVSAIMSTFGASNIVFV VNP
LQAYVLCPLLLAGTIVLTAWISIQSIKETSISKMIVE"

CDS 947603..948370

/gene="bceA_1"

/locus_tag="EFAGFIKM_00813"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34697"

/codon_start=1

/transl_table=11

/product="Bacitracin export ATP-binding protein BceA"

/db_xref="COG:COG1136"

/translation="MTTILEAKDVNKSVAIGENEEHNILKDINLQLKKGEFVSIMGPS

GSGKSTLLYNISGMDQISAGSVYFNGKKISAFEERDLASLRLTKMGFIFQNIHLLKNL

NLLDNIVLSAYLAKNSSRETINTRAMSLMKMGIDELAGHNITQASGGQLQRIAICRA

LINNPDILFGDEPTGALNSKSTYEIMDILGDINATGTTILLVTHDVKVAARSERVLFM

MDGKLVADR NIGKYARERQDLKTRESHLAQWLTEMGF"

CDS 948431..949066

/locus_tag="EFAGFIKM_00814"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRLIKNPEERRNEILDAAEILFITKGYTKATVMDILQACNIAKG

TFYYYYFQSKEEVMNAIVMRFILSGEASARHVVS NPKLNAHDKIFRIMMAQNQPDGRKH

DLIEQLHSVHNEMHQKSLVETVIRLSPIAEVVEQGIQEGVFHTPNPKESIEFLLV

SQFLLD RGIFQWEEEEELQKKVEAFTHIMERVLGAEKGSFAYVTRLYFPNQG"

CDS 949087..950415

/gene="entS_1"

/locus_tag="EFAGFIKM_00815"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01436"

/codon_start=1

/transl_table=11

/product="Enterobactin exporter EntS"

/translation="MEHTVQKSFKKFLVWFGQLISMIGIGLTAFSLGVYAFEKTNTA
TSVALITLFTFLPNILLRPIGGVLADRFDRRTMMIIGDLGSAAGLIFILSIMLTGDIQ
LWHIYVGVAFFSSVFSALQSPAYKASATDLLDKDQFSKGSGLVQLAESSKFLFSPIAG
ILLSITTIEVILVINILTLVAILAVLVIRKSMKVEREDREGKNWITDIQEGWREVV
NKGVLLLVIISLVTFYLGFLETIGPMLLSFTDAKTLGTFQSVSAIGMLISSLCIGI
FTITKRYASVLMGLILCGLSFSLLGISTNIYFIIFAGFLFLSSLPFVNMSADVLVRN
NIANDKQGRVWGIIGILSQLGFIIAYSLAGFLADHVFNPLLMEGGALASSVGQIIGTG
PGRGIAFLFIIAGLFVILIAITSRLKMIKSLEQSPDITAPSDVGGLAHD"

CDS complement(950577..951401)

/gene="melC_1"

/locus_tag="EFAGFIKM_00816"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34518"

/codon_start=1

/transl_table=11

/product="Melibiose/raffinose/stachyose import permease
protein MelC"

/db_xref="COG:COG0395"

/translation="MRLRKRLASIGLNALAWLLSLVVLIPFVWVVLNSFKSDAEAKVL
KLTLPEKFIFENYKIVYEQGHGGFFNSLLHSGASSLLLVFVVAFTAFTLSRNHSLK
SKFLYFFLILGITLPLNYIPLMEVMKSMGMINSHVGMILLYTAMGIPISLFITYAFVS
NIPKELDEAAIMDGCNGIKLFLRIIVPLLTSLVLTVFVLNFLSVWNEFTAPLYMLNTV
EMWPMTLAVYNFFGQFSAQWNLVSADIVLTSLPVLIVFLIGQKYIVGGTSGAVKG"

CDS complement(951403..952287)

/gene="melD_1"
/locus_tag="EFAGFIKM_00817"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34706"
/codon_start=1
/transl_table=11
/product="Melibiose/raffinose/stachyose import permease
protein MelD"
/db_xref="COG:COG1175"

/translation="MLRIMNANKIYPWYFSSGAIVLYLLFIVAPALLGIYYSFTDWNS
YSSEKNFIGLEHFRTILAGDPTYLLFIKNTVLFTLVTSIAKTVLGLFLALLLVSGVKA
ANLHRMIIFSPQVLSFLIVGLVFKSLDPNNGFVNVTLRSMGLDVL AQNWLGSLTWAM
PSIMAVDTWKGMGYIMVLFIAGLLAIPRDYYEAASIDGAGFGQKLFRITIPMLMPTIT
IATVLNITYGLRVF DAVYVLTNGGPGNATDVINTAVYSSFAKGYWGLGSALSTILFVI
MAISFFIIRLMNRKVEY"

CDS complement(952376..953677)

/locus_tag="EFAGFIKM_00818"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MRKRFLFSLASVLLLSTLLLAGCNSGKSTEGSGKVTLTFGTSQS
GIPRTGIMQTMKEYEQETGVKIDFQVVPDAQWRDLIKV KLASGEAPDIFNV DVDPLS
MPANVRPEEN AIDLTNEEFTGRMSEEILPTVSHNDKVYGVSFAPTKIWYVYYNKRIFQ
ELGIEPPTS YAEFKAISQKIKDKDIIPFYQAPASGWYQVLPLFETGPNYEQT TAGTYE
KLNNNEMKVADMTQLKT VIEQLKEFADLG YFGKDFLSNTVEAGIEAFGQEKAAMLLRV
PGTEKEVSEAYPEMEDNMGFFVMPWGD NQTIGVNP GGSAA MFGNKNSKHPEEV LKFFR
WITEHDHLQRVFDEGE GNLTICWPEIEPKLTQDYIDYEKNHEKG TVMQAAVKYIDPQW
MDIGKDL SGMFAGAMTPDQILQNIDKRRAEQAKVLKDEKWQ"

CDS 953858..955735

/locus_tag="EFAGFIKM_00819"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRYRFGTLQQLSFAYYSAVFIIFSLIVAGLLYVFLASDIRQRSE
EQQRQLGVSIVSNLDQEVVKMNNFSMNIVYSNLVKEHFHSHYLAEDSEQTMTSDPAL
YKDTTTLIDVILAISSSNTAKQANIYDVNGKMLGAGAFNGQLSVDLTQRPWYKETWE
RSGWRVIQLLEGGALPMPTGEGKSDQPYISLTRVYKDGNYVSQGVVEILQDAGTLFKH
LNELQTNNDLRIYVVEQNTRLFPLSSDADASPAGHFDDVDLIQNLSFPPDTMQETT
DPLSQSKQMMTYMTSQETGWTIVVMQSKQSLFASLNRMAVMFIGATFATLMLILILSY
LISKRVTLPLHRLQRIILKTGENDLLSGQDSGQLFKLEHPGSIREMDELNDTFIRLNQ
QLVQSFQDRLAMKSQETEARLLALQSQMNPFLYNNITNISIMAEEGMNEQIVAFCAN
IASMLRYISTPGKNGVPLSQELDYCERYLECMKIRFEDDLHYEFHIPEEMKYIQVPML
MVQPLENAMKYGLGDTTPWKLNITGMDAVQQTWQIHVEDNGPGMEPEALAKIMHYI
EQSQEWERMPPDLEINGMGLKNIWVRLKLWYGTAAHMQITNKPSGGVQITIGGSIRKEH
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CDS 955740..956549

/locus_tag="EFAGFIKM_00820"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q5HJF7"
/codon_start=1
/transl_table=11
/product="putative response regulatory protein"
/db_xref="COG:COG4753"
/translation="MTIKYRTIIVEDEALIRRNVSARKFRELDTRFEVIGEARNGQEAL
QLIEQSVPDLVVTDIQMPVMNGLELAKHLYFAYPHVKIVILSGYHEFEYARQAISYKV
EDYLLKPLSEEQLRTLDDAMELKLGSVDSLAVLSAVLDEQVKPEDIAEAIKLYLKQN
YMHEITLQDMAGQLHFSVDYLGKCFKKVTGETPLKYMTGLRINEAKRMLGTHENMDIK
TIGGAVGYSDSHYFSRIFKNKTGMYPSEYRLQLQERKKALSMDDENHVDLS"

CDS complement(956550..957179)

/gene="yfbR"
/locus_tag="EFAGFIKM_00821"
/EC_number="3.1.3.89"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01100"

/codon_start=1

/transl_table=11

/product="5'-deoxynucleotidase YfbR"

/translation="MGIHTYFRSLNDLERIIRTPGKFKFEEHSVSAHSWKVVQYAKTL

ADIEEQHGTIDWKKLYEITSSHDYGEIFIGDIKTPVKHYSLELRSMMLQKVEEGMVEH

FINENIPEEFQSIFRRQLREGKDQSVEGLILEVADKMDQVYEAFELQRGNTEKEFIV

MYRYALVKIKNIDLHCVQYFLEQILPDMIEEGIRSPFDIRKITEEALAQ"

CDS complement(957388..958170)

/gene="nirC_1"

/locus_tag="EFAGFIKM_00822"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AC26"

/codon_start=1

/transl_table=11

/product="Nitrite transporter NirC"

/db_xref="COG:COG2116"

/translation="MYTPSVEGIIEAAVKKRDQMNSNLSRYMVAALMAGAYVGLGIVL

IFSIGAPLLAAQSPLQTMLMGMSFGLALTLVIFAGSELFTGNNMFFTMSLAGRTTVN

ETLKNWGLVFGNLLGAILLSLLIVGSGLFKTATPEHLLFVVSAKKMAAPVSEFFRG

ILCNWLVLCLAIWMAARSKEDIAKIALIWWCLYAFIASGYEHSVANMTLLSLSWLLPNH

PDTITLAGWFHNMIPVTLGNIIGGALFVGMAWYTSPVRKKA"

CDS complement(958220..958546)

/gene="nasE_1"

/locus_tag="EFAGFIKM_00823"

/EC_number="1.7.1.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42436"

/codon_start=1

/transl_table=11

/product="Assimilatory nitrite reductase [NAD(P)H] small

subunit"

/db_xref="COG:COG2146"

/translation="MTTKQSGTYFPAGVVEEFLPRIGRVVEIKDHQLAVFRASDGTIF

AADNHNPHPKGGPLAEGIVSGHYLYDPLYDWKIDLTGTVVQAPDNGQVQMYPVKVENG

QVWIEI"

CDS complement(958604..961033)

/gene="nasD_1"

/locus_tag="EFAGFIKM_00824"

/EC_number="1.7.1.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42435"

/codon_start=1

/transl_table=11

/product="Nitrite reductase [NAD(P)H]"

/db_xref="COG:COG1251"

/translation="MNGKKEKLVIIGNGMAGISTVEQILKLTRFDITVFGTEPYPNY

NRIMLSYVLEGSKTLDDIVLNDLHWYEDYGITLHTGTTVTRIDAETHEVVTEDGTLVP

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AAKGLVQLGMEVTVVHLMEDLMERQLDPQASAMLKAELERQGIRFKMGAQTSELLGGE

RVEGIRFADDTVLNVDVFMVAVGIKPNTAVARESGMEVNRGIVVNDYMQTSLENVYSV

GECTEHRGVCYGLVAPLFEQGMILAKHICGVETAPYEGSVVSTKLKISGVDVFSTGEF

IDSPEHTVISHKDDWKRTYKKILLRDNKMVGAVLFGDITDSaelQKLIKNQTEMTEEL

YGSLMGTGCGGHKKTTSEVMAEDEIVCGCNGVTGKTIVDVITNQGLTSVDEIACTG

ATRSCGGCKPVVEQILQYVLGDSFSTGAKQGICGCTSMGRDEIVAEIREKGLQTTKEV

MNVLGWSQPEGCSKCRPAINYYLGMIAPDTHEDEKESRFVNERNMNIQKDGTYYVVP

RMYYGGVTTTPADLKRIADVSVKYDVKAVKVTGGQRLDLIGVKKEDLTKVWAELDMPSGY

AYAKSLRTVKTCVGSQFCRFGTQDSMAMGARIERKFERLDLPakfKYAVNGCPRNCAE

ACTKDIGIVGNDGGWEIFIGGNGGIKARLADSLCKVKTDEELIELCGAIMQYYREAGN

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MFHGIEVSARP"

CDS 961309..962016

/locus_tag="EFAGFIKM_00825"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMGRSHLIIGTGVSLSVLQLAGMPVTAPAVTVALIGSLLPDIDE

PNSLLVSRALPNSLIRLLQTILLPTAVFVYFYVHAKPWNLLLAILIALVSFLPSRSLR

KVLMFAIGLGLVFGYGHAFAPWNLIAGSLLMLCTTLTHRGLTHTFYGTAIWAGLLYSTT

QQQGPEIWWAGGTAYVMHLLADSLTNRGIRPLPPFKFRIRANLMSTGTKHGAVVENVC

IVLTLILAWFAFSSLFL"

CDS complement(962100..962219)

/locus_tag="EFAGFIKM_00826"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSDFDGIGFAELLIGVILVLLFVYGSTDIEGLSSTPTTS"

CDS complement(962244..962564)

/locus_tag="EFAGFIKM_00827"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS complement(962793..963866)

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/locus_tag="EFAGFIKM_00828"

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PICEFTPMANPKKIMAKAWDNRYGVGLALELVEALHKEKLPNTLYAGATVQEELGLRG
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CDS 964512..965015

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GFGGGHL"

CDS 965012..966028

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/codon_start=1
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CDS 966034..966384

/locus_tag="EFAGFIKM_00831"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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IFSFLAALVVRPKG"

CDS 966593..967549

/locus_tag="EFAGFIKM_00832"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MPVRKESIQIISAVRSNLESCIMGKSFEIQLLLTALLAGGHVLI

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LPEAQLDRFMLKISLGYPDKEIEKILLKQHQLGQPVDRLSVTHMDQISAIQQEIKEV

FIGDPVMDYLLDVVRQTRSHPSVLLGASPRAAISFMMAVKAF AFLQERDYVLPDDVKT

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CDS 967616..968800

/locus_tag="EFAGFIKM_00833"

/inference="ab initio prediction:Prodigal:002006"

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KEFEHESVPKTVLVLDALASSYEHGDAFEIAVSTAASLLEYGVRERMGMGLLTLSDQT
SFMAPSESLMERQKMMHHLVDIQYNGQDTHLLPGVERIARQLPQGAYFVVISPQKDEK
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CDS 968797..971010

/locus_tag="EFAGFIKM_00834"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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CDS 971121..971648

/locus_tag="EFAGFIKM_00835"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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CDS 971645..972772

/gene="yqeH"

/locus_tag="EFAGFIKM_00836"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54453"

/codon_start=1

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/db_xref="COG:COG1161"

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YIIDTPGIVYPWRFSEIVSRKDLAAIMPEKPLKPAVYQLNSGQTLFFGGMARFDFVEG
DRQSFTCFISTALDIHRTKLERADDLYRDHLGELLSPPTREDAAEMAIEWTRHEFRIKR
GSQSDVFISGLGWIKVNGDIGALVAVHAPKGIRVQIRPSLI"

CDS 972815..973684

/gene="aroE_1"

/locus_tag="EFAGFIKM_00837"

/EC_number="1.1.1.25"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5KWX7"

/codon_start=1

/transl_table=11

/product="Shikimate dehydrogenase (NADP(+))"

/db_xref="COG:COG0169"

/translation="MSEQNKFNSSLPVLLGVMGDPIAHKSPAMHNAALQAAGVNGMY
MPLHVHPDQLEAAVRGIVALGYRGVNVITPHKEQVMQYLDVIDESARLIGAVNTIVNE
GGTLTGYN TDGIGYVRSLKEEAVPELAGKRIAVLGAGGAARGVIYALALEKPERIHIL

NRTADRAIELASDLRGHGLGEISGSGMEDAATVLATADIVINTTAAGMHPHVDDVPVD
PALIREGAAVSDLIYNPLETRLLRESRKCGCTVHGGLGMFVYQGAVAFEHWLGIPAPV
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CDS 973767..974060

/gene="yhbY"

/locus_tag="EFAGFIKM_00838"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AGK4"

/codon_start=1

/transl_table=11

/product="RNA-binding protein YhbY"

/db_xref="COG:COG1534"

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CDS 974076..974666

/gene="nadD"

/locus_tag="EFAGFIKM_00839"

/EC_number="2.7.7.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54455"

/codon_start=1

/transl_table=11

/product="Nicotinate-nucleotide adenylyltransferase"

/db_xref="COG:COG1057"

/translation="MKIGIMGGTFDPIHMGHLLAAEAARDSHALDEIWFMPSHVPPHK
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IGADMVNYLPKWEQIEELAERLTFIGVGRPGFQLHLDDLDELQDRVLLAEMPLVDIS
STAVRRRLAKGHSVRFMIPDEVHQYIVRSGLYGTKP"

CDS 974650..975216

/locus_tag="EFAGFIKM_00840"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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EVINAIRWHTSGRVGMSLLDKVVCLADYIEPGRDFPGVDHIREQAERSLEEGLIAGFD
STISLLISQRRVIYPLTMLSRNDLIAQL"

CDS 975234..975581

/gene="rsfS"
/locus_tag="EFAGFIKM_00841"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9KD89"
/codon_start=1
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/product="Ribosomal silencing factor RsfS"
/db_xref="COG:COG0799"
/translation="MTVSSKELMNMMAVAAADDDKKASNIVALDLINVSLVADYFVICHG
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ERLWSDAKVVETV"

CDS 975578..976483

/gene="cvfB"
/locus_tag="EFAGFIKM_00842"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7A5Q1"
/codon_start=1
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VYKPLQMGTFFVLVEGGVLGFGAIGMIHSSERSHMLRLGEKVKCRVTLVREDGRVNLAM
TQLKQVGRNEDADKLLAFMKERPMGGMPYSATPPDIIKQRFGISKSAFKRALGKLMK
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CDS 976614..977384

/locus_tag="EFAGFIKM_00843"

/EC_number="2.1.1.156"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q83WC4"

/codon_start=1

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/product="Glycine/sarcosine N-methyltransferase"

/translation="MSYRKFAVVYDELMEDMPYPDWIRFARTAWEKHGMPSVAELGC
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RVPEPVDSVISFCDCVNYLLEQEDVIRTFQRTYEMLKPGGTFLFDVHHPNLIRYDEE
QPFVLDERSVSYIWTCDLDQDRCEIEHLSIFSRVDDGRKDIYQRFEEVHVQRAYNPD
WMKLELSKAGFRDVKVYADFEWKEAGDSAQRLFYVAVK"

CDS 977610..978566

/locus_tag="EFAGFIKM_00844"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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YSTWKEAFMNLMEDILADGEEAGITFSIDYPELRRRIEEKSNVLDDVKEPVLVSWDLW
DGNVLVDAGRITAIDFERSLWADPLMEHYFSHFNYTPGFVKGYGHATTESELKRRS
LYDLYFDLVLRIECAYRQYDNQEHVNWNTIHNLEEGIERFRLS"

CDS 979026..981470

/gene="leuS"

/locus_tag="EFAGFIKM_00845"

/EC_number="6.1.1.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P67513"

/codon_start=1

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DMFPYPSGSLHVGHPGYTATDIVSRYKMRGYNVLHPMGWDAFGLPAEQHALDTGE
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VAVNWCEALGTVLANEEVIDGKSERGGHPVVRKPMRQWVLRITEYAERLLEDLEELDW
SESIKDMQRNWIGKSTGAEEVFAIEGREEVIKVFTTRADTLFGASFAVLAPEHELVEA
ITDDQREAIQAYQEQASRKSDLERTDLAKDKTGVFTGAYAINPVNGAKLPIWIADYV
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DQLPLLLPDIDQIKPSGTGESPLANVTEWVNTVDPETGMKARRETNTMPQWAGSCWYY
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ANGVEGMHRFLSRVWRLFINEDTGAINDKITVDGGTDEFKRTAHKTIKKVTEDLEHLR
FNTSISQLMIFINDAYKADTLPREAMEKFVQLLSPLAPHMAEELWSRLGHEGGISYVA
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CDS complement(981451..982296)

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/EC_number="1.5.1.2"
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/inference="similar to AA sequence:UniProtKB:P0A9L8"
/codon_start=1
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/db_xref="COG:COG0345"
/translation="MKVGFITGSMGSLLIYALIQSGALEPRQIAASNRTPSKVRQLS
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HLESSLPCKVSKVIPSVTHQVGSGASLCIHGERMTSEDRAVLESLLSHIGRPYQVDEA
CTRITSDFSSCGPAFISFFLEQWIESAVKLTGIKRADACALAGEMLLGTGKLLTEGGY
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NRQQY"

CDS 982482..983120

/locus_tag="EFAGFIKM_00847"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MRWNKGMTIAAAVVGSIILWVGKSEQPPSGWEPLQLGTEKPTI

EQELPAVQSANSVQGNTGASSSGTEASGLQTGNDAKADESKELASVGVEGDSVVQTTS

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CDS 983161..983679

/gene="tadA_2"

/locus_tag="EFAGFIKM_00848"

/EC_number="3.5.4.33"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00972"

/codon_start=1

/transl_table=11

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/translation="MSTEVRKDWDTYFMDIAYMVSTRSRCSRRHVGAVLVQGKKLLGT

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REGSSVYVTDEPCWTCANMLANSGITIVFHRSYPKDTGKVTNMMQQKGITFRRLENY

QPPRETMMTVSN"

CDS 983782..986658

/locus_tag="EFAGFIKM_00849"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MKGRPLLSFTICWLCSGSMACALTGWTLIWGFIGALACLPLLLH

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QYNVLRWTDWTRHKLGSAVEQLFPEPHAGYMKGLIIGMANDINPGTYGQFSQLGLTHI
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IGLYMARRGLARDGLQMISAAAALLMMWWEPYFLLSVSFQLSFLVTAGLMIYMPINRL
FSSWPKSLAATASVTVTAQLISFPVTILYFNQFSLLSFVANFLLVSLISAIVLPLGTV
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GKETSLTTLGASIAWPEYTSFTARGAGYYSNERMSKAQQWLCGLLAISFIAGLWWAY
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KLLDTAMERKIPLYAIQQGMSYKVDKETS LHFIA PDLAHMDVNVSGNLPVSEHQNHDS
VVFLE MAGASMLFTGDM DAAAEQDLLYMIQDGLAAQFEQKGADIGVTEGVVQRVLT
RPLQVDSKDASAASASVSIDVLKVAHHGSKTSSTEAWLQYWNARTAVISAGVNNNTYGH
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CDS complement(986674..987123)

/locus_tag="EFAGFIKM_00850"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/translation="MTKTHRINRPRGKILAAVLTA VLISLAMGIYHYVPIDERLENTY

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CDS 987354..987620

/locus_tag="EFAGFIKM_00851"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MVPPAQIRRGRIK NMKYRCYRKSTTTKALQTTKRLIDPIGFSLV

RLSAFTA HSHKEDGTGFYCFYSGEGLTTEELKYFMLEMAGYRQ"

CDS 987880..988392

/gene="sigV_2"

/locus_tag="EFAGFIKM_00852"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O05404"

/codon_start=1

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/product="RNA polymerase sigma factor SigV"

/db_xref="COG:COG1595"

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IDLKLTLESLPDKYKSVIILRYFEDMKIEEVAAVLDENVNTIKTRLYQAHQLLRIKMN
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CDS 988389..989279

/gene="rsiV"

/locus_tag="EFAGFIKM_00853"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O05403"

/codon_start=1

/transl_table=11

/product="Anti-sigma-V factor RsiV"

/translation="MNNNMEQLRKEYHEIIPDELDNIVNQSIHKFSKEGRRGRGSKY
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CDS 989450..990226

/locus_tag="EFAGFIKM_00854"

/inference="ab initio prediction:Prodigal:002006"

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DLAQWEKDAAKTAKKAKVNHQKFHPYEFYVSYKLKSDGTGNPAGVVSLEVITEGYRGG
TSMPRIDTYNLKNASAAQRTLEDLLGSNYKEKLDANILAQMRKDPDQYFLEEFKGT
TEQSFYIEKGELVIVFPKYSIAPGYVGSPEFRFNLKNASL"

CDS 990942..992381

/gene="pdaC"
/locus_tag="EFAGFIKM_00855"
/EC_number="3.5.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34798"
/codon_start=1
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/db_xref="COG:COG0726"
/translation="MNKRKKTRWPVWLVGFIVLGGILGINLMVQNVLAGNHSVTE
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CDS complement(992628..992930)

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CDS 993282..993830

/gene="sigW_2"
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/db_xref="COG:COG1595"

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QDVEYEV MSTYVAQDIQDAINKLPEHHRTVIVLRYLQDLSYNEIADCLDLPLNTVKS
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CDS 993827..995110

/locus_tag="EFAGFIKM_00858"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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DGEESGVTETENGDAQSFTSQDTTPNITEDVPVEGNTVPDSSAGADASGGNKGFAAGP
DQGM TTTAAPKEWKSPDGSYVVMLIGDQISIYSKPVSEPDVLSLVEQRSIEGTLKSAS
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CDS 995367..996383

/gene="yqeN"
/locus_tag="EFAGFIKM_00859"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54459"
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/db_xref="COG:COG1466"
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VFSLVEELANLRLEKALALFYELLKQREEPIKIAALIARQFRIMIQVKELGQQSYSQQ
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RLGA"

CDS complement(996573..996845)

/gene="rpsT"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P21477"
/codon_start=1
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/db_xref="COG:COG0268"
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CDS 997021..998022

/gene="gpr_2"
/locus_tag="EFAGFIKM_00861"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P22322"
/codon_start=1
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GTTGIESSDIVQGIVDRTPDAIIAIDALASRSLERVNTTIQVADIGIHPGSGIGNKR
RGLTREILGVPCIAIGVPTVCYASTIVNNVIEMMRSHFRQETDQTKQIMGMLDDIGE
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CDS 998169..999464

/locus_tag="EFAGFIKM_00862"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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PNWRQNEAFAAKIHKKLEAKYPGVSRGVWGKDGGGANNGEYNQTLSPNSILIEIGGID
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CDS 999519..999878

/locus_tag="EFAGFIKM_00863"
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CDS 1000024..1001838

/gene="lepA"

/locus_tag="EFAGFIKM_00864"
/EC_number="3.6.5.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q2FX7"
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VVDGKIKSGSKIKMMATGKSFEVIEVGAFKPRMTIVDELNVGDVGFIVAGIRHVGDTQ
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PETSSALGFGFRGFLGLLHMDVIQERIEREFNIPLITTAPSVIYHVTLTNGEVMKID
NPSNYPEVGRIDYVEEPYVKADIIVPNDYVGTIMELCQTKRGEYVNMEYLDTRVTIT
YQIPLSEIVYDFFDQLKSGTKGYASLDYELSGYRQSNLAKMDIVLNGEQVDALSFIVH
RDRAYNRGRIVCEKLRELIPRQMFEVPIQASVGTKVARETVKAMRKNVLAKCYGGDI
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CDS 1001987..1003171

/gene="hemW"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54304"
/codon_start=1
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QLPLPHEDDELEMYLLLMRRMKEAGYGQYEISNFAKPGFESRHNTYWRNEDYYGLGA
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CDS 1003290..1003760

/gene="argA"
/locus_tag="EFAGFIKM_00866"
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/codon_start=1
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/product="Amino-acid acetyltransferase"
/db_xref="COG:COG1246"
/translation="MSVICRKAVPEDVEPLYEMIKGYAERGIMLPRSREILHRQLEHF
VVAEVDGEVVGCGSLCRLGNDLVEVRSLGISEGHKGLGIGSRLLDRLVEEAQKQIPK
VMALTYEVSFLLKNGFAVVEKEIFPEKVWTDVCVHCSKQDCCDEIAVLKELNVSA"

CDS 1004015..1005046

/gene="hrcA"
/locus_tag="EFAGFIKM_00867"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P30727"
/codon_start=1
/transl_table=11
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KTVQIPPEISVAEMENVVRLNNTKLVGVPYIKLSRLYTELQEMERHITRYEEVMQV
LNSAFDNEHDNRLFLSGATNMLTQPEFKDIEKVKDILDLEETPTLMKLMMPVPGGSG
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TAMLTHRFK"

CDS 1005091..1005654

/gene="grpE"

/locus_tag="EFAGFIKM_00868"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5KWZ6"

/codon_start=1

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/db_xref="COG:COG0576"

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CDS 1005815..1007659

/gene="dnaK_1"

/locus_tag="EFAGFIKM_00869"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5KWZ7"

/codon_start=1

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/product="Chaperone protein DnaK"

/db_xref="COG:COG0443"

/translation="MSKVIGIDLGTNSCVAVMEGGEAVVIPNPEGARTTPSVVGFKK
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EDQ TILVYDLGGGTFDVSILELGDGFFE VKATSGDNKLGDDDFDQVIIDYLVSEFKKD
QGIDLSKD KAAVQRLKDAAEKAKKELSGVLT TTTISLPFITVADGVPQHLELNLSRAKF
EEISEGLVERTLEPTRRALS DAGMTPNDIDKIVLVGGSTRIPAVQEA IKKLTGKEPHK
GVNPDEVVALGA AVQAGVLTGDVKDVLLDVTPLSLGIETAGGVFTKMIERN TTIPTS
KSQVFSTYADNQPSVEIHVLQGEREMAAGN KSLGRFMLGDIPPAPRGVPQIEVSFDID
ANGIVNVSATDKGTNKTQKITITSSSGLSDAEVEQMMKDAELHAEEDKKRRELVEAKN

SADQLIYSVDKTIKDLGEKADAGEVEKANAAKEKLQGVLASDNLEDIKAATEELTEIV

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CDS 1007789..1008913

/gene="dnaJ"

/locus_tag="EFAGFIKM_00870"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P17631"

/codon_start=1

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/product="Chaperone protein DnaJ"

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RIPAGVDDGAQLRMTGEGEGGLRGGPAGDLYIVIRVKSHDFFEREGDDIYCEIPLTFA

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SKLNDEQKDLLRQIASLDGEQTHEHEQSFFDRVKRAFRGD"

CDS 1009154..1009522

/locus_tag="EFAGFIKM_00871"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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VDESVHHRAMSIIEQAGGMI"

CDS 1009782..1009961

/locus_tag="EFAGFIKM_00872"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MAEHERPGKILTKTEKMKRMQSAKNEDVEFSAEAADHEDIEALR
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CDS 1009954..1010346

/locus_tag="EFAGFIKM_00873"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS 1010537..1011502

/gene="prmA"

/locus_tag="EFAGFIKM_00874"

/EC_number="2.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A0P5"

/codon_start=1

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/product="Ribosomal protein L11 methyltransferase"

/db_xref="COG:COG2264"

/translation="MLWHELTHTTEESVEMISNFLHEAGAGGVSIEESGTLNKKRDT
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TTSCLRLTLETVIQGGEEVIDVGTGSGILAIGAIIKLGAKHVLALDLDLVAVISARENV
ELNGLEQQITVKESDILLSVLGSQDPALGVQLPVKVVVANILAEIILLFVDDVYNALES
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CDS 1011506..1012186

/locus_tag="EFAGFIKM_00875"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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DGYRILEDVPPSISRKLQGV EQWSIFIFLLVIPPLQNVTIQPLYEFAQTMYVDLA
KVIIELYR"

CDS 1012324..1013088

/gene="rsmE"
/locus_tag="EFAGFIKM_00876"
/EC_number="2.1.1.193"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54461"
/codon_start=1
/transl_table=11
/product="Ribosomal RNA small subunit methyltransferase E"
/db_xref="COG:COG1385"
/translation="MQRYFVSAEQFNEHAVIITGDDARHIGKVMRGKPGDKLIVSDGN
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VSFVPFLSERTIVQYDAKKEGKRLEWRKIAKEAAEQSHRNRIPSVEQPLSWKGLLSS
FEGYSLVCYCYEKENGKQLRDALKPFIEQLAPDASAEVLIVVGPEGGFSEKETAEADQ
AGAVSVGLGKRILRAETAGMAALTCVLYESGEMGGM"

CDS 1013091..1014437

/gene="mtaB"
/locus_tag="EFAGFIKM_00877"
/EC_number="2.8.4.5"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54462"
/codon_start=1
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/product="Threonylcarbamoyladenosine tRNA
methylthiotransferase MtaB"
/db_xref="COG:COG0621"

/translation="MPSVAFYTLGCKVNFYDTEAIWQLFKNEGYDQVDFDEQTADVYL
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RDKILPYVNEIQESRQPVNAVRNIMKTRVFEEMDVPDFADRTRAFLKIQDGCNNFCTF
CIIPWSRGLSRSEANSIIQQAHLVHAGYKEIVLTGIHTGGYGDDMENYDLTDLLWD
LDKVEGLERIRISSIEASQIDDRMLDVIKRSDKLVRFHFIPLQAGDDTVLKRMRRKYT
TEEFYNKMLRIREAMPDVAITTDIIVGFPGETDEMYRNGYKLMRKIGFSEMHVFPYSK
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SGKLHGYSDNYIQLVFDGTMDMVGKVCRVKVEAGVNESQATLVRVLEENLKSAM"

CDS 1014551..1014985

/gene="ndx1_1"
/locus_tag="EFAGFIKM_00878"
/EC_number="3.6.1.61"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q75UV1"
/codon_start=1
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/product="Diadenosine hexaphosphate hydrolase"
/db_xref="COG:COG0494"
/translation="MNKKEISAGGVVYRTGEDGRLQIQLIVDRYGKTTLAKGKMEEGE
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CDS complement(1015043..1016044)

/locus_tag="EFAGFIKM_00879"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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GLQIGRASLPLLVLSTGWAMFVVLGERNLAAPERTRQTLFNIQYSFLAAAGFALVMT
GIQVMQSIALPLRSMGVFQWFLDRSADSLWWGFLAGACLTALIHSSAAVISMALTA
TGVLPVEIGIAIVIGSNVGTCTAVIAAAGGASAGKFVAASHVVLNIAGALLFMPLIG

QLHAASAWLSADNGAQIAHAQTLFNITSSLLALPFCYLPWHKKPPVHAPAAKSPVA"

CDS 1016604..1017980

/gene="rlmI_1"

/locus_tag="EFAGFIKM_00880"

/EC_number="2.1.1.191"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P75876"

/codon_start=1

/transl_table=11

/product="Ribosomal RNA large subunit methyltransferase I"

/db_xref="COG:COG1092"

/translation="MPSVTLERSRKKRLEHAHPWIFNNEIASVDGNPEPGDLNVNLNH

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GWGYKSGITLQTTEQDGTEQLLPVNKSGKVTFPYWDGATVLECFSGSFTLNACKY

GAKKVTCLDISEHAIESARTNVELNGFTDRVEFVVADAFQYLREQVKGLDERTTRARA

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CDS 1018180..1021683

/gene="addB"

/locus_tag="EFAGFIKM_00881"

/EC_number="3.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P23477"

/codon_start=1

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/product="ATP-dependent helicase/deoxyribonuclease subunit

B"

/db_xref="COG:COG3857"

/translation="MSVRFVIGRAGSGKSSLITREITSLLQKEPQGTPLILLVPEQSS

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HDLNLIYRDYEQELTHLYIDDEDLT ELTDLRLSESALLQDAQIWIDGFQGFTPQEMSV
IGRLMLQSSSVTIALTLDRPYDHGALPGELELFYPTASAYTRLKGMADDELGVPSDITL
LDSEIPPRYKDRPGLAHLEAGFDRRIRWKSEGLDSGIRLVAAENRRAEMEGALREMRR
LAQNEGARYRDMAVLVRQLD TYADIAEPLFRDYDVPVFLDRRRNELHHPLSEFIRSAL
DIVRRHWRYEDVFRVCVKTDL LPRDGSITREDMDQLENYVLACGIHGYRWT DGKPKWKY
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AGMIETGLTELKGLVPPALDQVLVGSMDRTRLQDIKYVFILGAVD GELPAVPQDDGV
LTELERALLTDRGVALGPGATRQMLDERFLIYTALTAASSQLWLSYPVADDEGKTLLP
SEIVRHVRKMFGLQEQLLAQPPVANSEEAHWSYVTHPGQSLSTLIGQLRKWRRGEDI
PEMWWAVYNWHVSRETSRPQLERLMGSIFYRN RALPLRTATSRRLYGTEVRTSVSRME
RFVACPF SHFASHGLRLKERQLYRLQAPDIGQLFHAALSQ LAMRLREENRSWGS LTPD
QCRQEA EQTVEQIAPQLQGEILLSTKRYGYIFRKLKDIVSRASVILGEQSRRGSFEPI
GLELDFGPDKTLPLPLRFELENGCVMEIVGRIDRVDVAEGENGLLLRVIDYKSSQTDLK
LHEVYYGLSLQMLTYLEVLLSAAEEWLGETAMPGGTLYFHVHNPLLQSANGMTSEQAG
QELLKRFKMKG LLLADRDAIAQMDNTLDKGYS AIIPVALKADGSFYSSAAVATPEQWD
TLLASVRSNIREIGTRITDGDVAIEPYRIQQEVACTFCPYKPVCQFDENIEGNEYNLL
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CDS 1021680..1026107

/gene="addA"

/locus_tag="EFAGFIKM_00882"

/EC_number="3.6.4.12"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01451"

/codon_start=1

/transl_table=11

/product="ATP-dependent helicase/nuclease subunit A"

/translation="MTNMPKPEGSFWSDDQWSAISESGKDILVAAAAGSGKTAVLVER

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GSTFRELVDWFSGERNDDAMHRLVQRLYDFSRSHSWPDHWLSEMASAFQVESVEALGH
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CDS 1026167..1027351

/gene="sbcD"

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/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AG76"

/codon_start=1

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/product="Nuclease SbcCD subunit D"

/db_xref="COG:COG0420"

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CDS 1027348..1030767

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/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/codon_start=1

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/product="hypothetical protein"

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CDS complement(1032404..1033537)

/gene="mccB"

/locus_tag="EFAGFIKM_00886"

/EC_number="4.4.1.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O05394"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0626"

/translation="MRPKTKLIHAGIVGDPHTGAVSVPIYQVSTYEQESVGVHKGYEY
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RIFTKVLNRLGIESTFVDTTSLQALEKALQSNTKAIYVETPTNPLLKVTIDIAAVAIWS
KQHELLFIVDNTFSTPYWQTPLALGADIVLHSATKYIGGHSDVVAGLAVVNGEQLGED
LHFIQNAIGAVLGPMDSWLLMRGLKTLGLRMEAQERNTEQLVIFLNQHPAVSKVYYPG
LPDHPQHKLASTQARGYGGMVSFDVGSAEKVDDMLSKVRYFTLAESLGAVESLISVPA
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CDS complement(1033539..1034462)

/gene="mccA"

/locus_tag="EFAGFIKM_00887"

/EC_number="2.5.1.134"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O05393"

/codon_start=1

/transl_table=11

/product="O-acetylserine dependent cystathionine
beta-synthase"

/db_xref="COG:COG0031"

/translation="MTVYQHVQELIGNTPLLELTRYPLPEGIRLFAKLEFMNPGGSVK
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EIWRDLNGQVDVYVAGAGSGGTFMGVSRYLKEQNPLIKTCIVEPEGSILAGGPSGPHR
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CDS 1034710..1035069

/locus_tag="EFAGFIKM_00888"

/EC_number="3.9.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P44956"

/codon_start=1

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/db_xref="COG:COG0537"

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CDS 1035303..1035476

/gene="rpsU"

/locus_tag="EFAGFIKM_00889"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A2RHW9"

/codon_start=1

/transl_table=11

/product="30S ribosomal protein S21"
/db_xref="COG:COG0828"
/translation="MSETKVRKNETIDAALRRFKRSIAKDGVLAEVKKRKHYEKPSVK
RKKKSEAARKRKF"

CDS 1035492..1035935

/gene="yqeY"
/locus_tag="EFAGFIKM_00890"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54464"
/codon_start=1
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CDS 1036179..1037540

/locus_tag="EFAGFIKM_00891"
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CDS 1037702..1038712

/locus_tag="EFAGFIKM_00892"
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/codon_start=1
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DRLVGGAGEETIARVGEIVSTNGSSNSHKDVLENPDLSRTVLSKGLDAGTAFEIL
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GR"

CDS 1038726..1039325

/locus_tag="EFAGFIKM_00893"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MGLFEWIFDONLYIVAVIGFALFSFLGKAASADPNKKRPANGMP
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SRPATDYRSEGTMAMANSLEEQMRGMEEQQRLEEERLNRISANRPVVSDDSSWDETS
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CDS 1039505..1039798

/locus_tag="EFAGFIKM_00894"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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CDS 1039795..1040988

/locus_tag="EFAGFIKM_00895"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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FALSSMVWSVEVKGNVTIPTDEVLAALKKEGIYPLQWGFRLQSQDKLSRQLALALPDV
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VKKGQVLISGILGDEENTKTIVAKGEVRGLVWREYQVEAPLVQKHNTMTGESKERFYM
VLGNWAIQLWGYGSTPFTSFDTESNHKPLTWRSFTLPMGWLTEKDLETQEHEQQQTIE
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CDS 1040995..1041966

/locus_tag="EFAGFIKM_00896"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WIA3"

/codon_start=1

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/product="PhoH-like protein"

/db_xref="COG:COG1702"

/translation="MSEQTRSIQISLQSAGEGQSLFGPQDTFLKIESEIPAQIASRE
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SGLVEANTILNEVNEIGFVYFAEQDVVRHSLVQKIIVAYNHAAENQA"

CDS 1041983..1044232

/gene="pgpH"

/locus_tag="EFAGFIKM_00897"

/EC_number="3.1.4.59"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A0A0H3GGY3"
/codon_start=1
/transl_table=11
/product="Cyclic-di-AMP phosphodiesterase PgpH"
/translation="MTSKEPSKGKSFQNKATGWKYSVWARYLLFLFLVILFYVSLASK
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VVQEQSYRIPEETYIKISRLTSDDIQEMKPVARDIVARLMTDQISDATTARAKVAEMV
SVSSLGKRTQREVQELARLVVTANRFYDEEGTKEAKVQARENTQTVFIKQGDTLVAK
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LHYFYHKALRQAEAGVEPDFTEEDFRYPGPKAQSKESAIVGIADSVEAAVRSLRKPT
VEQVESMIEKIIKGRLLDDHQFNDCDLTMRELDIVARTLKETVMGIFHSRIEYP EEIKK
PKPTSPEAG"

CDS 1044267..1044764

/gene="ybeY"
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/EC_number="3.1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00009"
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IIISVPRTILQSEYGHHSFERELGFLFVHGFLHLLGYDHDQDEASEAEMMGKQEAVALQ
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CDS 1044764..1045135

/gene="dgkA"

/locus_tag="EFAGFIKM_00899"

/EC_number="2.7.1.66"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q05888"

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FAVIIGCIVFIKPVMWSWLGLY"

CDS 1045437..1045850

/gene="cdd"

/locus_tag="EFAGFIKM_00900"

/EC_number="3.5.4.5"

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/inference="similar to AA sequence:UniProtKB:P19079"

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CDS 1045888..1046787

/gene="era"

/locus_tag="EFAGFIKM_00901"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42182"

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/db_xref="COG:COG1159"
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GGDRYIAEQLKNIRTPVILVMNKKIDKIEPEALLPLIEEYRKLHDFAEIVPVSAKHGNN
VSTLLEQLGKYLPEGPQYYPDQVTDHPEQFVCAELIREKILQMTREEVPHSIAVTIE
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CDS 1046892..1047032

/locus_tag="EFAGFIKM_00902"
/inference="ab initio prediction:Prodigal:002006"
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CDS 1047066..1047818

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/product="DNA repair protein RecO"
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QDEETGTFWFKQLKACLQALKEEKDPVVITSLYEMKILQASGYGPQFDECISCNQERP
DEQLFISPRLGGVLCRACKHFDPPAMSVSPKALKLLRLFAQLDLQRLGNISVSESTRD
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CDS 1048229..1049116

/gene="glyQ"
/locus_tag="EFAGFIKM_00904"
/EC_number="6.1.1.14"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O67081"
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/db_xref="COG:COG0752"

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MERLASIYQDKENVFDLEWVEGITYGDVFRQPEFEHSKYTFEVSVDVKMLFTLFNMHEE
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EEREKLGFP LIKKGGAEHV"

CDS 1049109..1051184

/gene="glyS"
/locus_tag="EFAGFIKM_00905"
/EC_number="6.1.1.14"
/inference="ab initio prediction:Prodigal:002006"
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/db_xref="COG:COG0751"

/translation="MSKDLLFEIGLEEVPARFMRAAIAQLQERVVKWLDASRIAYGEV
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RWIVAMLGSEVIDLEVTGIKSGNVTRGHRFLGKEAVISTPSSYVEVLRSEHVIADIQE
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SMREHQRYFPVLDNEGQLLPFFVTVRNGGSDSLDVIARGNEKVLRLARLSDAKFFYEED
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CDS 1051414..1051881

/locus_tag="EFAGFIKM_00906"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A8D3"

/note="UPF0178 protein Yail"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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CDS 1051929..1053749

/gene="dnaG"

/locus_tag="EFAGFIKM_00907"

/EC_number="2.7.7.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P05096"

/codon_start=1

/transl_table=11

/product="DNA primase"

/db_xref="COG:COG0358"

/translation="MSTGQGGIPESIIESVLQQNDIVDTVSRFVHLTKQGKYMKGGLCP

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WQGRESAHVNPETERLLEAYELTAKLYHFLLKNTEHGKSAMEYLRSRGFGDKLIDQFQ

IGFAPNRWDTLVQFLEKRNYPLEEMEGGLLSPRNEGQGYVDRFRDRIMFPINGRSGK

PIAFAGRILGDGQPKYLNSPETRLFNKSRVLYNLHHAKNAIRKQRQAILFEGYGDVIS

AWDQDIQNGVAAMGTALTENQALMLKGMCDVIIICYDGDRAQAAALKNFPILEEAGL
QVKVALIPEGLDPDDFIRKHGGERFRNQIVDGAUVTTKFKLINLKKSHILLEGGGQIA
YSKEAVKLIAPLPSPTEREVYLRELAEEVDVSFETLKQECNEEREAMKNNLQFGDNNP
KRWNNGRQQNRQVPTPNLLPAYHAAERKLIAWMLQDDEAAQYVNEHLGEAFNLDDHAA
IAAYLYAYYAQGKPSDTSRPMSSSLHDDRLEKTVSSISMMDGPGGEWSIQMLDDCIREVL
KHPRKKEYDLKKEEMIAAERAGDSVRAAQIAIEMIALERQ"

CDS 1053793..1054932

/gene="sigA"

/locus_tag="EFAGFIKM_00908"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P06224"

/codon_start=1

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/product="RNA polymerase sigma factor SigA"

/db_xref="COG:COG0568"

/translation="MANDQHTELETELTDQVKDQLIESGKKRASLNYKEIIEKLSPF
EQDAEQMDEFYEQLSDLGIDVVNENNEEVTLRPSSESENNTREGEDEFHDDDLSLPP
GIKINDPVRMYLKEIGRVPLLSADDEVQLAKRIENGDEEAKRRRLAEANLRLVVSIAKR
YVGRGMLFLDLIQEGNMGLIKAVEKFDHKKGYKFSTYATWWIRQAITRAIADQARTIR
IPVHVMVETINKLIRVSRQLLQELGREPTPEEIAAEMDLSVEKVVREITKIAQEPVSLET
PIGEEDDSHLGDFIEDQEALAPADAAAYELLKEQLEDVLDLTEREENVLRLRFGGLDD
GRTRTLEEVGKVFGVTRERIRQIEAKALRKLRHPSRSKRLKDFLE"

CDS 1055117..1055875

/gene="trmK"

/locus_tag="EFAGFIKM_00909"

/EC_number="2.1.1.217"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54471"

/codon_start=1

/transl_table=11

/product="tRNA (adenine(22)-N(1))-methyltransferase"

/db_xref="COG:COG2384"

/translation="MKLSNRLQRIHDQIPDGSCMADIGSDHALLPVAAIRSGKAASAV
AGEVNP GPYDAACKQVSDAGLKEKITVRRGDGLDVISAGEVDVITIAGMGGALIASIL
DRGLSKLEGVQLLILQPNVGEDILRRWLLEHHWVVVAEQLLEEDGKIYEITAMPQSV
SPIANVEVYRARPLQGGAELETEDLLRMGPYLVDRPTDVFFAKWESEIVKLQGVVNSI
SKSDQDSSRDKAAEVERLIANLKEVLACL PKVKL"

CDS 1055851..1056966

/locus_tag="EFAGFIKM_00910"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P67272"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0327"

/translation="MFAKGQTVIQLMEQLAPKHLAVPDDRIGLQLGSLQKEITHVLVA
LDVTDEVVDEAIRIGANLIIAHHAIIIFRPVKSLSTDTPMGKLYEKLKHDIAYVISHT
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SIGQYNKCSFNTEGTGTFVPGEGTQPFIGTQGQMERVEEIRIETIVPQSLRSKVVQAM
LKAHPYEEVAYDLYAMD LKGRTLGLGRLGPLREP KTLGELVEVVKTFNVP HVRVVG D
LNKQIKKAAVLGGSGSR YALTARFKGADVIVTGDIDYHTAHDALMAGMCIIDPGHNSE
KIMKPKTADWLRSRLEEKRYDTQVTASEVNTEVFQFI"

CDS complement(1057714..1058943)

/gene="lysN_1"

/locus_tag="EFAGFIKM_00911"

/EC_number="2.6.1.39"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q72LL6"

/codon_start=1

/transl_table=11

/product="2-aminoadipate transaminase"

/db_xref="COG:COG1167"

/translation="MSIPWSKMAQNTPSSVVRDMLQAAQAPGMISLAGGLPAQTSFPL
EAIRVAYEKVFM SGAAALQYAETEGYRPLRAKIAERLESKGIPASPDHMLLTG SQQS

IDLVCRILLDPGDRVLVESPTYLAALQVIHSYQAESHGVACDDHGMLPESLEEQLQLH
RPKLVYINPTFSNPTGKVWSRERRQQAVDLCRKYGVLILEDDPYGEIRFNPEQLDVPA
LAELDAVSYDGPSNVIYTSTFSKTVAPGLRTGWILAAPDIVKMAARAKQGADLHSSSI
DQRALHALLECFDLDAHIRHISEDYEQRMKLTTLMAAKAWEGISWNSPQGGMFLWLQ
LPEGMLASNLFTYGIQEKVCIVPGDSFYAGTPELNRMRINFTHTDPELLPEAVERMDR
AIQRWHASLTSDSVVTL"

CDS 1059051..1060571

/gene="dapL_2"

/locus_tag="EFAGFIKM_00912"

/EC_number="2.6.1.83"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01642"

/codon_start=1

/transl_table=11

/product="LL-diaminopimelate aminotransferase"

/translation="MHIELKRGSSTKLYVQIALTIADRIRSGLIEPGTRLPSVRKMTA

DLGVSLVTVSKAYAELEAIQLITCSQGKGCYVRGTLNVDQMEDVDRTQRNNANGESST

SWNWQMALVDYLPRAQLWRHFDTSQVRYELHMSAIQPELLPTREIIDSAYRLSSDHT

ERMAAYGSFQGDRELQRQFAEHFAARGLQAAPERMLITSGAQQGIDLVARFVGPBGDV

VYMEAPSYTGAI DVFTSRGAKIITVPMDDDEGMRIDLLTRLCDTYPKLIYTIPTYHNP

TGITMSARRRAQLLNLAQSYHCLILEDDPFADLYFREPPASIKSMDGTGHVVYIKSF

SKVLSPGCRIACAIADGSVLTRLVAAKSTADLGSPLLTQKALQSFIQNQYGAYVSRLR

DELYSRLCAASEVLEEHA TMGMQWRLPEGGLNLWLQLPSNLD MRELHHQSLAAGVSFL

PGSACYVGEMDTPSLRICFTVTSVELLCEGLRVLCGVIGKVTPQEGGTVADRLPLI"

CDS 1060658..1060915

/locus_tag="EFAGFIKM_00913"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNHYCPPLCPIVCDPIQVVEDYYIPQIVPVIHPIEVIKKHHHCVP

IHHHMYPVVVK EEDPCYVSSHNP KKKSVKKSSKARTTSRKR"

CDS complement(1061018..1062892)
/locus_tag="EFAGFIKM_00914"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSRPKWINWALAAGAGALATLLLPTSNRQEPKPSALSDSAHEE
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IHLMNTNGSFNKPFDHASTQGSKLEQQKLQHSLNLAKKAVNKRQSFESSFPLGKEY
FVMGQPSKD GKRAVIALFSQNVLNAVEQHQRKNLRMIPYPREGKFKIESVHPDTLNEI
TVKTGHDNANASHFYENEIVIRFRQDPGERDMRIKSDLRAQSARKLGYTYVFRSEHM
SYQLHSYFESKWNPLYMEPHYMYLTNDVTEQTDVTIPNDILFSDYQWNLPAIETNR
GWNITKGNKDVIVAVVDTGVDMNHPDLKGKLLEGYNVVEPGSQPMDDVGHGTHVAGII
GATVNNNEGVAGMSWYNKVLPVKVLDNSGSGTTYAVAEGIIWAADHGAKVINMSLGNY
ADAQFLHDAIKYAFDRDIVLIAATGNDNTERPGYPAAYPEVFAVSATDPDMSKASYSN
YGDYVDVMAPGSSIASTYPNNQYAALSGTSMASPHVAALAGLIRSLNPDLTNTEVMDL
MRQSVIDLGDPGHDKYFGYGQIDVYKALQAASGNSAPLQFWPQHVRQQMDNTMKKYTQ
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CDS 1063176..1063682
/locus_tag="EFAGFIKM_00915"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSAANVQKTCESTREKLKPAIDRIEFLNENALPELDQNQTEES
TAFYKGFLSDLRHLLVFSEVSYEKLGVVLRANFDVDFAEKALYNTYHQC VN SFFYPK
NECYSEDGRYAYTGQDAIRFRDKPIRAVRDVILEVSKTYEELRDDLAYYESDYLTQRR
MQNQRNHA"

CDS complement(1063779..1064018)
/locus_tag="EFAGFIKM_00916"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIMVIGVKCLTGKFLMQTTGGMLVDVNHGDISVAEVVLSPKVAV
GDAAFDNWVFLAHFLSPRLLSPRHKPDIPRQNAR"

CDS 1064102..1064515

/locus_tag="EFAGFIKM_00917"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKNDDNKFNFQDRPKINVDGEKQRMVDYPRKAHREEYGAEVAP
PTVVRTGGSEAEVPPEKHEADRVMESTGKVAGYMGLAFGLASLFMWSIVLGPAAAVL
GYAYVNGRKTAGAWSIGLGVVATLSYFFMIPFAR"

CDS 1064705..1065457

/gene="mltC_1"

/locus_tag="EFAGFIKM_00918"

/EC_number="4.2.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01616"

/codon_start=1

/transl_table=11

/product="Membrane-bound lytic murein transglycosylase C"

/translation="MQIDPNGSRQLLELQLSNVNNQTSGSQSDTGSTVDFANVMDGLL
GMGANSTSNSTDSTATVSKRSSDGLLWLQLGSTYNPDINTAGSSSVSNNIVESLLSSSN
TGIVDSGASVPTDYESLIAEASAKYGVPESLIKAVIDTESNFNPVSSAGAKGLMQL
MDGTAAGLGVSNSFDPAQNIDAGTKYLSLQLQRFGEVKMALAAYNAGPGRVSR LGVS
SDSELMSVLNRLPSETQNYISKVEKAQSKYVI"

CDS 1065508..1065600

/locus_tag="EFAGFIKM_00919"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MWEQKRLKRLFPVGLFVLYGYRVTMLTVDS"

CDS 1065631..1066779

/gene="iscS_2"
/locus_tag="EFAGFIKM_00920"
/EC_number="2.8.1.7"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A6B7"
/codon_start=1
/transl_table=11
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/translation="MKYFDYAATTPHPDVIRTMAEIMETQFGNPSSIHGYGERAHQL
LRRARSGCAAAGVKPEEIVFTSGATESNNLAIKGAALRYQSRGRHIITTATEHASVY
ESFMQLQQWGWEVTLVPVNSDGVVDTQQVVDALRPDVLVSLMHVNNETGAIHPIAEI
GKQLKKKAPRVLFHVDGVQGFGKMKATPAAWGADLYSLSAHKIRGPKGAGLLYVRSGV
ELTPLLSGGSQEQGLRAGTENVALLVGMAMRMAAEDQVDFARRTTVLRDRLMETIR
VIPEFELNSSPEGAPHIVHFSYPMKAEEVALHTLEQLGVTISTQSACSSRSAEPSRAL
LAMGRDAACAGGGLRISLGDEHTEEDVALLEQALHQMVAQLRPLERRM"

CDS 1066779..1068026

/gene="thil"
/locus_tag="EFAGFIKM_00921"
/EC_number="2.8.1.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q81KU0"
/codon_start=1
/transl_table=11
/product="putative tRNA sulfurtransferase"
/db_xref="COG:COG0301"
/translation="MDMNYDMLLLRFGEFMLKGKNRARFEKTIITQVKALLKPYPGAS
LRKEYGRVYVDLGGESHTELIKVLKRVFGVMSISPVKVTPSELDEIVKTAVAFMDERE
DEFKEGTTFKVNVRRVWKEFPNSSHEMNHLVGSPILRKFFQQLSVDVRQPDIELRVEIR"

DQGTYIFNETIPAVGGFPLGTNGKAMVLLSGGIDSPVAAWSSMRRGLEVECVHFYSYP
FTSERAKEKVIDLARALADHAGKIKLHLVPFTEIQTAFATQLGQDNLIITLMRRSMLRI
ASKLAERERALALITGDSLQVASQTLPSMNVIGRATDLPLLRPLVMMDKQEITLSK
QIGTYDISILPYEDCCTLFVPKSPSTNPNLRIVDKIESTMSHLSEWVDQAVEQTETIT
LHAGETSVVTNPTSDNGMKDDWF"

CDS complement(1068149..1068859)

/locus_tag="EFAGFIKM_00922"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MELFSPTFWLALLNVFIDLILAGDNAIVIGLAARNLHPSVQKK

AILYGTGGALLIRILATVVVLWLLKVPWLLLVGILLIWIAYKLLADQGDEHDDVQAG

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NHFPWIIYVGAIVLGYTASNMITTEEQRLLPYFTEHPALRILFIVVIGGVVFAGYRKR

SSSSSHKSGSGGEQQRSYS"

CDS 1068947..1069606

/locus_tag="EFAGFIKM_00923"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDTLWLLTEILMINLVLSGDNAVVIALASKDLPPVQRKKAVWWG

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CDS 1069904..1070392

/locus_tag="EFAGFIKM_00924"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MRNEKAIGLFIVAAGIIILLGKFGVFGFIGRNFWPLLILLPGIA
LHALYYARISPSWSLVPAGILTVYGVLFISITNTWGAGLMSRLWPAFLLGIAIGLLEYG
MAERRRPEYVLPAAILGAVSIILFGFTLLQTGIIYVLAVLLILGGVWLLLGRGRQGR
GW"

CDS 1070570..1072414

/gene="typA"
/locus_tag="EFAGFIKM_00925"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P44910"
/codon_start=1
/transl_table=11
/product="GTP-binding protein TypA/BipA"
/db_xref="COG:COG1217"
/translation="MHSREHIRNIAIIAHVDHGKTTLVDKLLQQSGTYRDHETVQERV
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EFPVVYASALNGTSSMDNDPAKQDDNMMAIYNTIVSHIPHTENVEEPLQFLVTLMDY
NEYLGRIGRNVNRGVIRQQQSVTVIMRDGKSKTARIEKLFQGLKRIETEEAGAGD
IVAIAIKDINIGETIADPNNPEALPVLKIDEPTLQMTFLVNNSPFAGREGKWWTSRK
LRERLFKELETDVSLRVDETDSPAFAIVSGRGELHLGILIENMRREGYELQVSKPEVI
VREVDGKKMEPVERLLIDIPEESMGSMESLGARKAEMVMNMVNTGSGQVRLEFLIPAR
GLIGYSTNFLTTRGYGVMNHAFDSPVVGQVGRHQGVLISTETGTSTFYGMMGV
EDRGTLFLEPGTEIYEGMIVGEHTRDNDIVVNICKEKQLTNVRSSGKDDTVKIKTPII
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CDS 1072719..1073015

/locus_tag="EFAGFIKM_00926"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MQAWFASHPIVAYIVIFVLITYVYNKVFRVRQKLPLGKEIVLYI

LMAMGTFMLLIFQIDKLPIIQCLLVAVGLMLLVVRVRYFIEGRQKKKAEEAAARNS"

CDS 1073106..1074167

/gene="tagU_2"

/locus_tag="EFAGFIKM_00927"

/EC_number="2.7.8.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01140"

/codon_start=1

/transl_table=11

/product="Polyisoprenyl-teichoic acid--peptidoglycan

teichoic acid transferase TagU"

/translation="MNSNSNGLPPRRQAPTQSGASGSKNGKGKQPKKKKRMNAFGRIL

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LSDVVMVASLNPETKTATIVSLPRDTRIQLDGYKSNKLNSYYPRFKAQEKTGKNAED

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GAQHLDGKAALDFVRYRKSNCNPKTDESNDFDRNKRQNQVLNSMLDQMKSLGGITKIS

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KQALQDTLSGKVTASPSGE"

CDS 1074266..1074718

/locus_tag="EFAGFIKM_00928"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSEAVTQLTESLLQQFKNETFVLLSTVDVESGGPTSTAISWIYA

ENASTFRLAIDHRSRLVNNMITNPLITVTVFGEETVYAVNGRAAVRQDPLLDVPFNM

CFDITIEAVRNALFYGAQLSSVPQYVKIYDQRAAEKLDEQVFAAMKKA"

CDS complement(1074726..1075421)

/locus_tag="EFAGFIKM_00929"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

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QVEGVEDANCVILGNTAVVGIDVDGELERARVGTIKYAVAEALRKDPEGIDSIVTADA
DVTERIKEIGEHIRQGHPISGFASELADMVGRIIPQLPKDVKVRQNPDEHVNQKQQMQ
QLHSSDKRQQKAQ"

CDS 1075574..1076908

/locus_tag="EFAGFIKM_00930"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKIFVLDTNVLLHDPNAIFAFEEHEVIIPAVVLEEIDSKKRNA
DEIGRNARNVSRLLDGLRELGHLSGVPLANGGNLKVLELNHRSFVKVQEMFGEVSNDN
RILAVALNYQIEENEKEVVERQVVLVSKDVLVRIKADVLGLFTQDYLSDRTAGLSELY
PGYTALKVHPSVIDEFYTYRFLPIKPLQLSYSLYPNEFVILKDEMGTNKSALLKVNTE
GTKLEPLFLSNDNVWGISARNAQQRMALELLLNDDIPLVTITGKAGTGKTLLALAAGL
LKVEDDHKYKLLIARPVVPBGKDIGYLPGEKEEKLRPWMQPIYDNLEFLFDTKKAGD
IDKILMGLGSIQVEALTYIRGRSIPGQFIIDEAQNLSRHEVKTIVSRVGEYSKIILM
GDPEQIDHPYLDASNGITYIVERFKQEGISGHIMLEKGERSKLAQLAADLL"

CDS 1077130..1078401

/locus_tag="EFAGFIKM_00931"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MKRRHQVVLFVALLSLTILSPSFDGRGSQLNQERDQEKDAFHG
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PFDFDPYILAAQSSFLKRALESPLRNKDQWVKLTQQAIAEGTPLITMNINDTYGTNA
WLNHLEPRMAPDQVKRTQIDSQTGDLQQGIQLMNQIQPLIRLESTNPDFSPTADQNDT
PMVVSLLSQLLSADQASKVGKDPLERISFEPLETVNSRSLVITAGSVEAEEASRWIEG

MTSATTQLKWYQQVKRLPAKQQELDMESEKLVGPYDMTKGQSWFPTTQDAPAAATTESH

ALITRFHKKIQQLKGEITANQYVDSIRTTN"

CDS complement(1078425..1079504)

/locus_tag="EFAGFIKM_00932"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRQYGISAFILCIILFLQLPLAHAYGESSPEDTREILQKSLSI

VEIDHEIERITERQKQLAQYETLSVQLQEQQEQIHIQQDRAGAVVRSYYTGERDSSL

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TNLQNQRERVVALQKEVDAQIATSGDAAAIQKLMDELTYWENIGIYEVKRYFKALAS

AMQNLPDFIQKQNGGISTGTITYTIRIGQDELNAFLRSQNPFIEDFAFQFNQDKIIAS

GQRDQLQLSIEGHYTVENEPQNSIRFHVVDKLVFNQLELPDTRRMLEKEFDLGFYPQK

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CDS complement(1079689..1079925)

/locus_tag="EFAGFIKM_00933"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MARMFRVLGFFTLAIGLMAFAGDLVEMALLFFLQTAFFVILGYL

KFTERTYILLFWGYMIVTFTGFSYWTVFEMGLPL"

CDS 1080241..1080891

/gene="rsfA"

/locus_tag="EFAGFIKM_00934"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39650"

/codon_start=1

/transl_table=11

/product="Prespore-specific transcriptional regulator

RsfA"

/translation="MTAVRQDAWSTEDDLILAEVTLRHIREGSTQLAAFEVGEKIGR
TSAACGFRWNNSCVRKKYDSAISNAKAQRQKRSYLKQPAMLGPQVAALSTLDTEEHLY
KSDGISDDSLSM DAVIRFLRQWKGTVQESNRQLKMLEKELREKEDELLELRLENDRLS
KEVNEVQTDYRVVNDDYKALIQIMDRARRLAFLSEEEEEELKTRFKMDANGNLERIE"

CDS 1081042..1082001

/gene="panE"
/locus_tag="EFAGFIKM_00935"
/EC_number="1.1.1.169"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A9J4"
/codon_start=1
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/product="2-dehydropantoate 2-reductase"
/db_xref="COG:COG1893"
/translation="MIIDIVGAGALGLLYGGKLLASGNQVRFWTRTTAQADLLSHNGV
TIVEQDEEIHILPDQIQAKPISKLTDTWKNTPGEWLLL MVKQTSIDDFIHEISPLQDH
VLNVACFQNGMGHLTKLQAALPKSLLCSAITTEGAKRTQSQVTRAGTGETRLGRYNIH
IGASTSIEEKRTFTLSGSLQQAGFDCTVSNEIDKLIYRKLLINSVINPLTALWRIPNG
ELIVKEERKRLMRQLYDEVLLIYSANGICLDQDMWDQLISVCRSTATNTSSMLADVLA
GRGTEVRSINGHIVKMAQKLDLVAPTHEILLHLIEGMQPEGVN"

CDS 1082001..1082375

/locus_tag="EFAGFIKM_00936"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGLFIVLSILPFFPFFLVYWGMYVWKKDKRKALRMAMDVTTFFL
VFSVSALFNLT FDSNFGFYLT LILILVALGFIGGAQNRLKGKVDRGRMFRAVWRMSFV
IMSGYVLFTLFGFLFRYFMQQM"

CDS 1082529..1084226

/gene="oppA"
/locus_tag="EFAGFIKM_00937"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P24141"

/codon_start=1

/transl_table=11

/product="Oligopeptide-binding protein OppA"

/db_xref="COG:COG4166"

/translation="MKRKSLVLLTLILAFGTVLAACGSKNEGNTDTGSANEGNGL
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EDGLKYVFNLPDAKWSNGDAITAEDFVRSWERALKPETASPYAYQLYYIKGAEGYNL
SKDETYKGTKVTDIFSQVGVKATDEHTLEVTLENPTPYFLGLTAFYTYYPVHASADTND
KFFTDYKNMIVNGPFVMDQYSKGQKIVVKKNDGYHAAADIKLAQIDMSLTNSSASELQ
AYKSGQLDYGAPNGEIPSDQIPSVKAELPDEFKATGIASYYYQFNVNEAPFNNVKI
RKAFAMAIQRQLIVDKVTQGGQIPAFGFVPPGIRGENGEFRDEHKDDYFTENVEEAKA
LLAEGMKEEGYTTLPAVTLIYNTSDGHAKIALAVADMWKQNLGVDVKTENQEWGVFLE
NRQNNQNFQVARAGWSADYNPYNFLEMWTTGNTNNDKFSNEQYDKDKVKETVKSADPA
ARMAAFADA EKILIQDEMGMPIYYYTNVSLTKPYLKGVQLDFSGAIDYTRAYLEEK"

CDS 1084416..1085348

/gene="oppB"

/locus_tag="EFAGFIKM_00938"

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/inference="similar to AA sequence:UniProtKB:P24138"

/codon_start=1

/transl_table=11

/product="Oligopeptide transport system permease protein

OppB"

/db_xref="COG:COG0601"

/translation="MVKYVLKLLFMLLSLFIASATFFLMKAIPGDPFTSEKKVSPE
IRVLEQKYGLDKPMYEQYLKYMGGIIKGDGFGVSMKYLNRDVAGMIGETFTASLKLGV
FAIVISIIVGVLLGLIAAVYHRKLIDDITMILAVIGIAVPSFLLASLLQYLFATKLGW
FNVMGFDGPLDYVLPVAALSASPIAFIARLTRSSMLEVLHADYIKTAKAKGLKWPAIM
FKHVVRNGILPVVTYVGPMTANIITGSVVIEQIFNIGGIGKVFVESITNRDYMIMGI
TIFYGILLMLARFFTDIAYVLIDPRIKLESRKGA"

CDS 1085351..1086277

/gene="oppC"

/locus_tag="EFAGFIKM_00939"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P24139"

/codon_start=1

/transl_table=11

/product="Oligopeptide transport system permease protein

OppC"

/db_xref="COG:COG1173"

/translation="MSGTNNKKNETANTNLTSQAAVKPQESVSLFKDAMYRLATNKAA
MISLSVLVLVVIFSLIGPTSLFTSYNYYSNDLLNANAAPSAEHWFGTDELGRDVWVRT
WVGARVSLTVGLAAALIDLVIYGAIMGFYGGRVDGIMNKFSEILYSLPYMLVVIL
LLVVLEPSLTIIIIALTITGWISMSWIVRGEIMQLKNRDFILAARSMGASTGRQLFRH
LLPNAIGPILVTLTSLIPNAIFAEFLSFLGLGVSAPRSSLGSMINDALTGWTLFPWR
MWFPAGLMVLTMLAFNLLGDGLRDALDPKLRK"

CDS 1086295..1088064

/gene="gsiA_2"

/locus_tag="EFAGFIKM_00940"

/EC_number="7.4.2.10"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P75796"

/codon_start=1

/transl_table=11

/product="Glutathione import ATP-binding protein GsiA"

/db_xref="COG:COG1123"

/translation="MEPILTVKDLSVSFSTRSGEFDAVKHVSFELGKGETLGIVGESG
SGKSVTAQTIMKLIPSPPSKVKSGETFHGQDLLNKTDKQMEAIRGKDGMIFQDPMT
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RQRAMIAIALACRPSLLIADEPTTALDVTIQAQILDVMKDMQQKLGTSIMLITHDLGV
VAGMCDRVVVMKEGEVVETGTAEIFSHPYTIKLLNALPRLDEPKKEKPAPAGII
KGSNKPLVQVKNLKQYFNLGKGNILKAVNDVSFDIFEGETLGVVGESGCGKSTTGRTI

LRLYEPTGGNVNFNGTDIYKLSRKMKEMRKDMQMIFQDPYASLNPRFNVMDIIGESL
DIHGLASSSSKERKRRVEELLDLVGLNPSHALRYPHEFSGGQRQRIGIARALAVDPKFI
ICDEPLSALDVSIQAQVVKLLEELQQRLGLTYLFIAHDLMSVVKHISDRVAVMYMGKV
ELAESEELYANPVHPYTKTLLSAIPVPDPEVEANKRRILLPEEHMSPIQNGSGGPAND
PYNLENSQLIEVSKGHWVAEPYV"

CDS 1088222..1089853

/gene="bshC"

/locus_tag="EFAGFIKM_00941"

/EC_number="6.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P55342"

/codon_start=1

/transl_table=11

/product="Putative cysteine ligase BshC"

/db_xref="COG:COG4365"

/translation="MNGITEALRSGSRLAEDYICSRDAARGLYEYDIRWESGLQARAE
WLDQSENARIDRRDLAEYLRIYNKRVNDHGEVHASITRLAEQDALVVTGGQQSGLLTG
PLFVIYKAASVAAAAREAEERLQRPVVPVFWIAGEDHDWDEVNHTYLPDHQGMKKVK
LQGRFAGRDSVSNVHVDSQQWVNVLEQVEHLLPDTIHKPGLMKCITEIHQSSSNLSDA
FARMISVLFASSGLVLM DASDPDLRRLEQPVFERLIRKNEVLR SAYTQGASLVQQAGY
AMPAEVAEDGANLFYIHEGTRLLLLLKDGLYSDRKGLVSFTEERLLQELGEHPERFSN
NVLTRPLMQDSVLPVAAVILGQGEIAYWGLTREAFRQFGLQMPILLPRLSFTIMEDIH
HKHMKQYGLSFQDVQYHMEEKKEQWLAQQETFQVDEQFDKVQEAFLDLYGPLLDEIAE
IHPGLERIGDTNLSKINEQMQLKQQTHKAIEDKHNVSRLRHWNIGIQNSLFPTGKPQER
VHNALFYLNRYGTEWIDELIKASSEFLGEHKVIAL"

CDS 1089898..1091163

/gene="ahcY"

/locus_tag="EFAGFIKM_00942"

/EC_number="3.3.1.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O51933"

/codon_start=1

/transl_table=11
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/db_xref="COG:COG0499"
/translation="MTTPALQNSIVKDMGLASEGHLKIDWVEAHMPVLNRIRRFQEQD
LPFKGLKVAICLHLEAKTAYLAKVIQAGGA EVTITHSNPLSTQDDVCAALVEDGVTY
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IRLKALAKEGQLKFPMVAVNDAYCKYLF DNRYGTGQSAFDGIIRTTNLVIAGKNVVA
GYGWCGKGVAMRAKGLGANVIVTEIDPIKAVEAHMDGFRVMTMVEAAKLGDFFIAVTG
NKDVITGEHYDVMKDGAILS NAGHFDVEVNKPELAKRSESIRTVRRNIEEYRFKDGRK
MYLLAEGRLVNLGAADGHPAEIMDTTFALQALGLRYVSENYKDLGKNVVNVPYDIDQQ
VASYKLESLNIGIDSLSAEQEKYLD SWKF"

CDS 1091437..1091874

/gene="mraZ"
/locus_tag="EFAGFIKM_00943"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P65439"
/codon_start=1
/transl_table=11
/product="Transcriptional regulator MraZ"
/translation="MFMGEFQHSIDDKGRVIIPAKFRESLGPSFV VTRGLDQCLFVYP
MEEWGVMEQKLKALPLMKSDARA FTRFFFSGATECELDKQGRVNLPGNLREYAKLDKD
CWLGVSNRVEIWSKGIWESYFNQSEEAFNDIAEKLVD FNF DL"

CDS 1091893..1092843

/gene="rsmH"
/locus_tag="EFAGFIKM_00944"
/EC_number="2.1.1.199"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P60392"
/codon_start=1
/transl_table=11
/product="Ribosomal RNA small subunit methyltransferase H"
/translation="MFHHITVLKEEATEGLNIKQDGIYVDCTLGGGGHSSVIASKLGP"

GGRLIALDQDDWALDNAREKLAAYGERVTLVKTNFRDLEQVLKDLDVPMKDGAPQVDG
ILYDLGVSSPQFDEGERGFSYNHDAPLDMRMDQDAMLTAKIVNEWPEEEIARILYRY
GEEKFSRRIARVIVGKRAQSTIETTGELEVELIKEGIPAAARRTGHPAKRSFQALRIA
VNDELGAFFEEGLHQA VRCLAPGGRVSVITFHSLED RICKQIFSSYLEKCTCPPDFPLC
VCGGKGTLRLVNRKPLSPTETELAENSRARS AKLRVAEKL"

CDS 1092871..1093299

/gene="ftsL_1"

/locus_tag="EFAGFIKM_00945"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00910"

/codon_start=1

/transl_table=11

/product="Cell division protein FtsL"

/translation="MAYTRGNLAVKEKASQERVTTQQRYKETTQVVTRRTGLPAREKIL

YLITLVAVILVGGALMSRYAHYDLNKQAQSTISDIKVYEKTIADLQVEKETLNNQVI

ENAKQLGYVEASGKDVIYVPRSTSTKSTGTESSSNTASSK"

CDS 1093312..1095654

/gene="spoVD_1"

/locus_tag="EFAGFIKM_00946"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q03524"

/codon_start=1

/transl_table=11

/product="Stage V sporulation protein D"

/db_xref="COG:COG0768"

/translation="MIKRIKMRTLLIGGCITLFFLVLVTRIFFIQVVNGGVWQERAAG

LVEREQTIKAARGTITDRNGNILATDAPAYTVSVNPLLINELGIQDVVTEKLSNLLGK

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AQESKRFPYEETLASHLLGYMSRDGKAVNGLEVSYDEALTGTDGYLNYQKDAKGIKLP

DSQDNYLPPQNGKNLTLTIDDTIQFYIEDAMKEAVAKYNPLSMTVIAADPNTMEILGM

ANWPTFNPNTYGSTPDQKNFINHATQSIYEPGSTFKIVTLAGAVEEKLFDPNASFESK

RM YIGGFPISDNGHSYGWISYLEGVKRSSNIAFVN LGYNMLGGERLRHYID EFGFGKK

TGIDLPNEAASPIKPLVYKSEIATAAYGHGLVQVTPIQQVAAISAIANGGKLLLEPHLV
KEIKNPNDGTTEVIKPKVVRQVISKESSKLVSGYLEQVVADQTIGTGRNAYIEGYRVA
GKTGTARKVVNGAYS KSKDVVSFIGFAPVNNPKIAILVVIDQPDGTNIGGGTAAAPVF
KKIVSQT LQYMGIPKDTAKTPDKKSKEVSVVQAKAPDL SGKTAKQARSQ LLSAGIAYV
TLGQGDNVIRQYPVAGASMNPGQRIYLLTEESSKMIPDLTGESLRDALEVL SLMKVG
VTVKGEGYVVKQTEQVAGEQRTVQLNLQTAKAAVTGIADEAPISSDPSSEAEVKEQEA
SAGEAKTDETDGTDETDNNKAPANESESSDDPATNGASLP"

CDS 1095749..1097701

/gene="spoVD_2"

/locus_tag="EFAGFIKM_00947"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q03524"

/codon_start=1

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/product="Stage V sporulation protein D"

/db_xref="COG:COG0768"

/translation="MKGSSVNLRRLLWSLMILVLLFSALMIRLAYVQLGEGPELSAK
AEESWRRNIPYSAKRGEILDRNGTSLAYNVTTPTIMAIPAQVKEAETTAKALAPLLGM
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HILGFTGIDNQGLTGVEKKYDDKLNGLNGSVSYLSDAAGRLMPGSSEKYVEPKDGLNL
KLTIDKSIQSIMERELDQAMVKFQANSALAIAMNPKTGEILGMSSRPGYEPADYQQYP
AEIYNRNLPiWMTYEPGSTFKIITLAAALEEKKVNLQQDQFFDPGYVEVGARLRCWK
KGGHGSQTFLQVVENSCNPGFVALGQRLGKESLFSYIKDFGFGTKTGIDLSGEASGIL
FKLSRVGPVELATTAFGQGVSVTPIQQVAAVSAAINGGKLYKPYVTKAWVHPVTGEVM
EEAKPELVRQVISENTSKQVREALESVVAKGTGRPAFIDGYRVGGKTGTAQKVINGRY
SSTEHIVSFIGFAPADDPQIVVYTAVDNPKGIQFGGVVAAPIVQNILEDALHYMNVPV
RKDQVAKEYKYGETKIVTPDLTGATVEDLYEDLNMNFMLAKSGSGKYVINQAPKPGA
RVDQGSTIRIYMGNVLNDAHDHTKDE"

CDS 1097842..1099329

/gene="murE"

/locus_tag="EFAGFIKM_00948"

/EC_number="6.3.2.13"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q819Q0"

/codon_start=1

/transl_table=11

/product="UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,
6-diaminopimelate ligase"

/db_xref="COG:COG0769"

/translation="MLLKQFASMLTTARLVGESNTECQNLQTDSRQVKPGDLFICLPG
HTVDGHDYAEKAVNAGAVLVERQLDLPVPQLLVKDSRFAMAVLADFFFDSPSQKMN
MIGVTGTNGKTTTTYIEKIMSDYGRKTGLIGTIQMRYDGRTYPMGGTTPEALDLQRS
LHDMVQKGTDCCVMEVSSHALEQGRVKGTNFRFTAVFTNLTQDHLDYHHSMEEYRGAKG
LFFARLNGYTEDVSQRKFAVINADDPADYFISVTAAEVITYGMGEKADVRSQISI
TSQGTSTFHVDTFAGSTDIRLRMVGKFNVYNAMAAISAALVEGIPLEEIKRSLETVPGV
DGRVEGVDEGQPFVAVVDYAHTPDGLENVLRVKEFAEGRVICVFGCGGDRDRTRKPL
MGKIAANYSDFLVTSNPRTEPDILKLDIEQGLIEESVPAERYTMIVDRRQAIHEA
IEMASPADVVLIAGKGHETYQIIGTTKTDFDDRIIAKEAIRGKSN"

CDS 1099326..1100741

/gene="murF"

/locus_tag="EFAGFIKM_00949"

/EC_number="6.3.2.10"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P11880"

/codon_start=1

/transl_table=11

/product="UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-
alanine ligase"

/db_xref="COG:COG0770"

/translation="MIKRTLAQLAEMCGGTLSVAAHGNVMVEGVFTDSRKPLEGSLF
IPLVGERFDGHEFVQACLEKGASGAIWQKDHGIPPQGAVIVDDTLVALQALASAYLT
ENKAAVVGITGSNGKTTTKDIVDAILSTTFKVHKTQGNFNNHIGLPLTVLSMDPDTEI
IILEMGMSGRGEINDLSVIAQPDVAVITNIGESHLLQLGSRLEIARAKAEIAAGLKPG
GLLIYNGDEPLIAQVLEEPATKQPDGLQRFTFGLQTDNDDYPTGLMNAQNGVWFTTKQ

SGEHAFTLPLLGTHNVVNC LAALAVARHFIVTTEQIAAGLSRLKLTGMRIEVTQGVSG
LTLNDAYNASPTSMKAAIDVLEGLKGYRMKVAVLGDMLELGPQEQLHYGIGEYITS
AKMDMVLVYGPLSAKIAEGASKHMPTEAVHAFIDKEEMTRYLLEKLHPRDVVLFKASR
GMKLEDVVEALQIAPLQNRVD"

CDS 1100754..1101722

/gene="mraY"

/locus_tag="EFAGFIKM_00950"

/EC_number="2.7.8.13"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2FZ93"

/codon_start=1

/transl_table=11

/product="Phospho-N-acetylmuramoyl-pentapeptide-
transferase"

/db_xref="COG:COG0472"

/translation="MDFQVLLLTIGVSFILAVIAAPLLIPLLRRMKFGQQVREDGPQS
HLKKSGTPTMGGVVILVAFTLAFLKFSVAVKNTDFYVLLVATLGFGFLIGFLDDYIKIVF
KRSGLGTARQKMLGQLFFSAVMCFLLIQNGHSTAISIPGTSFSFDWTGWFYYPFVVF
MLAITNAVNFDTGLDGLLSGVSAIAFGAFAIVAMQATSMPAAVCAAAMIGAVLGFLVY
NAHPAKVFMGDTGSLGIGGAIGAVAVTKTELLFVIIGGIFVIEILSVIIQVVSFKTR
GKRVFKMSPIHHHFELSGWSEWRVVITFWAVGAILAALGLYLNKGL"

CDS 1101726..1103147

/gene="murD"

/locus_tag="EFAGFIKM_00951"

/EC_number="6.3.2.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8E186"

/codon_start=1

/transl_table=11

/product="UDP-N-acetylmuramoylalanine--D-glutamate ligase"

/translation="MNHPESYRGQQVVVLGLAKSGVQVAKVLDRAGAKVTVNDKKERD
QCPEASELEALGISVVCGGHPDDLHSGVKLVVKNPGIPYHAAPVQQALALGIEVVTE

VEVAYHLCAAPMIGITGSNGKTTTTTWWGKMLEHAGLKPIVAGNIGTPLCEAAEQASP
DNWMVVELSSFQLKGTVD FRPRIASLLNVAETHLDYHGNMDDYVASKAKLFANQQPDD
VAILNWDDAVCRGLVPYIKGRLIPFSVTEKLD TGVYADPPYVDGEEDDVKRQVIYADE
NGDHHIIIDVEDIGLPGRFNVENALAAVAIAVAAGADPALLAAPLADFKGVEHRLEYV
LEYNGSAYYNN SKATNSKATVMALNSFKEPVVLIAGGLDRGSDMMELLPLFQERVKAV
VAIGETRRTKIAKIAELAGLKQIKVVDNEEDAARTLT VAVQEASKLATAGDVVLLSPAC
ASWDMFASYEERGRIFKEAAHNL"

CDS 1103196..1104293

/gene="ftsW_1"

/locus_tag="EFAGFIKM_00952"

/EC_number="2.4.1.129"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ABG4"

/codon_start=1

/transl_table=11

/product="putative peptidoglycan glycosyltransferase FtsW"

/db_xref="COG:COG0772"

/translation="MKQTRPAPDIWLLICILALLAIGIIMVYSAGSVLAFHDYGDSFY

FVKRQALFAVLGLVAMFVTANVDYRVWRKYAKPILIA CFIMLIAVLIPGIGVVRGGAR

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QPD LGTGTVM MGAAMLIIFTAGARMKHL SLLALGGIAGFAALIAA APYRLQRITAF LD

PWSDPLGAGYQIIQSLYAIGPGGLAGLGLGMSRQKYSYVPEPQTDFIFSILAEELGFI

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ITLPLISYGGSSLTLM LTALGILVNLSRYAR"

CDS 1104301..1105410

/gene="murG"

/locus_tag="EFAGFIKM_00953"

/EC_number="2.4.1.227"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P17443"

/codon_start=1

/transl_table=11

/product="UDP-N-acetylglucosamine--N-acetylmuramyl-
(pentapeptide) pyrophosphoryl-undecaprenol
N-acetylglucosamine transferase"
/db_xref="COG:COG0707"
/translation="MRVVLSGGGTGGHIYPAVAIARQCEAENPDSTFLYIGGTRGLES
KLVPQENIPFKSIDITGFRRKLSIENLKTVMRFIQGVRKSKKMLKEFKPDVVIGTGGY
VCGPVVYAATKLGIPSIIHEQNAIPGLTNKFLMRYVDTVAVSFEGSEKSFSGAKKVIY
TGNPRATTVAQASRDGRGFATLGVPMNSRVVLVVGSRGAKAINQAMVDMAPLLEQLDD
VHVVVYTGDTYFDETREAIRSSLGTMPNHLHVLPHYVHNMPPEVLACTSLIVNRAGASFL
AEITSLGIPSILIPSPNVTNNHQEANARTLEGGGASLTMLEKDLTGKVLYEAIKIMN
DESGRKRMAEASRKLGPDAAEVLVHEIQRLAARR"

CDS 1105560..1106465

/gene="murB_1"
/locus_tag="EFAGFIKM_00954"
/EC_number="1.3.1.98"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q65JX9"
/codon_start=1
/transl_table=11
/product="UDP-N-acetylenolpyruvoylglucosamine reductase"
/db_xref="COG:COG0812"
/translation="MHQWISLLSQNNVGRVLENESLAKYTTWKIGGPADALVIPENKE
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HSFVKLSVAAKKEWAGLEFGSGIPGTGGAVYMNAGAHGSDVSRIFKFAEIVLETGE
LVRYSKEDMDFAYRHSVLHDRRGIVLEAAFELQHGERNVISETMAAYKDRRRRTQPLQ
MACAGSVFRNPPGDHAARLIEAAGLKGMTQGGAQVSTMHANFIVNTGQATAEDVITLM
QQIQSTISSQNGINLVPEVFVVGER"

CDS 1106483..1107766

/gene="murA"
/locus_tag="EFAGFIKM_00955"
/EC_number="2.5.1.7"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q88P88"

/codon_start=1

/transl_table=11

/product="UDP-N-acetylglucosamine

1-carboxyvinyltransferase"

/db_xref="COG:COG0766"

/translation="MDKLVIEGGKPLSGSIRIHGAKNAALPIMAASLLADGEVTLHNV
PHLLDIEVMYILERLGCTCRHEQGTVTINTSSIRSVDVPEDLMKQMRSSIFLMGPLL
AKFGQVSVYQPGGCAIGERKIDLHLRGLEALGALIEEQDQIICHGQNLVGTDIHLDF
PSVGATENIMMAAAMAKGTTTICNAAREPEIQDLQHFLNAMGASIIGAGTDTITINGV
EKLKPCSYEIIIPDRIVAGTVMIAAAATRGNVTLTHCNPAHLTSLIHVLKRTGVQITVC
NDIMTVSCMSRPKSVDRIVTSPYPSFPTDLQSQIMVLLSLADGFSVMKETVFEGRFKH
VDELNVMGADISVDLNAAFIRGVPRLYGATVEATDLRAGAALVIAGLAAQGKTVEQV
HHIDRGYDQIEKLFQSLGASVERQSPVSKQLDFAN"

CDS 1107824..1108591

/gene="divIB"

/locus_tag="EFAGFIKM_00956"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5L0X5"

/codon_start=1

/transl_table=11

/product="Cell division protein DivIB"

/db_xref="COG:COG1589"

/translation="MPKSQIPVLKKNRPKGKTSRKIVIIILLFFIVLLAVLFFRSSMS
RISAEITGNVYTATSELLEKSGLKEGEQFFGTSTAEVIERLKTIKAISTVTVDKQFP
GIIHIKVQEYATVAYELGSDGTLKAILASGSLTVPATIGVAVEKPILTQWKADDPLK
AKLSQTLAKIPNELTTDISEIIPNPTSPFPDQIRMYTKSQFEVITTVSLLSDKVEYLN
QVIETERPGKITMLEADTYVPFIPDDPEDDAEPGASP"

CDS 1108885..1110168

/gene="ftsA"

/locus_tag="EFAGFIKM_00957"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P28264"

/codon_start=1

/transl_table=11

/product="Cell division protein FtsA"

/db_xref="COG:COG0849"

/translation="MSNNDIIVSLDIGTSKIRAIIGEMNNGTFNIIGVGSADSEGIRK

GVIVDIDQTVQSIRNAVDHAERMVGIQISEVYVGISGNHIGLMSSHGVVAVSNEDREI

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GAKTAIHNLLRCVEKAGLKVSDLVLMSLGAGQLALSKDEKTMGSVLVDIGAGATTIAI

FEEDSLVATSTLPIGGEFVTNDIAYGLRTLTDQAEKVKLKYGCAWLDDAAADVMFKVT

RIGSNVDKEFSQEDLAAIIEPRVQEIQMISQEVKRLGYNELPGGYILTGGTVSMPGV

LQVAQHELAASVRVAVPDYIGVRDPGFTSGVGILHSVIRSLRIRPSINNGGGNNNNNN

NNKKPTNRPKPNTAQESEQKPGLFERLKNMFSEFI"

CDS 1110319..1111434

/gene="ftsZ"

/locus_tag="EFAGFIKM_00958"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P17865"

/codon_start=1

/transl_table=11

/product="Cell division protein FtsZ"

/db_xref="COG:COG0206"

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AGMGGGTGTGAAPVIAEIAKECGALTGVVTRPFTFEGRKRSSHAEQGIEALKEKVD

TIVIPNDRLLIEVDKKTTPMLEAFRQADNVLRQAVQGISDLIAVPGLINLDFADVKTIM

HERGSALMGIGESTGENRAAEAARKAIMSPLETSIEGARGVIMNITGGVNLSLYEVN

EAAEIVTSASDPEVNMIFGAIIDEDLKEEIKVTVIATGFEDKPAPPPPGRKPAPATAE

TTDTRSPNLRPFGNQPSNDQLDIPTFLNRNRRNNNNND"

CDS 1111696..1112676

/gene="spolIGA"

/locus_tag="EFAGFIKM_00959"

/EC_number="3.4.23.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P13801"
/codon_start=1
/transl_table=11
/product="Sporulation sigma-E factor-processing peptidase"
/translation="MVVYVDLIFLTNLCIDGALIGMTAWMRKTKLVWWRWLLSAIVGA
LYVMMFVPEFDFMFTFLIKFGFSLVMLTIAFGFKGLQAFARTLGTFYVINFVAAGGI
LGVHYMLQSSGELFNGIWFTASGGMSFDLKIAFWFTFIVFFAVLFLFKAVQSSKRKTD
RMTTYLGKVEVCIDEVVISCTGLLDTGNQLTDPLSRMPVMVMEVSLWQDMLPASWKGR
LKDEAPDNLILELDQESFQWQDRLRLVPYRGINKGTAFMLAMKPDRVKVTMEETCYET
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CDS 1112688..1113410

/gene="sigE_1"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P06222"
/codon_start=1
/transl_table=11
/product="RNA polymerase sigma-E factor"
/db_xref="COG:COG1191"
/translation="MLVKWKLVAQLQYYRLLFLLGLKSEEIYYIGGSEALPPPLTREE
EEFLLQKLSSGDSAIRAMLIERNLRLVVIARKFENTGINIEDLVSIGAIGLIKAVNT
FDPEKKIKLATYASRCIENEILMYLRRNSKIRTEVSFDEPLNIDWDGNELLSDVLGT
ENDTIYRNIEEQVDRKLLHKALEKLTERRMIMELRFGLTDGEEKTQKD VADLLGISQ
SYISRLEKRIIKRLRKEFNKMV"

CDS 1113522..1114304

/gene="sigG"
/locus_tag="EFAGFIKM_00961"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P19940"
/codon_start=1

/transl_table=11
/product="RNA polymerase sigma-G factor"
/db_xref="COG:COG1191"
/translation="MTRNKVEICGVDTAKLPVLTNTEMRELFHSLQQHHDRSAREKLV
NGNLRLVLSVIQRFNNRGEFVDDLQVGCIGLMKAIDNFDLSQNVKFSTYAVPMIIGE
IRRYLRDNNPIRVSRSLRDIAYKALQVRDSLTKNSREPTIFEIAEVLNVPKEDVVFA
LDAIQDPVSLFEPIYHDGGDPIYVMDQISDDRNDKDVSWIEEIALREAMHRLGQREKMI
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CDS 1114479..1114871

/locus_tag="EFAGFIKM_00962"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKVNTSEVAARGMKISDFQTKDVINITDGKRLGQISDLELDLKQ
GRIEAIVPGYSRFMGLFGGGTDLVIPWRNIVKIGSDVILVKMDEVKENTYDERDREA
RLYDEQQHNRTERVERIERSERNRRTI"

CDS 1114923..1115822

/locus_tag="EFAGFIKM_00963"
/EC_number="1.10.3.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q89ZI8"
/codon_start=1
/transl_table=11
/product="Polyphenol oxidase"
/db_xref="COG:COG1496"
/translation="MEPFVLDKELLERTKNPNSDFGPDPLLLYVEPWTQQFEQLSVGF
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VITAEDRSRGLLDRESALQDQDGLVTNVPGLVLLTSFYADCVPYFYDPVQQAAGLAHA
GWKGTVAGIAVSMVETMEREYGSRRQDIRAAIGPSIGDCCYEVDEAVMQYVRVWFDDSD
PVNDKYKDSASKQAYRAVNNGKTMNLKECNRHIMMKAGIMPDHIECTTWCTSCHPEL
FFSYRKENGVTGRMASWIGLEER"

CDS 1115829..1116530

/locus_tag="EFAGFIKM_00964"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P44506"

/codon_start=1

/transl_table=11

/product="Pyridoxal phosphate homeostasis protein"

/db_xref="COG:COG0325"

/translation="MSLEERIQQVNQKIEDACRRSNRHRDDVNVIAVTKYVSLETTGS
VLDHGLEHIGENRWQDAQAKWEAFGQQGTWHFIGHLQTNKVKDVIGKFRYIHSLDRLS
LAKELDKKAASLGTQVETFLQVNISGEESKYGLQPEQASSFLRDIRSFNNLKVVGLMT
MAPHEEDPELTRPVFRGLRELRLDQLNGQALTAEPLTELSMGMSNDFEVAIEEGATWVR
LGSILVGKEEGSRWA"

CDS 1116521..1116988

/gene="sepF"

/locus_tag="EFAGFIKM_00965"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31728"

/codon_start=1

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/product="Cell division protein SepF"

/db_xref="COG:COG1799"

/translation="MGVMNKF MNFLGLQEEEEIVERERMAAQEENESEHQAETSSLD
KRRNQRGNNVVSISQKNVKVVLYPEPSYDEAQEIADHLRSHRTVVVNLQRIRQDQAL
RVIDFLSGTVYALGGGISKIGGNIFLCTPDTVEIQGSITEILADSEQDYNRMR"

CDS 1116996..1117265

/locus_tag="EFAGFIKM_00966"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYQIESVLYTYQIYFYMVIVYILMSWLPNARESFIGEWLGKLV"

EPYLRPFRRFIPPLFGVLDISPIVALIVLQLALNGLISILRYFAY"

CDS 1117504..1118286

/locus_tag="EFAGFIKM_00967"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSGEIYEHFSHDERDFVDKASDWVEQAGKYHDMKLTDFLDPRQV

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LLPLDQMRWSESKLETMDITVASLRDLGICADVRLSRSKVLAPIKAGRCRVNWKVEE

DPSKSLKAGDVVSIQGFGRFKVMEQDGMTKKGRCRVKIGKFA"

CDS 1118527..1119036

/gene="divIVA"

/locus_tag="EFAGFIKM_00968"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P71021"

/codon_start=1

/transl_table=11

/product="Septum site-determining protein DivIVA"

/db_xref="COG:COG3599"

/translation="MPLTPLDIHNKEFSRRLRGYDEDEVNEFLDQVIKDYEGVIRENK

ELSNQLLSVQEKLDFHSTIEETLSKTIIIAQEAADDVKGNKKEAQLIVKEAEKNADR

IVNESLGKSRKIALEVEELKKQASIYRARFRTLVEAQLELLTQDGWEVLESREQEVRD

REREMKEIY"

CDS 1119720..1122824

/gene="mupB"

/locus_tag="EFAGFIKM_00969"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:BARRGD:NG_048009.1"

/codon_start=1

/transl_table=11

/product="mupirocin-resistant isoleucine--tRNA ligase

MupB"

/translation="MIMQRVDVKEKARARELRVLDKWKTENTFKRSIENREGKPNFVF

YEGPPTANGKPHIGHVLGRVIKDFVGRYNTMKGyRVVRKAGWDTHGLPVELGVQKKLG

ISHKWEIEDYGVEKFINECKASVFEYEQQWRDLTEGIGYWTDMDNPYITLDNNYIESV

WNILATIHEKGLLYRGHRVSPYCPSCQTTLSSHEVAQGYKDVKDLSATAKFKLNDSGE

FVLAWTTTPWTLPSHVALAVNPDMDYSRVRQGDEVYIMATNLVEKVMKDKTKGEYEIIG

ALKGADLVGKTYDPPFNyVQAEKANIILGAGFVTDASGTGIVHMAPAHGEDDYRVCRE

NGISFVNMVDLEGKFVAEVTDFAGRFVKDCDIDIVRYLSEHGRLFSKEKEYHSYPFCW

RCDTPLLYYAMDswFIQTtAIKDQLIANNSEVDWYPGHVREGRFGKFLEDLVdWNISR

DRYWGTPLNiWVCEETGEQFAPHSIAELRARAVGDVPENLELHKPYVDDVKVMSSCGK

YEMKRTPEVIDVWFDsgSMPFAQQHYPFENKEVFEQQYPADMICEGIDQTRGWfYSLL

AVSTLLTGKAPYKAVMATGHVLDENGQKMSKSKGNVIDPWEVIEEYGTDAFRWALLSD

SAPWNSKRFSKGIVGEAKSKMVDTLVNTHAFLTYATIDGFDPQEHpFQLSAHKLDRW

ILSRLNSLiLVVEKALLVNDYLNSSKAIEAFVDELSNWyIRRSRDRFWGSGLTEDKLD

AYRTLTEVLVTTAKLVAPFTPMLAEDIYLNLATGESVHMEDYPVANEALIDAGLEQDM

ETARRVVELARNVRNETGIKTRQPLSELIVSLDKGFDLASyEEIIEEINVKGIRTEH

NDAEFVDFTLKLNLKVAGKKYGKNVGFLQNFFKGMTADETRKVVSEGVLNIVSPEGEE

LQVTSEELLVDKQAKSGFASASGYGLTVALNTEITPALEQEGWVREVVRVAVQDTRKRL

DLPIEKRVRLTDVDASLQEAIQAFDDVLRENVLVTEVTFGSNESMERVEAGGKSIGI

YIEA"

CDS 1122990..1123349

/locus_tag="EFAGFIKM_00970"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSEHDKQTASTSQQSTSDNLNSHDKIEELHTLTNRLANELERSR

IAQYTELLNRPWKLiGLNLLSGAARGVGIAIGFTFFAATIIYVLQLLGALNLPIVG DY

IADIVRIVQRQLDMNTY"

CDS complement(1123391..1124128)

/gene="dksA_1"

/locus_tag="EFAGFIKM_00971"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00926"

/codon_start=1

/transl_table=11

/product="RNA polymerase-binding transcription factor

DksA"

/translation="MSHFTNEQLQSLRSQMSDKRDIEHRLSENEHYGLGDSLKLQTG

ELSPIDNHPGDLATEVYEREKDISLLEHDEFQLERIDSALHSIEEGHYGTCAVCQQPI

PYERMEAVPYTKYCKKHQPETVVSSENRPVEEEFLAPAFGRITSLDERDDQNGFDGEDTW

QIVESWGTSNSPAMAEGRDIDSYDVMAIEATDEVEGCVEAYESFVATDIYGHDSIVR

NRQYRQYLENREGEGLLEPDMETDDTY"

CDS 1124350..1124844

/gene="lspA_1"

/locus_tag="EFAGFIKM_00972"

/EC_number="3.4.23.36"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9HVM5"

/codon_start=1

/transl_table=11

/product="Lipoprotein signal peptidase"

/db_xref="COG:COG0597"

/translation="MVYYILAFIVFLLDQGTKYLIATRMELREEIPVIGNFFVITSHR

NSGAAFGILQDQRWFFIVVTLIVVVALIWYLQVKVDTPHKLLPVALLVGGAGNLF

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EHHE"

CDS 1124786..1125799

/gene="rluD_2"

/locus_tag="EFAGFIKM_00973"

/EC_number="5.4.99.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P33643"

/codon_start=1
/transl_table=11
/product="Ribosomal large subunit pseudouridine synthase
D"
/db_xref="COG:COG0564"
/translation="MKDGAKKQPRRLKGMNIMSNPNKEQINDEELMNGNERMEWTVAA
EHKKERIDKYITEAVDNVSRSQVQLWIGDGMVTVNGAVVKANAKLSEGDLEVELQIPEP
AAVEIVAEDIPLEVVYEDSDLIVINKQRGLVVHPAPGHTSGTLVNALMHHCKDLSGIN
GELRPGIVHRIDKDTSGLIMAAKNDRAHASLAAQLKDHTVNRRYIALVHGHLNHDQGT
VDAPIGRDTNDRKMYTVTERNSKHAVTHFTVSRINDYTLLDLKLETGRTHQIRVHMK
FIGHPLVGDPYGRNKGIKMQGQALHAAILGFVHPTTGEYLEFSTPIPQDMEDVLASL
RSR"

CDS 1125910..1127163

/gene="dapL_3"
/locus_tag="EFAGFIKM_00974"
/EC_number="2.6.1.83"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A0LEA5"
/codon_start=1
/transl_table=11
/product="LL-diaminopimelate aminotransferase"
/db_xref="COG:COG0436"
/translation="MSIDKYQETYIQTNFADRIGGSNYGKDTNIYKFEEKIRAKASAK
KDFPDVELIDLGVGEPDEMADAGIVAALAEASRPENRGYADNGIPEFKAAAASYLKN
VFNVEGINADTEIVHSIGSKPALAMMPSCFINPGDVTIMTVPGYPVMGTHTKYLGGEV
FNIQLTKENNFLPDLTAPIEDIAKRAKLLYLNYPNNPTGASATVEFFTEVVEWAKKYN
VVVVHDAPYAALTYDGKKPFSFLSVPGAKDVGVELHSLSKSYNMTGWRIGFVAGNPLV
VKAFSDVKDNDSGQFIAIQKAAAYGLNHPEITEKIAEKYSRRHDMMLVAALNELGFQA
EKPKGSFFLYVEAPKGVVGRRFESGEDFSQFLIREKLISSVPWDDAGNFVRFSVTFE
AKGEEEEKRVIAEIKRRLSDVQFEF"

CDS 1127343..1128257

/locus_tag="EFAGFIKM_00975"

/EC_number="2.4.2.45"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WFR5"

/codon_start=1

/transl_table=11

/product="Decaprenyl-phosphate phosphoribosyltransferase"

/db_xref="COG:COG0382"

/translation="MLSSRTSTVSSPATGTGSTVSGLIRLLRPKQWTKNLLFAALLF
SFEEIRTETILATLLGFILFSLVAGCVYILNDFVDRDRDRQHPVKKYRPMASGQVNPS
HALMFGIILLIFSVGTAFMMNPLFGVLCIVYFLLNVSYFVLKHLVILDMMTIAAGFV
LRAIAGGVLIHVPFTPWFLECTMLLSLFLAIGKRRNELTLLEGNTGSHRKVLDNYSIT
LLDQFNTIVTTATIISYSLFTFTSDRTIHLMWTIPLVIYGMFRYLYLIHMKNQGGSPD
RVLFEDKPILITVMLYVISVITIFAIFE"

CDS 1128276..1128908

/locus_tag="EFAGFIKM_00976"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKSTKVAIFDIDKTIIRSDSMFQFVHYGVRRYPWQVWRLPVIAL
HTVLFKAGFMTVEQVKRSYFQEIERMSEKDLEHFFDTRLRTSIFAEASVEMQHRKEAG
YHVLLVTASPHAYMKYFNNFPWVDHVIGTELVRHENGYTCDVDGSNCKGEEKVRRRIQA
YLSKKNMVIDYDQSCSYSDSLSDLPVMQLVVSQRYFINKRVPDMEALTWGK"

CDS 1128896..1129225

/locus_tag="EFAGFIKM_00977"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGEIKSRHTGKWMLVSAFLTATGQLFWKWGLTEWIYLGVGVC
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TLTSVDR"

CDS 1129230..1129532

/gene="arnE"

/locus_tag="EFAGFIKM_00978"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01869"

/codon_start=1

/transl_table=11

/product="4-amino-4-deoxy-L-arabinose-phosphoundecaprenol

flippase subunit ArnE"

/translation="MVAVLIVMTLCGALGGAGLKAYASSRNRLHVLMLGFYGTGALL

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CDS 1129564..1130868

/locus_tag="EFAGFIKM_00979"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNFLDYLFYNRRGNWTAFYLFAGFALFYGLMNGSYVLYIENNAE

MLGAYSPFNTTLFPINLFNFDPSMYYGDNSSSVIHPLISFLAVTLAAVAKLLGGNWFF

LILQSLVNAGSVVLAYLFLSQKEDKPTIIPLLFALLFGFSSYLMYTALIPDSYPYVQF

VILLSVVYMQYTRERQDVRYPNALLASINFGLTSTNIVPFAAATFFNMHAWRNKANL

KKYIGIMALAVLIIVLTGIQYVAFGGRSWISNWLLGIQNGGTSYATPFQFAVHWKAL

NMLTINPMLTPKMHLDPGMAAFVTDLSRSNPYVQMTGIFILLAFMGFIKIRERE

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CDS complement(1130960..1133635)

/locus_tag="EFAGFIKM_00980"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRHIWHVYKTDWLHILKVPTGVFLIVAIILLPGVYDWVNVKSVW

DPYSNTQGIKIAVTSEDAGATVEGTHVNIGDELVSSLKHNEKLGWTFVDQAEANRGVQ
TGEYYASLLIPGDFSSKITGIVDGKLERPEVIYTVNEKVNAIAPKITGSGVSAITTQI
NENFTEAVSEAVLTKLNEAGVEINAQLPTLRKMENGIFTLEKNLPAIQAAGQKVLEVE
KAMPEIVKDAQKIVEIEKKLPEINKAAQYVLKVQEYWPQINDAASEVLTIQGRIPDIQ
KAVERIREVDENFGQVSGVIQTALDKTNKALSIVTAAEQDLDKVSQIAGNGIELAEGL
NQFVDSSEEFQTIGPTIRQNLLLVQQITNAAGDVFAQLQNSDLNNLPTVEDLDRIAS
RLGIAVKLVDSMAELLGNINLLPDQPLADKITQLNSISDNLQLQIRLAGIISDAMRR
NTTPPTDVIAQLNTLSKDISSGIGNILNTYESEISPALAAGADKLRSILSTSAETLQG
AKDRIPDIADILASAKEGITFGQTELMKIQSELPQIQSKIHEISETLTNKSEGFQAL
DTVSSLIRNDLPKLGKNLNEAANFVRNDLPNAEKQIGKASDFVQNQLPEVEKGVHRVA
TLVRDDLPALESAISKAADKLREVEGNNQFAELAKLLRGDIEEESAFLSSPVQIKEQQ
LYPIPNYGSAMSPFYGVLSLWVGSTLLISLLRAEAENPGGKFRGYELYLGRLATFTI
GLLQAICVTLGDILILGTYVADKLWFLVLFAMLVSAVFVTITYTLLSVFGNIGKIAII
FMVFQFSSSGGTFPISMTSPFFQALNPFMPFTYAISSLRESVGGILWSTAIDILWLC
MFIALSLIVALALKRPLSSLTKRSAENAKKTKIIA"

CDS 1134344..1134907

/gene="pyrR"

/locus_tag="EFAGFIKM_00981"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P41007"

/codon_start=1

/transl_table=11

/product="Bifunctional protein PyrR"

/translation="MSTETHVIMDETAIRRALTRIAHEILEKNKGIDDCVLVGIRTRG

VYLAERIAAKIEEIEGAKVPWGELDVTPYRDDRLDENKANRKEMLIMTPESLSIHNNK

VILFDDVLYTGRTIRAAMDALMDCGRPQNIQLAVLADRGHRELPIRPDFIGKNVPTSK

SEEIEVALMETDGQDEVKITQNRGEQA"

CDS 1134907..1135818

/gene="pyrB"

/locus_tag="EFAGFIKM_00982"

/EC_number="2.1.3.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P05654"

/codon_start=1

/transl_table=11

/product="Aspartate carbamoyltransferase"

/db_xref="COG:COG0540"

/translation="MITQTALRDRSLLGLKELSRGEIESILNRAAHWEAQKEKLPVL

ESRFVANMFFENSTRTRFSFEMAERLGVQVLNFTAAASSVEKGESYDVTVRTLESMG

IDAGVIRLKPAGVLQQLAQKVVNPLVNAGDGNNEHPTQALLDLYTMRKAFGELKGLRV

SIIGDILHSRVARSNLWALQKFGADVRFCAQTMQAPELAEYAPYVGLLEALDADVVM

MLRVQLERHQHGLITSAEDYREHYGLTEERASRLKPSTIIMHPAPVNRNVEVDDAVVE

SEASRIFPQMANGVPIRMAVMERAMKL"

CDS 1135945..1137249

/gene="pyrC"

/locus_tag="EFAGFIKM_00983"

/EC_number="3.5.2.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81WF0"

/codon_start=1

/transl_table=11

/product="Dihydroorotase"

/db_xref="COG:COG0044"

/translation="MLQIIKNANVLNQQGELERKTIIDEGKIKKIAGLEDQAVLDAE

KSAQSVTDASGKLVIPGLIDMHVHLREPGFEHKETIETGARSAAQGGFTTIACMPNTR

PVTDTAEVVKLVLDKAKEADLVKVLPYAAITKNELGRELTDFALKEAGAIGFTDDGV

GVQNAQMMKDAMNLAASMDMPVIAHCEDDSLTVGGYVTEGEFSKRHGIGIPNESEAI

HVGRDILLAEATGVHYHVCHVSTEQSVRLIRLAKSIGIKVTAEVCPHHLVLSDEDIPG

MDANWKMNPPLRSPRDVQACIEGLLDGTLDMIVTDHAPHSEEEKAKGMELAPFGIVGF

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CDS 1137678..1138820

/gene="carA"

/locus_tag="EFAGFIKM_00984"

/EC_number="6.3.5.5"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P99147"
/codon_start=1
/transl_table=11
/product="Carbamoyl-phosphate synthase small chain"
/translation="MQAQARLLLEDGTLFTGKAFGAEGETTGEVVFNTGITGYQEVLS
DPSYCGQIVTMTYPLIGNYGITRDDFESIRPYVHGFVRRHEPTPSNWRAEYSVDNLL
KEYGIVGISEIDTRMLTRRIRHHGTMKGILTTGSKPVEELLEMMGDTTIAELRNQVPM
TSTEHVYNSPGTAERIVLVDYGAKTGILRELSKRNCVWWPHDVTADIRRLNPDGI
QLSNGPGDPKDVPHAVNMISELLGEYPIFGICLGHQLFALAAGADTEKLKFGHRGGNH
PVKELESGRCFITSQNHGFTVNEESVKSTDLEVTHINNNDKTIEGLKHKSFPAFSVQY
HPEAAPGPYDNSYLFDRFIEMIREHKITNPQKPRQAVLAAAVKGAQ"

CDS 1138822..1142040

/gene="carB"
/locus_tag="EFAGFIKM_00985"
/EC_number="6.3.5.5"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P63740"
/codon_start=1
/transl_table=11
/product="Carbamoyl-phosphate synthase large chain"
/translation="MPINKDLKKILVIGSGPIVIGQAAEFDYAGTQACQALKEEGVEV
VLINSPATIMTDTNMADKVYIEPITLDFVTQIIRQERPDGLLPTLGGQTGLNMAVEL
ARAGVLERENVKLLGTQLTSIEKAEDRDLFRDLMRELEQVPVSVIVTTLEESLEFAN
EIGYPIIVRPAYTLGGTGGGICANEEELRETVAAGIRYSPIGQCLVEKSIAGMKEVEY
EVMRDKNDNCIVVCNMENFDPVGIHTGDSIVVAPSQTLSDREYQMLRSASLKIIRALN
IEGGCNVQFALDPHSFQYYVIEVNPRVSRSSALASKATGYPIAKMAAKIAMGYTLDEI
VNPVTGQTYACFEPTLDYIVSKIPRWPFDKFISANRKLGTQMKATGEVMAIGRTFEES
IHKAVRSLEIGVHRLYLKDAETLDEATLNERLIKADDERIFLIAEAFRRGYTLQQLQD
LTKIDWWFLDKIEGLIAFEDRIRREESELSSDILYQAKRLGFTDRAIAELRAQGQPGGT
LTTEAEVTRRREAENLRPVYKMVDTCAAEFEATTPYYYSTYETENEVIPSDKKKVVVL

GSGPIRIGQGIEFDYSTVHAWWALQKAGYEAVIINNPNPETVSTDFNTSDRLYFEPLFF
EDVMNVIEQEKPVGIVQFGGQTAINLAAPLRNAGVTILGTDLESIDEADRKKFERL
LSRLEIAQPKGKTVISVDDAVETAQSLGYVPLVRPSYVLGGRAMEIVYSDAELLTYME
QAVKINPEHPVLIDRYMMGKEVEVDAICDGETVLIPGIMEHIERAGVHSGDSIAVYPP
QHLSQDLKEKIVEITIKIAKELKTVGLVNIQFVIHDGQVYIIEVNPRSSRTVPFLSKV
TNIPMANLATQAILGVKLKDLGYVDGLWPESDHVSVKVPVFSFAKLRRVEPTLGPEMK
STGEVMGRDPNYAKALFKGLIGAGMKIPATGAIVTVADKDKDEAVPLLEGFYRLGYK
IMATGGTAAALEANIPVTTVNKLSEGGSPNILD MIRSGEANFVFNTLTGKGPQRDGF
RIRREAVENGIVCMSTLDTIRALLIMLQTINFSSEAMPVSVK"

CDS 1142143..1142883

/gene="pyrF"

/locus_tag="EFAGFIKM_00986"

/EC_number="4.1.1.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0CB75"

/codon_start=1

/transl_table=11

/product="Orotidine 5'-phosphate decarboxylase"

/db_xref="COG:COG0284"

/translation="MNHTNFMEMASRLMVALDYPGAEEAQELVQALEGIPCYLKVGMMQ
LFYAAGPDFIRELKTKGYSVFLDVKMHDIPNTVRGGAESITRLGVDMFNVHAAGGALM
MRAAREGAEEAIAADPSLSKPEIIAVTQLTSTSLETMNNEIGIPGSVEAAVVHYAGLA
QEAGLDGVVASPLEVPAIRAACGSAFHTVTPGIRPAGSGLGDQTRVLTPEAIARGSH
YIVVGRPITGAPNPRAVETILKEMLNA"

CDS 1142880..1143521

/gene="pyrE"

/locus_tag="EFAGFIKM_00987"

/EC_number="2.4.2.10"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81WF6"

/codon_start=1

/transl_table=11

/product="Orotate phosphoribosyltransferase"
/db_xref="COG:COG0461"
/translation="MIELNEIPNHASQLLKIKAVLRPQQPFTWTSGIKSPIYCDNR
LTMSYPEIRNDIAEAFATIIRNQYPDAEVIAGTATAGIPHAAWVAQKLNLP MAYIRDK
AKGHGKENLIEGLITEGQKV VVIEDLISTGGSSIKAAEAVRVAGATPLAVLAIFSYQL
DKGVKAFEDAGIPLQTL SNY TALMDVALAQGTIQESDFELLKSWREDPSSFGK"

CDS 1143800..1144741

/gene="btuD_4"
/locus_tag="EFAGFIKM_00988"
/EC_number="7.6.2.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01005"
/codon_start=1
/transl_table=11
/product="Vitamin B12 import ATP-binding protein BtuD"
/translation="MIAGMKNLFLRKRPASQSGDEHQGETPLEASTESGENTYNNE
HDYLTSPPLPESEIASDEVAATAVTTVDEPQKKIKPKK DMLPPYDGPVLEVRNVHRS
FQTGSRIIHVLKGIDMEVNPQQLVMLKGRSGSGKTTLLNMLGGLDQPSSGDILFSGQP
LQDWGDRRRTALRRKEIGFIFQAYALMPLLSAWENVELSLRMADVPRAEWKDRVGHCL
DLVGLSKRVKHRPFEMSGGEQQRVAIAKAIHRPRLLLADEPTAELDSKMGAQVMAVF
RNII EVEQVTICMTTHDPTILEVADH VYEMADGRFIK"

CDS 1144704..1145813

/gene="macA"
/locus_tag="EFAGFIKM_00989"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P75830"
/codon_start=1
/transl_table=11
/product="Macrolide export protein MacA"
/db_xref="COG:COG0845"
/translation="MFMKWRTADLSSKGAAPKR GKRAALIVLGAIMVATMSGCSLLPS
ETEE EVLPITPTISKKPEYEVRTETLEKKVSGSGKMMSQREEKVYFTLDGMHV KEL

NVKPGDKVKKGQLLAVLDVESVEKEIRGKKLAIRKSEVQMKETLRKKDEMDPVEFEEA
TIAFEELRQELADLEEQLGKATLTAPFGGTVIQVEKGAAYKAYDPIATIADTSNLV
VAATFAKEDLEKFSAGMKAEVDINGAGKVAGKIKVMPIAEASGSGSGEGAGEGGTPPT
KETLDKYVIVTLAKMPKGVVERGTPLSVSIVTQRTENAIVIPVSALRSIGSRTYVQVVE
SDGSKREVDVEVGQQTSTDVEILKGLTVGEKVGR"

CDS 1145813..1148734

/locus_tag="EFAGFIKM_00990"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGLPLLRLFRKMWNTRWMTFSTLIGLIVAVAFTVSIPMYADGA

LKRVAQTLQDNSEGLPAGSLLMSYQAPGGVKTDTRGLDEVDRYIREDVPRDIGFPFH

TYVNSRSIRSTEVSPEPTKVDASRARSMSLGTMSGLDAQVNYSAGVKPGNQVKDDTI

EAVMLEEGMYRNDLHIGDILEYPVYSGLDITLRVKITGSFKADDPNSPYWVQGFDGMM

NGLYVDESVDVLLKEKGIPLQNSRWYAFDLKEIQTSQLSGLTSMLERLDIDLYQR

LKDTKVDITFGDLLKQFRSLSLQTLFTLAAPMIAMVFYFIAMNARQSLQKQESDI

AVLRSRGASARQIFSLYLLEGIVLGAIALVIGPLLGWFMASIGSASGFLSFVDRKSI

PIGVSKEAILLGVA AVLVAIIASLIPAITYARATIVSAKRRQARTDRAPVWQRWFLDV

VLLGLAGYGYLFYERQMLTFQTGMTTDQLQVQPFVFPALAI FALGLFFLRFLPWI

LKLIQLIGRKFLPVPLYLTLTQLSRSSSSYYPLMILLVLTGLGVYNSAAARTIDLNS

TERTLYRYGSDVIMQTVWEGTPEVKPGGSGQNGGTGGGQGGGNGGGGSAGGGSGGGN

GGGGAPGGGGSSQPSKVIYSEPPFEVFRRLDGEHAARVLQTKGNIIVSGKSGGQGM

LVGIDNVDFQAQVAWFRNDLFPAPHPYKLDLLGKYEGAVLISSKFADKFKLKTGDLVSM

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CDS 1148737..1149600

/gene="btuD_5"

/locus_tag="EFAGFIKM_00991"

/EC_number="7.6.2.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01005"

/codon_start=1

/transl_table=11

/product="Vitamin B12 import ATP-binding protein BtuD"

/translation="MIQCEGLVKIFKSSDVEVVALQGLNLTVNQGEMMAIIGNSGSGK
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LENVETPMILGGKRDRAYAKQLLEWVGLKDRMHNKLHQLSGGEQQRVAIAISLSNRPK
ILLADEPTGSVDSETCDTIMGIFRRMNKELGVTIVIVTHDLTLAGKVDRIVAIRDGLT
STEFVKRNPNLDDDEHNLSEAGMPDIHEAFVIIDRAGRLQVPKEYLEALSIDNRATLEF
DGERIVITPPR"

CDS 1149621..1151072

/locus_tag="EFAGFIKM_00992"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKNSMWGKRVLAVIATATLALPLIAGCTASEAKDTEQRVLRVAT
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KIMTGDNPVDVIVADTATVKSLIQENLVKQLDPLMQEDKFDTSDIVPSVLEGIKDLGD
QSIYALTPTFSSSALFYNKGMFEKAGVEPPTDNMTWDDIFNLGTRLTKGEGKDHVFGF
SFTTYQGGSPYYSMQYYSSLQLKTFDDKAEKMTVDSPQWEKVVSTISKLAIDKVIPK
GDEPQDQNPNGRYDPVQGDLFLSGKSAMVIGDYSYINQLIDANKNADKMKDFTKVDWD
VTPPVHPEAPEIGGSIYLSNLMAINSAAQNPDDAWELIKYMNSDWAKIKARSSYEM
VSRKSFIPKDGLDYNIQAFYALKPIPTNTNLDKMYQKSPGLWQVNEKGMIFYNQVL
ENKKTPEALGEWAAKGNEMLEKLKDPKATFQ"

CDS 1151179..1151370

/locus_tag="EFAGFIKM_00993"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTTPERTSGMHWVYFSKLYATKFQAGCLAKRMEQDGWIYGHNEP

AEVEVYRSRKGRYGVRFIP"

tRNA 1151442..1151515

/locus_tag="EFAGFIKM_00994"

/product="tRNA-Met"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Met(cat)"

tRNA 1151572..1151645

/locus_tag="EFAGFIKM_00995"

/product="tRNA-Met"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Met(cat)"

CDS 1151825..1152250

/locus_tag="EFAGFIKM_00996"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSQFIDARTSQNASLANIAIPILVINTPQLFGQIGLVTGGSIG

ANPRVQFKGTVSVQLPLALAGITITIVRGTLATDPVIYSVTSTFSLSVLAPQIITFSA

DDFNPPITPQLTYTAFVSSNLLGTIRVGPENFDGVLYSD"

CDS 1152488..1154044

/locus_tag="EFAGFIKM_00997"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTSNESQRFYSEAPVWDWQRAYYEKGLQAWTENQVPQYITSN

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LPPFRYVMTDLVAENVLGWQEHPMQSFIQQGIVDFARFDAVADTELNLVVAGTVIRP

GDLKQPLLLIANYYFFDSIPQELIYIGDGEIYECDLLVQSPDRRLDLEPAEMLKNMTLS

YEYRRAPEYSAGNYPYQELITLYKEELED SHILFPAIGLSCLERLNKLSQSGYVLITA
DKGDHRLDNWKFAEPPEFVLHGSFSLTANYHAIQYVLEQQGAHTRFTTHHYKDLNVGC
MLMVDEPISYVNTRLAYHRFVERFGPDDFFSMKQWVDSRIESMELKHILPFWRLLGGYD
AEFLIHSATHISSLLPDASDEEMLDIQSGIHTMWSSYYVMEQQGGLAFLAGQLLYEMY
MYEDAKRFLEISLVADPSNHNSAVLYDLAVCCYELELEEETLSYTHKVLALEPDHEEA
AALLQSFELI"

CDS 1154183..1154350

/locus_tag="EFAGFIKM_00998"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKMLSIALYPLAWVLGALSILSGNENSVLLVKDIATDRSYDGQ

AIYDSIERRNA"

CDS 1154527..1155225

/locus_tag="EFAGFIKM_00999"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKIIIGQPRLEQHLLQLEAELKQHPDADVFFPEGYLNQNVEDA

CRLAAEYGTMIIVSGHRRLLHERPKDRSIIISTAGEIVLEKAKYTPAETVEEQEWAISTL

LCDELVLQGFRNENIGNVDIVMHSIGVGMFSEEQYSEWVEEARQIALKHQCIVMGTSH

ADGSYRDSEISIPIAYCITADGEVVLASRSDTRTRTILLDRGNTDPSPQESQEKQLKI

SITHPVKLPGMNPR"

CDS 1155317..1155439

/locus_tag="EFAGFIKM_01000"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSQVGYGCGNVGGFGGGWTSTSAIIVLFILLVIITKSFWL"

CDS 1155600..1155929

/locus_tag="EFAGFIKM_01001"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPFIRFKGFTGPQLEEVVPQITEQMALITHIPRERMKAERHDVQ
ALTPSPASIEILMFQRDQEIHNRIASSVQAILEEAYMPDVIHFFNILSPTLYYKKGRP
LTDYRLD"

CDS complement(1155971..1157194)

/locus_tag="EFAGFIKM_01002"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNIAFYYPYWAAKTLLSLINVIYIMVITTFIYGLTGSVLSAAIFP
LIQIVARIAGFTLPLLVRNRPFSRLLISISIAKTLMTCIAISLNHLISQLPLLLIG
VVILSFLDGWETPLLKTLTPRLVQGEDLIKANSLLSFSNQTVTIVGYAMTGFAVMNWW
ASQTFWAATSLSWAVLIFMIAMGSLTRDVEQPQKSAVSWNVLSEGWSILWNNRSLRLI
TLMEDIAQALAGSIWIGAVTLAFAKEALGRGEGWWGLMNSSYAAGTMLGGILALALAKR
IQKHLIASMTIGSLLFSLTIVVYGLNNLPWLALVLCILMGPVHQIRDVAQQTALQNSV
PVESLTKVYATHGVLIVMSVSIVIFGLVADQLGVRWVYLIAGALFILSAICSLSL
RVHRNQPIAKHTKNM"

CDS complement(1157335..1157523)

/locus_tag="EFAGFIKM_01003"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRTLFFIFMVLCIINLCFPKFGWYLYRYGWISRGAEPSRPYMTM
VRTTSLMLLIAFTLAMA"

CDS 1157837..1158985

/gene="rcsC_2"
/locus_tag="EFAGFIKM_01004"
/EC_number="2.7.13.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00979"
/codon_start=1
/transl_table=11
/product="Sensor histidine kinase RcsC"
/translation="MSQHNQLSLQWEFIISKVKSSVTVV DATLPELPLMYVNEHFTQL
TGYTYEESVGHNC RFLQGQDTPETVMQIRDALKKQQSIKIDILNYTKSGQKFWNELN
IDPIFNESGECLYFVG IQYDISERKYAEQQLKFATSMAEMNSRGQLEFIGKLNHELRT
PLNGIMGMIELASMGETTDEQKEYLELARQSGEALLNIINNSLDMAKLGRGKMDVENI
EFQPLKLIQQIVKTHEPAARNKQIRLLCHADLNVPDVLIGDPLRLRQVLDNLLSNAIK
FTEQGEVQLQVDVRQQ LMDTVVLVFSVRDTGIGIPQHQIEQLFDAFTQTDISHARRFG
GSGLGLTICKELLELMNGQISVESTEGKGTQFEVTLPLLRQQAIPNVG"

CDS 1159095..1159577

/gene="nucB"
/locus_tag="EFAGFIKM_01005"
/EC_number="3.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42983"
/codon_start=1
/transl_table=11
/product="Sporulation-specific extracellular nuclease"
/translation="MSKRRTSRKRGKQGFKKQVLT LVAMLLVALYAWAGGEWP EEIP
NPFVGTNKSVDHTITFPSERYPETAKHIKAAIKAGHSDVCTIDRNGAEGNRDLSLKG V
PVKKGKDRDEWPMAMCAEGGTGADIQYITPKDNRGAGSWVGNQLSTYPDGTRVKFVVK
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CDS complement(1159772..1159996)

/locus_tag="EFAGFIKM_01006"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MKKEVEIAIRRKQQIMVRNTSGQTVTGFPERTADTSILSLRTVH
GSLWIPFDEVEHVTRLLSIRSHHLSGMQLV"

CDS 1160204..1160653

/locus_tag="EFAGFIKM_01007"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTQLIIGLARTENEAILMLNQVKEEGIKDKYLGAVAKEQLNLEL
VSEKTGLPKPLKGAGTDGAFGALKGILAGLGKRMQTMSIGNAVRRLAGNEIGSETDD
LVLTLTEAGISEEDARYYEDWLLKDHILVIVECSEEEAARVRPILLF"

tRNA 1160889..1160977

/locus_tag="EFAGFIKM_01008"
/product="tRNA-Leu"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Leu(taa)"

CDS 1161348..1164269

/locus_tag="EFAGFIKM_01009"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLKQLKPYKVLQERRIEELKSDAYLLEHQKSGAKIVLLSNQDDN
KVFSIGFRTPPEDNTGVAHILEHSVLCGSKKFPKDSFVELLKGSLNTFLNAMTYPDK
TIYPIASRNDHDFHNLMDIYLDVLTNTNIYENKIFLQEGWNYNLTSADDELTYNQGVV
YNEMKGAFSSPERMVRREVLNSLFPDTTYSSES GGFPEAILDLTYQGLLDFHTRYYP
SNSYIYLYGDMDMEEKLQWLDENYLSAYDRIEIDSAIQLQPAFAERVDTVKTYSAGST
ESEVDNSFLTYNVIGTSLDKELNISFQILLYALLNAPGAVLKQALLDKGIAKDVYGS
YDDSLYQPVFTVGLKKS NLASKEDFLGTVKEVLERVVKEGFDPKALLAGINSYEFNHR
EADYGRMPKGLIYG FSSLQSWLYDEEAPFTHLEANDVFAELRTKMNEGYFEQLIEKYI

LQNTHTSFVALTPDKGLNSRKEEALKERLKTIQAGLSEEEVQTLIQKTEALAEYQNTP
STKEQQQVIPTLSIEDIEPKASTLHQTVNQVDGTTILHHNLYTNGIGYLRLLDIKEV
PRHLLPYAGLLKNVLGYVDTQNYSFNELSNEIHHSGGIQSGIGSYANAHKHNEFKAT
YEFNAKVLYDKLGFAFDMIKEIVFTSQFDNSKRLYEIISQMKGNLQRNLINSGHSAGI
GRSSSKHSAVADFREAVSGIAFYQWLEDLQANFEARKEELSSSLQELTGIFRPENLL
VSYTADEQGYEGLEQQVSDLKAKLFTHEVAKEEFTFTPATHEGFRSPSEVQYVVQTG
NYIDKGYQYTGSLRVLQGILSLDYLTNIRAKGGAYGCMSGFRRNGDSYVASYRDPNL
DKTYKVYEEIPQYLNDFRADEREMTRYIIGAIQDLDTPTPYGEGAFSLECYLSNVTE
ADLQQERDEVLTSTKESDIIGFAELLSTVLKQQQRCVIGNENKIEEQKQMFDETLDLIK
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CDS complement(1164415..1165122)

/locus_tag="EFAGFIKM_01010"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNNINQEVGKKIRNFRKWRGLTIQQLADQIFKSKGTLSKYESGD

ITLDLVTLHHIANALNIQVEQLLYQEPRHASPLMNAVPSSFFKNSTRFYSYFYDGRNN

SLIRCVIDMMAQSDANRYRTVMYMNVKDFENYQECENMYWGHTEHYDTLTTLILKNQA

TPLENLYINILASFQESEKKWGLMAGVSFRPFMPIALKMLFSRTPLPENQELYNELKI

SKEDLRTLKIYNMLAVT"

CDS 1165374..1166594

/gene="patB_1"

/locus_tag="EFAGFIKM_01011"

/EC_number="4.4.1.13"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q08432"

/codon_start=1

/transl_table=11

/product="Cystathionine beta-lyase PatB"

/db_xref="COG:COG1168"

/translation="MKYNFDEIIDRTGTNAMNTDGRQYIFNATEDMTFPFKDEEFIR

MWIADMEFATPPEILDAVKERLDRRIMGYSQVFDPAYYEAVSNWMKRYDWSFPKEQL
ETSNGIIPALYELVEYICQSDEKVLIVTPSYGFFKSAAEHNNLELVCSDMLNEQGRYS
IDFEDFEAKAKDEKVRVCIFCNPHNPSGRVWTEELQRVGEICLRNNVWIISDEIHCD
LLRTGKRHTPLAKLFPDTRITCMSPSKTFNMAGLMFSNVIIPNKALRDIWQARHYS
FKNPLSIAATQAAYETGDEWLKQLKAYLDANFACVEQYVKQHLPLAVFHIPEATYLAW
IDISAYAPQHVSLLPFFAEQAGVLLEDGHMFVANGEGCIRLNLACPRSVLQEGLRIS
SVLVKEVEEVPVQV"

CDS 1166837..1167505

/gene="ung"

/locus_tag="EFAGFIKM_01012"

/EC_number="3.2.2.27"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39615"

/codon_start=1

/transl_table=11

/product="Uracil-DNA glycosylase"

/db_xref="COG:COG0692"

/translation="MFGNDWDKVLQEETEAHEYFNKIRYTLAAEYKTQTVFPPKEDLFS

ALKLTPYHQVKAVIIGQDPYHGAGQAHGLSFSVRPGVRVPPSLKNIYKELHADLDLPI

PNHGSLVHWAQQGVLLNNAVLTVREGQPNSHQGLGWQTFTDAVIRALNERSEPMVYML

WGSHAQKKGAFINRDKHLVLESTHPSPLAAHRGFLGSRPFSKANDFLTSGIEPIDWK

IPEN"

CDS 1167525..1167944

/locus_tag="EFAGFIKM_01013"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRHWIGRKVAVYRATGIREPLKGTLEWDEEAECVRIGPKRIKV

SFDNIAMIRPLPEESLPLKKARSEVHKVGVMKKAIQFENAIYFKSQVMIWRRAKIVA

LSTILRHDEDQVELADGRVLRKDKHMFVRSRRGIR"

CDS 1168366..1168950

/gene="yvdD"
/locus_tag="EFAGFIKM_01014"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O06986"
/codon_start=1
/transl_table=11
/product="LOG family protein YvdD"
/db_xref="COG:COG1611"
/translation="MKRIAVFAGSNPGNHPDYTEKAIQLGKQIADSGYALVYGGSCMG
LMGAVADAALQGGGEVIGVMPTGLFRGEVVHGGLTQLIEVGTMHHERKATMAELSDGFI
ALPGGMGTFEELFEVLCWAQIGIHRKPVGLLNVNGYYGPLMKMVEHSVQEGFSNTSHL
SLWSLEADPAELIKQMSSYIPAELTQKWSQLNGE"

CDS 1169071..1169199

/locus_tag="EFAGFIKM_01015"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSELKGTGYGYGGGFSGGAWTSTGAILVLFILLVIISRTFIL"

CDS complement(1169418..1169684)

/locus_tag="EFAGFIKM_01016"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNPSKKKSIPTRPHTSQLQSASRLSTSSVHIKNKSGKTANQRS
LNSSPNTLDQLAIVAAILSLIAAAIGLYIAWKSLSPDQTAVVV"

CDS 1169916..1170653

/gene="glpQ_1"
/locus_tag="EFAGFIKM_01017"
/EC_number="3.1.4.46"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37965"

/codon_start=1

/transl_table=11

/product="Glycerophosphodiester phosphodiesterase"

/db_xref="COG:COG0584"

/translation="MRNMEIIAHRGASAVCPENTMSAFERSLELGATGIETDVQMTSD

GRLVLIHDETLSTRTGGAEGWVKDATYDQLRTRDAGSWFHADFTGERIPSLEELFKLVQ

GKGTLLNLELKNGIVSYKGMEEKVIQAIIRDWNLEQQVVLSSFNHASLVRCKRLAPEIR

TALLYMEKLYRPDYAAKLEATGLHPYKLAVTQEDVAAALAHGVVTYPFTVNDPAEMQ

AMIDMGVQGIITDVPDVLASLLTVHAR"

CDS 1170926..1171981

/gene="feuB_1"

/locus_tag="EFAGFIKM_01018"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40410"

/codon_start=1

/transl_table=11

/product="Iron-uptake system permease protein FeuB"

/db_xref="COG:COG0609"

/translation="MSSQASPEKHNPDSPTAKIHTRPWAATLILTGGVLLLALGMALS

ISFGAADIKLSVWWKAIFDFNPELTPHQIWEIRLPRILGGAMVGACFAVAGAIMQGM

TRNPLADSGLLGLNAGAGFALAVCFAPFPGLPFMYIIMYSFLGAGLGVLLVYGFGAAS

KSGLTPLRLVLAGAAVSAMLSSALSEGIALYFRIGQDLAFWTAGGVAGTKWSQLEVMFP

WVLAALIAGLLISRSITLLSLGEDIAVGLGQRTGLIKLIGLIVVLILAGTAVSVVGAV

GFVGLIIPHLTRKLVGVDIRWIIPCSAVMGSLLLVFADLAARMINPPYETPIGALVAL

IGVPFFLYLARKERRTL"

CDS 1171984..1173015

/gene="feuC_1"

/locus_tag="EFAGFIKM_01019"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40411"

/codon_start=1

/transl_table=11
/product="Iron-uptake system permease protein FeuC"
/db_xref="COG:COG0609"
/translation="MESSTIVGAERKKRTKSTIVLIVLALLIITAFVSMNTGFTKLS
PLEVLRTLFGGGTAKQELILFEFRLPRIVISVLVGAGLALSGCILQGVSRNALADPGI
LGINAGAGLVVMLFVSFFPTTTAAPVFLLPILALIGSGFAAFLIYILSYKKGEGILPT
RMLLTGIGVAAGISSAMIVLTLRLSPEKYQFVATWMAGSIWGSNWKFVTALLPFLIIL
VPLVLYKARVLNVNLNGDQTASGLGTPVERERLILLAAVGLAGSCVSVSGGIGFVGL
IGPHLARRLVGPKHQFLLPASALIGSLLVLVADTLGRVILQPSEIPAGILVAIIGAPY
FLYLLSKTK"

CDS 1173060..1174775

/locus_tag="EFAGFIKM_01020"
/EC_number="3.6.3.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q99T13"
/codon_start=1
/transl_table=11
/product="Putative multidrug export ATP-binding/permease
protein"
/db_xref="COG:COG1132"
/translation="MLRRFFAYYRPYKKLFILDFSCAILVALLELAFPLAVNRVDDL
LPGGRWDWILWACLALLGIYLLNSFLNFVVTYWGHKLGINIETDMRKSLFNHVQKLSF
RFFDNTKTGHLVSRMTNDLMDIGEIAHHGPEDVFIAMTLIGAFSIMMSINGNLAVLT
FIIVPLIIYLSLYFGSKMSKAFSRMFGDIADFNARVENNITGIRVVQAFANEEHEKAQ
FAVNNGRFRQTCLIAYKIMAWNSSVSYMLMKLVSLFVLVCGTWVFIQGSMTYGQFIAP
IMLSNVFLTPIQKINSVIETYPKGIAGFKRYTELLDMEPDVEDRPGAVTVSHLRGDIR
YEQVTFGYSDQEPVLKGIDLNVRAGETVALVGPSGAGKTTLCSSLPRFYDVLEGRITI
DGQEIQDMTLDLSLRSHIGIVQQDVFLFDGSIRENIAYGKLDASEEEIWMAARRAQMEP
LIQSMPEGLDTLIGERGVKLSGGQKQRLSIARMFLKNPPILILDEATSALDTETAAI
QQSLAELSEGRITTLVIAHRLATIKNADRIIVVAEQGITEQGRHEELLAAGGVYSRLHY
AQFGA"

CDS 1175008..1175337

/locus_tag="EFAGFIKM_01021"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQLNDMLKILITCLLFILIWWFLIQGIRKLSSTRAGSGFQRLGG

WSIGLFIVGAVPLGFSLYTEIFDKRLDANIGLGLAMFFVWAYCVILLCAALVWGRYV

YKRDMKK"

CDS 1175463..1176032

/locus_tag="EFAGFIKM_01022"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSNLRRVLILLSILIVCLTGCSGHIECNSVQTQANAPSEDGFTG

YVVERKDNSILVDPAYEDFSANGGGRYYPKWFSNAPDPQIGSYVEVWTDGGPENQ

PYPGQARAIEKIVSCLNTPDGAHLSEADAIRGGLYSPDGEKVRVPVIEDVQFYQDAGT

WAIRIRDAMSTTKNQDEIEIRVEDVEPVE"

CDS 1176077..1176331

/locus_tag="EFAGFIKM_01023"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDIRECLPRDKHDFEAVRKLNQFSDVELKVIIPELMEWLQDGNW

PISKPVENLLLRLGEDLVPHIKDVLQTQDSTWEYFIFWWG"

CDS 1176564..1176833

/locus_tag="EFAGFIKM_01024"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLKYQLLFPTFLSSEIYCLHIVQLLIELFDISEKEAFLRINSFW

EGNDFLSEEDLIFHESPEFWAKTIYYEESNWWNFPENELIPRKID"

CDS 1176926..1178011

/locus_tag="EFAGFIKM_01025"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MELSRSQQLAQEHVTNYARSRKNEAEQTIREILRMSNIELKTFE

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RDVWENKMFGGAYQINGSTNSERPKYGALNVMLHPDGPAPRFGSCYFLLSTEVSQRCT

YTYLDSHQDPEEKGTYYEFDLILAALMRDVFNSGFAIGERNLTVQKLIDHMLVNLEKP

FQNPSNQEPNRNLDYYIEAQIHGDISLEKDVKMLVADPSFKGHTHTGRILEQICLKYSI

DLHWHMGFTLLVNDVPIDFRGPSMPSLAKRIAKSDLIDANIIGSAAMDLDKQNP SHWSD

RGTYKEVLQELKLLWHVLVRYGKPMEE"

CDS 1178319..1178498

/locus_tag="EFAGFIKM_01026"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSAKKVGRPKSDKPKSRTIEIRVDEEIMNKLDISAEKLNTRSD

IVRKGIEMIYDELQK"

CDS 1178641..1178934

/locus_tag="EFAGFIKM_01027"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNSILEALYNGRLRPDEMMMPHPEYQALGRQIAALTEQWKNRL

SEEEFLELEQLFDLCGRCEGMHTEAAFAQGFR LGANMLIEVMSQREESVLEFN"

CDS complement(1179155..1180057)

/gene="ydbD_1"
/locus_tag="EFAGFIKM_01028"
/EC_number="1.11.1.6"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P80878"
/codon_start=1
/transl_table=11
/product="putative manganese catalase"
/db_xref="COG:COG3546"
/translation="MFKRLDEILIEIPNVEKPDPNAAAAIQELLGGKFGEMSTLNNYL
YQSFNFRSKEKLKPFYDLVMSITAEELGHVELVSHGINKCLRGSTEYREPDDTPLGSV
KDARLSYHYLAGAQGAMPFDSMGNPWTGANVFNSGNLVEDLLHNFFLECGARTHMKMV
YEMTDHPAAREVVGYLLVRGGVHV VAYAKALEIATGVNVTKLVPIPSLNNKAFNEARK
YEEKGVHTKLYTYSKDFNTIGQIWKGTHPEDGQPLEVIQGIPEGFPIPEAPAVEEEF
APGISQEDFKEIARRLKMAGNIAD"

CDS 1180320..1180628

/locus_tag="EFAGFIKM_01029"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNKRWIRITGIVMFLMIQMYISSEPATAYVVTNEVQVDEQTRQR
LEKKYGLDRPEEPKTQQHVFSGDWGMSFRTEPPDSFDRLVHVVPFSLRPLAWIFRLFV
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CDS 1180685..1181005

/locus_tag="EFAGFIKM_01030"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRMLIVTVMSVVLSLAGITSGTGAAIPDYAKWGIIAVKETQTKY
NVDILDYKHIGRTSLTADQSREQFKLWVRGKDGKQFAVYVNVDFNPSTQQLKKVQFSE

SDRH"

CDS 1181152..1181373

/locus_tag="EFAGFIKM_01031"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLGKYIGQMVELVYMDRAGQITQRQIRINSVRGGMIRASAGKEG

SPRTFLEQGILAWRPVTDLNGEVKYAERL"

CDS 1181357..1181638

/locus_tag="EFAGFIKM_01032"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLNDFERKILRIMVNYAGQRRRLPRMDELETKTGRSRAYIHESL

LELERTGHIAWENRSTLEGIQILQAWEQVQQPIRKSQPSGDSVKYFTDY"

CDS complement(1181714..1181950)

/locus_tag="EFAGFIKM_01033"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDQTTRESFTAVQKNGDGDLTAFQTSAGRVLDYQQALAEVKAGA

IAGVNVFKGKDGEMYIRGDADGDPTNNLDQLPHF"

CDS complement(1182063..1182506)

/locus_tag="EFAGFIKM_01034"

/EC_number="2.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5HH30"

/codon_start=1

/transl_table=11

/product="Acetyltransferase"
/translation="MAAEISYVSTEEQLEQALGIRHHVFVIEQQVPAEIEIDQYDVIS
PDVHHVLLSTDGQAVATGRLIYYSKDTAKMQRIAVLESHRSFGYGRVLLAMEELARE
LGLSYSVLDAQCQAQKFYEKLGYEVISEEPFYDADILHVRMRKSL"

CDS 1182616..1182729

/locus_tag="EFAGFIKM_01035"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGMTGIMVITLLMSAGMITLLYYVTKKAYSRKWDEDE"

CDS complement(1182745..1183002)

/locus_tag="EFAGFIKM_01036"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRNLTKRSKSNKYTFTKCFFLFAGLVILSTNVTGCGLEKDEHTV
QFQQLQQPHENSESLPVWLDVYSKSVIQDVYSPRGSSEVLP"

tRNA 1183205..1183276

/locus_tag="EFAGFIKM_01037"
/product="tRNA-Val"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Val(gac)"

CDS 1183512..1185725

/locus_tag="EFAGFIKM_01038"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNYSNPFTSKLARVGIAGTLALILATSPLANMGVVAAEADPAPV
STKIYNTQKDSLEQVPIQYHIQARLNEKDMTLRGNEKITYRNTSNDTLNQLVLHTYAD"

ANLSKSTQASMFQANENISKNSPDKKPEDFLGGMDIQGVTTAGGQSLDFKNENQALT
VQLNEPVQPGKSVSFQVSFQLNIPYGSQRISYYQDIINGAHWFPVMSVYDEGKHQWDT
APYSQTFESDYYTSADYEVDLNVPPDDYQVAMPGVITTREDTEHGRKIVSALAENTREF
VFFASPKFQVESVTRNGLTVEYYYFDNQPGKKEIVEQYIDQAFKAIDFFSDKYGKYPY
PEFRIVETYVQGVAVEYARLIQMGGIQNGAVPEEDTTFVHEIAHQWFHALIGNNSET
SFLDEGFADFSMVYFAEKQGDKLNGFRSLQFDDSSVEVAIASTNDEVEDLASLVFYQK
GRQAIYQLYRSVGEEKFDQFMKEYFNRYVYQNAIDGLLHTIEDVLGKEQRMEMETAL
YKPNFVLKPEYQLSLEERTAYLHDVFQLQYQTVMKLIPDLPFEVMNRMMDKVLQGERL
TIVLSDRVSKIADKQGEAIVSQLTSFLDMSGVKYDVVRDRKELKQKMKKEIGNSNLIV
IGNAKSNGVVQALKSSIMDRANQIGFDWKQTMKQPLAAGAYITKHPYNQNRMLLHYFW
NEDHLSEARFEPFMMKIQQTIGFTNDFYQYYVLDNQGKEKSNKKVVNPISSLFAE"

CDS 1185908..1186180

/locus_tag="EFAGFIKM_01039"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKDQHYPGVPMKGTLDYNCKGIKGMNKMKAYSYNARIRPIICN

TQEPAANEQNVVDFSILLKDTSAVLYSRPVNGNALLTKELSSHVYD"

CDS 1186167..1187165

/locus_tag="EFAGFIKM_01040"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSMTDNIAQAALDAAMKANRAVAPYDYCDAESRRMYTPQFDKKM

DNPMYTAAMAGLQSIYWFRAIKVKGLIPDAKADYYATYSTNHNHIGGIGLAYSNSPTG

PWTKHGGQVYLDTVVGNSTETPFVIWNDEEQLEFFMYQQNGLGINQSTALATSVDMINW

TRVGLILDKPPGFPGDGHTGYFSCFRNGGKWIGFSVMGGGDFGRKCIWHS HDGRSWLA

DPRPLMGGNDATLSAGENISRPNAGVFMYKGSWWLGMLSAYASGGVTTVARPAIAKI

SADFRQLLDKPTDIYFPALTWETTNMQSLMVSVMDGVVYVYNTDHNIGVAYSVGV"

CDS 1187168..1187854

/locus_tag="EFAGFIKM_01041"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLIRDAAGQIVPFGKVHKQLVADFLYGTLPDWVEVVGTPTFEPL
PDRGTITVTPPTTAGATAELKMKHLIDSSKVTAIAITLEALQLNGNIGISVQVGIKSK
DSKAGITFFQNVNQKYGMRAYKADGTYTDFNQNMVFFTHGVAGDEAQRKNLTVLL
CTGLQFSAGFERPSVWLGADDQYGGVAADLSGGLFQHGELQCLLKLTTSKAEAKYFKC
AQMKVDIWSN"

CDS complement(1187979..1189190)

/gene="chrA"
/locus_tag="EFAGFIKM_01042"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P14285"
/codon_start=1
/transl_table=11
/product="Chromate transport protein"
/translation="MENNSFLTPDKPKHTVRALSEVLAVSTKLGLTSFGGPIAHLGYF
HEEYVRRRKWMDERSYADLVALCQFLPGPASSQVGIGIGIIRSGLLGGLMAWLGFTLP
SVIALVLFAFLQGFDISSTGWIHGLKIVAVAIVAQAILGMGQKLTPDRYRATIAIFT
AAATLVWQTAFTPILFIVIAGIIGMIYFRKMTGIKTADLSVPVSRNLAIVCLATFFGI
LILLPLITPFDRSGWLLFFDSFYRSGSLVFGGHHVLPLLEREFVPTGLMNKSDFLAG
YGAAQAVPGPLFTFASYLGAMMRGIPGALVATIAIFLPAFLIVGALPFWNSLCKSSK
IQGALIGINAAVVGILLASLYDPLWTTAILAPVDFALVCMLFLMLVFWKVPPWIVVVA
GAAGGTIMNLL"

CDS 1189408..1189827

/locus_tag="EFAGFIKM_01043"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7A6M9"
/codon_start=1
/transl_table=11

/product="Organic hydroperoxide resistance protein-like
protein"

/translation="MKTLYETTVINTGGRQGIVQSPDNVFM LDVAAPPELGGQVTTAT
NPEQLFAAGYSACFN SALEFQLKKHKVEIERSTVAATV MLVTDSEDNGVKLQVDLEVK
ILGLDEETAQKFVKLAHDYCPYSKGIKGNVNVNVELA"

CDS 1189973..1190152

/locus_tag="EFAGFIKM_01044"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMDFSKPPHGSETDTHRQRHQENEQKYL SGGKSIWYEISNWLIL
GGILLVIFLLFKYVF"

CDS 1190627..1191181

/locus_tag="EFAGFIKM_01045"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKWKRILLCVTVFSL LGGSLLFADSVNEKIRVLINGKEAADGGY
LIDGTTYVPVREAGGVVKWDSSNKRVTVIKPNVHIFL FKGDTVFGNVNVGKLKFNVFS
QVDSL TADVA AVKVTITNPSGQVKDIQSQELTTQKDNFWFR TYDFTYDFSRAGKYQVG
FHIKENANSSYVLVAEKIITALND"

CDS 1191279..1191596

/locus_tag="EFAGFIKM_01046"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSDHTHEHGDGCGCGQDHDHDHEHEEVLLT LDENGQDVEMVLV
ETFDVEKHVYALLLERNNPEADGIILRMEEDEEMVLYNIEDEEEWNRVEAAYNELVA
SQE"

CDS complement(1191803..1193290)

/gene="speA_1"

/locus_tag="EFAGFIKM_01047"

/EC_number="4.1.1.19"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P21885"

/codon_start=1

/transl_table=11

/product="Arginine decarboxylase"

/db_xref="COG:COG1982"

/translation="MTALMNHHRTPFLTALKNHAALNPVQFHIPGHKKGLGADTEFRE
FIGDNAFSIDLINIAPLDDLHQPTGVIQEAQILAADAFGADYTYFSVQGTSSAIMTMI
LSVCSPGDKIIVPRNVHKSVLSAIIFSGAKPVFVSPSQDANLGIDHGVTTQSIRRALE
RHPDAKALLVINPTYYGVVTDLKEIVELAHSYQVPVLVDEAHGVLIHFHEDLPLSAMA
AGADMAATSVHKLGGSMQTSSVLNLTNGFVNPQRVQTILSLTSTSTSYILLASLD
TSRRNLALHGREIAQKAIELAEFARRSINDMDGLYCFGRELLGTEATFNYPDKVTIH
VRHLGITGYETENWLREHYNIEVELSDMYNILCLITPGDTDNSVDILLNALQDLSTRY
YQVNPAHELKVKVPDIPQLMLTPRDAFYGDTEVIPFKESAGRIISEFIYVPPGIPIL
LPGEVITQENIDYIIDHVEVGLPVKGPEDRSVTNVKVIVEADAIF"

CDS 1193456..1194748

/gene="ltaA"

/locus_tag="EFAGFIKM_01048"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2FZP8"

/codon_start=1

/transl_table=11

/product="putative glycolipid permease LtaA"

/translation="MQTDTKPAKILRSPFFIAMWLTLFLVEIIKGALLVAVLPVYMDN
ILGLSAGVIGVAFALQYLGDNLFRAPSGWAAERIGFRATMVTALICTLIAVIMILFLK
SAVGLAMACLILGIGTSPLWPCAMTGV TAMSGPQNKNGTAMGALEMAALGGTGLGPIG
MNWLLERTHHDYRTIFLVLMGCAILVILVAMILPGRVIVEGEHAEQAAKNSDVKYPK
PNLLTPFIRLQKSVKDTLQVRSTLVNPLVYPALFMQSFVIGLLSPVITLYTRTDLH

ISPNLYSLLLIAGGGITVIALLPVGKMVDVDFGTPFLNIGFLMAAASLFAFSSITSIP
VVFVWMLVGVISYAMILPAWNAFVATLIPKGERGAIWGFLLTLQGSGMVVGPIVSGLL
WDHVSHPPAPFIGSAIVMAGLAVVHFVLSRNPFRTPAK"

CDS 1195002..1195601

/locus_tag="EFAGFIKM_01049"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKSYEVEYCNLELRFNRRHIQNLIRDLIREGYSLYWSEDESFF

ILSVRTGRKLVKLRQQTTRTGNKMTGDYIHKDAKLAEWLEKLIGDTRGHAVVKRFKD

QQMTVENILFGEVIRLVEVSGFKQRVIFQKEPAPTAEEMEEMFLSREGEERLMLLRME

VDDELERLYTAMQMDNIDKANACRQVLKQLSGHLLMLEG"

CDS 1195774..1197183

/gene="gndA_1"

/locus_tag="EFAGFIKM_01050"

/EC_number="1.1.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80859"

/codon_start=1

/transl_table=11

/product="6-phosphogluconate dehydrogenase,

NADP(+)-dependent, decarboxylating"

/db_xref="COG:COG0362"

/translation="MTKQQIGVIGLAVMGKNLALNIESKGFSVSVYNRSPEKTNDLLK

EAEGKNLTGSFSIEEFVASLESPRKILIMVQAGKATDATIEQLLPHLDEGDIIDGGN

AYFPDTQRRSKELEDKGIRFIGTGVSGGEEGALKGPSIMPGGQESAYKLVEPILTAIS

AKVGDDPCCTYIGPDGAGHYVKMVHNGIEYGDMQLIGEAYHLLKSVLNVSVEELHAIF

TEWNQGELDSYLIEITADIFSKYDPETGKPMVDVILDAAGQKGTGKWTSQSALDLGVP

LSMITESVFSRFLSAMKDERVAASKILNGPATEAFSGDKKAFIESVRKALFASKIVSY

AQGFAQMRAASDEYGWDLKYGNIAMIFRGGCIIRSQFLQNIKEAYDKDAALKNLLLDLP

YFQNIVESYQGAWREVVASAVKQGVVPGFSSALSYYDSYRTERLPANLLQAQRDYFG

AHTFKRVDKEGSFHHNWME"

CDS 1197410..1198066

/gene="aroK"

/locus_tag="EFAGFIKM_01051"

/EC_number="2.7.1.71"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00109"

/codon_start=1

/transl_table=11

/product="Shikimate kinase"

/translation="MPGVTRSVLEVLADGRKEVGEEMVFPSPQGCVMIGQKCSRIALI

KGVYTLKSNNIILIGMMGTGKSTVADMLARELGYRLIDVDTAVEKEEGCTIPELFTG

KGETYFRDAESRMLCSVLEKKSQVIATGGGVLRSDNCDVMSKNGWVVALTADPAVIV

ERVSGCDNRPLLAGNAEERIKTIMEERKDAYRFAHYTVDTTELSAAEVTRLILAHYRV

"

CDS complement(1198203..1198508)

/locus_tag="EFAGFIKM_01052"

/EC_number="2.8.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:D3RPB9"

/codon_start=1

/transl_table=11

/product="Sulfurtransferase"

/db_xref="COG:COG0607"

/translation="MTQIAEIETSELRRRLQAGEKLQMIDVREDDEVAQGMIEGAKHI

PLGQIPDRLSEIEKSGEIVICRSGYRSEACEYLQQLGYEGCTNMVGGMLQWQQED"

CDS 1198614..1199909

/gene="aroA"

/locus_tag="EFAGFIKM_01053"

/EC_number="2.5.1.19"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q482G5"

/codon_start=1
/transl_table=11
/product="3-phosphoshikimate 1-carboxyvinyltransferase"
/db_xref="COG:COG0128"
/translation="MDVIVKPTPTLNGEIGALSSKNYTTRYLLAAALAEGTSTIHFPA
HSESDAMRRRCIRDLGAVLEEDDSKIVIQGFSGHPRDVRELVGNAGAVLRFLMGVTA
LCPDVTFVNTYPDSLGRPHDDLIDALGQLGVDVQHEQGRLPITIKGGNAKGGHIRVS
GSVSSQYLSALLFVTPLLAEDSTIEVLNDLKSQVIGQTLEVLEQAGIVIHASDDYMS
FRVPGGQAYQPTTYTVQGDYPGSAAVLAAAAVTQSDVKILRLMEQSKQGERAIVDVL
MMEVPLTHENDVVHVQGNRGLKAEFDGDAATDAVLAMVAAAVFAEGTSRFYNVENLR
YKECDRITDYLNELRKAGANVEERQAEIIVHGRPEGVEGGVEINAHYDHRVIMALT
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CDS 1199969..1200403

/gene="yccU"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P75874"
/codon_start=1
/transl_table=11
/product="putative protein YccU"
/db_xref="COG:COG1832"
/translation="MEFNNPTREEIGQLLRKAGNIAVVGLSDKSDRTSYMVAEAMQSR
GYRIIPVNPQVQGEILGETVYATLADIPEPVDIVNVFRREEFCADVARDAAA
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WLQLGIHSDEAVQIAAENGMTAVTNRCIKVEDSIVLRGAGRG"

CDS 1200600..1202480

/gene="gamP"
/locus_tag="EFAGFIKM_01055"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39816"
/codon_start=1
/transl_table=11
/product="Putative PTS system glucosamine-specific EIICBA"

component"

/db_xref="COG:COG2190"

/translation="MNWLGSLLQQLGRAVMLPTMVLPAAILLSVGSPLWDAWGGLDIVG
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LQHGLNGIATWEYSLGGFGLFIYGVLYRVLVAFGLHHLLNNVFWFQLGTFETPDGNIV
QGDLPFRFFAGDPTAGFFMAGLFPIMMFAIPAIAFAIIQEAREDLPKIKKTFLTSALV
CFLTGVSEQIEFAFLFAAPYLFIVHAVMSGVAMWISYWLDIRHGFSYSAGIIDYILNF
HLSENAWKLIPIGILYGLVYYFLFRWAIRTFKIPTPGREEGSMLEDWVGNIPYQAPLI
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SELIREEIAKLLERDLQQVLFCAVPVQGMPLIEEVPDQIFAAKLVGDGVAFVPEKGEL
VSPVYGTIMHLYPTMHALGISTREGLEVLLHIGIDTSQKKGHFEAFVQEGDTVEPGQL
LIKFDLAVLREQAASLTTPMVITNPDRVKSWSFAPFKQVKKGQASVMSVLYDRNVGG
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CDS 1202477..1204237

/gene="ptsI_2"

/locus_tag="EFAGFIKM_01056"

/EC_number="2.7.3.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P08838"

/codon_start=1

/transl_table=11

/product="Phosphoenolpyruvate-protein phosphotransferase"

/db_xref="COG:COG1080"

/translation="MKIQGINAAAGIAIGKAFVLPSWEWDLDPQKMDSVDLAQEFERL
YEGIRTSKDEIEYIKNEFKEVVGPEESSIFDAHLAILEDPVFMNEIRGIIERQYKAAE
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AKELSPSQLAHLNPTHVLGIVTLIGGKTSHSAIMARALGIPLVSGLEASLGMPVETGD
MLVVDGDNGLVFTDPDRKTIERYTMLRSKQLKKKEQLQVLATVDAVTKDGAVLHLASN
ISSVKELDLALKQGAKGVGLFRTEFLYMDRATFPGEQEYEVYRLVAEKTAGQSSVIR
TLDIGGDKQLDYFELPEEDNPFLGYRAIRISLDRKDLFKTQLTAILRASAAGNVKIMY
PMISSVEELQQANEILREAMSDLDERGLSYDPHIQVGIMIEVPAAVMIADLLAEEADF

FSIGTNDLVQYVLAVDRMNEQIAHMYHPYHPAVLRMLRATADAAHTAGIDVSVCGEMA
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LQVFNDSTGSPDEQSGSNAS"

CDS complement(1204358..1204882)

/gene="yfkM"

/locus_tag="EFAGFIKM_01057"

/EC_number="3.2.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80876"

/codon_start=1

/transl_table=11

/product="General stress protein 18"

/db_xref="COG:COG0693"

/translation="MRLTGKKVIALVDEEFEDLELWYPVHRVREEGAEVHLAGEKKGK

TYIGKYGVPAEAEYSFDELDSSDYDGILVPGGWAPDKLRRYPKVLELVKEMNADRKPI

GQICHAGWVLISAKILDGVTVTSTPGIRDDMENAGAIWKDEAVVVDGHIISARRPPDL

PPYGKAFCDALADK"

CDS 1205126..1205572

/locus_tag="EFAGFIKM_01058"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVRKSCRCGHVMELELRTVYAKKVEIRNVPVFACTDCVSYEVL

PPVKPDLTECINTLGEQPVKQDVSFGERNELADLFHELLLTWPDATDREMEHRMQQAV

EERINLLLDIMGYATKSGDAAWMETTERRLSQLSGFVWQEYFSNAV"

CDS 1205695..1206042

/locus_tag="EFAGFIKM_01059"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MADMTKMTSIEQLNSAVEATKDQPLLLFKHSTRCPISSNAYQEM
NDYLLNNANEQVKYGIYVVEDRPVSNEAADKLGVKHESPQAILIKKGIPVWHTSHSD
ITRTTLTNVLSSES"

CDS 1206135..1207148

/gene="ccpA_1"
/locus_tag="EFAGFIKM_01060"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P25144"
/codon_start=1
/transl_table=11
/product="Catabolite control protein A"
/db_xref="COG:COG1609"

/translation="MTVTIYDVAREAGVSMATVSRVVNNPNVVKPQTRKKVYEAIERL
GYRPNAVARGLASKKTTTVGVVIPDISNSTFAEIARGIEDIANMYHYNILCNADKKK
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HEAAAFDAVNTLIRHGHKEIAMISGTLQDPANGYARFQGYKKALEAAGIEYQEDLVRI
GNYRYESGVEAMKYFLGLKKPSAIFAATDEMAIGAIHSIQDDGLKVPDDFSIISVDN
IRMASMVRPQLTTVAQPMYDLGAVAMRLLTKLMKKENVENPRVILPHETILRLSVSHA
DVW"

CDS 1207268..1207963

/gene="mtnN"
/locus_tag="EFAGFIKM_01061"
/EC_number="3.2.2.9"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7A5B0"
/codon_start=1
/transl_table=11
/product="5'-methylthioadenosine/S-adenosylhomocysteine
nucleosidase"

/translation="MSETIGIIGAMDEEVELLLAGMKQLETVKQTGITYVAGEWLGKH
IVVCKSGVGKVNAAVTTQILIDRFQVNRIFTGVAGAVNPELNIGDMVISSVCVQHDM
DVTPLGFARGVIPYQETSAFPAEASLITLAEAEACKAQGANYLIGKVLSGDQFIANKDT

VNMLYTEMDGACAEMEGAAVAQVCYMNRPVFLVLRGMSDKADGSAHVNFAEFTVESSQ

RSHRIVEHMLENM"

CDS complement(1208073..1208705)

/gene="acuA"

/locus_tag="EFAGFIKM_01062"

/EC_number="2.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39065"

/codon_start=1

/transl_table=11

/product="Acetoin utilization protein AcuA"

/translation="MEHIKEHHMRSIFKSGHRITIEGPVQAEETRILAFHPDLDAFRR

PTEQQEALAEIAALPEGRIIIAHENETIIGYVTFHYADDCERWSEGNMTDLIELGAIE

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ETIDMTWYATDDPEICSHPANCLMVRIGSQVPITSEEQFDRVRFRHRFMY"

CDS 1208975..1210699

/gene="acsA_1"

/locus_tag="EFAGFIKM_01063"

/EC_number="6.2.1.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39062"

/codon_start=1

/transl_table=11

/product="Acetyl-coenzyme A synthetase"

/db_xref="COG:COG0365"

/translation="MSQAHGEMLQTVVSESNLGDYTEARSRFDWESVERHFTWHASGK

VNMAHEAIDRHVLEGRGGKTALLYSDASREEAYTFADLSEQSSRFGNVLRKYGIKGE

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RIKRSELPELKHIFIVGGGAQTEEGLIDFDAEMSAASDEMEVEWLNREDGLLIHYTSG

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GEPLNPEVVRWGWKAYGQRIHDTWWMTETGAQLICNYPGMPKPGSMGRPLPGIEAAI

IDDRGQELPPYSMGNLAIRTPWPSMMAKIWNPNVKYEEYFRLTGWYVSGDSAYMDEEG
YFWFQGRIDDVINSSGERIGPFEVESKLVEHPAVAEAGVIGKPDVTRGEIHKAFVALR
EGYEATPELKEEIYRFVKEGLSAHAAPREIEFKDKLPKTRSGKIMRRVLKAWELDLPT
GDLSTIED"

CDS complement(1210938..1214033)

/gene="mtgA_1"

/locus_tag="EFAGFIKM_01064"

/EC_number="2.4.1.129"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00766"

/codon_start=1

/transl_table=11

/product="Biosynthetic peptidoglycan transglycosylase"

/translation="MVDVNKKKPDEQPVRKRSFARRLGSFVKWMVVLGFMGALFVGGA
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PQKVIDAVISIEDNHFYEHKGVDMSGTLRAVKQKVLKESVQTGGSTLTQQLARRVFLN
LDRTEDRKVKEILLSRLRLERFLTDEIMTAYLNKVPFGNGSSGYNVYGIKAAAKGLFN
INDLEKINIAQAAYLAGLPQLPSSYSAFNGKGDFVEENFDRAINRQHVLRRMLELGK
INQSEYDKALAFDIKSALAPKTIKAYNTYPYLMETERQAAQILMKQLNSDTAESTDK
ATDADTPQKESSALLEEAQTQLRTGGYRIYTTINKSIYKTMRTIAEDDSNFSADDPVK
GKEQTAAMLINHKTGAILGMIEGRDFQDEQMNYATQMIRQPGSTMKPIAAYLPALDEG
LVQPASIIDDSPILKNGPSGYHIAKNANNRYQGLVTARRALNYSLNIPALKLFNEEV
GIEKAWTFAKKLGITTIQKEDYQAQTGVLGGLQYGVTVVEELTSAYGAIANNGVYNDY
MISKIVDSKGNIVYKHDTEPVQAFSEQTAYLMTDMLRTVITEGTADKVRENYKYSKSV
PIVGKTGSTQNYADVWFEGYTPDVTLGWVWGYKQPVNTLESKSQRKRAQQLWSKILNE
VIDTQKDLFVTDSFKKPSGIETRTVSAYSGKLPTSMTDKFVTDIFNSKFVPKDSDDGV
AKAKYITYNGVNYIPRDGTPSDMLKEKTVIKRKKPISDLIKELQNAFSRMSRHESLAY
YLPEDAGADMPTQIDPRTDNGKAPDAPGNVRISTSGERAVITFNATPENDVVGYRLYR
SVNGGGFQNNQGQVLTGESRSFSAYAAQGGNFAFYVTAVDVAGRESAPSATVNSAGVA
PPVEEEIDEPIEVPGTVVTPGETQTDNTTTTAPGTPGQVSVSALTQGLRIQWAASPNA
DSYTVYYSETGSAPYTKIGTTAGNTMDYGVPASTSGWFKVSASNSAGESEPSAALHFQ
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CDS complement(1214263..1215381)
/gene="mcpB_1"
/locus_tag="EFAGFIKM_01065"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39215"
/codon_start=1
/transl_table=11
/product="Methyl-accepting chemotaxis protein McpB"
/db_xref="COG:COG0840"
/translation="MAVLLLASVVYTYIISIVRQLNQVNIVAGQLAGGDLTQKLPVRS
KDEFGIMAGHMNQMMDLRHTISVISEHALSVGSTSQQLTAGAEETGKAAELIALTGV
ELADKAGKQVQELQESSRSMNEISAGIGRIAKAASDVSDSSRAVAERTTVGTDKIQSA
MRMVDSATSSVQTSMTALENFRQRSEEIGHITGMITEVSRQTNLLALNASIEASRAGE
NGRGFGVVASEIRNLAEQSRVSAAQIAALIHVSQQEVLSLVENMEHGNAEVSHIAEVI
NESGELFLSISSQISDVNEQIEHVSAIAQQMSAGSQQVDATLVQLKTIGHETADHATR
VASASEEQLASMEEITAASASLANLTQELLELIQRFKT"

CDS complement(1215519..1216367)
/gene="mcpU"
/locus_tag="EFAGFIKM_01066"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q88NI1"
/codon_start=1
/transl_table=11
/product="Methyl-accepting chemotaxis protein McpU"
/db_xref="COG:COG0840"
/translation="MHFFRNRKLAVKLGLLLGIVLLCCIGALIAFNKTSIYDKSLQYG
ETVAGQAANRATNEFMTDINQVKNTLDTMSTLLDAAQNGSLNREEVVRLLLEQYLKKD
EKVFGFYTGWEPNAFDGND AEHINKKEYDDATGRFVPYVIRDGNSLHFEPMPPTYEGSG
ETSTYYQQPKKTKSIYWSEPVYTVGGKETLLVSIVLPLLDENKNFLGIVGADFTIDR
FQQNIASLNPDQGYAMLITSEGQIAAHGSKPELANEGAVIPSEMRQSFSVYSLASLSF
TLQTLK"

CDS complement(1216556..1217155)

/gene="rpsD"
/locus_tag="EFAGFIKM_01067"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P81288"
/codon_start=1
/transl_table=11
/product="30S ribosomal protein S4"
/translation="MARYTGPKFKLSRRLGISLSGTGKELKRPFPQGQHGANKRRKIS
NYGMQLQEKQKLRRHMYGLGEKQFRTLFSKAQKMQGIAGENFMFLLECRDLNLVYRLGF
ANSRAGARQLVAHGHVTVNGKKVDIASYQVSTGDIVGLREKSRALSSIKEALEGRSHL
PAYVEYNEAAVEGKFIRLPERAELSQDIDEKQIVEFYNR"

CDS 1217621..1219612

/locus_tag="EFAGFIKM_01068"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLEHLRSLPASLNSRSSGDSASFAAPHSHEEHVLWMQKMDITPF
DFSYLGSLLAQAYS DWNSRVGSRLARPSTFYVWNTEGDCIGYDSDHEADPGVNARRL
VLECLDKRQVLSLKGTS EHG EYLIITHPLFSRTNKDMFAVFTAVIYESNGYETSEAVV
QSEALHYRTC FYRRFEYIFMTDLLHAHEQTAREEHRSILFQIVQRMHDKMDVDAILD
EVFDSMDYLYPATYIKLYMSQDQSNSDPRIKPLLVEHQGEDICVRSFMEGKLIVARSH
DAENRIVDVGIPLKGKQGIYGVFHIEMNEEIMEESDLQLITMMVDTAGTAFENAKLHE
QSNMLIQELRLINDLTQRLNKSLHLSEIYQLSEQLKEIFQAETCCILQLNDSTNDFE
VMSSNVKDVFHQSFSVDYGIAGLVYRTEEPLIIANYAQFDKVSSFFMEDTGSMGLIAS
PIRVNGEVKGAILLGH SREHYFSYDN YRLLQMLS IHGLALS NATLHAEVRRLANLDM
LTGLYVRHYLDSVIHERQAHEFCGSLIVDIDQFKQVNDTFGHQTGDQVLKQVSEIVT
SSVRSE DVCARWGGEELAIYMPQVSVRQALDYAEVIRKRVAEETRPPVTVSSGIAEWN
WMDEKVSVESLFYRADMALYS AKNGGRNRIVVEEQDVTR"

CDS 1219714..1220604

/locus_tag="EFAGFIKM_01069"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEKVHGRVKIDMFNRHSVRTLWLFVSIVIIGVPGCLIQRDQTP
EEVFSLALSGIAGKETLSFEGEAGLRRENSGLFENQFKFEGKLENHDRLTLQTRLPGE
VTAVGTGIQTTAVKNNGQPSGFSASFERKQGQWMALSAQHEPLRGSLSRFNPIAQLEK
IDGMHKTIQSEYGAGRRRTLRIELAPEDAKSWAVTQLNDEMNAIRAEYMHKAATVKG
ARKEKLEKDLEKVKQGETTMQQMMKQASVQTVYHLTVDRKSSLPLRLSSESQMSYTD
NNRKSNEALVTDVNFKSYQ"

CDS 1220716..1221831

/gene="pepS"
/locus_tag="EFAGFIKM_01070"
/EC_number="3.4.11.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9X4A7"
/codon_start=1
/transl_table=11
/product="Aminopeptidase PepS"
/db_xref="COG:COG2309"
/translation="MKDPRIQKLAANLVGYSVDVQPGENVLVEMIGSERDLINAIIEE
VGKKGGNVFVQLTDKTVQRAMLKNATEEMMKTWAEIDLNRMKQMDCYIGIRAGENVND
LSDVPEEKMKMYNSLYSHPVHSEQRVKHTKWVVLRYPNASMAQLANTSTEAFEDFYFD
VCNLDYAKMDKAQDSLNLNLMKRTDKVRITGPGTELSFSIKDIGAEKCSGQKNIPDGEV
YSAPVRNSVNGTISYNSPTLYNGVTFENIKFTFKDGKIVEATSNDTERLNEILNSDEG
ARHIGEFAIGFNPHILHPMKDILFDEKIAGSLHFTPGQAYEETDNGNRSSIHWDLVLI
QRPDYGGGEIYFDDVLIRKDGIFVIPELECLNPDRLK"

CDS 1221928..1222173

/locus_tag="EFAGFIKM_01071"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MSSNNAAVVEIAQTAGKFTSSIVLHSENKYIDVKSILGLFTTLI

STHSYELHVHGPDAVEAKAAMSEVFAKHGLNVSIASE"

CDS 1222399..1222692

/locus_tag="EFAGFIKM_01072"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07638"

/note="UPF0358 protein YlaN"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTSSDLQDQLSLKAISLLQEDADKIQKLEIQQMENLATRYCPLY

EEVLDTQMYGFSKEVDFAVRAGLLPEGAGKQLVSALERNLAILYEALNKKNEQ"

CDS complement(1222875..1223945)

/gene="chaA"

/locus_tag="EFAGFIKM_01073"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34840"

/codon_start=1

/transl_table=11

/product="Ca(2+)/H(+) antiporter ChaA"

/db_xref="COG:COG0387"

/translation="MRNRISSILLIAFFALSAIAHYLKWDSILQFVISAISVIFVAGF

LGKATENVAHYAGQRLGGFLNATFGNAAELIIAIFLVKEGLFDMVKASLTGSIIGNLL

LVLGLSIFAGGLKFKIQNYNVSLAGLNGSLMIVAIILFIPAVFLNTHSITQKDTNTL

SLIVAGLLILAYIAWLLFSMVTHKNYLADVTEDRDEELPHEHAPAWSKKKSILYLVLA

TVMVAFVSEWLVTLEVFTSEFGLSELFVGAFLVAIIGNAAEHSAAIMLAMKNKIGAA

VEIAGSSSLQIALFVAPVLIFVSYFTGRTMDIVFTTIELVAIGVSVFIAKSITQDGST

NWYEGLLLLLVVYIILGVSFLLV"

CDS 1224129..1224491

/locus_tag="EFAGFIKM_01074"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A0P8"

/codon_start=1
/transl_table=11
/product="Alkaline shock protein 23"
/db_xref="COG:COG1302"
/translation="MAEQLQLESGNIRIADDVVAKIAGMAAMETPGIAAMSGGLSEGW
AKRLSGKNVQKGVSVVEVGQLEAAIDLRIIVLYETPIHEVSRMLQQNVREAVETMTGLR
VVEVNVKVEGVSFKGDDL"

CDS complement(1224620..1225900)

/gene="ftsW_2"
/locus_tag="EFAGFIKM_01075"
/EC_number="2.4.1.129"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07639"
/codon_start=1
/transl_table=11
/product="putative peptidoglycan glycosyltransferase FtsW"
/db_xref="COG:COG0772"

/translation="MKQQTAQTKTKRGTPDFQLLILLLLVGFGGLVMVFSSSSSIAIA
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FIAGLIMLQPDFGTTFILVSTCGLLIYAGGASMKHILGSILLVVLGGALAFGANSLSFS
SMSPSDTTAATAEQNYKIGRIQAFLNPLSDINGGSLNLYRSLVAIGDGGMTGSGIGQ
GTMKLHYLPNAYNDFIFSVIGEELGFIGSALFLLVYLYFIWRGIIVSLRCPDPFGTLV
GIGIMGLIAIQAFINIGGVTTQIPVTGVTLPIFISYGGTSLFVMMVAMGILLSISRTNN
LDVIKEEKTksvtvqtqtrtspalrsresirrir"

CDS complement(1225914..1226261)

/locus_tag="EFAGFIKM_01076"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIFENTGLDGLKSDLAYLDESAEKVGFVRWQWEYYRATYDYKIE"

DEQTNSEYFVRINTRAVGGKLEKPDTVLAVEAVYLGKATFPHGLDYDSSVPQPVVKLA
AEKLQQLKELLEA"

CDS 1226472..1227641

/locus_tag="EFAGFIKM_01077"

/EC_number="3.5.1.47"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01692"

/codon_start=1

/transl_table=11

/product="N-acetyldiaminopimelate deacetylase"

/translation="MTNNIWWEDLQIHMVWRRHLHRNPEVSFHEEKTSSFVADMLES
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IHLWTPLPVGVVASKAGPMMAAADDFYIEIKGKGHHGGMPQSTIDSLIAGSALVMQLQ
TVVSRSDPLQPAVLTIGTMQAGSAQNVAEQCKMSGTVRTFDEETRNGMKERVLTMV
AQTGAAYGAETQVKYIMGYPPVWNDEQETARFFREATLFGAERVQASPMLMPAEDFA
YYLQKVPGCFCFMVVGAGNPDKNAIYPHHHPMDFDFEDAMQTAVRLFIA MAKGYTAE"

CDS 1227831..1229525

/locus_tag="EFAGFIKM_01078"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEGTEH MVSTDACIVQRDFTVLLEVGH PGFERAREQLGMYSELV
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LKLHSEADHTRMRLYSEDERLLDEL SGLKTIAAFRMERKDAHE LLLPREQRGLLKREL
TRLGYPVLDYVGYREGTKLSFDWRSNDPGDH SERFALRSYQREAVDAFEGSEG MGGSG
LLVLPCGAGKTVIGMAVLERLQCECLILTSNTTSVRQW IQEIQDKTTITSEQIGEYSG
QKKQVKPVTVATYQILTHRKSKDADFTHIKLLSERQWGLIYDEVHLLPAPVFRATAD
IQATRRRLGLTATLVREDGCEQDVFSLIGPKLYDMPWKQLEQQGWIADVQCQEIRIPFS
PELRSNYLRAEVKHQFRLAAENPAKVRVVKRLLERHRDLPALVIGQYLDQLELIAREI
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CDS 1229562..1231280

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GPDVIWMLEQYAERVTRDRMSIYRLTRERFISAIARGYALHEVIEFLDQYALTGIPEN

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LVDVPASLHGLERDHSVIEKKFSLLGFEEIPETWYKEWRRYHSSTARQIAAKAIEWQT

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CDS 1231433..1231870

/locus_tag="EFAGFIKM_01080"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MSVAEMNTVDMAQVLTGAYELGDMINQSAEVSDYLYWKQVETT

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CDS 1231898..1232164

/locus_tag="EFAGFIKM_01081"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"
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CDS 1232330..1232767

/locus_tag="EFAGFIKM_01082"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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CDS 1232900..1233823

/gene="cmpR_3"
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/inference="similar to AA sequence:UniProtKB:Q55459"
/codon_start=1
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CDS 1233891..1234760

/locus_tag="EFAGFIKM_01084"
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/inference="similar to AA sequence:UniProtKB:Q7NXD4"
/codon_start=1

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/db_xref="COG:COG0613"
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AFDQYLAEGKPGFVSVPRVAPEDACKWIRAAGGAAVIAHPGLYNDDDELVRRRIEDALP
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ERLAAAASQQRGE"

CDS complement(1234903..1235349)

/locus_tag="EFAGFIKM_01085"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MTVDIRETQPNDLKPLMALMHDYVVGFYNNPWPGDQSIQLLINN
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CDS complement(1235728..1237500)

/gene="rqcH"
/locus_tag="EFAGFIKM_01086"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34693"
/codon_start=1
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YTAPPEQHKSNPLEVSR TAFEDSYHAAEEDASRWLVNSFSGLSPLIAGEIAARGIAAE
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QDVEKTYDTMSKCMEDYYGDKAERDTVQQRVSDLLRFLQNERSKNIKKLDNLNKDLLE
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FKRYNKYKNSLAVIHEQLGKTKDEIDYLDNLLQQLSIASMNDIEEIRDELVQQGYLRD
RNKKGKKKKKSDRPTVHQFTSSEGIDILVGKNNLQNEYVTNRLASSNDTWLHTKDIPG
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HQTFLFVTPNDELIKSLPSTIKNG"

CDS 1237856..1240714

/gene="yloB"

/locus_tag="EFAGFIKM_01087"

/EC_number="7.2.2.10"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34431"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0474"

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RAERSLRALKQLSAPLAKVLRSGQEVHLAAKQLVPGDIIMVESGDRIPADVRWLQTN
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EMGKIADLIQNTTEEQETPLQHRLEQLGKILIFVALGLTIMVVVAGILHGQPAVGMFLA
GVSLAVAAIPEGLPAIVTIALALGVQRMIRKKAIVRKLPVETLGCASVICSDKTGTL
TQNKMTVTDVWLEGRNIKVTGDGYAPEGQMLENGRTVELKSDQSLRRMLQISALCNNA
SIVESAASEVGSKKKGKDTKKESKKNTKKGDLQEETVQRDNVFWELKGDPTGALVTL
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GLAGMIDPPRREVRDAIATCRKAGIRTVMITGDHGTAEIAHQLGILPRGGASLSGQ
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DIGIAMGITGTDVTKESALILSDDNFSTIVAAIEEGRNIYENIRKFIRYLLASNVGE
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ARRLGWKIVSRGVLIGLCTLGAFWLTQAAPDNPGQLIKAQSVAFATLVLAQLIHVFD
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AGIPTFLMGAGSVWGGRRNRRRMGGSGRFVPKSTKFSA"

CDS 1240897..1241730

/gene="dapF"

/locus_tag="EFAGFIKM_01088"

/EC_number="5.1.1.7"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81XR2"

/codon_start=1

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/db_xref="COG:COG0253"

/translation="MEFTKMHGLGNDFIVVFGEKELPADAAELAVKWCNRFFGIGADG

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NPHAVIYVDDAVNFDLTTWGPLLEVHPMFPPKINVEFATVRDRGYVDMRVWVERGAGPT

LACGTGACATLVSSVLNGHTDRTAVISLKGDDLHIEWNEADNHVYMTGPAEVVFKGIT

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CDS 1241945..1243834

/gene="yitJ"

/locus_tag="EFAGFIKM_01089"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O06745"

/codon_start=1

/transl_table=11

/product="Bifunctional homocysteine

S-methyltransferase/5,10-methylenetetrahydrofolate

reductase"

/db_xref="COG:COG0646"

/translation="MKADLRKVMQERVLVGDGAMGTFLYQMGPVGISYEELNLISPE

VVADVHRRYRDAGTEIFETNTYSANYDKLSKFGLESKVEDVNRAGVRIAKEVAGDIGY

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RKLSDLPVIGQFAVEDVGHTLDGYTMPEAFRIMREQGADVIGFNCRSGPNGIMRAMET

VSGRIGIPMSVYPNAGAADYVDGQFRYGATPEYFGQTAVQFAELGARIIGGCCGTPD
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VELDPPRDLIAKFMKGAETLKAAGADALTADNSLAVTRMSNMALGHLVQDRTGLRP
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MIKQLNDGVAFSGKPLKQRAGFVIGAAFNPVNKYLEKAVQRLEKKIASGADYIMTQPI
YDPELIVAMHEATKHLDPVIFVGVMPPLASGRNAEYLHNEVPGIQLSDEVRSRMAGLEG
EEGRAMGVKIAKELLDVATAHFKGIYLMTPFMFYGMTAELTQYVWEKSEHQPTCFNP
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CDS 1243854..1244753

/locus_tag="EFAGFIKM_01090"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P44726"

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/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSFSMTGYGQSAFHFGGYKVQLEIKSVNHRYCEVMMRLPREWTY
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GKPSIVDMLGLPDVMVHSDGTSSIPPEEQKGEWERVVLQEGLKEALSSLEQMRAREGLHL
ASDLERRITRLESLHTEMLDLAPTIVSDYRNKLRQRLTEMQEESFPFDEHKLGMIEA
MFADRSNIEEELTRLQSHFGQSRELLKSDEPVGRKLDFLIQEMNREVNTIGSKANHLA
LVNRVVEMKAELEKIREQAANIE"

CDS 1244805..1245065

/gene="remA"

/locus_tag="EFAGFIKM_01091"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7WY72"

/codon_start=1

/transl_table=11

/product="Extracellular matrix regulatory protein A"

/db_xref="COG:COG2052"

/translation="MAIKLINIGFGNIVSANRIISIVSPESAPIKRRIIQEARDRHMLI

DATYGRRTRAVIITDSDHVILSAVQPETVAHRLSSKDDDNDE"

CDS 1245079..1245651

/gene="gmk"

/locus_tag="EFAGFIKM_01092"

/EC_number="2.7.4.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P99176"

/codon_start=1

/transl_table=11

/product="Guanylate kinase"

/translation="MSKGLLVLSGPGVGKGTVCALRKRVPELIYSVSATTRQPRL

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VQGALKVKEKFPEGIFVLLPPSLDELKDRIQGRGTESQATIDHRMSVAVDEISLLEQ

YDYAVVNDEIDLACKRIESIIIAEHCKINK"

CDS 1245809..1246021

/gene="rpoZ"

/locus_tag="EFAGFIKM_01093"

/EC_number="2.7.7.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00366"

/codon_start=1

/transl_table=11

/product="DNA-directed RNA polymerase subunit omega"

/translation="MLYPSIDEMMNKVDKSLVVAASRRARQLREGEKSDLRGARSH

KQVGVALEEIYGDLLVVIKGQDEEEE"

CDS 1246160..1247395

/gene="coaBC"

/locus_tag="EFAGFIKM_01094"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ABQ0"

/codon_start=1

/transl_table=11

/product="Coenzyme A biosynthesis bifunctional protein

CoaBC"

/db_xref="COG:COG0452"

/translation="MLNGKKIVLGVTGGIAAYKAATLCSRLVQKGADVHVIMTASATQ

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GKGRLEEPESIVDVVERFFEQRESADISRQGGAPLLQGKKVVVTAGGTIERIDPVRYI

TNDSSGKMGFAIAAAARDLGADVKLVMGSTQAKPPENVELIPVQSAQDMYEAVTREWD

DADIVVKAAAVADYRPKEVYTEKIKKKGDTLSLELIKNIDILETLGKQKTHQFLIGFA

AETQSVEMYAREKLERKNCDLIVANDVTRTGAGFGTDTNAVHIYDREGLVEELPVIK

DDVAHRLLRIAAERIAGRN"

CDS 1247399..1249948

/gene="priA"

/locus_tag="EFAGFIKM_01095"

/EC_number="3.6.4.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00983"

/codon_start=1

/transl_table=11

/product="primosomal protein N"

/translation="MEIAKIVVDVPVKETDRPFDYLPESMREWIEIGSRVGVFPGHR

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QVPLQQLSRKYPNHAALIKKLLGGVLLESQAIKDKLNKTKMSVDLAVDIAAAQEAL

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FRDPYQGRTEFKATEPLVLTDEQKLVDNINGRLQEQRHGVFLLHGVGTGSGKTEVYLQT

IQQCIEQDRQAIVLPEIALTPQMVERFKGRFGDQVAVMHSRLSGGERYDEWRKIREG

QVKVAIGARSAVFAPFSRLGLIIMDEEHETSYKQEETPKYHARDVAVKRAQQHQAVVV

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SRALHKGLEERLERGEQTVLLNRRGYSTFVMCRSCGYVAGCPECDISLTYHQRSNNL

RCHYCGYAEAAPEVCPDCGSEHIRYFGTGTQRVEEELAKLFPGIRVIRMDVDVTTTEKG

AHEKLLKQFREKKADVLLGTQMVAKGLDFPDVTLVGVITADSALNLPDFRAAEKTFQL

LTQVAGRAGRHLPLGEVQSYTPEHYSIGHASQHDYVSFVREELLHRRNLQYPPYCR
LILVTFSEQLPVLIRLAENYTRILKEKANAAGWLGLDRFSNDAFDVLGPVASPIPR
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CDS 1250065..1250553

/gene="def"

/locus_tag="EFAGFIKM_01096"

/EC_number="3.5.1.88"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q4QMV6"

/codon_start=1

/transl_table=11

/product="Peptide deformylase"

/translation="MSIRIIVQEPDEVLHKKAKEVTKITPNVQKLLDDMADTMVDAEG

VGLAAPQVGILKRLIVIDAGDEQGLIKMINPEIIASEGEQFGPEGCLSIPGINGDVRR

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RN"

CDS 1250566..1251519

/gene="fmt"

/locus_tag="EFAGFIKM_01097"

/EC_number="2.1.2.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81WH2"

/codon_start=1

/transl_table=11

/product="Methionyl-tRNA formyltransferase"

/db_xref="COG:COG0223"

/translation="MNIVFMGTPEFAVPSLDMLMAEGYNVVGWVTQPDKPQGRKKVLT

PTPVKAAAERHGLPVFQPVKLRDPEAVARLAEWKPDIVTAAFGQILPKAVLDMPVRG

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SGSMFDKLSEAGSKLLQTEMPRLIAGETTAVPQDDAEASYARNLTRDDEKMDWSRTSR

ELFNQIRGLVPFSGAFTMWDDQVFKVWATANPDQVDLATSSDAGQAEPGTVLQLNKAG

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CDS 1251516..1252994

/gene="rsmB"

/locus_tag="EFAGFIKM_01098"

/EC_number="2.1.1.176"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P36929"

/codon_start=1

/transl_table=11

/product="Ribosomal RNA small subunit methyltransferase B"

/db_xref="COG:COG0144"

/translation="MSGNIPGRSSGKGQKANGNSSGREGNRRPNSGKSGGASRSQQPK
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FLERYVAKGVSKLQPWVRSLLRISVYQMIYLDRIPEHAVVSEAVNLAKKLGHQGISGM
VNGVLRNMIRNRDELRIPEHLPVAERISLEHSHPLWMVERWIAQYGEETAEAICRANN
EPPAVSVRVNTTMTTREKLMHEMTSTGAVVEASQLSSDGILVRSGGNMALTSWYRDGL
FSVQDESSMLVAEAVAPEVDQLVLDCCAAPGGKTAHMAEKMQDRGRIVANDVHAHKRH
LILDQAERLGLTCIDAVTGDALDLNERYPEASFDRILLDAPCSGLGVIRRKPDVKWTK
TVKDIEDIAGLQRELLDHVAPLLKPGGILVYSTCTIEPAENEDMVADFLNRHPEYSPA
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CDS 1253248..1254288

/gene="rlmN_1"

/locus_tag="EFAGFIKM_01099"

/EC_number="2.1.1.192"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A600"

/codon_start=1

/transl_table=11

/product="putative dual-specificity RNA methyltransferase

RlmN"

/translation="MKPFIYDYSLEQLQQWAVENGEPFRGGQIFDWIYVKRVNDFSE
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ICVTTQVGCRIGCTFCASTLGGLKRNLTAGEIVAQVVQAQKILDERGERVSSIVIMGS"

GEPFENYEATMTFLRIMIHEKGLNIGQRHITVSTSGIVPNYKFADEDTQINLAISIH
APNDALRSKLMVPVNRFPFEDVMESLRYYLAKTGRRITFEYALIGGVNDQPEHAAELA
SVLKNMLCHVNLIPVNHVPERKYVRTSRSDIFNFQKILSEQGVNVTIRREQGHDIAAA
CGQLRAKHMELR"

CDS 1254296..1255072

/gene="prpC"
/locus_tag="EFAGFIKM_01100"
/EC_number="3.1.3.16"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34779"
/codon_start=1
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/product="Protein phosphatase PrpC"
/db_xref="COG:COG0631"
/translation="MIKTVHVSHIGRVRSVNEDSAWIRNLDTGILGIVADGMGGHLA
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RRNVLTRALGTDAEVKVDLDTVKLEEGEVLLLCSDGLSNLVSNEQIIQVAGNLELAL
DRADRLQLALLAGGDDNITLALFELQREGSVD TETGCES"

CDS 1255069..1257285

/gene="prkC"
/locus_tag="EFAGFIKM_01101"
/EC_number="2.7.11.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34507"
/codon_start=1
/transl_table=11
/product="Serine/threonine-protein kinase PrkC"
/db_xref="COG:COG0515"
/translation="MIGHQLGGRYEVIERVGGGGMALVYKAQDLLNLRNVAIKVLRQQ
FVHDEEFIRRFRRREQSAASLSHPNVVSIYDVGQEDDVHYIVMEYVEGKNLNEIIKER
APLQVDESVRIASQIADALDHAHHNQIIHRDIKPHNILIGRNGRVKVTDFGIARAVTS

TTITQTGSVVGSVHYFSPEHAKGIVTGEKSDLYSLGIVLYQMLTGQLPFLGESPIVA
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ETKIDFPDEDDIDQTRVMPAIKPEPRGVTSTGAVPVMESDEETGKGKAKSKSWKKPAL
LISLTVLILIAMVGVVWYVKGMLVPEVTPPNVITQTEEKAREMLEEKGLVVSDEVIR
LYQEGVEPGIVYDQSRKEGDVVKEGSEVQISVGAEKELLMIDVKQVTYDEAVKKLTA
LGIKEDQIQRKDEFNSNDVASGSVISQTPGVNEEFDPAIVQIELIVSKGTETVKMPDLK
NLTRSEAEKKLSAGLELAQVQEESYTIIEKGKVTQQWPVEAGTEVSPGDKITIFIST
GYPPEALQYPFNINVSPKEEGKNSKIRITYEDARGKNQEWGTRTVNSTQTLTIPLVLA
PNENGAVSVYRDGQFLDTYLVSYSDAKNGTVNVPSIDPEQSTETPPENEPDPGEGSVD
EGSESVDPNQEGEPESTPADGEGDSVDEEDTSAMNNGKGHGKEKEKKKEVINASSRP"

CDS 1257347..1258255

/gene="rsgA_1"

/locus_tag="EFAGFIKM_01102"

/EC_number="3.6.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34530"

/codon_start=1

/transl_table=11

/product="Small ribosomal subunit biogenesis GTPase RsgA"

/db_xref="COG:COG1162"

/translation="MPEGIIVKALSGYYYYVMPVEDNGVPSVEGSAVQCRARGIFRKRG

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DKFLVHIEQAGLDALIVLTKLDLADPAKDTVAEVKALYEQVGYEVISTSSRTGEGSEL

LRDRLAGKISVFSGQSGVGKSSMLNALMPGLTLETNAISMRLGRGKHTRHVELIPLD

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CDS 1258257..1258916

/gene="rpe"

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/EC_number="5.1.3.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P74061"

/codon_start=1
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/translation="MIKIAPSILSADFARLGAEVAEAQAAGGDWIHVDVMDGHFVPNI
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CDS 1258920..1259171

/locus_tag="EFAGFIKM_01104"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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YFRKFDRTGHRVTFVIFGILYLLSVFMIAAYQYIPAQT"

CDS complement(1259614..1259802)

/gene="rpmB"
/locus_tag="EFAGFIKM_01105"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37807"
/codon_start=1
/transl_table=11
/product="50S ribosomal protein L28"
/db_xref="COG:COG0227"
/translation="MSRKCYVTGKKPGTGNHVSANNRNRRTWGVNVQKVRILVDGKP
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CDS 1260479..1262251

/locus_tag="EFAGFIKM_01106"
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/inference="similar to AA sequence:UniProtKB:Q7A5Z4"
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CDS 1262280..1263143

/gene="degV_1"
/locus_tag="EFAGFIKM_01107"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P32436"
/codon_start=1
/transl_table=11
/product="Protein DegV"
/db_xref="COG:COG1307"
/translation="MSHKVAIVTDSTADIPEELIRKYGIHIVPLRLLFGEETYADGVD
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LFFLVDTLEYLQKGGRIGKASAILGTLLNIKPILSIDEEGVIYAVEKVRGHKKAMARI
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VIAIFMWPVPE"

CDS 1263154..1265199

/gene="recG"
/locus_tag="EFAGFIKM_01108"
/EC_number="3.6.4.12"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P64325"

/codon_start=1

/transl_table=11

/product="ATP-dependent DNA helicase RecG"

/translation="MKLEEISVKQINGVSALKEGELHAFGISTVKDLLEYYPFRYEDY

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FQLKMQAYRALNRNRMDGVVHTTDNTTIREFVRSLPFELTDAQKKVELEILHDMRSPY

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MMERVLGFISREVDQGRQAYLICPLIEESEKLDVQNAIDLHVQMQQNFPKYRVGLLHG

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RVGRGAHASYCVLIADPKTEVGQERMKVMTETEDGFEVSRRDLDLRGP GDFFGTKQSG

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CDS 1265315..1265602

/locus_tag="EFAGFIKM_01109"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGYQQYGISPQLVERIKLKMKNPAVKERIKKLIDGVTKSDLQDK

AKVRRVLVKSSAVIMNENFSPAQEEQFVAFVLAQKIDPNNTFHLIKLWGMFR"

CDS 1266225..1270682

/locus_tag="EFAGFIKM_01110"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTLTRGFKQKIGGKVI AVITVVS LTWGSWGAMPLSASTTNTLKF

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FNETDEQGIPKNYPFAQEARDVRTSPPSDYNQVNHQEIALQAAQESVLLKNDGTLPL
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NVPVTEPVSYKISNANVTVKELGYVDVDADISAAVSGVHDLVLFHESDLRIDSLSFT
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VQTGDVADQAKAASIRSSGIRVIGDPWNVSIKDKQNTYVIAALPVNDVVAANSTAIAY
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GLMEEGQYLPNVPMSPREDMAMVLVRALNLSGVDMKLQEAIESRLGDFKDQDQLKPNN
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CDS complement(1270716..1272296)

/gene="cheB_2"

/locus_tag="EFAGFIKM_01111"

/EC_number="3.5.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00099"

/codon_start=1

/transl_table=11
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methylesterase/protein-glutamine glutaminase"
/translation="MYTYIVVDEPLIRKGLLKKIGTFEHSLELLGEADNGADALALI
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SSIKTPVFRSAEFAAIMASDQFILLTIYGPQPLTAQQLPTFSNGLYIPHPQTDQVLFF
LMHDLDCSGQLDLQKMAEQTASIILTKSETTECCVGISLPHTGIGGVREAHHQTILAL
DERAITDFGKCYVFSREQIPLHQLKWARTYELLFFIECGNVPKAEELITDFFAFYIRQ
PDALLAHLKEQCRDIITETKRLLSNYIQNGGSSSASSSLEAVLNVSFDMECIRHYMVK
VLTGTALLLKEDNPYASDQVIDNVRTYIDNHYTKDLTLEWVSSLFYLNPSYLSHLFKE
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CDS complement(1272304..1274112)

/locus_tag="EFAGFIKM_01112"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MILINIKTKLFLVLVLSIVPIIIVSVSSYRSYTKLVNEQTSLV
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KGDLYIGEVGVPYIINAKESIGFSRALYDPNNNEFLGVFMLDCSMNIFDGLKRNPA
SLSNLYLANDAGEILYSSDGSRVGTPLSDTLAAATHQVGNSSQYKSIQDNMMTVIQV
PGRNWNVIANISMDRLYEYENISQKLLFYVAVSCAVIFLLLSFFLSNLITKPIIELTK
LMRKTCKSHRFVTIKPQVTRQVDEIGILYHEFNKMMKDIDTHIRESYQNKILMLDSQMK
ALEAQINSHFLYNTLESINSIAEIEVESIVVMTKSLGDMFRYSIKTSELVAVSEEL
QHVENYMAIQIRYGDKFAFNLNVDPEIRSRRMLKLLLQPLVENAIYHGLENKRGKGS
VTITGLFQGDSIVFEIWDDGVGMSSTQAEELRQLLQQPPEFIAVGQRHKQSIGIKNVH
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CDS 1274244..1275575

/locus_tag="EFAGFIKM_01113"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKRKRLWFLTLVLLMMFLSACSSSSQEGSGTDTNNGSTDESEK
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LDFLGVYYNKELLQQAGYSEFPKDWPSFLDLCQKLQAAGVTPIAMGDKDPWMIQFGMY
PIAANVVYPNELDFDVKLQNGEKSLTDPKWVQTISKYKELYDNNYVVKNSLGIGSAQS
AQLFIDGKAAMTFTGTWDYASMTSKGATEFTRGFASLPGNEPEQPVFVSAATSAGYAL
NAKSANLDAAKEVLNLYLFDGESDLFKAFVEANSSISVYKDVKLENQLFKEVNDNYQQT
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CDS 1275661..1276539

/gene="melD_2"

/locus_tag="EFAGFIKM_01114"

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/inference="similar to AA sequence:UniProtKB:O34706"

/codon_start=1

/transl_table=11

/product="Melibiose/raffinose/stachyose import permease
protein MelD"

/db_xref="COG:COG1175"

/translation="MSSTVMKKSMYWFALPALIFYLTFWIFPILRLFQYSITDYNGYA
QAYNYIGFDNYKELFRSDILGISLKNTLIYFVTVIAGNIIGLAMALLLNMKIRGTGI
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FVEIWKTIGTTMIIFLAGLQTVPSDLLEAGRIDGCGSWRLLRHVKIPLLATAITINVT
LSLINGLKAFFDFPFIMTNGGPGTATNTLIYTIYKMAFTEQLFGKASALGVISFAVIIV
ITAFFVLKMNKREVS"

CDS 1276536..1277372

/gene="melC_2"

/locus_tag="EFAGFIKM_01115"

/inference="ab initio prediction:Prodigal:002006"

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/codon_start=1

/transl_table=11

/product="Melibiose/raffinose/stachyose import permease
protein MelC"

/db_xref="COG:COG0395"

/translation="MTLRKVLGKGSVQVVLLVMALNLIPLIIAFSTSLRDPSNNTNP
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KFMYLFFLSGLVPAQMVLPIVQMINALHIPTNQYTPIFMFITCSLPFSTFLYTGFI
RSGVPVEEVEEAHIDGAGLFQRFWTVVFPLLIPVTVSVIITQGVWIWNDYFFNMIFIS
SAGDSPLPLAMIGFLGDQQNPTQWNVLFACFLCALPMLLAFLFLQKYFIGGMTVGAV
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CDS 1277386..1278939

/locus_tag="EFAGFIKM_01116"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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PCEVGENFAEYSGWLSRSWLQDEIVNVDVLPGLTLDRRYAFRYLKIEVVETSIRYDI
RINDIYCMTVTSADIGAVPQLPEGIDTELLEIDRLSVKTLRDCMQTVFEDGPKRDRRL
WIGDLRLQALVNYETFGCNDLVKRCLYLFAGTRLEGGQVGACLYEQPEPYVDDIYLYD
YALFFIATLWDYFEATKDRETLEELWPVAREQIEIGLKRLDERGIVRDDDTWYCFLDW
HEELNKQAGAAVLIYSMKRGRSIAKELGLPEYEEWINAHIKDAEQAALHLWDGEGQ
FFISGEKRQISWASQVWMVLAEIMDAPAARQLLDRLTSSGEAIGMTTPYMVHHYVDAL
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SYFIRRNFS"

CDS 1279672..1281339

/gene="ypdA"

/locus_tag="EFAGFIKM_01117"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AA93"
/codon_start=1
/transl_table=11
/product="Sensor histidine kinase YpdA"
/db_xref="COG:COG3275"
/translation="MEMFTMLLGLFERAALLIIFLFLSRVPRFRQILQKGKLRWQEY
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FRSIDEDSLRKICRIIQEDIQADAVAITDTRNVLAYVGFGEERYHIGNEIISEMTKKT
ISSGEITISNDVIDEKTDPDIHSLLIPLKERGDITGALKIYYRKAYKITYPLQTMVAG
LSQIISTQMEVSRVEEIKAAANKAELRALQTTIHPHFLFNALNAIASSIRTKPDRARE
LIVNLSGYMRYNLELSDELIDIHKELEQVRNYVEIEKARFGSRLNVIYEIDEVAVHIP
SLVIQPLVENAIIHGILKVKGPGTVRIRVQDYPEFVRISVSDTGAGISADIIERVYHD
RMPGNQIGLYNVHRRVKLIYGQGVTTITRLEQGTDILFDVPKGDVVTR"

CDS 1281350..1282150

/gene="ypdB"
/locus_tag="EFAGFIKM_01118"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AE39"
/codon_start=1
/transl_table=11
/product="Transcriptional regulatory protein YpdB"
/db_xref="COG:COG3279"
/translation="MRALIVEDEILASEELNYLIQEHSQIEVDRLEDGLDVLKFLQE
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INLLRNDNIIVTDTADIYYAEAEQKVTKVYTKNGEFTMPVSISDFHSRLPQDTFFRCH
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CDS 1282271..1283566

/gene="yhjX"

/locus_tag="EFAGFIKM_01119"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37662"
/codon_start=1
/transl_table=11
/product="putative MFS-type transporter YhjX"
/translation="MKATISSVSSTPESTSAPTKMNRWLIVLGTIIVQMGLGTIYTWS
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LILSSQVTSLLYLILAGFVVGFDGTAYITSLSNLIKWFPERKGLISGISVGAFGTG
SLLFKYVNTALIGAVGPAQAFMYWGIIVLVLVAGSFLIREAVVREQAPASKEGSKQV
VARHDYTVKEMLRTKEAYMLFVIFFTACMSGLYLIGIVKDIGVQLAGLDVATAANAVA
MVAIFNTAGRIILGALSDKVGRMKVIAGALLVTAVAVMTLSLVPLTFGIFFACVAAVA
FCFGGNITVFPAIVADYFGLKNQSKNYGVIIYQGFQFGALAGSFISALLGGFHLTFIVI
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CDS 1283827..1284309

/locus_tag="EFAGFIKM_01120"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MKFIKYTQPDFDDYYALVSNMEVMKQITERAIPQEARTQFESM
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CDS 1284446..1285387

/gene="glsA"
/locus_tag="EFAGFIKM_01121"
/EC_number="3.5.1.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q5KY26"
/codon_start=1
/transl_table=11

/product="Glutaminase"
/db_xref="COG:COG2066"
/translation="MSNSTMERLNALLPEWLETSSLHTGQGVASYIPELIKASQDEL
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EVFQSESESGHNMNRSLGYFLKHNGVIKDDVEDVLAVYFRHCSIEVTCADLSRMSLVLA
YNGTDPITGEELIPRRYVQIAKTFMTTCGMYNASGEFAIEVGLPAKSGVSGGILTLP
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CDS complement(1285602..1285943)

/locus_tag="EFAGFIKM_01122"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSKKLQQNGIFESSRMMLPEHREAYILHQEQLAPRTRPSLDAQA
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NLITDVALADD"

CDS complement(1285940..1287184)

/gene="dinB_1"
/locus_tag="EFAGFIKM_01123"
/EC_number="2.7.7.7"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q47155"
/codon_start=1
/transl_table=11
/product="DNA polymerase IV"
/db_xref="COG:COG0389"
/translation="MPRQDRRVIMLADCQSFYASVEKSAHPEYKDRPLVAGDPARRS
GIILAACPLAKSYGITTAERLGEALAKCPDVVVVRPMSEYIRVSLHITRILQSYTDL
VEPYSIDEQFLDVTGSLDLFGSPETIARSIQSRVMDETGVYIRIGISDTKVFSKMACD
LYAKKVPGGICTLVRKDL PSTIWEKPVRDMFMVGSRMAQHLYKMGVHTIGDLAQTPLS
RLRERWGVNGEVLWRIARGIDDSPVKPGTYAHQQGIGHQMTLPQDYDSWEDIKVLL

ELAELVSRRSRDKSLMGHVSVSGCRGQDYDRPTGFSRQMKVNEPTNITDEVYDAAAAL
FLRHWDGLPIRRISVSLTGLVPDSEVQLSWFDDRERKRELERATDDIKRRYGDТАIMR
ASSLYSSAQAHERSYKIGGHYK"

CDS 1288096..1290267

/locus_tag="EFAGFIKM_01124"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVTGGIFAGWHYMQPKLVITYAENGTEMKFKTDGDRFMEYGPDG

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CDS 1290294..1291502

/locus_tag="EFAGFIKM_01125"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFPSLALAYLFLYICIALVVVGIVLFFAMKMSHNGKRRKTAFYE

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REAGFVEHDLKELGRLRYGRQIDAAYRLGGMRCPEAVPGLMELLKDEKPGPMAIMIGR

SISRCTTQQGELKDMLALLLTGKSIHHLAADILLETSLDTSRILIELLEDNRNPDFVK

VGLVAMWQGAVPEVMPALDRLVGAEHQDVRAEAVKLYLSASPALRDETILKLIQDPDP
EVRAEVVQALGSKHASGSIPLLRKALRDEDWRVRYNSAESLSKLGEPGFEALCQAAVQ
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CDS 1291525..1292925

/locus_tag="EFAGFIKM_01126"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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VPNTKIRGKIACQKIRGIYHNPEFPDLYVIDKENGGKADSLNAGINLSHYPLISSIDA

DSLLEKDALIRMARMYMEENPEETVAIGGDVRIANGCKIENGAVQDVSLPRKIWPMFQS

IEYLKAFLGGRIGWSHMNGLIIVSGAFGMFRKDAVIAVGGYRDGYPGEDMNIIIKLHR

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VMGMVTPMPYNVLFALNPYFRITGLLALAGYVLLDMTQWPILVLFLLNFVSGYLLSV

GALVLEEIAFKRYNKLSDLVKMLVYSALKFVGYHQLGVWLRLQGHVQFMQNNNSWGTM

TRQSWSEDEKKTSEAA"

CDS 1293201..1294004

/gene="rcsC_3"

/locus_tag="EFAGFIKM_01127"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00979"

/codon_start=1

/transl_table=11

/product="Sensor histidine kinase RcsC"

/translation="MPNTATLQREAAVNRYRSVEQGLKETGAETCGLMFIHCAGNSQP

EQQVRTHLEQTSESAFQVWKDGATQAIALLPGLTLDEVHYEGLRIKHELQETVPGAD

PQITLASFPEGERPSKATIQHMAESSKLVDSSSEIHYTLDNDADEPERILVDNDPTV

REFLQLRLKMQGYETYEAVDGLAALELIEKVTPDLVLTELNLYGIDGLPFIHHIQNLE

MEHPPKIVVLTEQ RVEQTISQCFRSGVDDYMTKPFSPVELDARIRRLH"

CDS 1294159..1295526

/gene="wbpA_1"

/locus_tag="EFAGFIKM_01128"

/EC_number="1.1.1.136"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:G3XD94"

/codon_start=1

/transl_table=11

/product="UDP-N-acetyl-D-glucosamine 6-dehydrogenase"

/db_xref="COG:COG0677"

/translation="MENQQFHTLLNAIENKEAVLGVVGLGYVGLPLAVEMVNQGFTVI

GIDLDASKVESIYQGDSYIHDISSDELKKVMQSGRFQPTTDYSMLRVIDALSICVPTP

LSENQDPDTSYIETVVDQIKLHMKPGMLITLESTTYPGTTEELIQQQLDKIGQEAGKD

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MSKLENTFRSVNIAFVNEMAMMCDRMGIDIWEVIDAAATKPFGFMPFYPGPGIGGHC

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EALLV"

CDS 1295535..1296458

/locus_tag="EFAGFIKM_01129"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRQRGKLVGMAKWAILAVVLCLLLLSWMFKWFSAEHKAATWLWD

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NMKAWTKAGEDAGLYMSAAIPFWLDARQSAEGEGTFSRWVISHFDAVIMAYRDSGQQ

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SSFAGVAVHHYEAUYAKENGIPLARKNEEKE"

CDS complement(1296717..1297589)

/gene="rhaS_5"

/locus_tag="EFAGFIKM_01130"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MTESMKEDHHEFLDIIFFTPSEFEKAGGAWPIRIGRNIAKTNYH
IGPRTTPYYYLLFVLEGEFTFIQNGQRHALRARDAFCLFPHVTHEYWTDPEDTLQKIF
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FLTLDRIARSPATKGLQPDSATPWLQKGKEYMDIHFAGGISVEGVSAHAGVDRTHFA
KQFRKAYGLSPVQYIQQLKMNQAKRLVQTPLSLTEVAHSVGYPDLSFSKAFKKQVG
LPPNRYRTAESTKE"

CDS 1298071..1298253

/locus_tag="EFAGFIKM_01131"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEGTSILKKRSGHLYPRIFTFKKGESKKFKDNSDRKNDSYPER
QGGVTVTFFNMRLYYs"

CDS 1298269..1299471

/gene="ssuD"

/locus_tag="EFAGFIKM_01132"

/EC_number="1.14.14.5"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80645"

/codon_start=1

/transl_table=11

/product="Alkanesulfonate monooxygenase"

/db_xref="COG:COG2141"

/translation="MSEQEDMKFGWFLPTAGDGKYVGVAPEEPSLDYLIDVAQTAEK
AGFEFVLIPTGGACLDWVVGSAVMSHTKTLRPLVAIRPGLVTPVLAARMGAALDQLS
GGRAMINVVTGSSVRDLEELGDPLAHADDERYVRASEYMEVMKRSWTQSTGLNLTEFA
GSGSKSGADAPSDPNPEFNGQYYNFKGPVGMPETVQNPHPPFYLGGSSPIAKKVAVEH
ADTFLMWGEPHDWIEQIEEIEVIRQQVKEETGQDRQLRYGMRAQVLIRDTEEAAWAA
AWEIISKVPPEAIEKAKAAFAETDATNQRRQNELRELSEKQQFVVGPNLWTGLSVVRS
GGAILIVGTAEQVAERLMEYGD LGVTTFILSGYPHLEAEIFGRTVMPIIREKWKTRQ
KQHQVTTN"

CDS 1299686..1300960

/gene="msmE_1"
/locus_tag="EFAGFIKM_01133"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q00749"
/codon_start=1
/transl_table=11
/product="Multiple sugar-binding protein"
/db_xref="COG:COG1653"

/translation="MKKNKKLILPLVSMMLVMSILLSACGGGDNASSGENGSSGSGKVT
ISFMHWRGEDSEALNKTIDAFEKENPNINVEMQTLPSDQYQSTVQSKISDGSVGDVFA
SFPGAQFEAFTKAGLFTDLTGSSFLSAYNSKLIESGQHDGKQYAIPYQLVYNDPIYNV
KLFEQYGLTPPTDWEGFLALCQKLKDNGIPIAFAGADIGPGQFMNTMVMNNAAPSDDI
FTKVEAGEAKLTDEFWVKTLTQIKELNDKGYFQQDALGTKDPAAGALFIQEKAAMLAS
GSYQLAQNKQQNPNEQKLLAPITVSADQAKYEGVHTTTFMLAVNSKSKHPPEAKKFL
EFLSNPEVASDYANQTGQNVTVNDVKYDTPELQVAGEWATKKTVFQPRFTILNGDNQK
AVTNSIQAVLSGTSPEEAAQQAQAIIDQHIGK"

CDS 1300964..1301836

/gene="melD_3"
/locus_tag="EFAGFIKM_01134"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34706"
/codon_start=1
/transl_table=11

/product="Melibiose/raffinose/stachyose import permease

protein MelD"

/db_xref="COG:COG1175"

/translation="MKNRLQLSLFLIPGLLLYVGLFVFPTLTGLFYSFTDWDGVSPSY

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QVWAHAGQMMIVFIAGLQGIPAELYEAARMGGSKWQVFRTVTWPLLAPSATIVVAYT

TIQSFKAFDLIFTMTDGGPNYATEILTTYIYHTAFGSYSFGLASAGSMIFLVLLALLT

LLQFKALRADRVSY"

CDS 1301886..1302701

/gene="araQ_7"

/locus_tag="EFAGFIKM_01135"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MFLKWFNRLILLVYALLILVPLYFVFVSSFKTSSNFFTSPFSWP

DPFTWDNITGMFRNQPMWQYFGNSLVTLGTVAIELLLSSMIAYAIVRWGGSVGKIVF

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SEILEAGSMDGASEWRLYTRIALPLAAPSLAATATFLLVMVWNDLLIPMLMLSSKSKL

TLPLALMQFRGEYVTNYPMMLTGVLVTAIPMIALFLLLQRYFVAGLTAGSLKG"

CDS 1302815..1304032

/gene="naiP"

/locus_tag="EFAGFIKM_01136"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34691"

/codon_start=1

/transl_table=11

/product="Putative niacin/nicotinamide transporter NaiP"

/translation="MSKLEVLRNPKQRKLLFSAGMSWLFDAMEVGMISFIVAALAKEW
SLSPGQVGVLTINSIGMALGALLAGALADRFGRKAILMWTLTLLIFTIASGLSALATGF
AVLCALRLVAGIGLGGELPVASTLVSESMPTAERGRAVVLESFWAGGWIVSALIANF
VIPEYGWRIAFAIGALPAFYALYLRRAIQDPPRYKNHTKLHKITFREKVATVWSAPHR
RTTLMWLWFTVIFSYYGMFLWLPSVVMAGFTLVKSFQYVLIMTIAQLPGYFTAAY
FIERYGRKFVLVVYLTLTAFSAIAFGLATTEATILTAGICLSFFNLGAWGGGLYAYSPE
LYPTSVRSTGVGLATSVGRIGGVLAPLMVGMLVQREVAISLIFTIFFVTILIGAAAVL
FWGRETKGQELAE"

CDS 1304311..1305198

/locus_tag="EFAGFIKM_01137"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMKNNIGMDQPNELNEMNMISELDSVSEIKEMKVSHMNSNERT
TV DSTNEGLDLLTFADNMEPITVSRKVTHGKGNTAGKRAGRVSMLLGACALTGLTVA
APSAGAQKLEQGVRSEHVLQLQEQLSDLGYFDAGMTGYYGTITKSAVRKFQQAQGLSA
DGVAGPATLNLNKKAKAEGETLRQLAKLIHGEARGESFEGQVAVGAVVLNRVHSSEF
PSSISKVIFQKGQFTAIDDGQFNTKPTQTSYRAARKALNGADPTNGALYYYNPKIATS
VWSKSRPTLLTIGQHDFTR"

CDS 1305792..1306154

/locus_tag="EFAGFIKM_01138"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYRMVMILAAMLVLILGGCAGVNEKKIKDQEIINRSEAMAIEY
LKNTYNLEVTITDKEIMPKMAMSWVTYVGHVKEHKEQTFSVSINYETNKQESFIYSQQ
LKSALQEEGYILNKNATQ"

CDS 1306170..1306463

/locus_tag="EFAGFIKM_01139"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEATVRQDITDLNYRTMSQIAYLKVEEGQEIDVPGWQVLDQKHN
VSGMDAVTFYNPETKQAVIAFRGTEGDAIPARSVPDFRTDALHIGFPEIGATI"

CDS 1306584..1307465

/locus_tag="EFAGFIKM_01140"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGSFNQLYEAESYVKSM TDQHKDLQFSLTGHS LGGANAQYAAVY
TGLNAVTF SAPT VVASLTPEMRRKAE EGVFDGQVTNFIHPGDGIASGFFGGYERHVGA
TFLIDSNYADGNENYGINVWAKVVD TFFEDGPKYHDMKHYSFDQDGYIDNPLYDEV TG
ERVNFSPRKPSEHNILDHAREAWDTLTKGFKSVANVVG GYSAGTIELTPEELQETADK
WRRQAQDM SCTFERIQRNFFEYTES SHSQRLVPIVWDLQMSIKQLDEWHLEHTSELVD
YINQKAEDFIQADSGAQ"

CDS 1307529..1308743

/locus_tag="EFAGFIKM_01141"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKIMLPIMSAVVVVSTLISSQASAATTTFKDVQANHWAKSAIE
SAVSKGYFKGYGNGLFKPNASVTRAEFASLISRVAKDMTLPEDAQTDSFKDLKGHWSK
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LPVKESFKPGIAQDKIPYLAVAMGTNLMNGFPDGSFGMDKTTTRAESSAILLRLENVL
KKEAVTFDDLNELRMMGT KKTNLELVSSLTGKTSIADISGKRKTRNGSGSLVFHRL
IGINTSEPKKKDSIYTS LFMTEFGMNKYKNSGLLPVFTEITIYPKKN GFAIGDLVSGV
IDMNGRGMTITNKLDEKYGYVTPNIETAKFFAKYKNGVKVWMVDYLEIKDFY GQFNM
DDGSYAVISNNN"

CDS 1308757..1312167

/locus_tag="EFAGFIKM_01142"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKKWTVLSLLVILIYSFGVMSIKTYANFKNGYPDKDIEVKPS
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KPNYKKGSLLVTIETRTGTDKVDADNNSDFKYKDKWDYGIRQDGDKKYQVEYLTPLEI
DYSGYVTETKEIRVREDMQLQLNDVKSLVAEIRTKAYDQEEFGNWINVSKRADQIEWS
SNKQNVVYVEPKTGQIVAKNIGTAVITAKWKNSEKGPYYIYENVTITVGDTPPPEIPE
TPDAACAESPVGEMTGERMDPNASAVIKADQRGSEPFVLRGIPTSESLYGNVFGLSY
LFQNKFVNMQGTCTYTVVEKTYNKTWTDERKVSDGKGGTTTVSTPRSRDVKVPYTYT
VKRDFEYWKIDTLLVYEITDAILKNYALPQIELYPADYRSPYIAAATNGTFYAPNTPA
VLTAPSQPVPGGTSEPPTPTDDLSSIAEDAVPKVQVKNDYLFNGAVVMDNAKVEETG
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EIPGINTVTVHTPVVNYSLVSDDQPHNQKTIPNMERSALILERPFTVRIPTSGQHLDV
NSYPGYGDRDYAKYYRIKQVRFPFDVYSADQTQFYPRSTWIDIPVYVLDTTFYLPVWV
DEGDYQVEFRNIAENAPADFESMSRSNAQPDANTDLTYHLASDEVSVIEGRLYDFEI
TDIADYNWELVFRRFKSGSIAPTWSYWTGTQGIDGDKRGNKPQFTVPIRPGSHPLQGY
QNVAVKTGYHFKFDFKTKGNMFGPRDGIRLTPTFDVSKDGKTHVPVDLYYSTNQRSF
IRIGSAEDQVKRFVILNDRLRQVPSEQLRDTATYKYNRYGEIHPGMMSERTYQEYYRD
KFTKMKTPVGGYSLLLMPEQLRTFIGPKTNIPTNASADVLRTNAAIQQWYGEYSLPAE
PYVVQAGTNLAEYGRTHGGLDAKSPIFLKNGYIVVNFNLESIQEGNLGAPHLQYIHAP
LMNQWLLEGFQRQVEDSYGNSFTLRDGDVVFYHADRSSRDDFSAQVPH"

CDS 1312275..1313459

/locus_tag="EFAGFIKM_01143"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSRIQVTPERLFEASREVERTRARMSDTREELVRLIRWMESMWS"

GMVRERFLERFEETQPRMIETLEHLTHIAKELRDIGVRFQQADEMSGAAVAGTVATMS
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GAVEPPNQDLIQLQIEALELRVNPFTGEPVTDDYAKMMISL KWSQIVAGIGLVTGGL
SGGKGPYKGRGTNPAIAKVQTIKDAKAKREKSSNDANGTSKGLKIPQGLTQKQFEKV
SAMIRKKVGHLSDDIVVQGSRAKG TAKATSDIDFAIRVSPEKFNELIKDSFSKIKAPN
PGSAKEKTMLHAIETGKIQS GEAKLSKFRELLQQELGIDVDISI IKIGGRFDNPPFTP
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CDS 1313475..1313852

/locus_tag="EFAGFIKM_01144"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEYQYDLFTKIFLDTDLEKTSVVETVSIMVKGSAAGSSIVTEQA

EILIFNNGDFDEERRNRGSDEFLYYKYLDIEPIEGVEETLYITEISKILTKLWDSGY

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CDS 1313943..1314671

/locus_tag="EFAGFIKM_01145"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVRKKSGVRKEEELFKGLAGIAMLGGSAGTYLLTSSWKASFVIG

LLGVVGVVVLMINIQSKRIKRLKKS GIAEIDQMDGIKFEHYLAYLFRSQGYKVQVTKA

VGDFGADLILSKDGKRISVQAKRYSKNVGIKAVQEAQSSVAHYGTAEAWVVSNSDYTS

AAYELAKSNKVKLFNREALIEMILAVNPQGTATPQVDVAEIDRDENICPKCGNDLIQ

SGPRGPFYGCSSFPKCRHTKSPNP"

CDS 1315175..1317157

/gene="rhaS_6"

/locus_tag="EFAGFIKM_01146"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaS"
/translation="MNWEEYIQMWDNSSIQLVDIRQLVISSGGKQQYLLPVSGFIYIV
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QLKLQGVTSKETDMVEEIIQYIHEHYNESISLES LAELWNYSIQYLSKQFKLRTGRSP
IEYVIQARMAKAKELMIRTDATAQEIASSVGYSDFYFTRLFKKQVGMPGQYKKKMK
DSLVDSDSPWEGFVSSMGKHSSSCYVINDNHYQYKTEGDWQMFKGTRSKMVLTLMLCF
TIILSACTSGNSSRTNNQGAAGGNSNQSAESTQNVTSTNEAKEDSTRKLSTVMGEVSV
PVHPKRVVVDWDLGPVLAVGVTPVGASSTQMNFAKFLKPYLPDVEDIGLEGSISLEK
VLDLSPDVITWNPAAYESYSKIAPTVMFETSKYSTIQEEITAMGDILGRREEAEKWN
ADFKRTEAARNKIKNVIPKDATISVDYVTVDKFLMVIGNAGERGGGRATYDILGLNP
TPKVKSDIIDKNEDRIEVSWEVNDYVGDYVIVLKVEGQEPTNLPATWTS LDAVKNNH
VIEIEMEKEYFAADSFSSLLQAEDIADKITKMAATAK"

CDS 1317380..1317661

/locus_tag="EFAGFIKM_01147"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKFLKESLIVITLIVIASVTWYGSYKNDMKELEDGLRTYLIVEK
GMDEHDIISITARRSKMPQYPVVVKLKDNPQEVVYTQREEQWVQLWPDP"

CDS 1317996..1318874

/locus_tag="EFAGFIKM_01148"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKNSKTFRVGAI AVALVIIVGVLMVTFFLTRIPNGYVGVVYSPN
GGVKDSTLSQGWL VGAFDKVTKYPIRIQTVEYRDIQIATSDGKNITIDFAYNYQVEP
SKVSSIFNTFGPISIQEIEDTYLKTRFRDAARKGISKFTVIDVYGEKSSEAGVDVQQR"

FSDDVKELGFIVSNVTVGVPQPDAKTQEAIKDRVEASQELERKTTELEIAKKEADRKR
VEAQGNADKLLIEAEGQAKANKELQQSLSSQLVEYETIKKWDGALPYVSGSNTPMIQL
PTTKTEQNSGAGSVSP"

CDS 1319089..1319841

/gene="yaaA"

/locus_tag="EFAGFIKM_01149"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A8I3"

/codon_start=1

/transl_table=11

/product="Peroxide stress resistance protein YaaA"

/db_xref="COG:COG3022"

/translation="MRIISPAAKMKIDTDLMAIAQMPRFINESEQLLSLLQELSYDE

LKAMWKCNDIAIEQNVERIQNMNIKANLTPAIYAYEGIQYQYMAPGVFQNEELAYLQQ

HLRILSGFYGMLRPLDGVTPYRLEMQGKLQGPFGKSLYQFWGSKLADQLQSESNYILN

LASKEYSKNILPFLSEETRFITCVFGQMVNGKLVEKATWAKMARGEMVRYMAEHKITD

VKDVRNFDRLNFAFSEERSDESTYVFIQAEGQ"

CDS complement(1319981..1320505)

/locus_tag="EFAGFIKM_01150"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMMKKQSKIIIVVVLLIIAASTFVLIENSISKKEIEINSKYTT

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INDFLIFRGEYGYLVRDQLKGSRADSEVLKMKVVKQVKLFLDLPNEYENSKEFSDQFS

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CDS complement(1320505..1321278)

/locus_tag="EFAGFIKM_01151"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MKNMNKSSIAIVIALIIFTAISSAPAHQNMGEYYHKGNAYSSY
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FTSGTEQNLSNPKNGLTFLNPTNASLSNNISWKDANQVIGSKKNSGAAAEFHFTVAN
GNQINVAPQARVQYGLYTTNTIIPKLSNYAYVNHTLN"

CDS complement(1321278..1321943)

/locus_tag="EFAGFIKM_01152"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRKKKVLISLGGLFLFVTSLSLFAGVGAASKPVT FDTSTPITFN
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LTS DGEYLVGSGGSIDL NMDGQKHNLSSILVSHFELKNGTHLLTGSFETEIKQDDG
TLVPSTVSFTSIVETGEGIYSVTMG TIEDGPVVL MFGDDSFATQEIRDIIRAQANFEE
DAL"

CDS complement(1322845..1323408)

/locus_tag="EFAGFIKM_01153"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRKLISLALILVLVLSFNVAAYADGDVTQAKPMTKEEIINSKEF
REAVKAAKA EFESQKADNAGGPVL FAPAPKVSHINVYGVVSPNGGQEIYGFNNNPLST
TNDHGGAWIQCITFQIGYDSSHYGTLAGNTMTNNWSE AIDL DGDRVVD AWAYS WVYEA
PTTGGQFVGT VYSINIPTQWTAWINIR"

CDS 1324192..1324659

/locus_tag="EFAGFIKM_01154"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MTQERFYDEFARSRPVLQKALESMVNTSMELKDIATRFENVDAE
KVSLGSAVSALGAGVMMKTSRYYAGSDDKGYRMAQVNVYGKLMWMPVNEGVTDQAAL
QAYKKDQGHLDINRMQATDAEAPGKIFMRCRSKLLKIEFIPSQASLYPISMLR"

CDS 1324656..1325078

/locus_tag="EFAGFIKM_01155"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MMLTSLKFSQLFMAFQMVRGSMPPGGKGPFLPSSHPAVAKIKKN
LEAAEARKANGQKRGSEVTGQVSKSVISGHVSDAEKLHRPYDHLNVVDGFKRGSRPV
SGGHNMNKFNETLQEDADKYGLNIKKDYIIGEPNKHNI"

CDS 1325091..1325387

/locus_tag="EFAGFIKM_01156"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEYQIPSLKRSESDKSIFEPITDTNGNVVGKRVNDPKTVYDPNI
ISNEKMYNWWGKAALEPQIQAGNVKNGIVKGELNGLKFVGFVDDKGNIKNFYPAF"

CDS 1325407..1325784

/locus_tag="EFAGFIKM_01157"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MMYKILTTKAEIDRSVESYFWIIDFPRALTYFGDHERHGYGSGP
LEVQFSSYHMPEEEEEYIGNQKVCFIGEPPAYDEDVMAVMEHDEFYNYLMIYSEKYVEE
HPEAKQEIYNLLDMVKKRLGLHS"

CDS 1326114..1326602

/locus_tag="EFAGFIKM_01158"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIKYRYTIEYKEDFNEVIVDLGIDSSLKNGYLISNSLGSDIFGD

FATIQEEIGNLIELLKGEITLYEGGGNVNLRSDQSFTTYEDIFAEDEEDSTCEIET

LEYVKILLLLWAKENFQYKSQRGVILKEEGQVALEWLNEKYIEVLVLGQKIERINNKL

IE"

CDS complement(1326959..1327474)

/locus_tag="EFAGFIKM_01159"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNIIIEKLKDTDIEDLYEFEIENRIFFEEMVPSRGDDYYISEVF

KVRNESLLDEQVKGLSFFYLIKDENNSILGRINLVDIDDSKIGFLGYRVGQIHTGKG

VAKKALKLLLNTIVDLDIKEVKAKTTNNVASQKVLEQNGFDHTETSDNEFEMNGQVL

KFITYTWTNKS"

CDS 1327735..1328028

/locus_tag="EFAGFIKM_01160"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MWAYIMGLFEHMSNYMNNDPAVLQLPDDDLTSQLTARKWSMTS

KGKILLESKKDMKKRGLKSPDRADAYVLTFGGYLMGTPQSIMLPTIGGVSIKR"

CDS 1328152..1328400

/locus_tag="EFAGFIKM_01161"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYKRYDFYTHQLERAQRLIKDEEARKAVDYRYIQGYSRKETILF
FRRALSDSTIKRKIDEGLESVANTLKLIGFFEQDDAEY"

CDS complement(1328445..1330163)

/locus_tag="EFAGFIKM_01162"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIILNVRIKNHKSIDDSGEIKLHNKMNVLAGKNNTGKSAFIEAL
YKVLQGMLNSPALDTQSTEIELELSLSDDEEVNYLNDNVPPGFTIQYSEKFRLFLRYFN
SHNVTVFNKKVQGYNDHFQDVYINSNYHKVGVAPKYMFPDQEDSVLPNSTFISNF
MNLNKKIVYITGSRHVPSTETSTLNNYLKIDGTNLNGFLYSMHNNEEETFDKIVETF
KQIFTDVITIRTPIDEGNQTFISVSFEGLDTPIPLSDCGSGYTHVLLLLCVLYTKENS
IVLFDEPQVFLHPSAEKAIYDLVSDSNEHQFVFTTHSPILINYP SDKYLIHVSKLNGI
SSFTQLEHIQEVLSDIGVSN SDFALSDKVIFVEGQTEELVIPMILTHFGLKQIGYNYR
ILNMKGTGNYFNKNSSMRAYKGKLDLILSGISESPIPYKIIIDADNKTDEKLLTLRES
YGDSIIILGRREYENYFLDCYHELSEIINRNSSIAAADPDLIKSKIDHLLLSIDDNKL
FPKKGSTNVLKDVVGSEVLERLFESYSLHYNKIVHGMELTELVLNNTPEKLEFFKSEL
QDFIKG"

CDS 1330513..1330776

/locus_tag="EFAGFIKM_01163"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDSTINEELQETAIAFLKWARNTLENEPANFETMNLVPQVSEVA
CTIITRLRDQGAGESPEHYVQKLQQPQIKELICKTISESLNKL"

CDS complement(1330748..1330996)

/locus_tag="EFAGFIKM_01164"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MSFEFD FDRVTKELVSELTDAIVDNLNEAIKGP NYANLQSLVGD
RAELIMLSSITLAASASLTNKVLKQYHKELTAYLETQK"

CDS 1331528..1331995

/locus_tag="EFAGFIKM_01165"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNYIDLASNISIGLV TGLVSGLFVTIYFRRRDKAQEARRLIREE
KQAMSTYITTIRFELKEIRENSDSYTAGDIRELRKSLNLIPKFYSYDFFESVPEETSK
YTSKIYNL NRELELYLESEEIDSHKILLFSSSELMRAQFDLLKYFRFSSMGKLK"

CDS 1332242..1332478

/locus_tag="EFAGFIKM_01166"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQPMNNKTLKLEGSDLQEIQDYLKTSNFDYFQALSTLAHV TYGG
SVQEFVNIETDEVTKGQYSDLIERLEDALRRHNS"

CDS 1332593..1333432

/locus_tag="EFAGFIKM_01167"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNKKHIALIVCGVFVWWAGSGIAINGLINASYRGTFGDMFGAVN
ALFSGLAFGGLIYTIFLQMAENRRQQQEAKDMNEKMMEQVRLSNVQRFESTLFLT VQM
HHDIVKNINIKGTSGRGAFFTFYNLLIKEYMLVLDEEYGIKTIDFPADINRELDDDYI
KESILHEQKVNYSLTHAIQRAILLNEQALGTYVRNL TNIYRMIDANASLSTDERNEYI
KLVNAQLSLY EYIMLFYYCFLTSREFKSYADKYHIFDVGNMNP GYLINIKHWFMYDK
LRW"

CDS complement(1333652..1334242)

/locus_tag="EFAGFIKM_01168"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNSFLIIGVLILLIVITILVEIQRFKVLKLNIEKNLPSGALKSN
VVSQEDIKLLRAYRTLQTNDSQKLKVARIHLKILKEKQSDNSPFEDIKLTIFITL
VGLMITTTLKIPKETIELLSIIKPISIVLLLMLIVSSVIFISYIFKFSTNRSTELIN
IHIVASDEITSDSELVINDITPENLNQDNAGIASSS"

CDS 1334342..1334611

/locus_tag="EFAGFIKM_01169"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSVKSYQKIIPATAIQFEGNSSTHADETFVQVQVPISIDLAGST
VKLRVIVDPLNPLVVPVGDYIVKDATGTLKHKMQAEFEAEYTVVK"

CDS 1334799..1335137

/locus_tag="EFAGFIKM_01170"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKWYHKAIFSFANSVLPAAVKRQMMGFGRMTSPRSSNGWDIFNW
LPKKYQSVHNIDLTQLQNTAEELLEILVSVHPDISHALYNFLRMGDTPLTFTAKKQS
GSDVKNGQHR"

CDS complement(1335569..1335787)

/locus_tag="EFAGFIKM_01171"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MYARIRNLRDKDLSQTQMATYLGCSQRVYSNYERGELDIPTAI
LIK LADYHQTSTDYLLNRTDVR RPYP SK"

CDS 1335901..1336170

/locus_tag="EFAGFIKM_01172"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSNLIEDLFHGNLGLDESIHPEQA EYQEINRQISDLMQDYKTQL
TEN EYDALEQLIDLIGQSTSMYVEAAFEQGFRTGGRLMIEVLAKP"

CDS complement(1336308..1337684)

/locus_tag="EFAGFIKM_01173"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKLFPSTSTHVSARSARSLKERSLKSKMAHICLSAAFPLLLIGG
GSAGAEELIESSLQNPSESVATSNIALAAGDLYVSPGGSASNPGTLNSPTSLANALTQ
IAPGKTIYLRGGNYTFSQTITIERGNSGTSSQRKNLVAYGSEKPVDFSAQAFAS TNR
GLQMFGDYWFVKGLEVKGAGDNGIFIGGSYNRLEQIEAHHNRDTGIQMGRYASTA AKS
EWPAYNEVIRSYSHNNYDPDDGEDADGFAAKLTVGPGNVFDGCIAAYNVDDGWDLYSK
TDTGAIGAVTIRNSIAYANGATSDGTSTNSDGN GFKLGGEKIAVNHIVENSIAFNNK
KHGFTYNSNPGSIQMKNNTSWNNGQSNFAFDVGTHIFTNNLSFQGGASDKTSGTDVSS
TNVWWKNKKSENAKGLLASAADFVSLVPSVTRSADGTPVLGNFLKLAGGSDLIGSGTP
AGKNIGAR"

CDS complement(1338241..1339833)

/gene="katA_1"
/locus_tag="EFAGFIKM_01174"
/EC_number="1.11.1.6"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q59337"

/codon_start=1
/transl_table=11
/product="Catalase"
/db_xref="COG:COG0753"
/translation="MNHQSSQPEHSSDKSAETLTDRQGHPITDNQNVRTVGSRGPTTL
ENYHFLEKITHFDRERIPERVVHARGAGAHGIFEAYGTAGSEPVSKYTRARLFQEKGK
QTPVFVRFSTVIHGGHSPETLRDPRGFAVKFYTEDGNWDLVGNNLKIFFIRDPLKFPD
MVHAFKPDPLTNAQDMERFFDFVSLSPETHMVTFLFSPWGIPANYRQMQGSGVNTYK
WVNQEGTGVLIKYHWEPLNQGIRNLLQKDASEIQGQNFNHATLDLYHAIEQGDYPEWE
LCVQVMEDGEHPELDFDPLDPTKLWPQDQFPFLPVGKMTLNRNPEDYFNEVEQAAFGT
GVLVDGLDFSDDKLLQGRTFSYSDTQRHRVGANYLQLPVNAPKNRVATNQSGGQMQYQ
VDRAPGQNPHVNYEPSSLGGLKEAAPRGKEHEPLVEGRLVREKIERTNDFGQAGDTYR
AFEDWERDELISNMVGALAQCKPDIRD RMISYFTQADADYGRRVSEGLASVPTDDSAT
VQPKHEPSVEQAEKRSRETDGY"

CDS 1340021..1342003

/gene="yoaA_1"
/locus_tag="EFAGFIKM_01175"
/EC_number="3.6.4.12"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P76257"
/codon_start=1
/transl_table=11
/product="putative ATP-dependent DNA helicase YoaA"
/db_xref="COG:COG1199"
/translation="MEADLGLSTQRYPFAYDPAEPFVSRLGEWVADVFDILPEFGFE
VRDEQIFMAYQLERAYGDKKTIMAEAGVGTGKTLVYLLYAVCYARYTGKPAVIACADE
SLIEQLVKPGGDIAKLAAHLDLEVDARLGKSPDQYVCLNKLSAVRFADEDAPVIEEVH
ESLPDFVNTPGTLQAFHPYGDRKQYPHLNDRQWNKINWDPFQDCFVCPKRQRCGLTSL
RDHYRRSKDIIICSHDYMEHVWTYDARKREGQLPLLPDHSSVVFDEGHLLEEAALNA
LSYKLKHRIFEELVTRLLEGEIRESLAECVDEAIESSERLFALLDTYTV AIPGSERKE
VRVEPPLLREIERLTSVLDAIGEELVFESGLFSLDGYQMRVVEEHLDMIQSALALFRK
EDGYICWAESEDETTLSIMPRTVKEMLNERVFNTGIPIVFSSATLSVDSSFRYVADS"

LGIDDFVSFSVASPYDYADKMKMKITDEAIPGHPENENRMRDAVSLLQESGGRALVLF
RTMEELRAFKQDIVHVPEAEGLRFMYEGDREISDLIAAFQQDEESVLCSVNLWEGLDV
PGPSLSNMIWSLPYPPQDPVFNARSASAPYEEIDLPMLLRVKQGLGRLIRTSTD
SGSAVILDESlyTKKEAKDRIAALLPEGVEWTTLTH"

CDS complement(1342494..1343450)

/gene="cysK_1"

/locus_tag="EFAGFIKM_01176"

/EC_number="2.5.1.47"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P63871"

/codon_start=1

/transl_table=11

/product="Cysteine synthase"

/translation="MDLNTHSIKRTPAHTGIAADVTKLIGQTPAVKLNRLTDSADSADV

YVKLEYFNPSGSVKDRAAYNLIVQAELAGHLLPGATIIPTSGNTGIGLAMNAAAKGY

KAILIMPDNMSKERINILKAYGADVLTAAERMPGAIRKAKELQADIPGSFIPQQFE

NQANPDIHRITTAPEIMQQMDGRLDAFIATAGTGGTITGTGEELRKQLPDIRIYAVEP

KGSPVLSSGEPGPHKLVGTSPGFIPDILNTDVWDIIQVSEDEDALDTMRQLAAREGLL

LGPSSGASVWASLRIAKELGPGHRVLCIAPDTGERYLSMGIF"

CDS complement(1343614..1343997)

/locus_tag="EFAGFIKM_01177"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTSSTFAPSPADEDHRLIKGLVVRTLLLDVLERDIRTLDTLLLK

MPEVYILSLTRIQQNNVLKEMLALRKQMRTRGVKVLEEKREAEGIETLYMCRGYWQRFY

MLWTFARNEVKKELSRHLQMDLAQT"

CDS complement(1344466..1344699)

/locus_tag="EFAGFIKM_01178"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKPETKKISKRWGSEKKVRLSSAPESSRPVPEPKEEDRFHKPAV
PLTTIGPSLKGKERPYKVILEKEAFYEKPQYLA"

CDS complement(1344696..1345733)

/locus_tag="EFAGFIKM_01179"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKTLPKPRVFIGCSLEAKPIAAVHENLRFSAEVPWYSGVFNPS
SYTMDDLEVEVRTTDFAI FIFHPDDISKIRGKYASVRDNTMLEMGLFMGRLGRKRIF
FILPEDITDIKDTTKVEGLRMPTDLLGLNPLVYEIRSDGKWAPAVSVACSKIADSIEE
QGRWSDPELENIIEKHKRTEGEARLQLLKLLRFFRELLRTRKADAKMLERMSDALRTA
FVSHPPFAVRGTAIYRTDDSGYIEQLCGNVGEPGRKYDLSANDDKQPDDPKRILVIDS
YRENKIKINLYDDYLEKEYLLCYPVAKKYVITVHIIGHIEADEAVFQQIDLQNRQLFN
AINDLLGGEPE"

CDS 1346684..1347418

/locus_tag="EFAGFIKM_01180"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRTSLTLQHVKTEAIKFAIMLLGTFILAFAYYHINFQNLHSEG
GFVGLALLGKYATGLSPAIGMLLLDIPVMILAWFLKGWKFMIQALLGVGAFSLFYDGF
ERYSTLVLSFNGLWIPAVLSGILTVGVGAGVVLRFGGATGGDDILAVLVSRWKGWKLG
TVFFVSDAFVLGLSLFFLPVKETLYTILAVWIASKVITYVVSVPARGTVVTTSVAKLP
MPSAAAKAVNAAAIQRTTVARGVSN"

CDS complement(1347544..1348014)

/locus_tag="EFAGFIKM_01181"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MPWNNKQDYPVSMKNLEPRVRHKAIEIANALLDDGYEEGRSIAIA
TAKAEEDWENHPAPESSKSDSTSSSDNSNPKSSSTDRRHSEPVSSSKSHDNIHVPT
NSGWAIKEEGKSTYLSTFDTKAEAVDKAKELSSKQNIIRAIHNQDGQIASSIKP"

CDS 1348406..1349206

/gene="amj"
/locus_tag="EFAGFIKM_01182"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P96581"
/codon_start=1
/transl_table=11
/product="Lipid II flippase Amj"
/translation="MFSLSLAIPMLFTMLIHGADSLSYALRLGGLRTRRIALAISLAG
ILLVSRSTNMAQGPMVGNLVDATRGANPHFAAQLHWLMGAATIGTALAILCFPTMV
KLSSRMVVHFEAAGSIPAMVRGMLKRSKIRNATYYITPPSWKMAKRLVQHGMPPRLMM
LNVVVTAIYTTGVLSSLYAAYLYPGQAVAASQSTGLINGIATILLTILIDPRISLLSD
KSLRGEIRLDRMNQIYGCMVLVSRLFGTLLAQLLLIPFAYWIGWIVSMM"

CDS 1349343..1349951

/gene="qacR_1"
/locus_tag="EFAGFIKM_01183"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A0N5"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator QacR"
/translation="MEVFPIEVKRRKDVAQIKKDIARNTKELFAQKGYSATSMEDICT
INNRSKGSIIYHFKSKEELFMYLIKLNNDWMDAWLDKESGYETAIDKLYGLADHYVD
DLANPLNHAINFVSGQVVSQEMLDMLSLIRIPYGTYESIITKGMEDGELKQDDPQD
VMHIIYGLFSGLTLLYEEKDLTDIRRIYHKGMAGLLAGIQQR"

CDS 1350032..1351267

/locus_tag="EFAGFIKM_01184"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNTLFRNKAFLIVTGSDLLQNLAIWIRNMAILYYVMDRTQGSP
AVSLITVLEYAPIFVFSIIGGALADRWNPKRTMILGDILSALSIVMIIGVLSSGYWQI
LYVATFVSSIVSQFSQPSSLKIVRRNVKGEHLHSAIAITQSGQSLFLILGPVGTFIY
TAMGIQASMYALLILFLTSALLLTFLPKDATQRETNTSLLADIREGWQYVARSQLKM
LSLVFICIGLSAGLISPLGIFLITERLGLEATSLQFLSGASGIGLLIGGGIAAAVSAK
LNQTLTLLVGVLC LAVATMGEVLSSWFWLTLISFLSSISLAFINVIISTYLVTRIDE
HLIGRVNGTITPLFIGSMLLGSSMAGVLMNSTSIFIVYAISVTVMIMGIVPAMRIQFR
NDQTASASQLNSEISSQT"

CDS complement(1351371..1352333)

/gene="msrA_2"

/locus_tag="EFAGFIKM_01185"

/EC_number="1.8.4.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01401"

/codon_start=1

/transl_table=11

/product="Peptide methionine sulfoxide reductase MsrA"

/translation="MEQHSSSELATFAGGCFWCMVSPFEELPGIHKIVSGYTGGHTENP
TYEEVCSETTGHVEAVQITFDPAIFPYKKLVELFWQQIDPTDTGGQFHDRGSSYQTAI
FYHSEEQRQIAEASKAELGQSGRFDKPIFTPLPAKPFYEAEEHHQNYHRKNPAHYKR
YSKSGSRVDFIERNWTGNVDKDKGLKERLTPLQYEVQTNSATEPAFHNEFWDDHGDGIY
VDIVSGEPLFSSTDKYDSGCGWPSFTRPLRDHNVKEKTDLSHFMRTEVRSREGDSDL
GHLFNDGP AEAGGMRYCINSAALRFVPKEDLQKEGYGEYAVLFQ"

CDS complement(1352515..1353126)

/locus_tag="EFAGFIKM_01186"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MRKWLWLLLYVLLAGVTFIYRYELLAWTDLHQSIPLLLAMATLF
ALVPVIPFKFVIIAFGYSYGTTTAAWICWLGTTLAAMLVYGGARTIFRHQARSYLERI
RGLNRFTTWMEAHFPMGVMMSRLLPIVPQMAVNIYAGITYTPFWVFMLATAIGKMPAI
FVFAYAGAQAETSIWLSLAILAGYLVFMAIILLFRFRSRNKA"

CDS 1353326..1354264

/gene="yceM"
/locus_tag="EFAGFIKM_01187"
/EC_number="1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P75931"
/codon_start=1
/transl_table=11
/product="Putative oxidoreductase YceM"
/db_xref="COG:COG0673"
/translation="METTQRKRVAIIGLGDIARKVYLPLTAHPNVEIVGIMNRSPEP
VKAVQEAYRLERGTDLKELLSWDLDAVFVHTATEAHFDIVMQCLEQGLAVYVDKPLS
YTIRESEEMTAFAEAQGLLLAVGFNRRFAPMYQKAKEWMQGGKGFESLTVTKHRTGIQ
DRPAAETIYDDFIHMLDLMLWYSDHNVELLHQWIRKNDLDRLLHVTGTAKLGRTAYGR
FDMVREAGADLEKIELHGGGRSVEVVNMDTISYMEQGSLETKETFGSWDTVLARRGFS
GAVDNFLACLDLPDDCLISASHVMDSHELAEQLIRK"

CDS 1354297..1354611

/locus_tag="EFAGFIKM_01188"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDEYEKERNKQIEEAHVETYKQEEEMMILVFAQWCVNHGLDPEE
MYRQAYPNQQSNERLQVQKLIVSKEEAGEIPDDTVLGVLSMFGNEDLAMVVSEIAIAA
RK"

CDS complement(1354637..1355455)

/gene="araC_1"

/locus_tag="EFAGFIKM_01189"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A9E0"

/codon_start=1

/transl_table=11

/product="Arabinose operon regulatory protein"

/translation="MPTDQSCQVLTAGFSFHRKPYAMVQPEGVKNYLLRLQTDGRCRA
RIDGDMSLVDAGDLLLFDPEPYELRIDNETNPMGERLVESGDYHIFNGSWVDEWWK
RHKRPTRIKVELTESLLVLFRQLVLEQRRISNPYPEISSYMRILCLEVDRLAEHPT
ITNTNYVAYEIKNYIEENASSLFLKDDVATHIGISVSRGVHLFKEAFGKSIMQYTLDV
RLNMARERII FSPMTLEQVSESSGFNNYTFHRVFRSRFGMSPKEFRVIHREQM"

CDS 1355645..1356757

/gene="iolG_1"

/locus_tag="EFAGFIKM_01190"

/EC_number="1.1.1.369"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01671"

/codon_start=1

/transl_table=11

/product="Inositol 2-dehydrogenase/D-chiro-inositol
3-dehydrogenase"

/translation="MEKMKAGIIGCGNISAIYLENLKNNPVIEVVAVADLIRERAQER
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HPNPEFFYVAGGGPMFDMGPYYLTALITLLGP IRRISASAGIQIADRKIGSGPKEGTA
LQVETPTHLAGTIDFAEGAIATMITSFDIRGASDLPRIEYGT EGTLSVPDPNYFNGE
VKVRRYGQDTWETVKQVFESGQNERGIGVTEMVESIRAGREHKASGKLAYHVLEAMHS
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CDS 1356959..1357927

/locus_tag="EFAGFIKM_01191"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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PDELLSNSTALKNFKNAVESRGLTISALSCHGNPLHPQKDIAGFHDDFVKSVELAEK
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RNVKVGLELHGGFSVHTPATLLRLREAAGEVIGANLDPSHMWWQGIDPVQAIHILGRE
GAIHHFHAKDTTIDPVNVNKHGVTDMQDYTNMLDRAWQFRSVGYGHDNKTWADIMSAL
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CDS 1357952..1358680

/locus_tag="EFAGFIKM_01192"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MINVTIWNEFVHEKIHDEVREVYPDGLHRALADGLGGEGFAIRT
ATLDQPEHGLSDEVLNSTDVLIWWGHMAHDRVSDEISQKVAQRLNMGMMIVLHSGHF
SKPFKALMGTSKDLKWRVADEQEIVWCVNPSHPIADGIEGKIVLEKEEMYGEFFDIPV
PDELVFVSNFQGGGEVFRSGCTFRRGEGKIFYFRPGHETYPTYKPEILRVISNAVKWA
YPARSKPEFGKSEPVVPFGGVLV"

CDS 1358986..1359303

/gene="yodB_2"
/locus_tag="EFAGFIKM_01193"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34844"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator YodB"
/db_xref="COG:COG1733"
/translation="MEGQDLRMCPRFETAFSFLGKRWNGLIIQTLMSGSKRFKDISNL
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WVD"

CDS 1359495..1360226

/locus_tag="EFAGFIKM_01194"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MREESLSREVRYGKKDIAELESASIQVHLIYKKAELFKRTAYS
RSVKDDLAEVNTHSVNSDGPKLAPAVLQKWIQTSRGWKCIGCELGQPDSTMSQMEETI
HGKQLVLDVGEGRVQAEMLIQAVVWSQYEKIRMFAPWLGDEPFYSLQELDVIARYIV
PTYFSERPLHEQGKVKVHQYQGQIPLYQEYVDAPSCCVQVDGGLLEGRLLTGVIYVSE
EQFFGLNPYLKDGDDGRTYMQACVQ"

CDS 1360424..1361137

/locus_tag="EFAGFIKM_01195"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MMKKIPGYIGVCLLLLAILAGCSETQPSEQPIVKETETANTITV
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CDS complement(1361225..1361941)

/gene="fnr_1"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P46908"
/codon_start=1
/transl_table=11
/product="Anaerobic regulatory protein"
/db_xref="COG:COG0664"
/translation="MRELTTVLEKRGNTNCFSESFNHLLVTMKDRYPEGTHLYWEG
DISDKLYYMKRGRAQITKSTDEGKELIMYMYQSGDMIGQADPFFGSKHSFSAEVLEDS"

EIGVLEHKDLEMLICQHCDFAIDFMKWMGIHHRLTQTKFRDLMLYGKSGALCSTLIRL
SNSYGEPHGHEHVIIHKKITHDLSNMIGATRESVNRMLSDLRKKDGI EYDNGMIVIKD
LKMLQGICHCELC PNEICRI"

CDS 1362372..1364984

/gene="adhE"

/locus_tag="EFAGFIKM_01197"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A9Q7"

/codon_start=1

/transl_table=11

/product="Aldehyde-alcohol dehydrogenase"

/db_xref="COG:COG1012"

/translation="MAVKNEVAPAKEPTAGQYIQTLDKANKAHAAFMKMDQKQIDRI

VQAMALAGLDKHMMLAKMAVEETGRGVYEDKITKNIFATEYVYHSIKYDKTVGVIEDN

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ALGVGPGNVPCFIEKSADINQAVTDLILSKSFDNGMICASEQAVIIEEPIFDQVKKKM

IANGCYFVNKDEAAKLTAGAINAEKCAVNPAIVGQSAVSIKLCGIEVPAGTKILVAE

IEGVGTFKPLSAEKLSPVLACYKVKTAAEGIERAAEVVAFGGMGHSSVIHSTNEEVIG

KFADRLQTGRIIVNSPSTHGAIGDIYNTNMPSLTLGCGSYGRNSTSSNVTAVNLINVK

RVARRTVNMQWFKVPNKVYFEKGATQYLAKMPDITRVAITDAMMVKLGYVEKVEHYL

RQRQMPVAIEVFSDVEPD PSTTTVDRGTEMMRRFQPD CIIALGGGSPMDAAKAMWLFY

EYPTDFNDLKQKFMDIRKRIYKYPRLGVKAKFVAIPTTSGTGSEVTSFAVITDKNQG

NTKYPLADYELTPDVAIVDPEFVYSLPKTAVADTGMDVLTHAIEAYVSVMANDYTDGL

AIKAIQLVFQYLEQSALQGDKLAREKMHNASTIAGMAFANAFLGINHSLAHKWGGQYH

TAHGRTNAILMPHVIRYNAKKPTKFASFPKYSHFVADERYAEIARILGLPARTTEEGV

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LADVYRNAFYGKFE"

CDS 1366083..1368341

/gene="pflB"

/locus_tag="EFAGFIKM_01198"

/EC_number="2.3.1.54"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7A7X6"
/codon_start=1
/transl_table=11
/product="Formate acetyltransferase"
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QTDAPFKRSIQPTGGIRMMIDACEAYGFEMPQGVIDIFTNIRKTHNQGVFDAYTSDMR
AARKAGIITGLPDAYGRGRIIGDYRRVALYGVDFLIRNKKGELNALEV DVIDEDVIRL
REELSEQIRALQELKQLGDMHGFDISLPATTAKEAFQWLYFGYLAAIKEQNGAAMSLG
RVSSFLDIYIERDLQEGILSEEQAQELVDHFVMKLRIVKFLRTPDYNELFSGDPTWVT
ESIGGMSVNGETRVTKNSFRFLHTLHNLGPAPEPNLTVLWSTKLPEAFKDYCSKVSIE
TSSIQYENDDLMRPIYGDDYGIACCVSAMKIGKQM QFFGARANLAKALLYAINGGRDE
KSGAQVGPEYPAITSEVLDYNEVMKRFKPMMEWLAKLYMNTLNVIHYMHDKYSYERIE
MALHDRDIVRTMACGIAGLSVTADSLSAIKYAKVKPIRNEQGIAVD FEIEGDFPCYGN
NEDSVDSIAVELVENFMGMIRKHKAYRNAVPTQSVLTITSNVVYGKKTGTTPDGRKAG
EPFAPGANPMHGRDKK GALASLGSVAKLPYEHSLDGISNTFSIVPKALGKEETTRKSN
LTAMMDGYFGQNAHHLNVNVFDRQQ LIDAMDHPENYPQLTIRVSGYAVNFIKLTREQQ
LDVINRTFHGSM"

CDS 1368431..1369183

/gene="pflA"
/locus_tag="EFAGFIKM_01199"
/EC_number="1.97.1.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7A7X5"
/codon_start=1
/transl_table=11
/product="Pyruvate formate-lyase-activating enzyme"
/translation="MVNGHIHSLETFGTVDGPGIRFVLFMQGCLLKCYCHNPDTWAL
DGGKEMTLEEVLAIEPYLSYRSSGGGLTISGGEPTLQAHFVAEIFKEVKRRWGLHT
TLDSNGFNEPERIHDLLDHTDLVLLDLKHIDDEKHIKLTGKSNERTLKTAKWLSEQGR
KMWIRHVYVPGIHNEEEDLLNLGRFIGTLNGVEKFEILPYHQMG IYKWEALGKVYPLD

GVPSPSEEEVERAYRLIEQGRQETAGMACSGK"

CDS 1369405..1370772

/gene="msmE_2"

/locus_tag="EFAGFIKM_01200"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q00749"

/codon_start=1

/transl_table=11

/product="Multiple sugar-binding protein"

/db_xref="COG:COG1653"

/translation="MKKRMTLLLSLLLITSWTLAGCASSSNEPQQGAGNTPVEETSKE

PVEMLLRHTQVGADKQKRLAILQDVVDKVEGEIPNLFTLDGVESDVNRKEKLRGEMA

AGNPPDIFELFGSPDSKVYAKEGMLLDLTPILQELGIQDQFTSLEPFTYEGKVYGLPI

GGSGEGFFYNKEYFEQKGWKAPTTMAELDHILAEIKADGKLPLASASKAGWVPLMLTN

HLWSRYAGPEITAKFATGEAKWTDPGVVQGFAKHKEWVDKGYFKKGELGFEYAEYTTQ

FTSGEAVLMYDGTWKSSVFKEGQSGESLIGKVGFNMPVENGAGDQTSLMRDVNNGY

GFSAAVADDPQKLEAVKAFIKNFYNEDMQIRGLVEDGVLPAMKLDEKVLTDSDDL

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CDS 1370824..1371708

/gene="ngcF_1"

/locus_tag="EFAGFIKM_01201"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O50500"

/codon_start=1

/transl_table=11

/product="Diacetylchitobiose uptake system permease
protein NgcF"

/db_xref="COG:COG1175"

/translation="MNTSLRSPLIYTLFVMPALILFVMFFLYPIGSSLYSLTSWNGV

SAEPRFVGLSNYMKALTDERFWISTRNNGFFIGFSVLIQVPLIVLFSLLIANVKRLKG

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VTNAWQWTGFYIVMVLAAILAIPRDLDEAAIDGATAVGRAMRITLPLIRPIISVIM
LSIAGAMKAADIVIVMTKGGPAGSTEVLATYMIKYAITNFKYGYGNTIAVLIFALTLV
LTAVYQLLVARRSEKVEY"

CDS 1371708..1372538

/gene="ngcG_1"

/locus_tag="EFAGFIKM_01202"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O50501"

/codon_start=1

/transl_table=11

/product="Diacetylchitobiose uptake system permease
protein NgcG"

/db_xref="COG:COG0395"

/translation="MAKSIKSSIPHVLLMLYLIALFPFLFVIFSSFKQDNNEIALNP

FGLPTTWEFNNYVEAWVNAKIGTYFWNSLYISVLSSACTIVLGAMFAFAVTRMRHRKW

SLFLYSLILAGMLIPNNALMLPIYLLVRKMGILDTHLALIVPYVANAIPTIILAAF

MRSLPGEIEEAAMVMDGLRAPGIFAKIVIPLTVPAIVTVFIVNFLGNWNEFLANYFLS

TDKLRTLPGMVQFRDQYQMNYAQMSAGIVYSVVPVLVIYAILQEKIIEGVTAGGVKG

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CDS 1372571..1374406

/locus_tag="EFAGFIKM_01203"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNLRMKLALAFMLLIIVPMCALGIGMFLVTSHTIEKKYNQQAQY

ALQAISYNIENVFQQINNVTDNGIATSVFQMALNAKDPTKQDLGTGNQLSLNASQRNF

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PKWLAPLEYPELTGVEPVFTQIRLVKELSYFQNIGVLVVQIKKGEIDRIFRHLQISDS

AQDTSFLLINEEGLIVYDPAGIYNGENMQNLGAESGSYGGFSSVRTVFDGKESIISQ

YHLKNYNWSLVSVTSWEALSAETNAFAGWSVIIIILLCLAAMIFNLFFMNRITGNIAV

LVRFMRRVDDGDFNARVEGKGFDEMQLLAQGFNELLDRIIGGLFRRVRAEQEQKAQAE

RVLQAQIKPHFLFNTLESINGLALRGEGRKVSEMVTRLGNMLRISIQDQEEIPLSEEI
RHLQSYLEIQQYRFSDLFTYEIDIPPHLYSSILLKLTQPLVENS IQHGFEGITYPGV
LRISAYAERGHVLVLCVEDNGIGIPQEMLARFEYMAEDLPEDMLTEGAESLSSITERRG
LGLRSVADRIRIQYGAGYGIFICSAPGYGTVIRCIIPLYEQEEAG"

CDS 1374403..1376034

/gene="cheB_3"

/locus_tag="EFAGFIKM_01204"

/EC_number="3.5.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00099"

/codon_start=1

/transl_table=11

/product="Protein-glutamate
methylesterase/protein-glutamine glutaminase"

/translation="MNLTAMLVDDELPILENLNFILPWEEMGIEITGTARSGVEALGK
VTECHPDILLCDIRMPMDGLELIRLLREQGETCEIILLTGYYQQFEYARTAIKYNVHE
YICKPIDYLNLEHKLREL AQIQKRLENESQRYRSQEMESWIRHKQLIDLLRGEAPL
KVAYPASVPEFITTATPYTLLLVDAVG YFRHSIGWSELQHQRWHETISSRLKEVAERI
TEDCQILSTRKGEWCILLEASGEWKRRSEELAHQLCLELNAILSLDSSVKVRVVQDDV
PVNLESKILERYRHCQKILMFHSESEDRVLKASCPETTLSYDHMVSKGANSWITREDL
EFVTRWIRQGKNKQGLRDVLDRLKQQMGNSGQSFNRIDETNLRFMLVHMLRELREVQAL
AEEHEVNFWNALQGAVSMRELLELAEVVTHASQGKQTQLRPSVSELILSACEYMDARL
QQDLGIDEVSDWLGISPGYFCQLFKTQMGVTFVEYMTQKRMESAALLSTTEWSITAI
GEATGFKERRYFSKV FHKHFHMKPSEYRQSKQLGS"

CDS 1376063..1377700

/gene="nagZ_1"

/locus_tag="EFAGFIKM_01205"

/EC_number="3.2.1.52"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40406"

/codon_start=1

/transl_table=11

/product="Beta-hexosaminidase"
/db_xref="COG:COG1472"
/translation="MKPLNDLTLEQKVGQLLMCGFHSQHADEQITRLIRDYHVGGVIY
FRRNVESVDQLTRLSAELQDMAAEAGALPLMISVDQEGGMVARIDKEGMTQVPGNMAL
GATGNPEYTLCAQILGRELKNIGIDMNLAPVVDVNNNPLNPVIGVRSYGEHAESVAT
HGVAAITGYQSQGIAATAKHFPGHGDTAVDSHLGMVTVPHNRNRLEQMELLPFRKAIE
AGVDAIMTAHVMFPSIEPEPIPATLSHKVLTGLLREEMGFEGIIITDCLEMHAISKPY
GVAEAAIRAVEAGADLILVSHTLQDQVTALEAIVEAVRTGRISEEVIHQAVRIMTWK
RKRCGQQNDHLVSPKASETVEATDVEPVDCTESTKPTENESTLTKIASSSITIVHND
GLLPDPEKDVYVIWPEVVQRTEVDEPWSHTESLGMALSQLRGRVREHKITTQPTYDE
ADRILADVSDSEQVIVCTYTSAGHLPKGQQYLVEKLSKNHSLIVIALRNPYDLLEISR
PRSYVCTYENTPAVVRALSHVLTGGLQPTGSLPVRLC"

CDS 1377975..1380227

/locus_tag="EFAGFIKM_01206"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNLKKKLSILTAFAVFQAFVIPANAQSDQSDTTSVNTAKVKS
VEVVKKEQTIAESEVKSGTNTPTSNNETTEEVNPETDVPTGTDATPVEPVIEPTDEEG
TAEETPAPAPVEVEQPSTGGSSVAGGGGGDLTYMNSNKMMQDGKTYLAGQPMKNG
VSYVAIRALVDRVGYNVKYDNTTKETIIISGEDELRFKTNSKIYTVNGVSRMTMGAAY
QQKNTFMVPLTSITQALDITYKVNQSAKTVVLNLSTKPVASFVQKEVFAGDQVYTT
RSSSPKGLSIVDERWTGRQDSFDQPGVYTVYAVQDSSGQWSDPYSVTIKVERPNLPP
VAMFTTDKEEYKMGEKITYIDQSTDDENAIVKTEWDNNAFFVPGPKTVTITVTDKH
GASNSYTKMINITGETLYSVTDFNQLFTPVGKFTFDGGGVPALKVPFTYYDEPSLL
IRSNSPETVNTGIVYKESSFGQTRFMIHHVNNTGKNVKMYVATNNNAYTASIDQQN
MGFAGPSPFATVAGKLSIDRWFQSMQNGTGQKKVYIQPGESKLILNDLSVLPMKQGQV
ISLYSDVFSDYELDYNIIEMIEENKDPMEVLSSLPVLD RDGVHNRGTYPNATRIITYDQ
EVGSKPARLPLGDNASDPNLVGTDP MAYTEASNAGNFGVLYKITLNNVAPRTLISFNP
RGGRYSGVALVNGQVVQISTGKSVTAPNEQSVMYRTGSYGESVTILFSAAPGSNLPVN
LLFTPLPAEK"

CDS 1380566..1381030

/gene="zur"

/locus_tag="EFAGFIKM_01207"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54479"

/codon_start=1

/transl_table=11

/product="Zinc-specific metallo-regulatory protein"

/db_xref="COG:COG0735"

/translation="MLSTEQIISTMSSQGLRITDQRKTLARLFAESPGYLTPKDVVEY
MGKTYSGLSFDTVYRNLRVMQELGVLEQVIFEDGVKFKAHCSDDHHHHHMICLKQCQT
YPIIFCPMQLADAEQFQVVDHKFEVFGYCKDCAEHAPAKAASGHQHAHGKH"

CDS 1381033..1381284

/gene="yidD_2"

/locus_tag="EFAGFIKM_01208"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A8C8"

/codon_start=1

/transl_table=11

/product="Putative membrane protein insertion efficiency
factor"

/db_xref="COG:COG0759"

/translation="MKLSRRIAQVPIRVYRNYISPLTPPTCRFYPPSCSAYAMEAIEVH
GALKGSLLSAKRIAKCHPFHPGGVDLVPPKAEEKSMMVSE"

CDS 1381785..1383809

/gene="metG"

/locus_tag="EFAGFIKM_01209"

/EC_number="6.1.1.10"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P67579"

/codon_start=1

/transl_table=11

/product="Methionine--tRNA ligase"
/translation="MADQKTFYLTPPIYPSDKLHIGHAYTTVAGDAMVRYKRLRGYD
AHYLTGTDEHGQKIERKAQEKGQTPQAFIDDIVVGIKELWNKLDISNDDFIRTTEERH
KTIVQDIFDRLLKQGDIYKGEYEGWYSIPDETYTETQLVDVEKNEKGEIISAKSPDS
GHPVELVKEESYFFRMSKYADRLLKYYEDNPGFIQPESRKNEMINNFIPGLEDLAVS
RTTFEWGVKVKGDPKHVVYVWIDALSNYITALGYGSSDASLYNKFWPADVHLVGKEIV
RFHTIYWPIMLMALDLPLPKKVFAGHWLLMKDGKMSKSGNVVDPVTLIDRYGLDALR
YYLLREVPFGSDGTFTPESFVERVNSDLANDLGNLLNRTVAMVDKYFEGKAPAFASNV
TEFDASLEEAGHATVEKVEQAMENLQFSVALTAISQFVSRTNKYIDETQPWALARDEA
KRDELASVMAHLIESLRIASILLQPFLTRAPLKIWAQLGIQEGELTAWDTAKQWGLVP
TGNALQKGDPIFPRLDSEQEIAYISEAMTGGQKAAQPETSQTDAGTSAAVEPVTAPEG
TEEIGIDDFAKVELRVAQVIACEPVKKADKLLKLQLDLGYEQRQVVSGIAKFYSPEEM
VGRKVICVTNLKPVKLRGELSQGMILAASHGDQLTLATVPDNMPNGAQVK"

CDS 1384053..1385111

/gene="znuA_1"
/locus_tag="EFAGFIKM_01210"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34966"
/codon_start=1
/transl_table=11
/product="High-affinity zinc uptake system binding-protein
ZnuA"
/db_xref="COG:COG0803"
/translation="MTFYKVQHQVEDNQTGTTSKRGSMKLLWTGLLILTLLVLSACGQ
DSSNSAKIVEGKVNVTTFYPVYAFTTAIGGEDANVINLLPTGVEPHDWTPKSQDIVN
TСКАQLFFYNGAGLEGWVPNFLKSLNSDTQVKSVAVSDGVKLLTAEGDDGHGHGEEHE
DEHADEHTDEATSEDVADHHIDPHTWVSPKSAMIMAENIKNSLVEADPDHKAGYEQRY
EELRTKLETLDQRFTDELANVPNNEIVVSHQAFGYLARDYGLTQHAIMGLSPDAEPTG
QDIVKLAKLVKDEGIKYIFFEELVSDKLAKTLASEAGVETMVLNPVEGLTKEQATNGD
DYFTLMEKNLQNLLIALK"

CDS 1385211..1385969

/gene="znuC_1"

/locus_tag="EFAGFIKM_01211"
/EC_number="7.2.2.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34946"
/codon_start=1
/transl_table=11
/product="High-affinity zinc uptake system ATP-binding
protein ZnuC"
/db_xref="COG:COG1121"

/translation="MQQIMPLCHDPIIEIKLSFSYGDQRVENLDFMAQERDFVGII
GSNGAGKTTLLRMLVGLLPPAQGDIKLFGQSIRRFKDWDRIGYVPQKNAFNPLFPATV
REVVMISGLYNNKNMFRMRSRKCQQQCMDAMQVMRIEDLANKRIGQLSGGQQQRVFLAR
ALINHPDLLILDEPTVGIDAESQASFFELITHMHEHHRMTFLMVSHDMDRMESYLGSE
AVVTNGKINFHVRHSHEVQDCAETNLQHTTAQVR"

CDS 1386022..1386825

/gene="znuB_1"
/locus_tag="EFAGFIKM_01212"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34610"
/codon_start=1
/transl_table=11
/product="High-affinity zinc uptake system membrane
protein ZnuB"
/db_xref="COG:COG1108"

/translation="MEILMSDFFQRALAGGLLIGITAPLIGLFLVLRRLSMIGDTLSH
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LFFTLGKGYNADVMSYLFSGSIYTLDATDLKLVGVVTLIVVIVVALLHKEFFLLSFEED
AAAVTGLPVRILNMLITVMTALVISTAIVGALLVSALLTIPVAVSLLMARSFKSAI
ILSVVIGEIAVVLGLVAGIWNLAPGATIVLLLIMMLILTMIGKKGFRA"

CDS 1386875..1387588

/locus_tag="EFAGFIKM_01213"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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/product="hypothetical protein"
/translation="MPDVNVWMAFVAGLVSFISPCCLPLYPSYLSYITGMTVQQLKDD
RNQREVRFKTMHTLAFILGFSAVFYSLGLGAGLFGQFFNDNRELIRQLSAILIMLMG
LFLLGVFQFLMKERKLDKWKWPAGYLGSFIFGIGFSAGWSPCIGPILATIIAMAAS
EPTTWLALITGYTAGFAIPFFILAFFIGSTRWILRYSNVMMKVGGALMLFLGVLLFTD
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CDS complement(1387735..1388805)

/gene="splB"
/locus_tag="EFAGFIKM_01214"
/EC_number="4.1.99.14"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37956"
/codon_start=1
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/db_xref="COG:COG1533"
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TGCMGHCHCYLQTTLGAKPYVRVYVNTTEEIIQAAKG YIEERAPEITRFEAACTSDPV
GLEHITENLSDLIRFMAEEEEYGR LRFVTKYHHVDPLLNIKHNGHTRIRFSVNSDYVIK
NFEPATSRFEERIEAAGKIAHAGYPLGFIIAPIMWYEGWEEGYSDLLQKLADTLPEEA
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LREFITERIFEHFPLASIDYFT"

CDS 1388998..1389426

/gene="mntR"
/locus_tag="EFAGFIKM_01215"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54512"
/codon_start=1
/transl_table=11

/product="HTH-type transcriptional regulator MntR"

/db_xref="COG:COG1321"

/translation="MPTPSMEDYLERIYKLIDEKGYARVSDIAEGLEVHPSSVTKMIQ
KLDKDEYLIYEKYRGLVLTPKGKKMGKRLMERHHLLEQFLTIGVQEQNIYNDVEGIE
HHLSWDSITCIESLVEYFRQDESRLRDLKNLQDVMSNTES"

CDS 1389636..1391246

/locus_tag="EFAGFIKM_01216"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNVRKGLMLLLIFVLGLQTAGMTAQAAGQKEIAIFLDGNRLESD
VSPYILPKVNVMTMVPLRVISEGLGASVLWSQATRTVTIQKSDSVISMTSGRQQATVDN
TVVGLDASVELKQGRVMVIPRFVSENLRVNVNQAAQTIDLYTGDESVPTPEPTPVT
PVEPGGTGTVPAEEMRGAWISTVNGDWPSSGAKGNVEKQKQEYTKQLDTLQGMGINA
VFVQVRANGDAIYPSGLVPWNSVLTGTQGKDPGYDPLAFMVEEAHKRGLEFHAWFNPF
RATNSASTSNLAANHISKLHPDWIVNASGKMYINPGIPEARQHIIDTIMEVVNQYDID
GVHLDDYFYPSNVTFSDDAAFKTYNTLNTKDRAEWRRDNINQFVKQLGQSIHSAKANV
EYGISPFGVWRNKSVDLTGSDTKAGVTAYDSMNADVRTWINQEWIDYVAPQVYWSMTL
SVARYDKVVDWWANEVTNTNVKLYIGHSPYKLGTPDIGWQTSQEIIDQLNYNKKHASV
KGDIFSSQYLTKNPLGLIAKLKAYYGL"

CDS 1391336..1392337

/locus_tag="EFAGFIKM_01217"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLINAVFEGGGVKGISLAGAVQGAQDCGIQFN RVAGTSSGSIVA
ALLAAGYRAEEMKVIIENTPFVSLRRSPIFNTRWIGPAARLFLKKGLYSGEALESWI
RKMLEQKGIRTFADLPQGKLLITASDISNGTILVLPDDIRRFIDPAKLDVAKAVRMS
CSIPYFFDPVVIRKSPVFSKGLPFQDQFVYVVDGGLLSNFPLWLFDGDRSERGGDVIP
VVGFKMVGKTEVEPARIKGPLSMLQALVETMLTAHDERYIEQINRFRTVKIPTLGIKP"

TQFHLSLQDSTALYRSGATAGNEFFNGWNMKNMYDEQLDKQRKELRKKQAEAPPLIPV"

CDS complement(1392399..1392731)

/locus_tag="EFAGFIKM_01218"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKQAILFWTFIALAAVGVLTWLGSASPSRIIPLVVFGAVFLL

YKYPPRRWASKTKSPKIKPSARTMAKVNAQSSARKSSGSSKKRKDYFPQVIQGQKGKS

DEDIPKFH"

CDS complement(1392737..1393729)

/locus_tag="EFAGFIKM_01219"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPQQSKPVSYGGQAVIEGVMFGGKHVNVTAARRKDGEITYLEVP

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LLLAYLWLISQTPMIKRLFQYHGAEHKVISAHEAGEELTPENVQKYSRLHYRCGSSFI

MLTVIIGVFLYSLFTYDNLWERMGQRLLLPVVLGISFELLKLTNSVRDIPVLRYLGY

PGLWLQLLTTKEPTNEQVEVSIAFNRMRREDAKLANVSATSEVPVATLDPVKG"

CDS 1393943..1394521

/locus_tag="EFAGFIKM_01220"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTERKHEDTSQDEGQRPNERQQKDKGRRPTQRQGQAHYYTKPFS

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FSILASLLYTFTIRKLKGPLPGMVYGIWWLILFILVGPKLGMMKPLNGLTWDSIITE

LCFFLLWGLFIGYTVAMEYTDERKREPEQAGA"

CDS 1394598..1395041

/gene="yqhS"

/locus_tag="EFAGFIKM_01221"

/EC_number="4.2.1.10"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54517"

/codon_start=1

/transl_table=11

/product="3-dehydroquinate dehydratase"

/db_xref="COG:COG0757"

/translation="MKRIIVINGPNLNMLGVREPGIYGTLSLKDIEDKIRRQADEIGV
SIAFYQSNHEGDIIDRIHAAMGEADGIILNAGAFTHYSYAIRDAINAVKVPTVEVHLS
NIHAREAFRHHSVIAAETIGQIAGFGEVSYELGLLALVRHLDKQT"

CDS 1395081..1396154

/gene="ypdF"

/locus_tag="EFAGFIKM_01222"

/EC_number="3.4.11.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P76524"

/codon_start=1

/transl_table=11

/product="Aminopeptidase YpdF"

/db_xref="COG:COG0006"

/translation="MENKRVNKLREAMREHELTAMLITNPINRRYMTGFTGSAGYVLI
TEQDAYLLTDFRYMSQAPQQAQGFTVVEHGAKPMDTVRELLTSANIKEVGFEQDSVTF
GTHSAYAEALQSIELKAVSGIVEQLRMFKDEDEIAVMQRAADLADATFSHVLKFAKPG
MTEREVDLEMEFFMRKHGATSSSFDTIVASGERSAMPHGVASSKVIGQNELITFDGA
LLDGYCSDLTRTIATGTPVPELRKIYDIVLEAQLHTLENLKPGMTGREADALARDIIA
GHGYGDQFGHSTGHGLGMEVHEAPRLSKLSDDVLKPGMVVTVEPGIYIDGLGGVRIED
DWWITETGIHILTKSDKKFTVIG"

CDS 1396468..1397025

/gene="efp"

/locus_tag="EFAGFIKM_01223"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P99066"
/codon_start=1
/transl_table=11
/product="Elongation factor P"
/translation="MISVNDFKTGLTVQVDNDIYTVLDFQHVKPGKGAAFVRSKLKNL
RNGNTVEKTRAGETIGRAIIENRGVSILYASGTEHTFMDNETYDQFTLTSDQLEWEL
NFLKENMVVKIVSYQGEILGIDLPTSVELKVIETEPSVKGNTAQGATKNAKVETGLNV
QVPLFINEGDVLLIDTREGKYSSRA"

CDS 1397216..1398469

/gene="lysC_1"
/locus_tag="EFAGFIKM_01224"
/EC_number="2.7.2.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q59229"
/codon_start=1
/transl_table=11
/product="Aspartokinase"
/translation="MSLYVMKFGGSSVGDTERMKRVAGRVVEKADEGHRCVWVVSAMG
DTDDLIDQAKQLNSDLPAEMDMLLTGEGISISLLSMAIQALGRKAVSFTGWQAGF
RTEPVHKGARIHDIQPDRVNAALAEKNIVIVAGFQGMTEDEITTLGRGGSDDTAVAL
AAAIKADACEIYTDVDGIYSTDPRIVKVARKLKEISYDEMLELANLGA AVLHPRAVEY
AKHSGVPLIVRSSFNHNHNEGTVVKEEAAMEQGVVVSIGIAYDKNVARISILGVPDVPGL
AEVFGALASNQLDVDIIVQSGVMDGKADFSFSVALSDRENALRVIEGLHSRLPYREVT
SEENLVKISIVGAGMVSHPGVAAKMFKVISAEGVSIKMVSTSEIKVSCVIDGDKLHDV
IKALHTAYDLDTAEQAVIGGPQDRR"

CDS complement(1398557..1399306)

/gene="comB"
/locus_tag="EFAGFIKM_01225"
/EC_number="3.1.3.71"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9WZQ4"

/codon_start=1

/transl_table=11

/product="putative 2-phosphosulfolactate phosphatase"

/db_xref="COG:COG2045"

/translation="MRVDVVGNVNEVRTIDIAGRSAVVIDVLCTTSTIITALAYDASA

VIAVETVPQAKQMEVKDCIRGGERFDKKITGFEVGNSPYEYMTAGIADKTIILTTTDG

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DELHRQSCSPLQLNDLGIVLHQAVSQCKESIPELVQGSVSGRRLEKLGRVHDISYCSQ

LNLLDCVPEMGEGNRMQPYRGIRGGKMFKLM"

CDS 1399569..1400573

/locus_tag="EFAGFIKM_01226"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKVNWRELFPEPIRTILGRMPPALLEQVEEVRIREGRPLEINAG

NTYHFLTPQGCPTGNPEEAYVPQKEVTHRLDLISNHSLYTLEEELRKGFITIPGGHR

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PQQGKTTLLRDLARQISSGKLTGGTELVQGIRPRLKVGIVDERSEIAGSYKGVPGFD

VGPRTDVMDGCPKAEGMMMLRSMSPDVLIVDEIGRPEDAEAVMEALHAGVSVIATAH

GRDLSELSARPALRTLITEQMFQRYVQLQRTSRGMTFRLADGKMRALQQTGAGGEAFG

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CDS 1400566..1401084

/gene="spolIIIAB"

/locus_tag="EFAGFIKM_01227"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q01368"

/codon_start=1

/transl_table=11

/product="Stage III sporulation protein AB"

/translation="MVNMFGAVIILLASTLAGFYKARQYALRPRQLRELIAALQRLMT

EINYGLTPLPDAMGKMGAQTKEPVKTLFLHAATQMEPPHGLTARESLSQSGVDLAWGRS
AMKADEKEVMLQLSFSLSGTSRQDQTKHISLAIQQLMHEESRAQADQMKYERMSSRLG
MLVGALIVILIF"

CDS 1401114..1401317

/locus_tag="EFAGFIKM_01228"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNLEVNAIFQIAGIGIIIAMIHTVLKQMGKEDMAHWVTVIGFVV

VLFMVVRMLDSLLQEIKSIFLFQ"

CDS 1401350..1401739

/locus_tag="EFAGFIKM_01229"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEIIQVVGLALIAITVLILVIKEQKPMFAFLIAAATGIVIFMLLI

GKIGAVIEVLKRLAENSGMESIYLKTVLKIIGIAYIAEFGAQIVRDAGQESIASKIEL

AGKVLILVLAIPISIIIIETVMKLMPV"

CDS 1401760..1402950

/gene="spolIIAE"

/locus_tag="EFAGFIKM_01230"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P49782"

/codon_start=1

/transl_table=11

/product="Stage III sporulation protein AE"

/translation="MKSMHHKPQWRLTVVLMCLFLGILGQVTATSPSGEWMEQQADQ

LPKDQVEKYWDQLMQYGGFFPEGKTPSFM DMLIPGNEGFSLSVFAIGTFMLHEIL

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KDAITGMINFMMAMVPLLFTLLASMGNVITSVTHPLIIFMIHLVSTLIHLLVFPLLF

FSAVLHLVSSLSDKYKLTQLADLLRNISVALLGILLTMFLGVISVQGASGSVADGVSL
KAAKYIAGNFVPVVGRTFADATDTVITASLLVKNAIGLTGVIIILFLCAFPALKILAL
ALIYNVTGAIMQPLGDTPIVGCLQAIGKSMIYVFAALAAVGLMFFLAITILLTAGNLT
VMMR"

CDS 1402982..1403812

/locus_tag="EFAGFIKM_01231"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGWLSNWLQELIMIVLLVTFVDMLLPNRSMERYVKLVLSLLILL

TLLSPITKLLKSDPVGELKRAMSAMDAPSNGNATLEQILAQGKRLQSNEQEQLQWTA

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EGEVKAGQQEVPANTQPIFGTDESEKDKSHQIQPIQIQIEVPDVQIDVSREQRDG

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CDS 1403828..1404466

/locus_tag="EFAGFIKM_01232"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKQWFKKMETWMGGGEGGARRSQTFRWLIILGLIGVGIMLFNSF

VNVKKIDSENIGREPPDPATSMASIQSDPSEQNPFQAIEIAFEDKIKGVLENIVGVGT

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IVTKKLKPQIRGVLVVARGAENKVVKDLITDAVEKGLNVAAYRISVVPRKQD"

CDS 1404533..1405363

/gene="spolIIAH"

/locus_tag="EFAGFIKM_01233"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P49785"

/codon_start=1

/transl_table=11
/product="Stage III sporulation protein AH"
/translation="MNNKRQTVWLVSMLSLMVILSAYYLFTEDSGPVNTPVADSQQVD
GIKQGEAKETAGILDPTEGLVVNEVNSGEVESDPSAAGAVEEPAATEGKEAGNTEKT
PVVEPGENKGEAGKETNKETDKGATTPETDGQAGGTATKTDEEVLKEMEEQNTTASA
SSQFQNYQWQREESNNRKYEELMTVAGDLSKTPEENAKATEQLRTL EEKEAKITGIEE
TLSQQFANAIVQEDADKYKVVVLSDKLDVKQAVSIVDLVMKELAVSQNKISVQYVTEQ
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CDS 1405497..1405967

/gene="accB"
/locus_tag="EFAGFIKM_01234"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P49786"
/codon_start=1
/transl_table=11
/product="Biotin carboxyl carrier protein of acetyl-CoA
carboxylase"
/db_xref="COG:COG0511"
/translation="MEMFKLSEIKELIKLVDESSVQELEIENEGSRLSIRKPGKTEYV
QAAAVQPQMIAAPQVQPAAVVSEAAPQVDTTSHLHKIVSPMVGTFYRASSPETGPFVS
AGDKVVEKTTVCII EAMKLMNELDADIKGEIVEVLVENGQLVEYGQPLFLVKPE"

CDS 1406023..1407366

/gene="accC"
/locus_tag="EFAGFIKM_01235"
/EC_number="6.3.4.14"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37798"
/codon_start=1
/transl_table=11
/product="Biotin carboxylase"
/db_xref="COG:COG0439"
/translation="MKFQKILIANRGEIAVRIIRACREIGISTVAVYSEADKDSLHVR"

LADEAYCIGPTLSKDSYLNFTNLMSVATLTECDAIHPGYGFLAENADFAEICESCNIT
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TAGGGGKGIRIAEDEETLIKQITAAQQEAQKAFGNAGVYLEKFLTGMKHVEIQIIADK
HGNA AHLGERDCSVQRRRQKLVEEAPCPILSEDVRTLMGEAAVRAALAVDYSGAGTLE
FLLSPNGEFYFMEMNTRIQVEHPVTEMVTGVDLIREMISVAEGNPLSFRQEDVINGW
SIECRINAEDPDRNFMPSPGKIGFY LAPGGPGVRVDSAAYPGYTISPFYDSMI AKLIV
WGANREEAI AKMKRALGEFAIEGISTTIPFHQKLLEHPTFIRGDFDIKFLEENEI"

CDS 1407584..1407994

/locus_tag="EFAGFIKM_01236"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTLPTEFERTDIGEIQIAPEVIEVIAGLATLEVKG VAGMSGGF

AGGFAELLGRKNLSKGVKVEVGQREAAVDVSVIIEYGYRLPQVATEIQQNVKRSIENM

TGLNVNEVNVHIHDVQFKSTEKVEEIDLNSQRVK"

CDS 1408141..1408680

/locus_tag="EFAGFIKM_01237"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAKILDRLLLFIYSISVGAISAAVILLISGVLPYELNYQQEQNV

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RFRGVRDVKARIRVVESGLEIMIRAVVDGETPIPALTS DLQKAIHDHVQEITGIPVSF

VTVYIANVTQSPNYKSRVE"

CDS 1408695..1408928

/locus_tag="EFAGFIKM_01238"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLWKEIWDSHRGRITGIIGGIFFGFLYVWIGFWDMLFFALLVFI

GYTLGRRSDSKLGSSIPWREWGQWLGDWRPFPK"

CDS 1409151..1409603

/gene="nusB"

/locus_tag="EFAGFIKM_01239"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9X286"

/codon_start=1

/transl_table=11

/product="Transcription antitermination protein NusB"

/db_xref="COG:COG0781"

/translation="MKRRLAREIAVQSLYQMEMNEVGAAEAVNMLINEAAEDNETEVV

IRDADVMTYVTEIVQGAWNNKEAIDGLLDYLGWQISRLSRVDRQILRLSTYEMVF

RDDIPAKVSVNEAIELSKYFGTEESGKFVNGVLGRMIQEVDIAKAKLS"

CDS 1409721..1410578

/gene="fold"

/locus_tag="EFAGFIKM_01240"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A697"

/codon_start=1

/transl_table=11

/product="Bifunctional protein Fold protein"

/translation="MTASIINGKEVSQEIRASMTTEVKQLSEQGVVPGLA VLVGEDP

ASQVYVRNKEKACHDLGFYSEVHRLDADTSQEDLLALVDKLNNQQSINGILVQLPLPK

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AVVIGRSNIVGKPVSLLLQRENATVTMCHSRTANMKEITRQADILVVAIGRANFVDAD

FVKPGAVVIDVGMNRLENGKLAGDVFESVKEVSGPITPVGPGVGPMTITMLMQNTLI

AAKRAHGLA"

CDS 1410589..1411953

/gene="xseA"

/locus_tag="EFAGFIKM_01241"

/EC_number="3.1.11.6"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P04994"
/codon_start=1
/transl_table=11
/product="Exodeoxyribonuclease 7 large subunit"
/db_xref="COG:COG1570"
/translation="MADQKIYSIKDLNRYIRMKLESDQVLSDVWLRGEISNFTHHSSG
HMYFTLKDKDSRIKSIMFASHNQRLPFVPKEGARVIARGNVSVYERDGGYQFYATHMQ
PDGIGSLYLAYEQLKKKLEDEGLFSPSRKRKIPRYPQTIGVVTSPGAAVRDIMITLQ
RRYPSAKVVLYPVLVQKGGAAPSIVKAIGNLNRMGEADV LIVGRGGGSLEELWAFNEE
IVARAIVASDIPVISAVGHETDFTIADFAADLRAATPTAAAELAVPNRAELLDQIGQR
QRQLQHSLRQRAVHNRRERLARLQRSPVLVHPRRTLMQHTERLDMMHQRLRLRTVDTRMK
WTGEKQERLRAALQRFNPREQVNAARRENAARRQLELAIRSIARSKQQQWKSSVRHL
DALSPKVM SRGYSLVYDEQEQRLIKSTKDVQPGDSIKIKLTDGQLDCQVWGMKEDDN
THGE"

CDS 1411943..1412200

/gene="xseB"
/locus_tag="EFAGFIKM_01242"
/EC_number="3.1.11.6"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A8G9"
/codon_start=1
/transl_table=11
/product="Exodeoxyribonuclease 7 small subunit"
/db_xref="COG:COG1722"
/translation="MANEPELNFEEMAALEDIVGQLEHGDVPLEQAIDLFQRGMKLS
QLCGLKLEQVERKIEMIVEEDGELRKKPFGTADDESGEVHE"

CDS 1412193..1413098

/locus_tag="EFAGFIKM_01243"
/EC_number="2.5.1.10"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q08291"

/codon_start=1
/transl_table=11
/product="Farnesyl diphosphate synthase"
/translation="MSNRPSFQAYLEEVTAAVTEALKHTLPDHWDPQSLTDAMQYSL
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LTNHKVYGEATAILAGDALLTHAFYSIVQAGRRSGVAADALLSIVEDMSELAGARGMV
GGQVADMEGEQGM TDLSQLQYIHLHKTGDLIVFSLIAGARIGGATEGQLEALRVFGRD
LG LAFQIQDDILDLTGDEQKMGKKTQSDVNQQKVTPYFIGMEASVDEVKSLTQSAKD
ALERAELPDASRLLEIADYLMSRDH"

CDS 1413383..1415290

/gene="dxs"
/locus_tag="EFAGFIKM_01244"
/EC_number="2.2.1.7"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9KGU7"
/codon_start=1
/transl_table=11
/product="1-deoxy-D-xylulose-5-phosphate synthase"
/db_xref="COG:COG1154"
/translation="MLLPQIKQPSDLKSMSQDDLALLSAEIRQFLIEKLSVTGGHLAP
NLGVVELTVALHYCYN SPADKMIFDVGHQAYVHKVLTGRMDRFD TLRQHNGLCGFVKR
NESEHDVWEAGHSSTLSAAMGMALARDLKGEDNQVIAMIGDGALTGGMAFEALNHIG
HEQRKLMVILNDNEMSIAPNVGAMHKYLSKIRSDRH YLKAKDDVEGMLKKIPAIGDRL
AKSASWIKDSVKYMMVPGVLFEELGFTYLGPIDGHDIPKLIETFKQADNVDGPVLVHV
LTTKGKGYQPAEADSHKWHGISPYKIESGQVLKAVGKPMYTEVFGQTLIDLAKQDKRV
VAVTPAMPTGSG LIPFSKEFPDRMIDVGIAEQHAATMCAALAMEGLKPVFAVYSTFMQ
RAYDQIVHDICRH NANVMFAIDRAGFVGP DGETHQGVYDVAFMRHIPNIVLMMPKDEN
ELRHMMKTALDYN EGPIAYRYPRNNVVGVP LDDVLVPIPIGSWEQLRPSEGYAVIASG
SMVQLAEAAEMVKREGITAGVINARFLKPLDEQMLRDLAVRGTKLIVLEETSQAGSM
GSAVLEFYAEQGLHDVHVQLMGIPDRFIEHGSIKEQREEVGLTVENVCAELRKMAVQS
SYGIPKTRFPS"

CDS 1415313..1416158

/gene="tlyA"
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/inference="similar to AA sequence:UniProtKB:Q06803"
/codon_start=1
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/db_xref="COG:COG1189"
/translation="MSLPKERIDVLLVEQGYYESREKAKAAIMAGLVYANNEPIEKAG
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HGASHVYAIDVGYNQLDWSLRNDERVTVMERTNFRYVTPEDLAGPVPNFASIDVSFIS
LRIILPPLLALLKQPADIVALIKPQFEAGREKVGKSGVVRDTKVHKDVLQTMLHFASQ
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KGNSS"

CDS 1416243..1416728

/locus_tag="EFAGFIKM_01246"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDGQYDTIVIGVLAVCLILWLFFGLRNWVNRPMPSLSGMQLNG
KIQDSPALDLLEAQGYEVIGGKMKVPLAFEANESVYYSRLFIDYVAEREDLRYLVKTS
RRRQPIEMTGPALRDRFLNYLLLYPGCEGLLYVDVENS DIKLIRLMDYQEDVYDGDDL
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CDS 1416813..1417262

/gene="argR"
/locus_tag="EFAGFIKM_01247"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9K973"
/codon_start=1
/transl_table=11
/product="Arginine repressor"

/db_xref="COG:COG1438"

/translation="MKGQRHIKIREISQNEIETQDDLVEALRKSGFQVTQATVSRDI

KELLLIKIPMDDGRYKYSLPTDQRYNPIQKLKRALVDNFLHIDHTNNLVMMKCLPGTA

NSIAALLDNIEWNEVMGTICGDDTILIICRTEGNSVTVIERIMGYIA"

CDS 1417541..1419259

/gene="recN"

/locus_tag="EFAGFIKM_01248"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P05824"

/codon_start=1

/transl_table=11

/product="DNA repair protein RecN"

/db_xref="COG:COG0497"

/translation="MLVTLIRNLAVVEEVDVVFHPGFHVLSGETGAGKSIIDALGL

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VKLSHSEKMMDSVAGAYDLLSGQRGLEAVSIALSRIEDISGYDNKGLQPIVEQLQSAF

YQLEDATFQLRDYREKIEFNPARLEEVEQRLNLISGLRRKYGDSVELILSYDQISHE

TDQLENKDERLEKLRAERDKMLNLVMESAEELSKVRKQCAEELAAQVESELKDLQMER

TTLRVQITPFEDPKGIEWNGRRIRLNRHGADNAEFLISPNPGEPLRPLGKIASGGELS

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AEAKKG"

CDS 1419380..1420708

/gene="spoIVB"

/locus_tag="EFAGFIKM_01249"

/EC_number="3.4.21.116"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P17896"

/codon_start=1

/transl_table=11

/product="SpoIVB peptidase"
/db_xref="COG:COG0750"
/translation="MNSPLRKLLGLLFAFFLCVISQAIQPVQSYASLPDELQVFAGR
QADVRLAVPAVSSAVVDRPDIVGLDDQAAMHVTRQQPLHLHPQQTGHAKLTLKLWGKI
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LGLYIRDSAAGVGTLTIFYAPDQGVYGALGHVITDMNTQTSIVVSGSQIVQSNVTSISK
SETGDPGEKRAHFLKESKILGNIERNTAFGIFGKMSGNPEHSLYSKGIPVAFSHEVKE
GPAEILTVVDGQQVERFSIDIVHVADQTEPATKGLVLRITDPKLLDKTGGIVQGMMSG
PIVQNGKLIGAVTHVFNDPKSGYGCFIEWMLQDAGVMMKKENDKNLKAG"

CDS 1420904..1421710

/gene="spo0A"
/locus_tag="EFAGFIKM_01250"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P06534"
/codon_start=1
/transl_table=11
/product="Stage 0 sporulation protein A"
/db_xref="COG:COG0784"
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LEQTRDVPDVLILDIIIMPHLDGLGVLERLRDLNLSPQPKVIMLTAFGQENITQRAVQL
GASYIILKPFDMEVLANRVRQLVGTQTAMSTSSGSSMFMKSNVVPMGKHKNLDANITS
IIHEIGVPAHIKGYQYLREAITMVYNNIEILGAITKTLPAIAEKFKTTPSRVERAIR
HAIEVAWTRGNIDSISHLFGYTINISKSKPTNSEFIAMVADKLRIEHKVS"

CDS 1422136..1423092

/locus_tag="EFAGFIKM_01251"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MFTQIGEIAEPIPVVQSDTKCDIVYHLFKSNPSLEGIAVMGEKG
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IYDLVLVTSGESFFGAVSIRRLLLAVADVRAEMAIFMNPLTGLPGNHIIDERLSQALQ
MDQFSVLYVDLDQFKSYNDSYGFKMGDQLIQATANLLRKLFVPPEAFLGHIGGDDFIT
ILNHHDYKYISEEVISGFEEMKKTFYNEHDWHHQYVLGEGRSGLNRPIPLVSVSIAVV
TNSKRKYENIDQIIDEATRIKKGCKAIAAGSIICANDTATTPC"

CDS complement(1423285..1424097)

/locus_tag="EFAGFIKM_01252"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNSISSATKSSFTPGNQVSNRDKEIQGLMQQKIRLNEEIQGVKT

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KSMMLENSERTVFQAKRETVQDINSQLNKVNQKIGELVEEIHQSAPKESAQPPISAAS

GEDNQEVNEGRKTGSKEHPSDGGTTDQESGNGPQTTASTSPATSYPVSDIRI"

CDS 1424304..1426265

/gene="rhaR_6"

/locus_tag="EFAGFIKM_01253"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MWNDYYILWNYAAVSITDIRYMELEAYEEMKYKFPTSTFVLTIQ

GDAGVTIDNQTYEVSIFYIHHGGKGSQLVQAGESGLRLYYLMYKANLPSGGRNDLGR

LMERINPFQMNYGFTPDMPTILYEQLKKMHFLWDQKNPIQHFQAKSLFYAFVEQISSQ

IPRISNRYPMSMLDQVSKVIEIVESSYTQPLTLHVLAEMIGTSPRSLSRKFKQSTGTSP

IDYLIQFRLFKAKEMLLQTDATLDEIAAGIGYPDGYLGRMFKKHTGLSPLQFKEKSS

APLYWPDLTSGVARNDIFRGGSGRYVYTDGDNHYQYKHGGSINMNRQTRTGMLLSILL

SLTLLLSACSTGVASNSSGDASRSNSTSSSTNTVTAENQSKSLEPRTVSTVKGDITIP

AEPKRIVVDLYLGSIALGIKPVGTPEMNLKNPYFIKSLEGVQNIGEYETISLEKYLE

LEPDLIVTGNPDLFDSFSKIAPTLVVPYGELKNTHEEIAYFGEVLNKEKESEAWLTDY

DARIADAKKRVGEAIDPQAEVSVMQFYDKAPLAFGDNFGRGGQAVYSALGLNPPADKK
EILMKDQLVEVSSEAIPEFAGDYIILTADNLTLEELKSKPVWSSSLDAVKNDRVFIWNP
DRSWYFDPIATLDQTEELAAWFTKISEPN"

CDS 1426461..1428434

/gene="rhaS_7"
/locus_tag="EFAGFIKM_01254"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaS"
/translation="MQLDEQMKCWNHAAVKVLDIRRIVMEAGQLSSYTL PANGFIYT
IRGSAVLQLDGGQTYKAERFYMLHGAKGSSLDIQTNE DFEYILLYRAFLAFPSYRKKW
LLAQPEVAPFSLQYGFAPSSPLGLLRYLDELEGAWSQSGSLDLLHTKSLFYQFIHEMM
VQLAEQEIKTELADPVKQTLRYIQNH YREQVTLDFLAEQFNYSSRHLSMQFKRQTGYS
PIDYLIQTRIAKARNLLVRSDATLSEIAAEVGYS DVVYFSRIFKKHVGISPIQYQRKI
REEARTEDRPLVISESSIGRRWKSGYIDYENHYQYIDGGSTPMKRRKTSSSMIMVALL
SITMLLAACSSGTATTPAAGEGTGASSNNSSTAVSTDAGSQTNKDNETRTVSTVKGDV
VVPANPKRVVVLYLQGDVVALGVKPIATSDVYDGAAYKSELEGVNALGTWFE PNPEAV
IDLDPDLIIVPSEETYTLTKDIAPTVYIPYEKLTTEERLHDIASIFGKEQEAETLLTN
LNNKVEESKKT LADAGILDKTISIVEGGLKGMVIVESKQFGRGSQAVYEYLG MKAPEV
VQKKIDVVSDAAGSTISMEVLPEYIGDYVFRSVYEGADNL TENPIWSSIPA IKEGRLI
EIDFDFFYSDIYSINKQLDFVVEKLLAAPRAQ"

CDS 1428594..1429631

/gene="ycgT_2"
/locus_tag="EFAGFIKM_01255"
/EC_number="1.18.1.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31475"
/codon_start=1
/transl_table=11
/product="Ferredoxin--NADP reductase 1"

/db_xref="COG:COG0492"

/translation="MNQQLELYDVTIIGGGPAGMYSAFYSGMRDMKTKLIEARDRLGG

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GGGDSAVDWANELEALAEQVTVVHRRDRFGGLERNVLRMRESSVDVRTPYAVETLHSM

SGDVIEQVTISHVDTGETEMLEVDVAVIVNHGMKSDFGPIRDWGLDLGEWHVTTTERLQ

TNIPGVFAAGDFVDYGSKLYLIAGTFTDAALAVNSAKLYMDPEAEKVAYVSSHNSRFK

EKNKALGVVEE"

CDS 1429837..1430487

/locus_tag="EFAGFIKM_01256"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKGSQPQRGFTFIQRWFKRSDKKKIKWSEMYLALAGALHRLLV

EGRRERSAAKRLHQDLPINALGEMKLEPGDIVYTPSSESTYYAGHMGIIGLDGKVYHV

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RSIERNYCSKFIYQAYQFTSGLDLWSRKFTRMNQGYIYPFRIERSSELVDLGTfYK"

CDS 1431022..1431498

/locus_tag="EFAGFIKM_01257"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYSGRQDDTLYIMTYTLNSGIKGTVPLSNKQIIEWLDCYRNEKR

FVTEIGKEFFGLNAGLVADFKVQNHLSDYQQTIMPTQQQDNLERLSSAYKSTELLMKI

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CDS complement(1431620..1432219)

/gene="tdk"

/locus_tag="EFAGFIKM_01258"

/EC_number="2.7.1.21"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q814U0"

/codon_start=1

/transl_table=11

/product="Thymidine kinase"

/db_xref="COG:COG1435"

/translation="MQTGRITVITGPMFSEKSGELIRRCQKLIQFGRKKVVAYKPAED

NRFAQDEIVSRIGYRLPAHSIPRQLTPESVEMILNQITADVVAFDEVQFFSSAIMEL

VSELAYCGKHVIVDGLNMDYRGKEFGYVGGLLAMADDIEKLSAFCVCGSPDAAFTQR

IVNGEPVTLGPVVMIGDSEAYEPRCRCCFIPPHKVECSS"

CDS 1432396..1432608

/locus_tag="EFAGFIKM_01259"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSEALTSLQERYESLKEQGSLEATQALFAELFAEAERLQASNL

TLRRITLKSSSKESRMSTKLRDALYE"

CDS complement(1432617..1432964)

/locus_tag="EFAGFIKM_01260"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVSFLITLQRLKGFHAFKDPKFLALFALTAATLLSGTLFYTR

VEGLHWIDALYFCAVTLTVGHPEFVPTTGFSKAFVIYMFAGIGLTFAMIARITAGI

LFPRKLKTEEDPE"

CDS complement(1433028..1433345)

/locus_tag="EFAGFIKM_01261"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLMNTRLVFARFLAIVVLVIPGLMAMKGFLMMKDALFLYYAEHG
NELISPGFQWLSFGGGLVLFAAGMSFLGGWILFRDRKRNYVGPRFRSKSVPEKAETPG
RTP"

CDS 1433570..1434994

/gene="lpd"
/locus_tag="EFAGFIKM_01262"
/EC_number="1.8.1.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q8NTE1"
/codon_start=1
/transl_table=11
/product="Dihydrolipoyl dehydrogenase"
/db_xref="COG:COG1249"
/translation="MPITCDVAILGGGTGGYVAAIRAAQLGKQVWIEKDKLGGTCLH
RGCIPSKALLKSAEVYAEIQESETYGIETAGAKLVFPKVQARKDAIVEQLHQGVQYLM
KKNKIQVWHAKGRVIGPSIFSPQSGAVAVEFEDGEMDTVVPTNLIATGSRPRVLPGL
EPDGKFIMSSDEALRMDLPASLIIVGGGVIGLEWASMLNDFGVDITVVEAAAHVLP
A
EDEDVAREMQRLLGKRGVRFLTGATVLTETYNQDQEGIQIDVQLGDDKQETLRAEKML
VSVGRQANVENIGLENTDIKLERGFIAVNKQLQTGEGHIYAIGDCIGGLQLAHAASHE
GILAVEHLAGEKVHAVESHRIPCVYTRPEAASIGFTEREAKERGYDIKTGKFPFSAI
GKSLIHGSRDGFVKVIADAKTNDILGVHMIGTHVTELIAEASLAQMLDATPWVEVGQTI
HPHPSLSEIMGEAMLAVDGKAIGM"

CDS 1435134..1436162

/gene="bfmBAA"
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/EC_number="1.2.4.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37940"
/codon_start=1
/transl_table=11
/product="2-oxoisovalerate dehydrogenase subunit alpha"
/db_xref="COG:COG1071"

/translation="MSSQGTADAVHRHQQLGLSDGEVLDMYKYMLLARKFDERCLLLQ
RAGKINFHVSGVGQEAQVGAAFGGLDRDHDYLLPYRDYGFVLAVGMTPRELMLSAFA
KAEDPNSGGRQMPGFHGHKKLRIVTGSSPVTTQVPHAVGFALAAKMKKQEFVSFVTFG
EGSSNQGDFHEGANFAGVHKLPVIIMCENNQYAISVPIHKQLSGKISDRAQGYGFPG
RVDGNDALEVYAAVKEARRRAIAGEGPTLIEAMMYRLSPHSTSDNDLAYRTKEEVEEN
WKKDGVPRMKNYLIDCGIWDEARDADLASQLAMEMKEATEYADNAPYKPEDTLTHVY
ADSEEGGR"

CDS 1436165..1437151

/gene="bfmBAB"
/locus_tag="EFAGFIKM_01264"
/EC_number="1.2.4.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37941"
/codon_start=1
/transl_table=11
/product="2-oxoisovalerate dehydrogenase subunit beta"
/db_xref="COG:COG0022"
/translation="MAVMEYIDAIRLAMKEEMERDENVFILGEDVGLKGGVFTTTKGL
QDQFGEMRVM DTP LSESAIAGVAIGAAMYGMKPIAEMQYSDFMLPATNQIISEAAKIR
YRSNNDWSCP I VIRAPIGGGIFGGLYHSQCPESIFFGTPGLKIIAPYSAYDAKGLLKA
AIRDPDPVLFFENKKCYKLIKEDVPEDDYIVPIGKANVLREGADITVIGYSQPLHFVM
QAAEELEREEGITAHVLDLRTLQPLDREAIASARLTGKVLIVHEDNKTGGVGAEVAA
IISEECLFELDAPIQRLCGPDVPAMPISPTLEKFYMLSKDKAKAAMRTLAEF"

CDS 1437199..1438650

/gene="pdhC_1"
/locus_tag="EFAGFIKM_01265"
/EC_number="2.3.1.12"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P65636"
/codon_start=1
/transl_table=11
/product="Dihydrolipoyllysine-residue acetyltransferase"

component of pyruvate dehydrogenase complex"

/translation="MAERMKWIEVIMPQLAESLVSATIGKWLKKPGDRVEQYEPICEV
ITDKVNAEIPSTVDGIMGDLLVEEGTTIAVGEAICRMQVAASDEEAAEQVTQVSQQQE
QVQQHVSHTPVAASNTAAHDPNQPMRNRYSAPVQSLAAEHGLNLQSIQGTGAGGRITR
KDVLAFFVAQGGNASGTSASAQASSAAVQHTPSGVPSASPFSGVNRGNGEMGLTAGEAI
SASDAGVPVRLSGIHLTESPKIPQIEVEGGGQGRSEYFIDVTPVRNAIARNMRQSVSE
IPHAWTMIEVDVTNLVMLRNKLKDEFKRKEGINLTYLSFMMKGVVNAIKDYPIMNSVW
AVDKIIVKRDINLSMAVGTEDSVLTPVIKHADQRNIAGLAREVDELARKTREGTLKLD
HMQGGTFTVNNTGSFSGSILSQPIINYPQAAILTFESIVKKPVVINDMIAVRSMANLCL
SLDHRILDGVISGRFLQRVKENLEGYTMETKVY"

CDS 1438762..1439469

/gene="lipB"
/locus_tag="EFAGFIKM_01266"
/EC_number="2.3.1.181"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q5SLQ3"
/codon_start=1
/transl_table=11
/product="Octanoyltransferase"
/db_xref="COG:COG0321"
/translation="MSKPLDVAYIPMLDYEEAWNRQKAIVQRLDEGEAEQMLLLQHP
PTYTIGSQNHPEHLLLSPEELREQGISLFQIDRGGDITYHGPQQLVGYPLILGRDED
LDLHGYLRKLEQVLM DYLADQGIEAGRKEGYTGVWIGDMKIAAIGIKFNRCKHRRGFV
TSHGFAFNISSGIQHAGFQGIVPCGIEQYGVTSLEDITGKS YAVEQVAQEIVPYFNRI
FPYQINWWTEKEALQRL"

CDS complement(1439496..1439597)

/locus_tag="EFAGFIKM_01267"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQKKKWFKIIIIYLM LIAMIGSTLFIALEPLLFG"

CDS 1439681..1440814

/gene="pepT_1"

/locus_tag="EFAGFIKM_01268"

/EC_number="3.4.11.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29745"

/codon_start=1

/transl_table=11

/product="Peptidase T"

/db_xref="COG:COG2195"

/translation="MIKQQRVIDQFMELVQIDSETKNEHNISKVLKEQFTDLGLHVYE
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TTILGADDKAGIAALFEAIRVIQENKIPHGKIQFVITVGEESGLVGARAMNPKDIDAE
FGYALDSNGAVGTICVAAPARAEIQMSIYGKSAHAGVNPEDGISAIQVAAKAIAAMTL
GRIDDETTANIGKFQGGSALNVVCFVQLEAEARSIVQEKVELQVAQMRDALETTCKR
YGATAEFRSEILYPAFGFHDEHEVVQLAQRAIRSIGLETSTFASGGGSDANIFNGFDL
PTVNLAVGYEDIHTTKERIRAEDIVKLSQVVVAIIQETAADKK"

CDS complement(1440961..1441095)

/locus_tag="EFAGFIKM_01269"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNSYMTPQSVHVVGQARQVQLILKQWLREWGPDAKLIDLLAGRK
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CDS 1441218..1441811

/gene="act"

/locus_tag="EFAGFIKM_01270"

/EC_number="3.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8KP10"

/codon_start=1

/transl_table=11

/product="Methanol dehydrogenase activator"

/translation="MKPNQSAQSIHAAQPANPKLDEVTVSTKPIFEGKVISLQVDTVK
LPNGQTATREIIRHPGAVAVLALNGDRMLVVDQYRQAMGRTEVEIPAGKLDPGEEPEV
AAARELREETGYVAKSLRHLRSFYTSPGFADEIIHLYIAEELEAGDMALDEDEFLEVA
EITLEEAYALMDENRISDAKTMMAVYAWDLYRTTGRF"

CDS 1441814..1443034

/locus_tag="EFAGFIKM_01271"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQDQLETSTMWEPCYTDLHIHIGRTSRGEAVKISGSRDLTFENI
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LREPGMREFHMLAYFRDLKTMKSFTDWMKRYMKNVNLSSQRVYVPALEMQAEIKARGG
LIVPAHVFTPHKGIYGSTAPRMGDVLDTSLVDAVELGLSSDSSMASYIRELDHVPFLT
NSDAHSLGKIGREYNELQVAAPSFDEFMALQGEAGRKIAANYGLNPRLGKYHRTYCS
ACGSIMDEQAMSAERCPHCGSLKLVQGVLDRLAISDRESPHV PANRPAYHYQVPLEF
IPGLGKAKLRQLLDHFGTEMNVLHRTREEELAAVVG PVLAGLIVAARNGQLELSSGGG
GTYGKVAVQEKASE"

CDS 1443196..1443825

/gene="spolIIM"

/locus_tag="EFAGFIKM_01272"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37873"

/codon_start=1

/transl_table=11

/product="Stage II sporulation protein M"

/db_xref="COG:COG1300"

/translation="MRSSYFTFKGQTSLYVFVAVLFLVGVIFGALMVNALSLEQRQDL
EGYLGNFFMTVQHSAQVTETGAYWDIAMLHLKWVGLIFILGLSVVGLPGILVLDFLKG
VLIGFTVG YLVGQYSWKGLLFALVSVAPHNLFVIPILLICSVAAMTFSLYIIRNRVLM

QRTPGRQRPFASYIVLTLVMAALLLGVASFETWVTPAMMRWVTPMLLPA"

CDS 1443933..1444400

/gene="fur_1"

/locus_tag="EFAGFIKM_01273"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54574"

/codon_start=1

/transl_table=11

/product="Ferric uptake regulation protein"

/db_xref="COG:COG0735"

/translation="MEARIDKIKQQLQSQGYKLTPQREATLRVLLENEEDHLSAEDVF

MLVKEKAPEIGLATVYRTLELLSELHVVEKINFGDGVARYDLRGDTSKHHHHHLCVQ

CGSMDEIREDWLGPLEERLEREFNFSVVDHRLDFHGICYRCKAKNEQKPKDEE"

CDS 1444558..1444800

/locus_tag="EFAGFIKM_01274"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIISVRRGLRFIRFIFFAALVYLFYHVLDLFNGWISPVDQYQM

PTGNAIKVFQETDWPGNGEGRPTMAERLRLFYWYGE"

CDS 1444876..1445766

/gene="xerD_1"

/locus_tag="EFAGFIKM_01275"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A0P0"

/codon_start=1

/transl_table=11

/product="Tyrosine recombinase XerD"

/translation="MKQTIHAYALYLEDKGMSSSTLESYLRDVKFIEFADKEYGIR

EADQVRRTHVVLFAQQLKQAGRANATIARSIVSLRSYFHFLMRRGDIIQDPTFDVEAP

KADKTPPQVLSIQEIEQLLTAPDTRSPQGVRDRSMLELLYATGIRVSELIALDIRDVQ

PGMRFIRCGGAGKERILPIGAPAAHWASVYVEEFRNKLLKTDSDQALFVNVSGRRLT
RQGFWKLLKKAAMDAGISEEITPHTLRHSFAAHLIANGADTRAVQDMLGHVEQPGQQY
GNHGRKTMKEIYETHHPRAR"

CDS 1445896..1446720

/gene="punA_2"
/locus_tag="EFAGFIKM_01276"
/EC_number="2.4.2.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P77834"
/codon_start=1
/transl_table=11
/product="Purine nucleoside phosphorylase 1"
/translation="MTALNQQMISEAASYIQSKSSIKPEVGLILGSGLGVLAEIEDG
VSIAYQDIPHFPVSTVEGHEGELLVGTIKGRPVMKGRFHMIEGYGPELTAFPVRVM
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AYSRRLRALAKDTAASQGFNVREGVYAGMLGPNYETPAEIRMLRTLGAADAVGMSTVSE
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CDS 1446969..1448144

/gene="dacF"
/locus_tag="EFAGFIKM_01277"
/EC_number="3.4.16.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P38422"
/codon_start=1
/transl_table=11
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/db_xref="COG:COG1686"
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KDTHFANCNGLPVDNHYSSAHDIAVMSRELLKHSGITKYTGAYQDYLRKDTEKPFWL
NTNKLVRFYEGADGLKTGYTSEAKFCLSATASKDGLRVSVVLGEPNTKTRNSEVSSM"

FDYAFSQYTMKALYKAGDLLGSLRIEKGEVAELPLNATQNYSVLMRKGAKSNDIRHEL
LVAKELKAPIKAGQSIGKLVVYQGNDVIKEFDIQAPQDVNKAGWWKLFKRTTSNLFD"

CDS 1448290..1448643

/gene="spolIAA"

/locus_tag="EFAGFIKM_01278"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P10727"

/codon_start=1

/transl_table=11

/product="Anti-sigma F factor antagonist"

/db_xref="COG:COG1366"

/translation="MNLHVEMEHHRGILIVRLSGELDHHTADMVRMQMDEAIQRRQSE

HLVLSLKDLQFMDSSGLGVILGRYKLIKNGGKMVVCVNSPVYRLLMSGLFKIMPI

YENEGTALSGLEVVS"

CDS 1448640..1449095

/gene="spolIAB_1"

/locus_tag="EFAGFIKM_01279"

/EC_number="2.7.11.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32727"

/codon_start=1

/transl_table=11

/product="Anti-sigma F factor"

/translation="MNEGTGTNFMNLQFAAKSENESEFARVTVAAFISQLDPTMDELS

LKTVISEAVTNSIIHGYNNSSEGVVSIQAEIREDMITIIVEDRGEGIEDLELAKQPLY

TSKPELERSGMGFTIMENFMDEFVSSEPGRGTSIKMKKRIESKKALYN"

CDS 1449110..1449865

/gene="sigF"

/locus_tag="EFAGFIKM_01280"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P07860"

/codon_start=1

/transl_table=11
/product="RNA polymerase sigma-F factor"
/db_xref="COG:COG1191"
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WSVVQRFMNRGYDPEDLFQIGCIGLLKSVDKFDLSYDVKFSTYAVPMIIGEIQRFLRD
DGTCLKVSRSLKEMANKVRKKRDELSKHLDRPTIKEVAAELGVTPEEVVFAQEANKPP
TSIHETVFENDGDPITLMDQIADESQERWFDKLALNEAIGGLSERERLIVYLRYRDQ
TQSEVASRLGISQVQVSRLEKKILQSIRDQIAQ"

CDS complement(1449953..1450882)

/gene="yicL"
/locus_tag="EFAGFIKM_01281"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P31437"
/codon_start=1
/transl_table=11
/product="putative inner membrane transporter YicL"
/db_xref="COG:COG0697"
/translation="MTTSAKSKISGIILVLTGAICWGIGGTVSQKLFQLDGIEVNWYV
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GNSAVATLLQYLSPVMIMIIYALRKQSVLTRNDLACAVLTLSGCFLLLTNGSLTQLSV
SSLAVIWGLLSGVSAAFYTNAYVQLIKKFDSL VVGWAMIIGGLGMSFIHPPWKMNFA
NITLETYGYLIFTILFGTMIAFWFYIASLSLTPKETSLLGSAEPLAAVGTTVIWLHE
PFGFYQWIGMACILGMMLVMQSNRSRSPRINNK"

CDS 1450991..1451899

/gene="melR_1"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0ACH8"
/codon_start=1
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/product="Melibiose operon regulatory protein"
/translation="MQKIEFIIDQHLKEMTQHRTDLSIGCYETTIVQNVHGHIPLHW

HDELQFVAVLQGTALFHINDQKMILSKGDGIFINSGIMHMAEDHGVSENCIYLCLNLS
PHVIMPSDLYIKYVHPYVTATNLPFLYIERANAWGEQILDAIAWIRKELVHQVPFYEV
NIASAVLNMWKLIMNGYSLEHDPSEMSRNNRMKDMLQWINLNYADPIKLENIAGQ
LSRSETCRYFKQILKTTMPQYVIEYRIQRSIELLQSSKRSITEIAYEVGFNSTSYIN
QFRKTMNSTPLRFRRELNKRGENNS"

CDS 1452381..1453037

/locus_tag="EFAGFIKM_01283"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSQTPTPMVYIRLSRIRIQRGRAVKLGDIHVLTSSEDQEGRL

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CDS 1453024..1453446

/locus_tag="EFAGFIKM_01284"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSVLNGAISIVLGIAGGIAVGSGVIALILVLDMIPRLAQLTQSY

DKTHWYEGALIGGSLLGTVADEFWHWKMHGVLLLSPIVGLFCGVFIGLLAAALTEVLNV

LPVLAKRLGMKPYLFGLLLAMILGKMTGSLFDFFIYQR"

CDS 1453471..1455138

/gene="gerBA_1"

/locus_tag="EFAGFIKM_01285"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39569"

/codon_start=1

/transl_table=11

/product="Spore germination protein B1"
/translation="MDERTEHTGQENSEGITEEMLHKSAYEIQKEEEEKAYNKKKQNE
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TGFAKDEILLEILKRLTYLTPDQVSGHALKSYFECYIPHIQVEKVDKMSAVINKVLTG
MSAMFVEGDRSVLIMDTRSYPVRSPEEPSLERVVRGSRDGFETLLTNVTLVRRRIRD
PGLKFEIMQVGRRTQTDVCVVYIDDIVDKVQVDSVREKIQRVDIDGIPAADKQLEEI
INKGWNPFPLVRYSERPDVTASHLLEGRVVFVDTSPSVMILPTTFFDLCEHAEENRQ
TALMGTYLRWVRFAGILISLFLPLWLLMVIDPSIKPMGLDFIGPQENVKLPLILQFL
LIELGVDLLRMAAVHTPTPLASAMGLIAAILVGDIAVKTYGVNEVLYMAIAAIGMF
ATPSYELGLANRLVRLVLLVAVAIKVPGLVVGCTLLILALTVHRSYNSSYLWPFIPF
NAKALGNFLFRLPLENKKRPSFNKTRDNTKMSDDPDGELQSKKKHK"

CDS 1455242..1456573

/gene="lysA"
/locus_tag="EFAGFIKM_01286"
/EC_number="4.1.1.20"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P09890"
/codon_start=1
/transl_table=11
/product="Diaminopimelate decarboxylase"
/db_xref="COG:COG0019"
/translation="MYLHGTSKINAQGHLEIGGV DATDLKEQFGTPLYV VDEQLVRER
CREYMEAFRASGLGFQVAYASKAF CVMAMCALAAEEGLSLDV VSDGELFTALQAGFPA
ERIHFHGNKNTLEEIEMALDAEIGCFVVDN FNELHLLQAVAADKNRKVNILLRVTPGV
EAHTHEYISTGQTDSKFGFDIGNGTAFE AIDLASKQSNLVLLGVHSHIGSQIFEVEGF
QMAVQRVAEFAASVYERLNVAFKVVNLGGGFGIRYIDGDTPLEVAQYVKAITDAVKNH
FAQIGYAVPEIWVEPGRSIVGEAGTTLTYVGT SKDIPGVRKYVAVDGGMTDNPRPALY
ESKYEAVLANRANEA AQETVSVAGKCCESGDMLIWDLDLPKVESGDLLAVACTGAYNY
SMASNYNRIRRPVAVFVKDGGQGDVVVRRETYQDIIQNDLVPARIGKQPVTR"

CDS 1456821..1457252

/gene="ppiB"
/locus_tag="EFAGFIKM_01287"

/EC_number="5.2.1.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P35137"
/codon_start=1
/transl_table=11
/product="Peptidyl-prolyl cis-trans isomerase B"
/db_xref="COG:COG0652"
/translation="MAKQAKIKLANGGEVLIDLFDQEAPNTVANFEKLANS GFYNGLT
FHRVIPGFVAQGGCPNGSGAGGPGYTINCEINPNKHERGTLAMAHAGRNTGGSQFYIC
YQPQPHLDGQHTVFGKVTKGMEFVDALEGKDKMETVEVVEA"

CDS 1457357..1458670

/locus_tag="EFAGFIKM_01288"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDMVTQLSLLKQIYSERTLWDEELQASRHVVPDSLSVKDREVLE
AAGHEPNRNFVRPQHDETITELKKVANQWTINDAAQAFVSSLWSAPMIWRSLLTGKLI
SSMPSHEHTPYSSNTCKICGLSVDQATDTTLQWFWRM TNGTPLDGD PFGYVLALREL
AAAQELPIPNEYDRWTFSAVLTVLRDLPPKTRYSKAAVALKKERLLPTQKEYAYRDLL
ETLALIGILDTPEHPGMITEFTSYIQRDARNIRVEVQAPLAWWDSSVGINENNLNKI
FHD FDLNNISLADKPEESPAVKDTILGALEKKRSVRGKVPKASPDAGTGEVQSGDVYA
VRVREGVWVTVYCHEVRDKRVIVEYLDGVFPMPGKADLHGTFRPRANGRWKCSAIAI
DSTSWVRRVAREFPLPTSPLQEPDRTPFHNAKELKHMASWC FPD M"

CDS 1459335..1460432

/gene="ribD"
/locus_tag="EFAGFIKM_01289"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P17618"
/codon_start=1
/transl_table=11
/product="Riboflavin biosynthesis protein RibD"

/db_xref="COG:COG0117"

/translation="MINDEFYMALALDMAERAQQGTGINPVVGCVVVKEGRIVGLGSH
LKRGTGHAEVHALNMAGSDAEGSTVYVTLPCSHYGKTPPCSERLIHEKVKRVVVCCE
DPNPQVSGRGISMLRQQGIEVEVGLRERGRRMNEKFIKFITTGLPFVTLKTATTLTG
KIATRSKWDKSNPAREIVHALRHRHQGIMVGVDTVIADNPELTTRLQVEGISPVR
IVVDSKLRLPVGAKMVKDGLAPTWWLTDEASPEAAERLEAYGVEIIRCGPGPRVDLL
NGLSKLGEREIGSILLEGGGTNGAMLEARLVDRLLMFIAPKIVGGYDTPGSFRFEGV
ERMNQAIQLNQLEIEQVGDNISIGGIPVWPE"

CDS 1460494..1461162

/gene="ribE"

/locus_tag="EFAGFIKM_01290"

/EC_number="2.5.1.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P16440"

/codon_start=1

/transl_table=11

/product="Riboflavin synthase"

/db_xref="COG:COG0307"

/translation="MFTGLVEEVGQIRRIGRKGEAMVLNIGASAIMDDLKIGDSVAVN
GVCLTATTLEGGGFTADVMPETYRHTNLSQLQAGSKVNLERAMQSGGRFGGHIVQGHV
DGTGVIGSITRDQNAIVFEIKPDDHQLFKYLIPKGSVTLTGISLTVVHTSDTAFTVSI
IPHTIGETVLNVKKTGDTINIECDILGKYVDHLLQYGRGHRETGAGKPRSISEDFLSN
HGFA"

CDS 1461195..1462427

/gene="ribBA_1"

/locus_tag="EFAGFIKM_01291"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WHF1"

/codon_start=1

/transl_table=11

/product="Riboflavin biosynthesis protein RibBA"

/db_xref="COG:COG0108"

/translation="MSEQSILDTIEEAIYDLMRGKPVIVVDDDEDRENEGDFIALAEKA
TPEVINFMITEGRGLVCPITQQRADLNKPMVQQNTDFHGTFTVSDHKDTTGI
SAHERSITVKGLIDPEAKAGDFRKPGHMFPLIAKDGGVLRAGHTEAAVDLAIMCGSY
PAGVICEVIKEDGTMARLPDLQEIARKHDLKLISIQDMIRYRNEKEQLVQREVAVRMP
TDFGEFQAVAYTNAVDNKEHVALVKGEIDGTPVLVRVHSECLTGDVFHSHRCDGPQ
FDAALKQIHEEGNGVLLYMRQEGRGIGLINKLKAYKLQEEGMDTVDANLSLGFAADLR
DYGIGAQILKDLGVRQIRLLTNNPRKIKGLEGYGLEVVERVSIQMEENEDNTVYLHTK
QAKLGHMLKFDDIEQNEQ"

CDS 1462530..1462997

/gene="ribH"
/locus_tag="EFAGFIKM_01292"
/EC_number="2.5.1.78"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q81MB5"
/codon_start=1
/transl_table=11
/product="6,7-dimethyl-8-ribityllumazine synthase"
/db_xref="COG:COG0054"
/translation="MPQFFEGHLVSEGSRYGVVGRFNEFITSKLLSAALDAFKRHGV
QDDEVDVAWVPGAFEIPLIAQKMAESGKYDAVITLGTVIRGSTTHYDYVCNEMAKGVA
AINLKTGVPTIFGLVTTENIEQAIERAGTKAGNKGWDAATAAIEMANLTKQLK"

CDS 1463102..1463902

/gene="scpA"
/locus_tag="EFAGFIKM_01293"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P35154"
/codon_start=1
/transl_table=11
/product="Segregation and condensation protein A"
/db_xref="COG:COG1354"
/translation="MTVVTYKLETFEGLDLLLLHLIDKAEIHIQDIPISDITDQYMAY
LHSMQELELDITSEFLVMAATLLSIKSKLLLPKPPVIEDFEDYDFMEEEDYDPRAELI

ARLIEYRKYKGIARHLHEREWERSLIFSKEPEDLRPYMPVEAQSNPVEGLHTSDLIAA
FQKALRKA EKRTTVTRIKRDEISVKDRIRDVIGALESMGPGGRLLFSKLMDEHIYRHE
IVVTFLAVLELMKMKQIVCYQERMFEDIVMEWRGETKNHGFSEIEIDY"

CDS 1463871..1464527

/gene="scpB"

/locus_tag="EFAGFIKM_01294"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P35155"

/codon_start=1

/transl_table=11

/product="Segregation and condensation protein B"

/db_xref="COG:COG1386"

/translation="MDFPKLKSII ELLFLSGEEGLSIKQIAEIVDQRVELVTDAIEE

MIHEFSQQGRGVQILKIAGVVQLGTLPDHAVYFEKLAYSPARTSLSQAALETLAIVAY

RQPITRVEIEEIRGVKSERAIHTLVNKDLIIEVGRAEAIGRPILYGTTKSFLDYFGLA

SIKDLPEPGLFEDSENLEEETQLLFNKLDLQQLPEIVDPADDLSLIDNEDDNTDSSL

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CDS 1464717..1465448

/locus_tag="EFAGFIKM_01295"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MWIWLGGIGLLFALLIAAVLISNVHVHFTFSKHKSDDYANINVR

LLYGIVRINYEIPSIVFRNMKEGFLVKTEQSMNHSRGEAQGSERVNKRKVKKWAKDVK

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YQIRFDETPVLQVMPVWSDEMEFRTELDFRVKIRITAVLIAGVTLLTRVLQVEGGWRM

WFKLLQEQRRRHKEKQKKKLSGTTV"

CDS 1465596..1466078

/gene="ytfJ"

/locus_tag="EFAGFIKM_01296"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34806"

/codon_start=1

/transl_table=11

/product="putative spore protein YtfJ"

/db_xref="COG:COG3874"

/translation="MSDHPIQGLMETAMENIKAMVDVNTIVGDAVETPDGTVILPISK
VGFGFAAGGSDFHVNGESSGKSGATGTSTEHASSAKVASPFGGGSGGGVSIRPIAFLV
VGKQGVHIVPLDNSTHLFEKLIDSTPYVLDRIQGMFQRNTTPTNTTGVPVTPDPSTYS
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CDS 1466209..1467396

/gene="dacB"

/locus_tag="EFAGFIKM_01297"

/EC_number="3.4.16.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P35150"

/codon_start=1

/transl_table=11

/product="D-alanyl-D-alanine carboxypeptidase DacB"

/db_xref="COG:COG1686"

/translation="MRKITKVIACMLIPVFLSSLGVTQAQATIQGPSTHAQSAALID
VTSGRILYSKDGDKELRIASLTAKIMTAIVAIEHSLDEKVKVSPTAFAKEGSSLYLKL
GEEMTLENMLYGLMLRSGNDAASAIAEHVGGSEEGFVLLMNKKAEQIGLTHSHFMNPH
GLDAEGHYSTANDLARLTAYALHNPVFKRIVATEDKSAPNPNESWEYSWHNKNRMLRM
YEGADGVKTGYTKAFRCLVSSATRNGQQLAAVTLNDGNDWWDHARMLDFGFEYFPLV
EVAKQEQPVQNTDVTGRGFWYPLAESEKSSLTKKLILHENRGQSETEGKEQSTDPSF
GLAGRIDMQLDGKLVGSIPVYRKGSYIPPEPKTEDATLGGIGNVSSWAAAWRAVLGHL
LSP"

CDS 1467428..1468054

/gene="spmA"

/locus_tag="EFAGFIKM_01298"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P35157"

/codon_start=1
/transl_table=11
/product="Spore maturation protein A"
/db_xref="COG:COG2715"
/translation="MINLIWLLMILIGFAFAAVNGNIEVVTQAAFDGAATGVTVCFGL
ISVLVFWMGMMKMAEDAGLLARIAKLLGPVVGFLFPDVPKNHPAMGYILSNMSANLLG
LGNAATPMGIKAMQQLQELNPDQKTASPAMCTLLALNTASITIIPTTLIAIRLNYHSA
NATEIVGTTLMATIIATLAAIIADRWYRNRLHKPPRIQKSGNPGMKG"

CDS 1468061..1468594

/gene="spmB"
/locus_tag="EFAGFIKM_01299"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P35158"

/codon_start=1
/transl_table=11
/product="Spore maturation protein B"
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DVVGFIALAICLLVFG"

CDS 1468658..1469476

/locus_tag="EFAGFIKM_01300"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQKSWKRMLRVGMSGVLAIAMLAGSTGLAAAQAVQTIHFTGYFD
KQLRAQMAVTADSFVNVRLVKQDEPDMVYYDVGTSILISKDEVLTYHVVQSFAEL
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YTIGFPKNPAGDLVILDEDFPSTYNTVAKSRVFSSQASDVPGKKIGSIVKSMAQGNS
GGPVLDQNNRVIGMMTFVYGGRTYYITSKTLQTFIKESTKPAKKQVAVAGKVS"

CDS 1469664..1470422

/gene="rluB_1"
/locus_tag="EFAGFIKM_01301"
/EC_number="5.4.99.22"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P35159"
/codon_start=1
/transl_table=11
/product="Ribosomal large subunit pseudouridine synthase
B"

/db_xref="COG:COG1187"
/translation="MTNMERLQKIIAQAGIASRRKSEELILSGKVEVNGEVVTELGTK
ANPEEDMITVNGKPIRSEKKVYLMLNPKGVITSASDPEGRKIVSDYLGVKERVYPV
GRLDYDTEGLLILTNDGEFAHLLTHPKHHVPKTYHATVKGVPHTALEKLKTGIMLDD
GMTAPAEVEYKDVRTAANESVISITIEGRNRQVRRMF EAINHPVTRLKRISFGGILL
QNLKRGLTRHLTKEEVNNLITLAQSEPAKKMKKR"

CDS 1470557..1471084

/gene="resA_1"
/locus_tag="EFAGFIKM_01302"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P35160"
/codon_start=1
/transl_table=11
/product="Thiol-disulfide oxidoreductase ResA"
/translation="MGKSRRTVQIVILLILVLGGYAITTSVSGSNGKPKEGDKSPSF
ELLGLDGQVHTSDEYK GKAMVINFWGTWCEPCVKEMPALQAQADKWKDQGVQFVGINV
GEDQMTVDNFRVQVGVTFPIMLDREKNSVRDFGISPMPTTFFVSDTGKISTIHIGQLD
LDTLDAQISQLAKQP"

CDS 1471099..1472772

/gene="ccs1"
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/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01392"

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GLDENGQPKSKSPSPNAPAFLLIKGPDLP EEGIQYLYFAKQIDKQRFQQDAINQQLI
GADIPLQLEVDSMDKVDIIQSVSYLNIRVDKAMPFVWVGAGIVMLGLVMGFYWHHRRI
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CDS 1472769..1474031

/gene="ccsA"
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/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01391"
/codon_start=1
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/translation="MRLLDFSSDAFIVSFFLYCAAFLLYAVAVMGKKWSNRDPLDHMN
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AGFMYLLRTVDFSGKDKSSRRQRGWVEFTLV TIVVVIGFIGTVFAFR TAGYEAVFVQK
TVSIDTEVQENSTIEKVIYRMPPIFAPYNSEVESMT PFLGMKKPLLET PSWMNGVNAG
RKLNTVWWSLIVGLILY GIVRLLVRRPLGQALQPMMDGIDADDLDEISYRAIAIGFPI
FTLGALIFAMIWAQIAWSRFWGWDPKEVWALITWLYYSVYLHLRLSRGWQGQKSAWLA
VLGFLVVMFTLVGVNLI IAGLHSYAGAD"

CDS 1474078..1474887

/gene="srrA_2"
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/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9L524"

/codon_start=1

/transl_table=11

/product="Transcriptional regulatory protein SrrA"

/db_xref="COG:COG0745"

/translation="MYLFIKGYSNIVRQIEHNRSDEELLQRGWRGMAEHENRILVVDD
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RQVKSTPVLMLTAKGEEINRVQGFEVGADDYVVKPFSPREVIYRVKAILRRASATAYL
SKESNSSNNIVFPHLVIEHDAHRVTAGGEEISLTPKEYELLHYLATSPDKVFSREELL
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CDS 1474907..1476340

/gene="resE"

/locus_tag="EFAGFIKM_01306"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P35164"

/codon_start=1

/transl_table=11

/product="Sensor histidine kinase ResE"

/translation="MVGKLWITIICLVGCVLIALGLFLLPYIDTNFAESES RDIKRLF
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DLDWAKMDEGQESEQSDKTSRDVPELLPLFRMVMEQGGDQNSNVHVQQGVWSVQMAP
LYADSVVRGAVAVLRDVTEEVRLEKMRRDFVANVSHEIRTP LSMMQGYSEALLDGMAT
SPEESEELIQVIHDESLRMGR LVKDLLDARMEAGHTDMVMKEVDLGELLERVYRKFS
VRSKEQGIQLQFKFEQPTIELQQAEDRLEQVFTNLLDNAFRHTPTGKNVMISAERV T
YLRAPFVRVSVKDQGVGIPSSDLPFIFERFYKADKARVRGESVGTGLGLAIVKNIVDA
HQGMITVNSVLGEGTEFILQFPLDSSK"

CDS 1476535..1480947

/locus_tag="EFAGFIKM_01307"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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GAGLTGAVAFNPVLAPGYPAGQVITYNGSTYITSVAGPLGTPGSSSDYTLIAAAGATG
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SGVTGVTGATGIGLNGAVPFDPAVAPTYAGQVVFNGSTYITTVASPTGTPGTSPDY
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AVAPTYAGQVVFNGSTYIANVASPTGTPGTSPDYTLIAGAGATGVTGATGVGVTGS
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GVTGSTGVTGATGATGTSVTSNSAFAENTNGTIVVILGGTLVPLPNNQNIGTGITVNG
TNDTFTLTNAGRYYISYKINLTAALAIQSRVLLNGAAIPASVVSPVLSLSQLQSDFMV
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CDS complement(1481143..1482738)

/gene="serA"

/locus_tag="EFAGFIKM_01308"

/EC_number="1.1.1.95"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WNX3"

/codon_start=1

/transl_table=11

/product="D-3-phosphoglycerate dehydrogenase"

/db_xref="COG:COG0111"

/translation="MYKVLVSDPISDLGIQQLVDANDVVVEKKTGLSEDELVAIIGEY
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CEHTFAMMMALARHIPQAYAKTIQGTWDRKTFLGVELRNKTLGVLMGRIGSEVAKRA
KAFGMDILAYDPFLTEERAERLQVKLASVDDIIRNADFMTVHTPLTPETRHMISRPQF
EVMKKGMRIINCARGGVVDEMALVEAIDQGIVAGAAFDVFESPPAADHPFLNHPSII
VTPHLGASTVEAQENVAIDVSEQVLHILRNEPFKNAVNM PAVAPTVMNKLQPYFKLGE
TLGSFAAQITQNAVQEIRIDYAGELSEVDTSPTRYIVKGILARHLGGEANIVNSMHL
AKIRDLNVVVSQTSTTKGFTNLITVTLVTTQDAEERRVAGTLLAGYGERIVRLDKFPV
DIAPESHQILISHNDKPGIIGRVGTLLGQNDVNIASMQVGRKII GGAAIMILTVDKAV
PKDVLVQLAALPEINTAVEIVLE"

CDS 1483504..1484097

/locus_tag="EFAGFIKM_01309"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKFKFPKFKIQKAEPQQLTERLLLINLYFTQGLTLIIGVWWIL
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PIWHIVCIAAIVAVCEELLFRGAIQHAIGPYWTSILFAVIHIRYLRHWIPTGWV FVSS
YGLGWIYLQSGTLWAPILCHF IIDLVSGLAIRFRGRS"

CDS 1484094..1484546

/locus_tag="EFAGFIKM_01310"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MNQPLSRMKTYGSQRHRQSDKKEKSERQVASQVSIVAETAAAAE
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ELHPSRRLKLSKRFVNSLIFVMLTISLVWWGVEGAPALNTFLPLPW"

CDS 1484546..1485373

/gene="ypbG"
/locus_tag="EFAGFIKM_01311"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P50733"
/codon_start=1
/transl_table=11
/product="putative protein YpbG"
/db_xref="COG:COG1408"
/translation="MLLLAGLIILMGVLLVFHMWREAHIHQMIEEEVEVPHLPTSFDG
AKILYVSDTHKRKLKQKDLENVKNKVDWVLIGGDVAEKGISWSLVRHNMKILSNIAPS
FTVYGNHDKRAGTAQLARILRESDVKLLQDNVEYLQRGNDRLSLIGIDYRSKQGDVLL
QQIGNRFCKIAIVHDPLQALRLEENADLILSGHTHGGQLVLPFFGPPVFLSKAYRPVSN
GWYSLKRSPEDVHQEGKMLVSRGYGTNHLPLRLGCPAEMHIITLRVPAEKALTEKQP"

CDS complement(1485418..1486314)

/locus_tag="EFAGFIKM_01312"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
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/translation="MFRHTAALIAASLLLSACGTAEKTSNDSTPAGESTTTVQKEQ
GNSNPTETGEPGSGVPEPSTEDSTATEEELESSEKVSTEEKVEKTYHMNENYYIKPND
EASPNKVLLTFDDGPKEEKMITSLIDTLDKHNAKAIFVNGYRVKSHPELLKLIHER
GQIVGNHAWDHEDLKKMSNAEAAKQVTDVQKIVKETIGEEPQFFRPPFGSGNDALKAV
VKKNGMLYMTWSNGSLDWDKSTKDKPEKVIQNVLDQLNPGSNILMHELPWTVEALDEL
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CDS 1486409..1486762

/locus_tag="EFAGFIKM_01313"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKTSSFFWGIVIGVAASSWLSKGKLPMMSSGSSRNMDQAKHKM
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VEQILSQTNTTVPGL"

CDS 1486950..1487564

/gene="mecB"

/locus_tag="EFAGFIKM_01314"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P50734"

/codon_start=1

/transl_table=11

/product="Adapter protein MecA 2"

/db_xref="COG:COG4862"

/translation="MKIERLSHDKIRIFLTDDLSEIRGIQKEDMWQEIPKVHELFTM
MDQAYSELGFDATGPLAVEVFALPAQGMVVIVTRGKYDPQQYGLGHEDDLPEEVYEME
VTLEQSDSIVYAFKDFEVLIEAAHMLRQHVTDAGRLYSYKDKWFLHLEPDEV DSTKHA
ALIALLAIEFGEGSSVTPAVMEEYGKVVIPAQAIDVICTHFKRQD"

CDS 1487608..1488303

/gene="prsW"

/locus_tag="EFAGFIKM_01315"

/EC_number="3.4.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P50738"

/codon_start=1

/transl_table=11

/product="Protease PrsW"

/db_xref="COG:COG2339"

/translation="MLLFSVLAAAVAPGLALLTYFYLKDRYDYEPLHMLRVFLMGIL
MVLPMIIRGMMMWLGDNPYLEAIMISGGVEEFVKWFLYHIIYNHTEFDEPYDGIL

YAVAVSLGFATVENVLYAFAGNASVSAMFLRALLPVSGHAMFAVIMGYMGKAKFIGG
KKKRWYLVLSLVLPPFFWHALYDVIMNTMVNHWLWFIAPLMAGLWYGAMGKITRANNRS
PFRFVKREEEVKL"

CDS 1488418..1488588

/locus_tag="EFAGFIKM_01316"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRIKIKIRCKQCGERFTLRGKKERGRIETGFKQCLCDNRDQFEI

EEEGMATGIQLN"

CDS 1488710..1490056

/gene="ypeB"

/locus_tag="EFAGFIKM_01317"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P38490"

/codon_start=1

/transl_table=11

/product="Sporulation protein YpeB"

/translation="MYKRLSSVMFPIFAVLLVGALVWGYQENQEKNAILIKAENQYQR

AFHDLFSFHMDKLHSEIGNTLAVHSTSQGMHRKGLMNWVRLTSEAQNEINQLPLTMLPF

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DRLRWMDAETAMATQEQTMDNTIVDGFRTVNKKVQEYPELDWGPSVSNIYAKRSVKKL

DGLPVTKEQIQSAAKFSDADRSKIQQVQENGKGTDWESYTATIDHANNGKLMMDFTRN

GGMLISYSDTRPIGTTKVSQRNAMAKADQFLMNKGKDKMAVNYDEYGNLGNLTYVRK

QGDTLIYPEKMSVRVGLDTGEVTGFQASDFVYEHNDMRKIPKATLTEQQARKKLNSEF

EENYVRKSLIENDYSKEVLCYEFGGKINGSRYRIYINANTGLEEAVEEIKPVNATS"

CDS 1490205..1490858

/gene="ypfA"

/locus_tag="EFAGFIKM_01318"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P38491"

/codon_start=1
/transl_table=11
/product="putative protein YpfA"
/db_xref="COG:COG5581"
/translation="MFPKINEILYIQIASADEKEEYKEYKSRIADMDDSSFLIEVPMQ
QGSSRLKRLFFGDELSISYITEDGVRHYFNTYVTGFEEDEVRLVRIRKPLPSDISKIQ
RRSFLRVHANLELAIQSEDLTRAVGLTEDIGGGGLSIYGETGFSIAEGQKLKCWLLVP
YRNSTIEHVNFEAEVVRICKTLETGRQLCMLKFVQISDSERQKIKFCFERQLDYRTK"

CDS 1490922..1491146

/locus_tag="EFAGFIKM_01319"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNHRHATRRYDRLYYVFSRRMERKVTILITALIILLVVYQLLLL
VPGFKKYM TIDRLEGTPIHVQTVNDYKRR"

CDS 1491250..1491954

/gene="cmk"
/locus_tag="EFAGFIKM_01320"
/EC_number="2.7.4.25"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P38493"
/codon_start=1
/transl_table=11
/product="Cytidylate kinase"
/db_xref="COG:COG0283"
/translation="MASQNTSENGKMNVAIDGPAGAGKSTVARLVAEALAYVYVDTGA
MYRAVTLHMLRKDISPEEVTQVLQEAQKLVIDLQPDGQKVFCEGEEVTSEIRSREV
TGIVSRYAQIEGLRTQLVDTQRQMALRKGWMDGRDIGTTVLPDAEVKIFMTASVEER
ALRRFKELDPSEGLTLQQLERDIATRDRLDESREISPLRCAEDAIVLDTTEMNIHEVV
DKIVSYCTMVRGEIGL"

CDS 1491951..1492538

/gene="plsC"
/locus_tag="EFAGFIKM_01321"
/EC_number="2.3.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07584"
/codon_start=1
/transl_table=11
/product="1-acyl-sn-glycerol-3-phosphate acyltransferase"
/db_xref="COG:COG0204"
/translation="MIYTF CSTLLRIIYTILFRLEAVGRENIPKEGGVLLCSNHISNF
DPPTVGIKLRQVRFMAKSELFIPVLGRIIKAVGAFPVKRGGVSKESIKTSLNILRD
GQVLGIFPSGSRHNDGGIGKKGAASFALRSGATVIPTAIIGNYKVFRKMKVVYGAPVS
LDEFKEDPSGEALEKATEKIMSKINEMVQTGVPSK"

CDS 1492681..1493895

/gene="ypfD"
/locus_tag="EFAGFIKM_01322"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P38494"
/codon_start=1
/transl_table=11
/product="30S ribosomal protein S1"
/db_xref="COG:COG0539"
/translation="MSEEMKNQEATQDELDQFVSLKKGDTVKGTVKLEDNQAYVSIG
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QLQKH FEDQDVFEVVVG DVVKGGLVADVGVRGFIPASMVERHFVEDFSDYKGRTL RVK
VKEIDRENNKVILSQKDVLEQEFEANKATVMAGLQEGQVIEGTVQRLTQFGAFVDVGG
VDGLVHVSELA WTHVEKPSDVLSEGDKVS VKLVKDPEKGKISLSMKAVQPGPWETAS
EKFNSSDIVTG VVKRLVDFGAFVEIAPGVEGLVHISQISHKHIGTPHEVLKEGQEVQV
KILDMNPSEQRVSLSIKETEEAPAQPQKSERPSRNNAPREEINNPVSLNNQGMSTTL
GELFGDKLSKFK"

CDS 1494081..1495403

/gene="der_1"

/locus_tag="EFAGFIKM_01323"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P50743"
/codon_start=1
/transl_table=11
/product="GTPase Der"
/db_xref="COG:COG1160"
/translation="MARPVVAIVGRPNVGKSTIFNRIIGDRLAIVEDKPGITRDRIYG
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EVAEMLYRSGKPIVVAVNKNVDNIGRSELIYEFYGFSGDPIGVSGSHGTGVGDLLDAI
VEKLPELEEETDDEDVIRVALIGRPNVGKSSLVNAILGEERVIVSDVAGTTRDAIDTP
FEKDGQRYVLIDTAGMRKRGKVYETTEKYSVMRAMRAIERADVVLIVINGEEGIIEQD
KHIAGYAFEAGKASLFVVKWDVVEKHDKTMKEFERKIRDHFLFMTYAPVVFLSALT
KQRLQKLLPVVKRVADQHSLRVQTHLLNDVSDAVAINPPPTDKGRRMRINYVTQVAVK
PPTMVVVFVNDPELMHFSYERYLENKIRAAFD FEGTPIRIFTRKKSDS"

CDS 1495415..1496038

/gene="plsY"
/locus_tag="EFAGFIKM_01324"
/EC_number="2.3.1.275"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O66905"
/codon_start=1
/transl_table=11
/product="Glycerol-3-phosphate acyltransferase"
/db_xref="COG:COG0344"
/translation="MILQIAAIVLSYLLGSISFSVLLAKAIRGIDIRQHGSGNAGATN
TLRILGKGPAIAVLLLDVLKGVAAVWIGIWLNDGSAWIPALSGIAAIAGHNWPLYFHF
RGGKGVATAIGVLVSLAFLPALCAGVIAILSIVLTRYVSLGSLIFVAFTPIFILVLP
YSMNIFWGSLIICLFAFWRHRTNIAKLAKGQENKLGSKNPGGGKRVV"

CDS 1496031..1497071

/gene="gpsA"
/locus_tag="EFAGFIKM_01325"

/EC_number="1.1.1.94"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5XE03"

/codon_start=1

/transl_table=11

/product="Glycerol-3-phosphate dehydrogenase [NAD(P)+]"

/translation="MSKKVAVLVAGSWG TALASVLAANQLDVM MWTRGEDQANEINNK
HTNTRYLPDAELSSRIQATTDMEA AVEGAIAVLIVAPSSAMRAVTNQLKAYYKPEMLV
IHATKGFETESLKR MSTVISEELECEEGRV VVLSGPSHAEVVKRCPTTVVASLDKA
SAESAQALFMNAYFRVYTNRDMIGVELAGAFKNIIALGAGMSDGLQFGDNAKAALLTR
GLAEITRIGVEMGANPLTFSGLAGIGDLVVTATSQH SRNWRAGSMLGQGQKLDDVLKS
MGMVVEGIRTTQAAYFISQKYGVQMPIADQLYH VLFQERQPRDAVEALMGRDPKTEME
VMKLETWEQWHS"

CDS 1497175..1497450

/locus_tag="EFAGFIKM_01326"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGNNISKDALNAINKKTGKTITEGAVKKLASTVKPTTIQNEAQL
RQLIKQVSAMAKVPVSEDTVKDIVSAVKKSG LNPSSMESLMKMMMCK"

CDS 1497623..1497802

/locus_tag="EFAGFIKM_01327"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSAMDKMWLSLVAILIMGLSVFLITFARA KTKGIVRGILSLIAF
LIMLIGFFGGIASLT"

CDS 1497886..1498503

/locus_tag="EFAGFIKM_01328"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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/product="hypothetical protein"
/translation="MRPHDTEGRTERYPELHAALLETAKAWNTQPQTWLLGGSCGLLL
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ELVGGFEIWARSWYRIEYVLAPHAPVAQVGSYSRLMPLAHELLFNLLRGREDRY
VPIASQMREQPDAHQPIMMLLSQQNVWTSRFRAEVEELVGFTWPQ"

CDS 1498520..1498870

/gene="nqrF"
/locus_tag="EFAGFIKM_01329"
/EC_number="7.2.1.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00430"

/codon_start=1
/transl_table=11
/product="Na(+)-translocating NADH-quinone reductase
subunit F"
/translation="MDYKVTFLPMNKSIALKPGATLLHAARRAGVKITTRCDGKAACL
MCKVNVDEEHRAELYPPTDAEKHKLGSLLEAGTRLSCQAKVCGSLSVHVPEDPLKAAI
RKQLERQQQEDDWF"

CDS 1498917..1499696

/locus_tag="EFAGFIKM_01330"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIRNKPKEVEGSRRLKHQTGGLLLFLFAFTASGCMYPSQSN
SDPKIAYRESVSRIQSAVEAFQQDEGILPIINADMETPKYEKFRVDLPKLKQLGYLDE
IPGTAFESGGSAYFLIQDEEVNPTVKVMDLLTVQKVNDVQRMVNQYKSVHNNKLPRGE
ELYPGLYAVDMEQAAQAGTPSITLNSVYSGQALPFMMDDDEGKVYVDYAFDIMQAVEKS
DVSPAETEDVRDLLVEHSYFVPVKSVFYAWQNNAPVAQPIK"

CDS 1500150..1501628

/gene="spoIVA"
/locus_tag="EFAGFIKM_01331"
/EC_number="3.6.1.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P35149"
/codon_start=1
/transl_table=11
/product="Stage IV sporulation protein A"

/translation="MEKVDIFKDIAERTGGDIYLGVVGAVRTGKSTFIKRFMETIVLP
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ARSSYVESEERVIAELKEVGKPFVLVINSTRPRSEEALQLRSELAAKYDIPVMTLSAA
TMTEDDVTGVLREVLVEFPVHEVNVNLPWVMVLNETHWLRSNYENSVRDTVKDIRRL
RDVDRVVAQFMEYEFIDRAGLSGMNMGQGVAEIDLYAPDELYDQILVEVVGIEIRGKD
HLLQLMQEFSHAKREYDRFAEALEMVKTGYGIAAPSLAEMALDEPELIRQGKFGVR
LKATAPSIHMIRVDVESEFAPIIGTEKQSEELVRYLMQDFENDPIKVWDSDMFGRSLH
SIVREGIQGKIAMMPDNARYKLQETLGRIINEGSGGLIAAIL"

CDS 1501846..1502943

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/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"

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ELTLEQMKKDINGQGNIVKVVWAGFAPMERRQIAYGEFMKANPDIKEIATFGSAQNPA
LDTQAKMEAILKQYPKGEITAVWTAWDEFAKGAARAIQQAGRDEIKVYGIDMSDEDLQ
MIQDPKPNPWASAAVDPTDIGRVQVRYAYQKLNGDETEDAVLNPVYVQREALPDKQI
STSELSEFVEGWGGSTQG IKDWMSEYGITAK"

CDS 1503058..1504575

/gene="rbsA_1"

/locus_tag="EFAGFIKM_01333"

/EC_number="7.5.2.7"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P04983"

/codon_start=1

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/product="Ribose import ATP-binding protein RbsA"

/db_xref="COG:COG1129"

/translation="MSTAPTLLQMEHIHKQFSGIPALKDVDFSVKGGEIHALLGANGA
GKSTLMKILSGAYPLDQGTIQLSGQALHLNSPGDAKASGIHCVYQEVDAALVPQLTAA
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ILIQDAKVIIFDEPTAPLSQEETDAFFRIVHLLKDRGVACIFITHRLAEVTVHCDRVT
VMRDGQHVFTGEAKGLTINDLVTQMLGKPFEEFFPKTEAPLGELLLEARGLRGVKVK
GVNLSVSRGEVLAVVGLVGAGKTESSRLIGADRLEGGEIRLNNRNLRLSQPADAAAL
GIVSVPEERRKQGILIQENVERNLSLPLLSRLSTLGFVSRKRERLNAESLVKQLGIKT
SSVKQEVKYLSGGNQQKVAIGKWLNADADVFIFDEPTKGVDIGAKSDIFRIINELALA
GKGVIYFTCELDEGMGIGDRIAVMCEGVIVKEFKRGETNQEQLLYASGGQEVQS"

CDS 1504572..1505558

/gene="rbsC_1"

/locus_tag="EFAGFIKM_01334"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AGI1"

/codon_start=1

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/product="Ribose import permease protein RbsC"

/db_xref="COG:COG1172"

/translation="MKDKSLDFAFRYGAIIVIGVIAFFGIKLPYFFTYSNLTDILGS
ISIVTFVAIGVTLSLIVDGFDSLVSATVSLTTVVTASLMIWYQQPLAIVIVPLIIGA
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PTFLLIGQGKWLGMPIVIMLLIAVIGVHIFLTYTKYGRQMYITGGNEEAARLSGIKV
KKVRTLAYVAAGVFAAIGGIIYASKVSGSQIDAGSPLLMESVAAVFVGFSVFGAGKPN
VIGTFIGSVLIGVLVNGLTMMNVQYFTHDIVKGGVLVLALAVTFYVLNRNRT"

CDS 1505665..1506048

/gene="ihfA"

/locus_tag="EFAGFIKM_01335"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00380"

/codon_start=1

/transl_table=11

/product="Integration host factor subunit alpha"

/translation="MFSAQDVRRFFAYERIFRYKTETQYNIQDIDTGGEKQMNKSDLI
THVSEATELSKKDVTKAVDVFEAISEALQSGDKVQLVGFGNFEVRERSARKGRNPQT
GEEIEIPASKIPAFKPGKALKDGIK"

CDS 1506218..1506439

/gene="mtrB"

/locus_tag="EFAGFIKM_01336"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9X6J6"

/codon_start=1

/transl_table=11

/product="Transcription attenuation protein MtrB"

/translation="MDHPTGNDYIVIKAEENGVQVIGLTRGQDTRFHHTKLDKGEVM
FAQFTTHTSAIKIRGKATLITKHGQIESE"

CDS 1506561..1507112

/locus_tag="EFAGFIKM_01337"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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LGFRSLDNVDQVLLRVMAEDEWMHKRHLLLAADIRRGWPLYAIETLRNWKSAAFSDE
LKDWFFHLMETELWKKQFEMTSQG"

CDS 1507214..1508077

/locus_tag="EFAGFIKM_01338"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MNSYRVPQLAKKYTDYDMIRQHTEIPSPDSRARLLQIFVGRTD
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IQHNEESLWNSLLTEFSSCETIVEELKRMND AKQYLHSYAYWHIYEHGND DERNVLRQ
SEPDARAWNAMVLKHRVGEVLLDKLRECTHRIQLLLQDEEGRMGLHEIHAILEPYLAY
LQPSHAAVRED"

CDS 1508093..1508821

/gene="menG"
/locus_tag="EFAGFIKM_01339"
/EC_number="2.1.1.163"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P67062"
/codon_start=1
/transl_table=11
/product="Demethylmenaquinone methyltransferase"
/translation="MGSGETKPKEEYVHSVFQSIAGKYDVMNDILSFRRHKAWRKFTM
KKMNMSKGD TGLDCCGTCDWTLAMAEASETG HMGHGLDFSSNMLEVGQTKINAVQRQK
QITLTQGNAMSLPFEDNSFDYVTIGFGLRNVPDLRQVLSEMKRVVKPGGMVVCLELSK
PTWQPFKGIYYFYFEKVL PNLAKVFAKSFEQYKWLPDSL AIFPGRQELADIFAETGLQ
QVQAYPLTGGIAALHIGTKENQH V"

CDS 1508814..1509680

/gene="ubiA"
/locus_tag="EFAGFIKM_01340"
/EC_number="2.5.1.39"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AGK1"
/codon_start=1

/transl_table=11
/product="4-hydroxybenzoate octaprenyltransferase"
/db_xref="COG:COG0382"
/translation="MFRKIRIFLEMIKIEHTLFALPFAFMGAILGSMVVNDTFPSWMQ
IMWVLLAMVGARSAAFGLNRIIDQAIDGKNPRTAMRAIPAGLLKNGEVVIFVIISFIL
LFWASSNLNLVLSMQLLPIAVFMLVLYSYTKRFTWLCHIVLGMTIGLAPLGGWVAVTGT
MDWTAIVLYVTIVFWTAGFDIIYACQDLEFDQGEGLHSIPSRFGLVKSLQIAKFFHVI
TAIGFLALLLMTDLSWWYGAGMLVTYGILFYQHYIVSPNDMSRVQTAFFTMNSLLSLI
VFTFTLIDLAVK"

CDS 1509681..1510301

/gene="ubiX"
/locus_tag="EFAGFIKM_01341"
/EC_number="2.5.1.129"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9HX08"
/codon_start=1
/transl_table=11
/product="Flavin prenyltransferase UbiX"
/db_xref="COG:COG0163"
/translation="MVQQPDNKRLVVGITGASGSIYGIRLIETLLDLEYNVHLVISNA
GWRVLKEELDWDVTNRDAVLEEKFGNRAGSLIYHPVSDIGASIASGSYLADGMIIMPC
SMGTLSSIAQGSSDNLMSRAADVMMKEGRTLILVPRETPLHAIHLENMLKLSRLGVRM
IPAMPAFYYPQTMDELILFLVGKVLDSLRIHQFTRWGPDERG"

CDS 1510645..1511619

/gene="hepT"
/locus_tag="EFAGFIKM_01342"
/EC_number="2.5.1.30"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P31114"
/codon_start=1
/transl_table=11
/product="Heptaprenyl diphosphate synthase component 2"

/db_xref="COG:COG0142"
/translation="MKLLDIFGLKKDMDYIEKELYRSVRGEQKLLSETSLHLLKAGG
KRLRPVFLVLLGGKFGTYDIERLKLVAVPLELIHSASLVHDDVIDNAETRRGKPTVKS
WDNRIAMYTGDYIYGKALEMTAGLSDPAIHRILAKAMVQMSIGEMEQIRDFNTGQSV
RNYLLRIRRK TALLIAVSCQLGALATRAPEHVSSLLYTYGYNVGMAFQIQDDVLDLVG
TEKQLGKPPGSDMKQGNITLPVLYALEESDLREPLLKEISRVQHEEGRASASDAIGMI
RQSQGIKAEALADRYMKKALDALDQLPNIKTTKNLRDIAHFVVKRTH"

CDS 1511774..1512217

/gene="ndk"
/locus_tag="EFAGFIKM_01343"
/EC_number="2.7.4.6"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P31103"
/codon_start=1
/transl_table=11
/product="Nucleoside diphosphate kinase"
/db_xref="COG:COG0105"
/translation="MDRTFLMVKPDGVQRGLIGRIISRLEDKGFKLVAGKLVQMSEDQ
AKRHAEHEGKPFDDLVRFITSGPVFAMVWEGDDIVALARIVIGKTNVKEAAPGTIR
GDFASHTPHNLIHGADSPESASREANFFASDELVVYDKSIAAWL"

CDS 1512243..1513037

/gene="cheR_1"
/locus_tag="EFAGFIKM_01344"
/EC_number="2.1.1.80"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P31105"
/codon_start=1
/transl_table=11
/product="Chemotaxis protein methyltransferase"
/translation="MLEQEQLLDPDYTGFIKIKESTGIDLAQYKEGQMKRRLTTLRN
KNGFHTFSNFFEAMQKDKSLFYEFDRMTINVSEFWRNPNRWEVLRDEILPELLGSKR
RAKVWSAACSTGEEPYTLAMILDTMGILKDSSITASDLDEGALAKAKEGRYMERSLKD"

VPKETANRYFKQDGLVYRIDEQLKNSIKFMKQNLLVDRFDDGYDLIVCRNVMIFYFTEE

AKNLLYHKFAASLRPGGILFVGSTEQIFSPGQYGLETAETFFYRKK"

CDS 1513216..1514385

/gene="aroC"

/locus_tag="EFAGFIKM_01345"

/EC_number="4.2.3.5"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P31104"

/codon_start=1

/transl_table=11

/product="Chorismate synthase"

/db_xref="COG:COG0082"

/translation="MSLRYLTAGETHGPQLTAIEGLPSNLTIDFEELNFQLHRRQKG

YGRGRRMQIEKDQANFVGGIRHGYTTGAPVALVVQNNDWKHWQNIMNIEPIEGSDEEK

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GRVLRIGEIEAPYQDLPIDELIAVTEASSVRVTD AET EKKMEAYIDQIKQEGDSIGGI

VECIVEGVPIGLGSYVQYDRKLDARIAQGVMSINAFKGVEIGIGFEAGVIRGSQVHDE

IMHTDERGYHRATNRLGGFEGGMTNGMPVVVRGVMKPIPTLYKPLQSV DIDTKEAFTA

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CDS 1514387..1515481

/gene="aroB"

/locus_tag="EFAGFIKM_01346"

/EC_number="4.2.3.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9KNV2"

/codon_start=1

/transl_table=11

/product="3-dehydroquinate synthase"

/db_xref="COG:COG0337"

/translation="MRQLTVQLEERSYPILIGSGLLAQAPQYFEQYGLTKKSPLLIIT

DENVAPKYLSGLEQTLRTAGYTVVSAVVPSETSKSLSVYQDMMTVAIEGKLDRSSAI

LALGGGVVGDLAGFVAATYMRGIKFVQVPTTILAHDSVGGKVAVNHPLAKNMIGAFH

QPELVLYDVDTLQSLPPRDVSAGLSEMLKHGLIRDEAFAHWCEEHAEELLALNPEALG
YGLERGCIGIKAEIVSRDERENGERALLNLGHTIGHAIEAIAGYGEFLHGEAISIGMAG
SALLGEKLGAPAGLYEDTVRMLRSLRLPTTMPAHLDTDALMEAMMHDKKFREGHMFVI
IPDRIGAARIVKDVPVSAVRDVIEMLRKGE"

CDS 1515487..1515864

/gene="aroH"

/locus_tag="EFAGFIKM_01347"

/EC_number="5.4.99.5"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P19080"

/codon_start=1

/transl_table=11

/product="Chorismate mutase AroH"

/db_xref="COG:COG4401"

/translation="MVTRGIRGATTVTQNNEEQILKETAVLLQEIVDRNEIQPEDICS

VWITLTGDLDAAFPAKAIRQLDGWELVPLMCALEVPVKGALAQCIRFMVHVNTNKAQN

EINHVVYLNQAQALRPDLATPSGS"

CDS 1516368..1517936

/gene="trpE"

/locus_tag="EFAGFIKM_01348"

/EC_number="4.1.3.27"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P20580"

/codon_start=1

/transl_table=11

/product="Anthranilate synthase component 1"

/db_xref="COG:COG0147"

/translation="MITPNVNQVLKMSNDYNLIPVVKRILADMETPIRIFRRYADNDR

AFLLESVEGGIQWARYSFIGTDPFLMISAKKGRIVVEEAGKTRELPGKPIEELKALLR

KYRSPKDELPPFTGGAIGFFGYDLLSYYEKLPAHALDDLNMDDIRFMFCDQIIVFDH

VKQQMLLVGNVHVKGATDDEIRQAYAVTSEKLEQAAERLQQQGPGENLNPRSIPGDV

ELGDIRSNLTKEQFIGNVEQAKDYIRAGDIFQVVLSQLFHIDTEVSPLHVYRVLRTLN

PSPYMYYLKMDDEIIVGTSPEALVKVDGNRVETRPIAGTRPRGATEAEDRALAADLLQ
DEKERAEHLMLVDLGRNDLGRVSSFGSVKCDMFMEIERYSHVMHVMVSNVTGELREDKD
FFDAFLSCLPAGTVSGAPKL RAMEIIAELEKEARGAYAGAIGYLGFSGNMDSCITIRT
IIFKKGKAYVQAGAGIVWDSVPENEYEETVNKAKALLKAIRTAEMFPAKEKDSTLRL
ANADYFVTPAAAKN"

CDS 1517954..1519045

/gene="trpD_1"
/locus_tag="EFAGFIKM_01349"
/EC_number="2.4.2.18"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P00500"
/codon_start=1
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/product="Anthranilate phosphoribosyltransferase"
/db_xref="COG:COG0547"
/translation="MNINPIMNENPVTPIAEITREEGMKNGLAKILEGSHLEQAEARD
LMYSIMRGEATPAQIGLLMALRMKGETVDEITGFAEAMRGQGGRILTDGSGLLDTCG
TGGSGIHKFNISTASAIISAVSVRVAKHGNRSASGKAGSADVLEALGVNIHLNGEQA
RQCLDDIGICFCFAQVYHPSMRHAAGPRKELGVRTIFNMLGPLTNPAGADRQLLGLYD
RSRTPMIAEVLNRLGLKRALVVASHDGLDEVSIAPTQVSELRNGEVHTYDIDPRDMG
LSLHPLEAVLGGDAAQNAEIIKRIFQGEQSAYRDVLLNAGACIYVSGLADSIAEGVT
LAAEAVDSGKAAGKLEQLIHTTEAYSHVS"

CDS 1519035..1519823

/gene="trpC"
/locus_tag="EFAGFIKM_01350"
/EC_number="4.1.1.48"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q2YRR4"
/codon_start=1
/transl_table=11
/product="Indole-3-glycerol phosphate synthase"
/translation="MYLDRIVATKHKEVEVLAQTFRMDEAIQKIEQLPATRGFEQALS"

SGRNRKLGLIAEVKKASPSKGLIRPDFHPVEIAEAYERAGADCISVLTDVSYFQGSNE
YLQAIHQAVNIPLLRKDFIIDERQIAEARLLGADAVLLIASILTPEQIRQYLEFAKSL
GLDALIEVHDRTELEQVLEIPQATLVGINNRNLKTFETSLNTTLDLMELIPSGVTLIS
ESGIDGPESTVPLIQAGVHGILVGEHLMRKDDVEAAVYDLMGPK"

CDS 1519820..1520560

/gene="trpF"
/locus_tag="EFAGFIKM_01351"
/EC_number="5.3.1.24"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q56320"
/codon_start=1
/transl_table=11
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/db_xref="COG:COG0135"
/translation="MMNTSIHDGTGDSMSELRNPLPAAVKICGLQDVEVLKSMINLPV
DYIGVVFAKSRRIEPEQAAALRTVLFEWSTYDRPKLAGVFNPTLEELEHIMDIAQL
DVIQLHGGQETAFCQVKQRWNAKVFKVFSFPKDETGPEADDAAIRALDITYDKFVDAI
LLDTHDPLYGGGSGKTFAWERIPAYA EWAKSREIALFVAGGLQPDNVQQLIQTYAPFG
VDVSSGVETEGVKDIAKITAFVERVKQA"

CDS 1520557..1521756

/gene="trpB"
/locus_tag="EFAGFIKM_01352"
/EC_number="4.2.1.20"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q81TL8"
/codon_start=1
/transl_table=11
/product="Tryptophan synthase beta chain"
/db_xref="COG:COG0133"
/translation="MTHQLPDQHGRFGHFGGRFVPETLMNALIELEEAYSHFSEDEEF
NKELNYLLSEYSGRETPLYHAEQLSRRLGGPKIYLKREDLNHTGAHKINNAIGQGLLA
KRMGKKKVIAETGAGQHGVATATVAALLGLECKVFMGEEDTERQQLNVFRMKLLGAEV

IPVTSGTRTLKDAGNEALRYWVSNVEDTFYVLGSVVGPHYPMPMVRNFQRVIGDETRR
QIQEIEGRLPDVIVAAGVGGGSNAIGMFYPPFIGDQDVKLVGVEAAGKGVETHEYHAATMT
KGTHGVFQGSMSYLLQDEYGQVQPAHSISAGLDYPGVGPEHSYLKDIERAKYVPITDQ
EALDALQLLCRTEGIIPALES AHAVAQVVKLAPELTADDIVVICLSGRGDKDVESIMK
YTGGDLG"

CDS 1521753..1522559

/gene="trpA"

/locus_tag="EFAGFIKM_01353"

/EC_number="4.2.1.20"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O67502"

/codon_start=1

/transl_table=11

/product="Tryptophan synthase alpha chain"

/db_xref="COG:COG0159"

/translation="MNLMDQTFQQLKEQNRTALIPFLTVDGPDVDTTIDIKELEQAG
ADILELGVPSDPLADGPVIQRASERALKSQITIRVMETAARKAGVKLPFVLFTY
YNPVLQTGLDVFFDELVKHDISGMIIPDLPIEEAEEMRERANRAGVHLVPLVAPTSNA
RIERIVTGARGFIYCVSSLGVTGERASFFDGVESFIETVKSLTDLPVAVGFGISSHEQ
VAHFSRICDGVVVGSAIVRQVEDAIPLLENPDTRAAGLLQIRNFVAQLKG"

CDS 1522646..1523746

/gene="hisC_2"

/locus_tag="EFAGFIKM_01354"

/EC_number="2.6.1.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q92A83"

/codon_start=1

/transl_table=11

/product="Histidinol-phosphate aminotransferase"

/db_xref="COG:COG0079"

/translation="MKPKSQIVNLPVYQPGKPIEEVKRELGLEQVIKLASNENPYGSS
PAALEAITKEMTNISIYPDGSSVELTGVLAKHLGVERNLIIFGCGSDEIIALITRAFF

LPGDETIMADQTFSVYKSNADIEGAVSIEVPLKDGTHDLSAMLAQINDKTKAVWVCNP
NNPTGTIIESEQELTAFMDCVPAHVMVILDEAYYEFVTDEAYPQSIPLIERYPNLVILR
TFSKIYGLASLRIGYGIARPEIIDLINRVREPFNTSRFGQVAAKAALLDQDFVQECSK
RNATDRDYLQNEFTRLGLSYFPSQGNFIMVDLNMPSAIAFQSLLKQGIIVRSGFHVYP
TYIRVSVGTSEQNRAFVTALENTLAEKAVARS"

CDS 1523773..1524867

/locus_tag="EFAGFIKM_01355"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLKIAMIGVGLIGGSLALCFKGKPDVTVMGYAHLDELKDKYIA

SGVVDDATLSLEEAVEDADFIFLCVPVGLLESYFEKLSKLPLKKGCIITDVGSTKASI

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ELLAYTRAQIVRVEPLLHDDIVGAISHLPHVIAVALVNQVREYNESNPLYKMLAAGGF

RDITRIASSDAIVWRDILLSNRDVLLGLLKDWNSQMTAFTDMLEHKNGEGIEEAQRQA

REFRSILPERRKGMISPLFDLYTDVQDAPGMIGKIATELGANDINLSNLEIENRVDV

PGIMRLSFRQEEDMERAKTLLDSLGYQVWI"

CDS 1525594..1526187

/gene="algU_1"

/locus_tag="EFAGFIKM_01356"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q06198"

/codon_start=1

/transl_table=11

/product="RNA polymerase sigma-H factor"

/db_xref="COG:COG1595"

/translation="MTDSQLIREIKEGNLELYSELMSRYQRKILAFVYHMLKSSNMEL

LAEDLCSETFYKAYRSLHSFREVDASFSTWLYTIARNTVLSELRKQRSGNIPLEESGF

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VSSVKSLFRARSSVKTLQLEPYFFEPVYEPYEGMKNR"

CDS 1526184..1526819

/locus_tag="EFAGFIKM_01357"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNCNEAQELFALVWDLPETHPQRIAFHAHLAGCEECSEQFEVWE
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AAFLAIFLCSFLYMAMFKPDVSEAEQTKVTTGILETGIAGSGPSSSGMYQYNMTGAD
RGSIIEPFVSMGPAYPQYWMALSLLAIGMALFSLGRMHRTTNKRKQGASA"

CDS 1526863..1527462

/gene="gpmA_1"

/locus_tag="EFAGFIKM_01358"

/EC_number="5.4.2.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01039"

/codon_start=1

/transl_table=11

/product="2,3-bisphosphoglycerate-dependent
phosphoglycerate mutase"

/translation="MRIGLIRHGLTDWNAAGRIQGQTDIPLNGEGREQAERLGRRLLT
EEYQWDYIITSGLSRAQETGEIISKLLNVPLLEPDARLKERAQIEGLTSEERVARW
GQAWETLDLGQEADIQIRALAFLEDLWSAYPDQNVLIVTHGAFLANLLTALFKDRY
TERIGNLSLTILEKERDDWSPLLYNCTRHLSDTAKQPE"

CDS 1527697..1528815

/locus_tag="EFAGFIKM_01359"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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VRFNKSGWLFNGTTQQTRYLYQVPQDLKLRFRDVLSTHLRAGITKTTEPPMYRDEYHL

LADDLKLFLQFVQQHEIALNAEGMMYRRSQQQIMEHLHISEELVGKGGWRFGYGRSFK
DYPDRFALLYDYAFHHRLVREEQGTLLKSPAGEDKLGAEKTAEMIQLFRFWLRLYKGA
IPNLSSIVYWTGEC AQEWSTAESLFRQIGPFIQPFYYDTAEAIYDNRIVKMMLHLGMV
RIGEHEEGRTIQMTAWGTRLAASCRSISGDITPIMFDK"

CDS 1528860..1529366

/gene="yrdA"

/locus_tag="EFAGFIKM_01360"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A9W9"

/codon_start=1

/transl_table=11

/product="Protein YrdA"

/db_xref="COG:COG0663"

/translation="MIIPYKGLQPQLHPSVYMAEGAKLIGDLRMGEESVWFNAVLRA
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CDS 1529390..1529569

/locus_tag="EFAGFIKM_01361"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDKMKVTYEVMLGLAAEMVWDEALRKQRSEKLYLEIDKALATGD
EVAFRSLTDELRTIN"

CDS 1529723..1530145

/locus_tag="EFAGFIKM_01362"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKFSEMTQDSWAELQLYLDTCIPYTALSGEQSPVEATEALERL

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VEIPAADLVLSRSLTHEVGEEGIARFIGEKIRELWKK"

CDS 1530338..1530880

/gene="petC_1"

/locus_tag="EFAGFIKM_01363"

/EC_number="7.1.1.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01335"

/codon_start=1

/transl_table=11

/product="Cytochrome b6-f complex iron-sulfur subunit"

/translation="MSSEHDHHEASLKLPSRMEMSRRQFLTYTLGGATAYMAAGAILP

MVRFAVDPIQLQHKGEGTSVKVAEISKITNEPQEFTFELKQQDGWYLSNASLVAWIRKD

EQGKIYALSPICKHLGCTVGWNSDKQYPDEYHCPCHGAHYDKEGKNLAVAPKPLDEYV

VKEEQGWVYLGDIVPNTRVN"

CDS 1530896..1531567

/gene="qcrB"

/locus_tag="EFAGFIKM_01364"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P46912"

/codon_start=1

/transl_table=11

/product="Menaquinol-cytochrome c reductase cytochrome b
subunit"

/db_xref="COG:COG1290"

/translation="MFKNVYDWIDERLDITPIWRDVADHEVPEHVNPAHHFSAFVYCF

GGLTFFITVIQILSGMFLTMYYVPDIINAYASVEYLQTKVAFGQIVRGMHHWGASLVI

VMMFLHTMRVFFTGSYKAPREMNVVVGMLIFFVMLGLGLTGYLLPWDNKAYFATKVTL

EIANTVPWLGPIIKEFLQGGTIVGAQTLTRFFALHVFFLPAVLLVLLVGHFIMIRRQG

ISGPL"

CDS 1531589..1532473

/gene="petD"

/locus_tag="EFAGFIKM_01365"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01344"
/codon_start=1
/transl_table=11
/product="Cytochrome b6-f complex subunit 4"
/translation="MAHGHKKDDEEKVIFVGDSRVRKGAGFITPPDYTAYPGKSEAFI
PNFLLKEWMVGVVVLVGILVLTISEPAPLGYPANPSASVIPMPDWYFLFLYQYLKYPY
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AWTHYEHELEASGQKPEHIQREEEALERREQGLPPVSNAPGQQEEVAIVEQDDPAMET
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CDS 1532525..1533211

/locus_tag="EFAGFIKM_01366"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MFFWTALYRAQYMMKEGAGNVALSYFWSREFLTNRYFLWLLFWC
NAVGTVYGYIWYGEQMKLTAEQPWWQIVFVPDSPTASLFFTLALLWVLYPPRSIIK
RFGHVIQALAVVTSVKYGVWAVSIIFAGWMQGGTQHWQDWMLIASHSAMAIEALIFVR
FFGFRWTSLVVAGLWTLNNDTMDYTYDIYPWLPASLYDHVDGVRNFTFGLTLVSILCA
WLALRQAKRT"

CDS 1533278..1534147

/locus_tag="EFAGFIKM_01367"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKRTFGIKTGLLVVSFIALLWTNLAYRVSAQSEALNSNSDQQV
STSNSIAKLNEEAAILYRQALENNIEEVRGSILRISKSLEHISFEGQTTVEGIHALSE
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TNQGQTAAVLANRYTVLEEHYETIRPAALIRREPYEIAQMDAWLSHTKGLTNAKQPDL
AQLKSMVGHGEELVNQLFGREKDESAFVPFVQGPDRRAAGLLISSVIVATLSYAGYRK
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CDS complement(1534268..1535137)

/locus_tag="EFAGFIKM_01368"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTAKTWIQVKLVPIVLGTALYAFGLLYFIIPNQLMEGGTGV

TVLINYAFGISPSLTTLILNVPLFLIGLKILGGRQMIYTGIGIGALTVFLWLFELIH

LGWIEPLHTENDLLLAALYAGVTLGAGLGIVFRWGGTTGGSDIARILNRKYGWSMGR

VLLGIDFIIIGLSLIYIPKEKILYTLVAVFIASKVIDFIQEGAYSARAFMIISDHAP

IADQITRDMDRGVTLPAGAYSKQAKHMAYCVISRQEFRRQLQTIVRSIDPRAFVIIS

DVHVDVHGEGFKES"

CDS 1535309..1535638

/gene="ypjD"

/locus_tag="EFAGFIKM_01369"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42979"

/codon_start=1

/transl_table=11

/product="putative protein YpjD"

/db_xref="COG:COG1694"

/translation="MEKSIAEMQREVDQYISQFKEGYFSPLAMLARMSEEVGELAREV

NHEFGKEPKKSSEAANSIELELGDILFITICFANSLGIDLAEAHDKVMHKFNTRDANR

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CDS 1535689..1536213

/locus_tag="EFAGFIKM_01370"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MMKP E E Y M Q Q A Y R C I L Q N D F E Q A I R W F E S A I H A H P K H A E L Y Y R C
S I T H A R S K H L V P A L E Y A R K S V E L S P G T E E Y I L H L Q T L E S K Q L T S R A K L L L E Q A G I A T Q
E R Y V E A S T L L Q E A V K L D P L S V E A H V M L A L A Y S D L N E F D Y A I Q A L R E A I L L D P Q N G Q L H
Q M L Q E I K Q R M K S I Q"

CDS 1536294..1537097

/gene="dapB"
/locus_tag="EFAGFIKM_01371"
/EC_number="1.17.1.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P63895"
/codon_start=1
/transl_table=11
/product="4-hydroxy-tetrahydrodipicolinate reductase"
/db_xref="COG:COG0289"
/translation="MSEVIRVAVIGAAGRMGREVVKLVLQDPELELAAAVNRSGAGTD
AGTLVGLPECGVLVTDDIEMAFAETKPQVMVDFTVPQFAFAHTEIAIRHGVRPVMGVT
GFTPEQIEQLDKQCQDKGIGGLIAPNFSIGAILMMRFAAQAAKHMPNVEIIEYHGDQK
LDAPSGTAIKTAELIAANREELRQGNPNEETIEGSRGGYYNGFRIHSVRLPGVFVAQQ
EVVFGDYGQSLKIRHDSYERAGYMPGVKIGVQKVM EYTGMIYGFDFHID"

CDS 1537109..1537549

/gene="mgsA"
/locus_tag="EFAGFIKM_01372"
/EC_number="4.2.3.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42980"
/codon_start=1
/transl_table=11
/product="Methylglyoxal synthase"
/db_xref="COG:COG1803"
/translation="MLKIAFIAHDRKKEEMVNFVTAYEPVFTDHQLYSTGTTGLRIME
GTS�KIHRFESGPLGGDQQIGALVAQNEMDLIIFLRDPLMAQPHEPDINALLRLCDVQ

GIPLATNIATAEILVKALDRGDFAWRELVHKYKPEAGLNSGDSE"

CDS 1537546..1538244

/gene="bshB1"

/locus_tag="EFAGFIKM_01373"

/EC_number="3.5.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81ST8"

/codon_start=1

/transl_table=11

/product="N-acetyl-alpha-D-glucosaminyl L-malate
deacetylase 1"

/db_xref="COG:COG2120"

/translation="MSLDILIFGAHADDAEIGMGGTIAKHTAAGLKVGVCDLTRAEMS
SNGTVERRTEEAQASRVLGLSCRTNLGLPDRGLYLTPEHVQAVTAEIRRHAPRMVFA
PYWEDRHPDHVNC SKLVQEAVFNAKL RNYMPDMPAVQVKELYFYFINDIGPTDLIVDI
TEHYEQKETSLLSYRSQFELGDGAVSTPLNQGYIERVRARDSLLGQRSLIPFAEGFAT
ITPYVVHQFGSGAQ"

CDS 1538344..1539504

/gene="bshA"

/locus_tag="EFAGFIKM_01374"

/EC_number="2.4.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81ST7"

/codon_start=1

/transl_table=11

/product="N-acetyl-alpha-D-glucosaminyl L-malate synthase"

/db_xref="COG:COG0438"

/translation="MDKKLKIGITCYP SLGGSGVVATELGKLLAEQGHQVHFANSIP
FRLGTFQKNIFYHEVEVNDYYVFRYPYDLSLATKMAQVAKSQQLDLLHVHYAVPHAV
CAFLAKQMVGDGLKVVTTLHGTDITVLAQDESLKDLIRLAINESDAVTAVSQDLIRET
VELLDIQRPIDLTYNFIDKRIYYPRDAASLRDFAAPDEKILMHISNFRPVKRTQDVV
EVFRQVQE QVPAKLLFVGEGPDL PKMQWKINDLGLNDKVHFLGKQDDIAQVISMADVL

MLPSEKESFGLVALEAMACGVPTIGSQAGGIPELVLHGKTGFLSAIGDTQSMAENTIR

LLTDDRLAAEFREACLQRAHHDFCNDKIRLEYEQIYYRVLGREVPNLKPVCG"

CDS 1539564..1540865

/gene="cca"

/locus_tag="EFAGFIKM_01375"

/EC_number="2.7.7.72"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7SIB1"

/codon_start=1

/transl_table=11

/product="CCA-adding enzyme"

/translation="MVVQWTQVDREMAMQSENVLTTLNKHGYKAYWVGCVRDPELLER

VVDDMDITTSASPQQVMELFDDCIPTGLQHGTVTVRSGGYFEVTTFRTESEYQDNRR

PAAVQFVQDIKKDLQRRDFTMNALAMDVTGTIVDPFGGQADIKEERVRCVGSAMERFG

EDALRMLRCVRFASVDFKIAHNTWKGLVRQKDLLQHIAMERVRTEMVKMMSGPHPLR

GLELLYRSDSLAHIKAPVSSTRFNKMLLSNLEQLSGQHVLRLWSLILIAAGGYSKDEAD

VLLRQWTFSENEHRSRITGVLQVEQLIHTFVQEPKDTVSLRSDWIVTVLACGVQAADDW

LRIQSTLPAGWRNQSEQAEIQVVLVQELAGEWSQSIPVHDLKELDITGEQVLQMVQRK

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CDS 1540852..1541829

/gene="birA"

/locus_tag="EFAGFIKM_01376"

/EC_number="6.3.4.15"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0CI75"

/codon_start=1

/transl_table=11

/product="Bifunctional ligase/repressor BirA"

/db_xref="COG:COG0340"

/translation="MTKHEDLLHMLLNAEGRFVSGEEISRNLISRTAVWKHVNLKLRD

MGYEFEEAVSRKGYRLLTKPDSIDATGLQLALDTTVFGRKAVLLTSTLSTQGDLKLAE

QGQAEAVVIAEEQTGGRGRFGRQWFSPPGKGIWMSVLLRPDLPLQHTPQLTLTGVA

VCRAVRACSGADAGIKWPNDVLIDGRKVCGILLESTVEDHEVRYCIAGIGVDVNFDP
DYPEDLTTIATSLKMETGQSVDRTKLTAAILTELEQLYFLYQKEGFGVISALWEALSV
SMNREITVTNPHGVIEGKAIGLDPGALIVEKHDGEHTLIISGEISWKS"

CDS 1542174..1543052

/gene="panB"

/locus_tag="EFAGFIKM_01377"

/EC_number="2.1.2.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WIL7"

/codon_start=1

/transl_table=11

/product="3-methyl-2-oxobutanoate
hydroxymethyltransferase"

/db_xref="COG:COG0413"

/translation="MANKQALNIVKMKKYKQDGVPLTMITAYDYPTALLAEEAGIDLI
LVGDSLGNVVLGYNSTLPVTIDDMVYHTRSVMRGAEKTFIVADMPFMTYHGSVDETLK
GVRRLMQEGHAHAVKMEGGVEIADTVRAVVQAGVPVLGHIGLTPQSVNQIGGYRIQ GK
DAADAKRLMDEAKALEAAGAFGIVLELVTEEVARAISEELSIPTIGIGAGRGCDGQVL
VFHDVVQYASPYTPKRFVKTYGDVGTLIRTSIEAYVKDVKDRSFPAEEHVFNAADGVL
DQLYGGQRKEKVG SNS"

CDS 1543049..1543945

/gene="panC"

/locus_tag="EFAGFIKM_01378"

/EC_number="6.3.2.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9X0G6"

/codon_start=1

/transl_table=11

/product="Pantothenate synthetase"

/db_xref="COG:COG0414"

/translation="MKVLRITAE LRQELSLKRQAIRSSASVVGLVPTMGFLHQGHASL
MQAARQQSDIVVLSIFVNPIQFGPNEDFDSYPRDEARDVETARSQGVDIVFIPSVEEM

YPQATQTTVSVSKLTERLCGASRPGHFDGVTTVSKLFNIVQPQRAFFGMKDAQQVAV
IQQMVNDLNMPVEIVPCPIVREEDGLALSSRNVYLSAEQRTQALVLSKALRAAQEAAD
TGVATTAADIRRLREHIATSPLAVIDYAEIQAFPSLEPLTDQEEVQGRDDLIALAV
KFGKTRLIDNIRLQKSEVLSHV"

CDS 1543938..1544321

/gene="panD"

/locus_tag="EFAGFIKM_01379"

/EC_number="4.1.1.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WIL3"

/codon_start=1

/transl_table=11

/product="Aspartate 1-decarboxylase"

/db_xref="COG:COG0853"

/translation="MFRTL MKSKIHRATVTEANLNYVGSITIDEDLMETS DLMENEKV

QIVNNNNGARLETYVIPGPRGSGVICLN GAAARLVQPGDNV IISYAMMSQEEANTHK

PTVVFVDGQNKPVQTMKQEVHATIM"

CDS 1544415..1545062

/locus_tag="EFAGFIKM_01380"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFQHVFAEMNDMLDEI IKSYP SAEGLNKQELLQKWNLLKRMSDG

MLDEWLMFEEKMSQVREREMDKPASLEPEQEAVTALPELHLECF SRGGYFKLQMY PQ

AIMQFSRVVTDHPESALTRFY LALAYLNLEQMAEAGTHLQQIMY LKGS PRLKGLVCNA

LGCIQAKLANPEAACSLFAQALQYDPTLTEPLYNMEACRLNRGKLQYANQLTTLH"

CDS 1545205..1548066

/gene="dinG_1"

/locus_tag="EFAGFIKM_01381"

/EC_number="3.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A5K4"
/codon_start=1
/transl_table=11
/product="3'-5' exonuclease DinG"
/translation="MKFAVLDFETTGTQSDGEIIQAGLAIIDHDYSITQIYSSYVNPG
VPIPPFISGLTGITDEDVADAPSLEEMMEMVPLLNDVVLVGHNVAFDFHFLQNALDR
CGYLPFTGRILDTIDFLKITFPSLGSYQLGYVSSEFGFQHDRPHQADSDALATAYVLL
KCLDELKELPLITIQRLSDLFAPEDSDLGWFLDGMRSEKEAEPIQDLDGHTYYRQLAL
NVSDWTDIGAPRDEREANPLDGVSFEQFMDQVRENKDTLDHYEEREATQMFSVVRQ
ALDEEKHLLIEAGTGTGKSLGYLLPAIYESVKQEQQVMVSTHTINLQEQLRERDIPML
TQVVPFPFKA AVFKGRGHYLC LRKFEHKINKREFATPKEDYFTAAQMIVWLTQTETGD
DEELNLSGRGGDFWETVQSESESC LGRSCPWFRKCFYHRAKHEAGLSDIVITNHSKLF
TDVKA AHQLLPAYESLVIDEAHHLEDVAGKHLGMHMKYFTLVHTLTRLFKDSRNGQLP
MLRSQ LSGHENS VQWGSMDQMFP LALEV KELWDRMSDALFGLLPERSDASPGETGQF
SLRLKASQKPAKWQELQDLENQIYVTLGDLVRKGDKLLLEV KEDQDDYQSDSLITDIT
GLLKDLTTLKENLRFFMRMDDAKTVYWMEASGQFRSKSLQLYAVPVDVSAQLKDLFFD
KKKS VVLT SATLSVDKSFQFMIEQLGLQEASENNRLLTSM LPSPFN YRDQALLVIPRD
FPSVKGSVGD AHFVNMLVQSLAETAIATRGRMMVLFTSYKMLRQVYDPLKEALSGNDI
SLLGQGVDSGSRSKLTRRFQDAKATVLLGTSSFWEGVDIPGEALTCLAIVRLPFQPPN
HPLVEAKSELLQEQQKNP FMKLSVPQAVIRFKQGFGRLVRTAKDRGIVIVYDTRVIEA
YYGKFFLYSLPGPKMEHMLTEQMVP RITEWLEKPANEQK"

CDS 1548286..1548939

/gene="rex"
/locus_tag="EFAGFIKM_01382"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O05521"
/codon_start=1
/transl_table=11
/product="Redox-sensing transcriptional repressor Rex"
/db_xref="COG:COG2344"
/translation="MKSDKISEAVVRRLPVYLRYLNELHQREVATVSSQELGQRLDLN
PAQIRKDLAYFGDFGRKGIGYDVSYLIEKIRHILKIDQQIN VALVGAGNLGQALSNNY

AYLKDNMKIVAVFDAYGPKIGSQINSLTVKPMDELTEAVKMENIRIGIITVPDTEAQN

VADQLIESGIEAILNFAPTILKTPPHIRIHHADFTDLLSLAYYLETGKDDEEDDNK"

CDS 1548926..1550233

/gene="mtaD_1"

/locus_tag="EFAGFIKM_01383"

/EC_number="3.5.4.28"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9X034"

/codon_start=1

/transl_table=11

/product="5-methylthioadenosine/S-adenosylhomocysteine
deaminase"

/db_xref="COG:COG0402"

/translation="MTTNRWVIHNGKFAVNEGGTTWNVVQGYMVVENDKIVHIGETLP

DEKKNCTKVDGKGLFFLPGLINTHGHAAMSLLRGHGDDLALQVWLQEKMWPM EAKMTS

EDVYWGTSLSVLEMLKGGTTAFLDMYDHMDQVAKVVEQSGVRAALARGVIGLCSEEEQ

LRKLEESAFAREWNGQADGRITTVISPHAPYTCPPDYIEKLVQVANDLNLPLHTHMS

ETLREVEQNVADYGLRPVAHLEKLGFFSRPSLVAHAVHLNDEEIDILARHDAVSHNP

GSNLKLASGVARVPALLKAGVTVSLGTDGPASNNNLDMFEEMRLAALIHKGVSGDPTA

VPAGEALLLGTSYGAKSIFLNNTGALQVGMKADFIALDIEQAHFYPHTDLISHTIYSA

SAKDVEHVWVDGKQVVKHGECLTLDEERILRESQLAFDGLLAR"

CDS 1550271..1550801

/locus_tag="EFAGFIKM_01384"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKKKKKIWIWISLLALVLILFGLQRYVHVHTQDQRKEEALAIQAA

QEQLGITSYDELKRYIWGDKEGSDNIYWTLIGKNKDTQDVMVWVKFDANNQPAKGANA

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FSNGEQVDLVYTL PNS"

CDS 1551103..1551630

/locus_tag="EFAGFIKM_01385"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKLKVLPIALTAVISAVVLFGGWVFYRQVAVQNPIEKMVTQYDG
VNDVQLTINRNEVQLKLDLQPDVDLGRVLQYIHKEGQTLIGTRSLKLDVVDHSSEALE
SWWGDAMFTVAQAMENKQYTEITPTLSKMATNGIKVNTAMDDNNVYVSLRDGDASKFI
ILPRVPGQIGVWPNA"

CDS 1551623..1553125

/gene="ftsH_1"
/locus_tag="EFAGFIKM_01386"
/EC_number="3.4.24.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9WZ49"
/codon_start=1
/transl_table=11
/product="ATP-dependent zinc metalloprotease FtsH"
/db_xref="COG:COG0465"
/translation="MPKWTKEVAIGFFPVLIIFLAFTGVNIVPILIAGVLVGALLFMM
QMRGGITVGAAQERKRKKKGPSKLTFFEEIGGQDSAKQELREALDFLIKHEEIRKFGIR
PLKGILLTGPPGTGKTLMAKAAAHYTDVSFVAASGSEFVEMYVGVGASRIRDLFKDAR
TRATKENKENAIIFIDEIDVIGGKREGGQQREYDQTLNQLLTEMDGIYTSDTPRILVI
AATNRKEMLDSALTRPGRFDRHIQVDLPDKKGRKHILELHAVNKPLMKEVNLEKTAE
SYGFSGAQLSVMNEAAIYAMRDGLLNIEQRHLSLAIDKVMGKTDRESSVEEKKRV
AIHELGHAIMAELVRPGSVSQVALSPRGQALGYVRHNPQQEQFLYTKRFLEEQIMIAL
GGAAAEEEMYGGRRSTGSRNDFDQATNVVQTMASGLTSLGIVNMDMVTTEELMRENKL
ILQELMEQTKQLLEEQRITFDNSLDILIREEVLSGEQFRCQFRDSALLPA"

CDS 1553259..1554131

/gene="hbd"
/locus_tag="EFAGFIKM_01387"
/EC_number="1.1.1.157"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P52041"

/codon_start=1

/transl_table=11

/product="3-hydroxybutyryl-CoA dehydrogenase"

/db_xref="COG:COG1250"

/translation="MFFKKIGVVGGGTMGQGISQMLAAKGLDVLLVEHTTQKLDHAYD

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QLDQVCPSNVILASNTSTLSLTELASSTKYPERVIGMHFIHPVSRVDLVEIIRGLKTS

DTTFEETRRFVEEVADKKGVMIYESPGFVTSRLICLLINEALHVLQEGVASAEDIDDA

MRIGYNFQHGPLEMADRFGGLDSVEAALERMFRFEGELKYRPSTVLKKMVRAGHLGAKT

GEGFFKYDKDGDRL"

CDS 1554128..1555333

/gene="ackA"

/locus_tag="EFAGFIKM_01388"

/EC_number="2.7.2.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9WYB1"

/codon_start=1

/transl_table=11

/product="Acetate kinase"

/db_xref="COG:COG0282"

/translation="MKVLVINAGSSSLKYQLYNMTDESVLAKGLVERIGMDSSILTHK

PTGREDVTEVSEILEHTTAIRKVIDILTHKENGVLDSVSEIQAVGHRVVHGGEAFKES

ALVDDAAKAEIRRLFDLAPLHNPAAMMGIRAAELNMPGVPQVMVFDTAHFQTMPEKAY

LYAIPRVLYKKYKVRRYGAHGTSHDFVSKAAAEYLDRPVEDLKIITCHVGNNGGSVTAV

KGGVSVDTSMGMTPLEGLMMGTRSGDLDPAIVPYVMNKEELSVSEVNSMLNKHSGLLA

ISGISSDMREITEGMENG DANSTLAFEMYEYRLRKYIGSYAAAMNGVDVIVFTAGVGE

NSVVLQRQKVCEQLTYLGVELDEALNAIRSGEPRRITTANSKVEVLVPTNEELVIARD

THRIVLNSQ"

CDS 1555435..1556730

/gene="asnS"

/locus_tag="EFAGFIKM_01389"
/EC_number="6.1.1.22"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P67572"
/codon_start=1
/transl_table=11
/product="Asparagine--tRNA ligase"
/translation="MNTNCVIRNVNEHVGETVTIGAWINNKRSSGKIQLQLRDGTGY
IQGVVVKSEVSEEIWNNAKSLTQESSLYVTGIIREEPRSASGYEMTVTGVEIIHLTEN
YPITPKEHGVDFLMDHRHLWLRSTKQRAVMVIRAEIIRAVQQFFDGNNGFTQVDPPILT
PSSAEGTTNLFHIKYFDEDAYLTQSGQLYMEAAAMALGKVYSFGPTFRAEKSKTRRHL
IEFWMIEPEMAFVDHEESLRVQEKFAHVVSQSVVKNCRAELESIGRDVSKLEGIVAPF
PRITYDEAIEFLHGQGFDIPWGEDFGAPHETAIAEKYNTPVFITHYPAGIKAFYMKPD
PNRPEVVLCADMIAPEGYGEIIGGSQRIDDPELMQQRFEHNLSDEAYQWYDLRLKYG
SVPHSGFGLGLERTVAWICGLDHVRETIAFPRMLYRLYP"

CDS 1556751..1557455

/gene="dnaD"
/locus_tag="EFAGFIKM_01390"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39787"
/codon_start=1
/transl_table=11
/product="DNA replication protein DnaD"
/db_xref="COG:COG3935"
/translation="MEDTTSKAWLDGAAYGMTSGTAHLPYALLRFYHQLGLSDAEVLL
LIQLLGFRQAEFNEFPTLEELATRMGLAPEGIARMLQRLMRDGYIAIDEHRDEERDIQ
YERYDLHGLYAKLAACTAEVAAFRAEQQSINTARQDSNSVQKEEEERNMFSIFEKEF
GRPLSPMECETISGWLDQDRYQEELILMALKEAVFAGKVHFRYIDRILLEWSRNRVKT
VQDAKAYTQRFRNGGR"

CDS 1557703..1558203

/gene="algU_2"
/locus_tag="EFAGFIKM_01391"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q06198"

/codon_start=1

/transl_table=11

/product="RNA polymerase sigma-H factor"

/db_xref="COG:COG1595"

/translation="MRTLIDKYSQHVVYHVAYSVLRNDQEAQDAAQEAFIQMYKSLPDY
RSEGFKTWLTRIAFHKAIDAKRKLGRRTAEDLGGEKIINMPGRDEDVLTSLVREERQ
DKLRERINQLPAQHRDIITAYYLSEKNYEQIASDAQVAVKTVESRLYRARQWIRKHWK
EDEWRE"

CDS 1558196..1558648

/locus_tag="EFAGFIKM_01392"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKQEKYTAGQWTDYIEGHMSETQANQMEQLLEDPDAMDIIYLE
ALGIHGELPPLPDPTGFADSVMHRIEIQPTKSQRKPRAGNRNRWLEHKVFHYAVAAC
LTLIFLSSGLFDKVAPYHKFQDGDHRGSFTEKWTEAATSWLDNLKPKP"

CDS 1558686..1559975

/locus_tag="EFAGFIKM_01393"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHSDRNKLLAFLNLIPGLGFMYWGRPTRAVVYPLLFFGTGIGF
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GAAYQKAYAGQEEPLGQMDQEEPHQDHGGVYGVPEGYPYQPMYRKGSEGERFFTILLS
FVPGLGHLHLGLLHRGLSFLMAFFGSFAMMVVASITNESVFLMFLILPVIWVYCMF
DAVQHVHRKQAGEILQDRTLFEELMGRVAGRRSKVLATLLSAFPGAGHLYLGLQKRG
MQLMFLFLGSIYVLDLLHLSVFLFMIPLIWFYSFFDGLQCSSRYGREPLVDQPIFKDW
ARHQRLIGFGIAALGLYYLTIRLVIPQLNELFPNAFMTYEIRSYLNTVIVSLLLIFGG

LKLLFGKQRGTGIQSAAHQNDEGADSLFLFKDRDDRL"

CDS complement(1560139..1560792)

/gene="mtnB"

/locus_tag="EFAGFIKM_01394"

/EC_number="4.2.1.109"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31668"

/codon_start=1

/transl_table=11

/product="Methylthioribulose-1-phosphate dehydratase"

/db_xref="COG:COG0235"

/translation="MGFEKITLEHKRQVLEELADIKALFASRNWFPGTSGNLSMRVGD
FDPEQFYFAVTASGKDKSLRTPEDFLFVDKHGKAIETTLKPSAETLIHCEIYRLTGC
GAVFHVHTVFNNLISEFFGADGHVPIQGIELIKAFNIWEENAEIRVPVLPNFADIPSI
AELVPGVLDANVPGILLRNHGIYAWGKDAFEAKRHLEAFEFLFEVMYRQLLLKGATK"

CDS complement(1560796..1561473)

/gene="mtnX"

/locus_tag="EFAGFIKM_01395"

/EC_number="3.1.3.87"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31667"

/codon_start=1

/transl_table=11

/product="2-hydroxy-3-keto-5-methylthiopentenyl-1-
phosphate phosphatase"

/db_xref="COG:COG4359"

/translation="MRSDKKTVIFCDFDGTITLSDNIVAIMKHKPEGIEAIMKDTIE
QKISLREGVGAMFALLPASRKDEIVEFVLGQAGIREGFSEFLDYVRSEGIEFNVTSGG
MDFFIEPLLAPFHIPQDHVYCNGADFSGETIQIEWPNPCQPPCENGCGMCKTTVIRTF
PEDQYNRILIGDSLTFEGAKIADLVYSRSILTDKCIELGVDHVPFATFYDIIDMKQ
KQTQGVL"

CDS complement(1561470..1562693)

/gene="mtnW"
/locus_tag="EFAGFIKM_01396"
/EC_number="5.3.2.5"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31666"
/codon_start=1
/transl_table=11
/product="2,3-diketo-5-methylthiopentyl-1-phosphate
enolase"
/db_xref="COG:COG1850"

/translation="MNNMCTATYRLHDDHADFRKKAQSIAIGMTVGSWTELPQAQREA
MQKHLGEVISIEVNEAEGIAAGERYADITIGYPDVNFSRDIPALLVTVFGKISMDGRI
KLTKLGFSDGFLSAFPGPKFGLNGVRDLLGVHDRPLLMSIFKSVIGLDADELREQFIR
QALGGVDLIKDDEILFENKLTPIEKRVEVCMKAAEQARQETGKKLLYATNLTGPTSRL
KEQAERAIGAGANALLFNVLSYGYDVLHELSSNPDINVPIMAHPALAGALYSPHYGM
SASVVLGQLMRLAGADLVLFPSPYGSVTMPKEENMAITEQLLTADLPVRTSMPVPSAG
IHPGLVPLILRDFGTDVIVNAGGGIHGHMPMGTEAGGRAFLQAIEAAQRSIPLAQYATE
HPELKSALDLWGGER"

CDS complement(1562690..1563550)

/gene="proC_2"
/locus_tag="EFAGFIKM_01397"
/EC_number="1.5.1.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7A5G8"
/codon_start=1
/transl_table=11
/product="Pyrroline-5-carboxylate reductase"
/translation="MSSEQQTLLQKQKTFHGAGAMAEIVRGLISRLVVRPQDITMLN
RSNQKRQEELSTRYAVHTGTASHSLDHLASTPVIVLCMKPKDAAAALRELGPLLSPDQ
LIVSVIAGLSIRTMQSLLGRKQPIARTMPNTSSTIGLGATGLAFSAEITDEQRSTVMT
MFEAVGIVTIVPEDKLEVLTGISGSGPAYVYYLMEAMIAAGIRGGLSSQQSRDLTVQT
VLGASRMVQQTGLEPMKLRSDVTSPGGATQAALKTLDEGDFFENVIAAVNRCAERSRE

MGAALEGDLK"

CDS complement(1563587..1564834)

/gene="proA"

/locus_tag="EFAGFIKM_01398"

/EC_number="1.2.1.41"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9WYC9"

/codon_start=1

/transl_table=11

/product="Gamma-glutamyl phosphate reductase"

/db_xref="COG:COG0014"

/translation="MSEVREKAIKAQATVPQLNRLNTEQKNTALRVMADALIKETDSI
ITANAEDLARGREQGTPDSMLDRLALNKERIAEGLRQIADLPDPVGEVLETFTRP
NGLHVEKLRVPIGLIGIIEARPNTVDAAAGLCLKTGNAVLLRGGSSALSSNRKIVEV
LHQALTITDMPADALQLVEDADRASVDEMLKLNGLLDVIIIPRGASLIRNVVANATVP
VIETGAGICHTYVDESADPVMAAEIAINAKAQRPSVCNSMETLLLHAAYAEHLPALA
EQFREANVVLKGCDTVRRLLVPSALEATEEDYATEYNDYILNIRVVENLEEAMQHIAHY
GTKHSECIVTRDTAHAERFMHDVDAAAVYHNASTRFTDGFEEFGYGAIEGISTQKLHAR
GPMGLPALSTSKYRITGNGQIRQ"

CDS complement(1564893..1565996)

/gene="proB"

/locus_tag="EFAGFIKM_01399"

/EC_number="2.7.2.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39820"

/codon_start=1

/transl_table=11

/product="Glutamate 5-kinase 1"

/db_xref="COG:COG0263"

/translation="MTSRIVVKIGSSSLTTEEGGLDRSSITFFAGEIAALADQGHEVL
LVTSGAVAAGFREIGYPQRPKLLHEKQAAAAVGQALLMQAYQQAFAAHRVTTAQILLT
RTDFHSRKRMGNAGMTVEELLKQRVIPFNENDTVSVDELKFGDNDLLSALVANLVKA

QHLIILTDNGLYTADPRKDPSAMRYDRIPEITAEIYAFAGGSGSTVGTGGMRSKVDA
AKVATRGGVPVVFVGSVKEPGDMQKAVEGTGKGTYFETRLASLSRKKQWLGMSTPLGT
VVVDDGAEELVHGGHSLLPVGVKRVLGTFHAGDVVEVIGMDETLLGRGIVNYDDDQL
RLIAGLPSGEVMKQLASIHRLVIHRDEWITLK"

CDS complement(1566358..1567566)

/gene="bacF"

/locus_tag="EFAGFIKM_01400"

/EC_number="2.6.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39643"

/codon_start=1

/transl_table=11

/product="Transaminase BacF"

/db_xref="COG:COG0436"

/translation="MTQSDHTSARSFAKIPTSDVMTQLPTQFFATLVQNVNREIASGH
DVINLGQGNPDTPPPHIVKTLQESAENPLYHKYSPFRGHSFLKEAVAKRYKEDYNVD
LDPETEVAIFLGGKTGLVQLPQILLNPGDVLVPDPGYPDYWSGVALAKANMSFMPLL
ESNAFLPDYEAVTAEDREKAKLMFLNYPNNPTSATAPLSFYEDTVEFAIQNQIVIASD
FAYGAIGFDGHRPVSFLQAPGAKEVGIEFYTLSTYNMAGWRVGFALGNAEIVSKINL
LQDHIYVSLFGGIQAAATEALTASQECVTSLSRYESRRNTFYDALSSIGWQASKPAG
SFFSWLPVPAGYTSASFADLLLREAKVAVAPGIGFGSHGEGYVRAGLLSDENRLREAV
ERIGKLNLFK"

CDS 1567826..1568821

/locus_tag="EFAGFIKM_01401"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKGIRNTGVLLTITWLSILLACGNQAATPAAGADDSKAATET
TETQTATEETNEGETRIFKDWTGHEVEIPVNPKRVIYHGEVTGDLLALGVVPVGILRQ
EGTVFDDQVAQSEDEVGFPISVEKALDLPDLIIFSNSDEAQYDQIAKVAPTFTFDSFG
LIEDRMRLGDLLNKKQEAEDWITAHQKATEEMWTQLHENGLKEGETASVFTMYPGNR

LFVMAGAGLPQLLYGEDGLKPTAEIQKVLDEDMGFVEISTEKLSEFAGDRIFILDPVT
DDAKQSTKELL DSTIWKNLPAVKEGKVYRFNIVKASSDALSREWLLQELPKQMIQ"

CDS 1569024..1570646

/gene="btr_2"

/locus_tag="EFAGFIKM_01402"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40408"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator Btr"

/db_xref="COG:COG0614"

/translation="MQALDADGGALFFSAFMFRLDHLVRRIEPPEQVMLEVACEKHTF

LICEEGDGRLYIGHEQFPFTTGCVYPLSPGEGYQIEHRNNSSELKYIVMAFDVIHVLTG

DPELFTRAVFEHRNQLNGYPYAPLSGLLEQMYVIRNYKTD AEYSHLNAQFQKWMELII

TRYTSPKTEQSMEARLHSTIQYVDDHYAE EITVQKLARLAEIRPVQYTTLFRQLTG HK

PLDYVNHVRIKHAKDWLRKSDEPLRDIASRVGFKDEY YFSRRFRQMTGLSPRQYDRSI

QQQTLVQDWLGHVDNIPV NPERIMYYGDSAGDLLVLGIQLLGDQTYDAVAPVNVEAAV

IMKPDLIIFDSSNKQQYEQLYRIAPT LAYNSHATLEERMHRLGSWFGRQPQAEQWLTS

YAERTEQMWAKIHTVIEEGETASVFTYHRGARLFVMGNIGLAPMLYHPMGFRPVIVK

EALASGRAYKEISAEAVRQYAGDHV FVMLPEEVVARQATEMLMKSPSWQALPAVQNGR

VYPVEESTWNVGDALTSDRLLALLPELLCASS"

CDS 1570720..1571541

/gene="yafV"

/locus_tag="EFAGFIKM_01403"

/EC_number="3.5.1.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0DP65"

/codon_start=1

/transl_table=11

/product="Omega-amidase YafV"

/translation="MTEKQQGEMRVALIQGDIQLGDPEANHKHMQTL LERAVEQYPDL

GLAVLPEMWNTGYALTQIHELADPEGQKSREWLSAFAQKHQISIVGGSIAEKRDGQIY

NTMYAYDREGKQVTRYDKLHLFRLMDEEKYLQPGAPEIFELQNGLTAGASICYDIRF
PELARTLALNGAKALIVPAEWPKPRLHHWRTLLTARAIENQMYVIACNRVGKGGETEF
FGHSLIIDPWGEIVAEGGEGEEIVTGIIRPSLVDEVGRIPVFEDRRPGVYFGGK"

CDS 1571633..1571818

/locus_tag="EFAGFIKM_01404"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDNHVKDTLRRLEQDNTREDHLRAFLENGAGGLSPDSTVQDEG

RVMNQQRNLTSDRNLRK"

CDS complement(1572068..1572994)

/gene="oxyR_1"

/locus_tag="EFAGFIKM_01405"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ACQ4"

/codon_start=1

/transl_table=11

/product="Hydrogen peroxide-inducible genes activator"

/translation="MTMEFRQLQYTLQIAAERNFSRAAEKLHIAQPSLSQQLSKLEKE

LGVLLFQRNTSTVELTHAGVTFVEQAQKIVDAVELLRQEMSDISQLRKGVVVGSMPI

TGSHLLPHVLPFQAYPEIEVTLLLEDSTGLTLEKLTASGKADLSLLSLPLQEPSLAYV

AIGEEKIDLAVPPNHPLARRADPEHPLPVRIEELRDEPFVVLKKGQGFRKLTFDLCEQ

AGFDPQVVFESTNIETVQSLVATGMGITLVPRFIARAPRSEFVPVYVPLAEPTPSRTL

VVAYRQGRVLSKAAEAFIHTFQQTVAELSKGD"

CDS 1573355..1575268

/gene="bglF_3"

/locus_tag="EFAGFIKM_01406"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P08722"

/codon_start=1

/transl_table=11

/product="PTS system beta-glucoside-specific EIIBC

component"

/db_xref="COG:COG1263"

/translation="MNSKKLAQEILEHVGGNNNINQVIHCSTRLRFTLKNSKLANTEE

IKRLDGVIGAVDSGGQYQVIIGNDVSYYNELAPLINMETASDEVKSPRDYSPKGLFN

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MLLAFSSANKFKANPYIAVLLGGVLLHPNMIGLLGGEEPVYFLGMNVPNVAYATSVIP

IILTVWFMSYIERFADKVSPGPVKIFLKLPLIVLIVAPISLIALGPLGTYIGTMSEA

VFWIQDKVGWVTVMMSMLMPFIVMFGMHKVFYPVIFGAIASPGYETLFLVSMLAANM

AQGGGALAVAFKSKDPKMKQIALSAGISGMFGITEPAIYGVHLRLKKTFLACLIGAGA

AGMFAGIVNLKAYTAVGPGLATLPIFVSDDPNNILYALITVAISSVIAFVGVFLIGFQ

DTVASAESGKAGKPSAEPVSPVRMDSQPQTSASGMKSKKVVFAPLEGKVLPLREVKDE

AFSQEAMGQGMAIQPSVGKVFAPFDGTVETVFR TKHSIGLRSVEGVELLIHVGLD TVK

LKGQHFDVKVNEGEQISHGQLLIEFDLEAIQAAGYDTTTPVIVTNSSDYLEILGNETA

ATTGPGKPLITVL"

CDS 1575305..1576144

/gene="licT_2"

/locus_tag="EFAGFIKM_01407"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39805"

/codon_start=1

/transl_table=11

/product="Transcription antiterminator LicT"

/db_xref="COG:COG3711"

/translation="MEVIKILNSSIVLARRGEDDKEIIVMGKGIGYRSKPGDVVGED

IEKIYVLENETISSDLTALMKETPKEYLILADEIISHAKHTLSRHLSDHLYVALTDHL

YMAMKRFKDNMTIQNRMLWEVKKFY PQEFSIGLHGLSLIQQLGLSLPEEEAANIAFH

LVNAQQNDDNMNQVMMMTNTVKDVLNIIKIHYQVELDTHSINYSRFLTHLQFFIQR LF

EHKTLNTQDHELFEQIANKYPQEEACVLLIKDYIEARFEHTISNEEMMYLIIHINRVM

SRN"

CDS 1576190..1577647

/gene="bglH_4"

/locus_tag="EFAGFIKM_01408"
/EC_number="3.2.1.86"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P40740"
/codon_start=1
/transl_table=11
/product="Aryl-phospho-beta-D-glucosidase BglH"
/db_xref="COG:COG2723"

/translation="MKNTTRTFPEDFLWGGAIANQAEGAWNVDGKGLSTADIAIYRK
GVAKSEYKKHNAINEEQIKTAMESTSDREYPKRRGIDFYHRYEEDLALFGEMGLKTLR
LSIAWTRIFPNGNETEPNEAGLQFYDRVIDGMLKQGIEPLITLSHYEMPMYLVNHHGG
WTDKVVVDYFVHFCKTVFTLYKDKVKYWITFNEIDSIVRHPFTSGGIVPERFENVEQA
VYQGLHHQFVASALAVKYCHEIIPGSQIGCMLTKLTTAHTCNPEDVLVASRDNQFNL
MFTDVQVRGAYPYFTKRFFAEKGINLDMLEGDEEILKVHTVDFISFSYMSLVSSVDG
DRLEQVSGNTTGGVKNPYLQTNWGWQIDPVGLRISLNELYSRYEVPLFIVENGIGAV
DTIEADGSIQDDYRIDYFRSHIEQMHEAILDGVELLGYTSWGVIDLISYSSSEMEKRY
GFIYVDQDNDGNGTLERKRKKSFYWYKDVIANNGL"

CDS 1578018..1579439

/gene="leuC"
/locus_tag="EFAGFIKM_01409"
/EC_number="4.2.1.33"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P80858"
/codon_start=1
/transl_table=11
/product="3-isopropylmalate dehydratase large subunit"
/db_xref="COG:COG0065"

/translation="MSKKTMFEKIWENHVIHQEEGKPSILYIDLHLVHEVTSPQAFEG
LRLSGRKVRRPELTFATMDHNVPTKDRFNITDPISKQQIDTLSQNCRDGFKLYDLDT
IDQGVVHVMGPELGLTHPGKTIVCGDSHTSTHGAFGALAFGIGTSEVEHVMATQCLQQ
AKAKTMEVRFVVGKRNPVGTAKDMILAVIAKYGTDFATGYVIEYTGESIRELSMEERMT
VCNMSIEGGARAGLIAPDETTFEYLRGREYVPADAKFDEAVEGWKQLVTDEGAEFDHV

VEIDVETLIPQVTWGTSPGMGTDISSKVPVPAELPTENERKAAEKALEYMGLEPGTPI
AEIPIDYVFIGSCTNGRIEDLRAAAQVAKGHTVSSQVTAIVVPGSGRVKIQAEQEGLD
KIFTEAGFEWRDAGCSMCLAMNPDVLKPGQRCASTSNRNFEGRQGRGGRTHLVSPAMA
AAA AVKGHFVDVRDWNFKTEAAI"

CDS 1579471..1580073

/gene="leuD1"

/locus_tag="EFAGFIKM_01410"

/EC_number="4.2.1.33"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P04787"

/codon_start=1

/transl_table=11

/product="3-isopropylmalate dehydratase small subunit 1"

/db_xref="COG:COG0066"

/translation="MEEFKTLQGIVAPVDRVNVDTDAIIPKQFLKRIERTGFGQFLFY

EWRFDEEGNNNASFEMNKPRYEGASILISRANFGCGSSREHAPWAILDYGFRCVIAPS

YADIFYNNCFKNGILPIKLSEEQVEDLFQRTATHEGYEMNVNLENKTITDAYGLHIDF

DLDEHRRQFLLQGLDDIGLTLQHDDEIAAYEQRHAAKLFG"

CDS complement(1580273..1581748)

/gene="flp"

/locus_tag="EFAGFIKM_01411"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A3Q5"

/codon_start=1

/transl_table=11

/product="Protein flp"

/translation="MLKLKKRMYITTISCLLLCIAWAPPLSATEARDRTEVLQEIDEY

MNRSMKANHIKAASLAIANNDDEVFYAKGYGTFADGQKVTGNTPFPIASLSKSFTALAV

LQLVDKSRIDL DATYASYFPELSPQDPHVLDITVRHLLNQTSGLNDKINPDMTKTPQF

QSLAEANQLLNTVQLAHIPGTAYSYHNPNYVLLANLVESVSGERFSDYLKEHIFEPLG

MNHTFSVSTTQQFYKNNTIPLGHYLSLGRAISQSEPLWFIEGPASIVSTAEDMSLWML

SQYHGRLVSPVLMKQYHASGDISPYGMGWLADQDASNGQTISHSGIFWTYKSEERVYL

NEQMGIAMFNSGINAYVNYS AFLDGIADIMRGQKPQTSFVN GRNMEMIMIALIVATL
SWG IYGYSRILRNYHRLTISK LILITVGR LIPVLILLSLSHLVTFIGGGRVLPWFGIW
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CDS complement(1581800..1582897)

/gene="sasA_2"

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/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"

/codon_start=1

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/translation="MAKFMTRLLFLKRLSLLHSFMLLCVVTLIAVLGIITIEFAWAEN

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KGNAELLATYLPKKLSEEKVLDIHTMNLHILRLESYAEAMNSIQRLEDLPLNIQSM

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CDS complement(1582882..1583556)

/gene="arlR_1"

/locus_tag="EFAGFIKM_01413"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9KJN4"

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/db_xref="COG:COG0745"

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SIRELGARVEAHIRREQRIQTKSSVRFNNELVIDYTARELYYLDKRISLPKKEFDIVE

LLSTHPDMVFGKERIYEKIWGMDEQGDSNVIAEHIRRIYKLYKEYGCDNQIETVWGVG

YKWPSS"

CDS 1583832..1585238

/locus_tag="EFAGFIKM_01414"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKWSAAVVFLFLCLFPVMAHADTTSPSIVLDGVTINQQTGAPA
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DSPPLIKQGTTLVPLRFVGE GMLRVGWDNGTKTVSLFSIPPVETEGSDPVEAPVP
DGLTELQGISFSGDRLIVATNGNISPKVSSIGGPDRIIVDLPSAKFSQEFIQGQASNP
DGSGQILVTGSSIVSKVRYAMFSKSPSTVRVVLNQTATAKWSVGDNNVLLVDLTAT
SGEPTSQPAVPTNDGKTIVVIDPGHHGGRQSGAVSLSGAYEKDFNLAVGLKVQAILQQY
PNIQTVITRQDDTELSLKQRVDIAELNQADVFSIHGNKFTTPVPNGIETLYSRKESK
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CDS 1585497..1586906

/locus_tag="EFAGFIKM_01415"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKFGFLVLLVFVGLVFPGYSHAATDTKIILDGKEIVQPSDTKA
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DAPPLVKNGTTLVPLRFIGEEMGLKVGWNNNTTKTVTLVTQNSGSGNGTTTPPNSGNEG
GGSDQEGFLVLVNGISFSDNRFMIATSGSTKPNVFTMTGPDRIVIDLPNTAFADSFSEG
QALDSNQNGQLVVS GYPDVSKIRYSLYNSPSTIRFVIDLSSSKGYSVQND SGLVMIN
LDNQSGTPAPPVGNNGKKVVVIDAGHGDQDPGAIGVTGKREKDFNLAMALKVEALLKK
ESKIDVVLTRSDDTFLALKERVKIAQDIKADIFISIHANSGPAAANGVETFYTRSNSK
ALATVMHKYLLQSSGLKDRGVKTASLHVTRETTMPAVLLEGGFLSNKSDEAALFTESF
QSSVAKGIVAGIKEYLGIK"

CDS 1586942..1587619

/locus_tag="EFAGFIKM_01416"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNKKIWIAALLVTMVAAGCGSKPTAAPNQTQGAGTENNVTEV
EGETITEPVTAEP EENTTPTESTEGSSEEATTTTPPSDTSTEKPATSESNEKKTITVF
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HPMTRSE"

CDS 1587692..1590430

/locus_tag="EFAGFIKM_01417"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MTFKYNHTSHSKKVSAVLGMMALSAGGAAMAAESTETGQGQT
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GNKFNPTGSVTRAQLATFFSRGESLTD TYPNTSTGYVTGLKDGQITLVVDGKAVNFA
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LSGNKIGIFVGENYETYSYDEATAFIDQNGNAIKLSDITADSIIEVQRETFTADKKT
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LKAGSAVKYTVKDSVLQTITLSQGVESV RGT LVEIGGNQSTLTFKREGGSLEAKLLT
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SGQTITPSQLTAGNLINVT FEGATPKAVQVVKRTLAEVTAVDASSVTLKQFNGQTETV
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ILVKRETTADTNYRFALGSSVFVHHGDNTLSVQSLRDNDNIVLYLLNNVILEIQKQ"

CDS 1590594..1591289

/gene="nth_1"

/locus_tag="EFAGFIKM_01418"

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/inference="similar to AA sequence:UniProtKB:P9WQ11"

/codon_start=1

/transl_table=11

/product="Endonuclease III"

/db_xref="COG:COG0177"

/translation="MNAATVRHILETMEAMFPDAHCELNHSNAFELTVAVLLSAQCTD
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DVPQEHDQLVTLPGVGRKTANVVVSNAFGVPAIAVDTHVERVSKRLALAGWDDSVLEV
EKKLMKRVPRDEWTLTHHRFIFFGRYHCKAQNPAICHICPLLDICREGKKRMKTSQIRK
DKERVTTTRKRKIN"

CDS 1591313..1591585

/locus_tag="EFAGFIKM_01419"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKCISVYTDNFEAFSDIFEQIVEQEMAENEEKEVEGITVSHSGD
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CDS 1591794..1592138

/locus_tag="EFAGFIKM_01420"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MILGGDIFMAKKGQTFQTYTEEFKLNAVRSYVEGSSSYKVAER
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KKRYPNLVKEKR"

CDS 1592303..1592998

/locus_tag="EFAGFIKM_01421"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISBth8"

/codon_start=1

/transl_table=11

/product="IS3 family transposase ISBth8"

/translation="MMAIHFANREFGYPRMTTALWEAGLNVNHKKVWRIMRELSIQSV
IRKKRKKSSYTPSVIYPNRLKRQFHATAPQQKMVTDITYISDGSFVYLSVIQDLFNN
EIVAWQLSKRNDVQLVLDTVEQWTQKRDVSEAVLHSDQGFQYTSQAYNSRLEAFGVKG
SHSRKATCLDNACIESFFSHLKTEKLYLNQCNSEAEIRQAVEDYMYNRYRRFQAKLK
QRAPIEYRCALAA"

CDS 1593199..1596885

/gene="der_2"

/locus_tag="EFAGFIKM_01422"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00195"

/codon_start=1

/transl_table=11

/product="GTPase Der"

/translation="MSRTDYPKEMAKPLLPLREAMEQTGDHTAVQAITDLISKAEMKH
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NGAGTLEVSPEELEAYCKNGGAYSSIEVWDDIPLLKDDAVLLDTPGVDSTDRGHSLAT
HSALHLADVVFYVMDYNHVQSETNLSFAKSLSDWGKPLFLIVNQIDKHRERELSFDQY
TEGVEAIFAWEVRYDGLLFTSLRDKQHRYNQWDVLPELIGHMMQEKEALITHSLASS
ASHVTEQHILTREAEREDEENSLGGEIGGKEGIERLERELELLDQQATDIRTGPSRVR
EKFRAELEPLLANANLTPADIRASAAAYLESRKPGFRVGLLFSGGKTEQEKQRRASEL
VRLQDQASGQVEVHIRTMLRQLGESHQLWGAWEQALNTELPVDEALLEMKRSASA
EVSPEYVIQFSKDVGEIEARYRRSAMMLADRMLEALAARGEAAALQALDASRAALLAQ
SAAAARYTALQRSAAAEAGLRSLPHAGPLPSGLLPEVKGPHVPAVPEPGEVPGSHA
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VTEQGIVLVDTPGADSVNARHTGVTFNMYMKNADALIFVTTYNHAFSQQGDRQFLNQLGR
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KMAGDSKLLEQSGFIRFEEEFNQFAGRELADLAVGGASEEMARVIQRLKKRAEDAAQG
EEVLQQRRDELETIQGQSRQRIQQLAARSMKEELSQETAELLFHVQRQLAYRLGLFMA
EAFHPSVLREDRGNLKMAFAACGRELLRMIAIELEQELLATTLRLEQAGQTWLMKQVT
DCIDEVRQLSGGVDVSLPLNERWSTPVLEEVRLEEPSGWKSYLNYFRNPKQFFEGDGR
QRLQEALDPVLKQMIIEVLPAAQDKLIQFYDNQICQSLQHQSRQLEERLDEAVSGIQD
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CDS 1597210..1598982

/locus_tag="EFAGFIKM_01423"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9WYC4"

/codon_start=1

/transl_table=11

/product="putative ABC transporter ATP-binding protein"

/db_xref="COG:COG1132"

/translation="MDVLRQLQIFFWEKRTYLFVSILFLALATALGLVYPYMLRILID

DIIVPRTFEDVPIIALTVLGVVILKAGMQFLHGFYGGRLGNFLAYRLRNACYEKLQFL

SFRYYDTAKTGDLM SRLTGDL EAIRNFIGFGFAQILNMVFMVVF GAIMMMTMSWQLTL

FTLICIPLLAFVALRFESKIHPAFQEMRLALSSLTAVQENITGVRTVKSFAREPYEV

EKFSIRNERYKTNQIHAATLWSRYFPIMEILASVSIVLLLVIGGRMVIQKTLTLGELV

AFFSLIWYIIGPMWNLGFHINNYTQSKASGERVLELLNTPVDVEETQDPVIVEADQVN

GHVTFESVTFAYGNKMPAVTDINFDAAPGSVIGFLGGTGSGKSTIIQLLMRAYNVNSG

TIKLDGKNIKDIGIRSLRSQIASVFQETFLFSSSIRNNISYGLKNVTMDEIIRAACKLA

KAHDFIMEFPDGYD TVVGERGMGLSGGQKQRIAIARALLKNPKILVLD DATSAVDMET

EHEIQSGFQEV MRGRTTFIIAHRISLRHADEILVLDEGRVVQRGKHTELIEVPGPYQ

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CDS 1598979..1600829

/locus_tag="EFAGFIKM_01424"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9WYC4"
/codon_start=1
/transl_table=11
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/db_xref="COG:COG1132"
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SIFVLYLIQWAANTYRIKLTNIIGQRVIYDLRSDLFKHIQKLSFNFFDKRPAGSVLVR
VTNDINSLQDLFTNGAVNVMIDCVQLLGIIVILLINWKLGLAVIITVPIMFIISTKL
RVLIRRAWQDVRMKNSRINSHLNESIQQIRVTQAYTQEKENMKYFDNMNLSSKKSWDR
ASAMNQGGFGLIEITGGFGTLILFWFGAYLIQHDQLTVGLLVAFANYVGNFWDPINRL
GQMYNQLLVAMASSERIFEFMDEKPSIADKPGAKPLPSIKGDIAFENVVFEYEKGRQA
LKGISFSAAAGQSIALVGHTGSGKSTIINLISRFYDISGGRLTIDGQDVRDVTVESLR
SQISIVLQDTFIFSGTIRDNIRFGRLDATNEEVEDAACKAVNAHEFIMKLPGGYDTEVE
ERGNVLSMGQRQLLSFARALLADPRILILDEATASIDTETELKIQEALKVLLQGRTSF
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CDS 1601040..1602680

/gene="rhaS_8"
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/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1
/transl_table=11
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/translation="MQMDNNEINSKHLHDHDMNFRLLHVNYTSDPATEWLLRKHFIE
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ALEQEGGTALEMMKQLLRNEVNGEVSSSSPVAVGVICQMIYHHTLKKDGLQRYYGQIR
FQELLYTMFYDVACAECTDLASPIEHVKGYMEQNYSKRLTIEELANVARMSPRHFMR
FKKRYGYSPVDYLTLYRIKQAQILMRNDHSYQLKDVASYVGYQDETYFRRKFQISGI
PPAAFIRNSKQKIAAIHSVSIGILLALQIIPCAAPASHPWYTYRRKYETDKVMPLAE
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DRSDIAEVWLQRYEEKAKIIKNQLTDFIRNDRLLVVKVHGEALQMLGPRSIASVFYVD

MQMEGPEGVETYWERGTVTIKELSVLNVERILLIVGEDEISRQTWSAVRKSEEWLALL
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CDS 1602812..1603801

/gene="yfiY_1"

/locus_tag="EFAGFIKM_01426"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31567"

/codon_start=1

/transl_table=11

/product="putative siderophore-binding lipoprotein YfiY"

/db_xref="COG:COG0614"

/translation="MRFRWLTVLCTMMLVLIISACGTAGQDEATSEGQKTGSDNTSTT

ETSQVKKVTTKMGEIEIPVEPQRVVGLSLVPEFLYALGIVPVAVQNYHEDHPSYLEE

PFANTMKMGIARTPNFEAVMETMPDLIIPDWWSEKDQDQLSLIAPTLLPQRDDWRD

ELRDIKILDKEEQAQKVEDLVAKKVAADKLNEMIGEETVLYIRVMEKEIVLHGEN

LDRGNFVHKRLGMNPLPNFPKDQVAMSVSMEVLPEYDADHLIVQLDDDKNPEIKKKFE

EMLATSLWKNLKAHKNDHVYMGVGGKEWLNLMGMSPLADQYVIDDIVAVFEEKNK"

CDS 1603864..1604886

/gene="ycgT_3"

/locus_tag="EFAGFIKM_01427"

/EC_number="1.18.1.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31475"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0492"

/translation="MNKEDIYDLTIVGGGPAGLYAAFYAGMRDMRVKIIDGKDQLGGF

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GGNSAVDWAIELAQLARSVVVVHRKNEFRAMERNVSEMNNVTDVTRTPYSITRLHNHGE

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KQIPRF"

CDS 1605139..1606326

/gene="purT"

/locus_tag="EFAGFIKM_01428"

/EC_number="2.1.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P33221"

/codon_start=1

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formyltransferase"

/db_xref="COG:COG0027"

/translation="MWGAPFTAQAKKMLLLGSGELGKEVVIEAQR LGVETIAVDRYEN

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KGQSVCRTPGDVEDCWNIALSGARGKSVRVIVESFVQFDSEITLLTVRSVSGTVFCPP

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EVSPRPHDTGMVTMVTQDSSEFALHVRILGFPVTGVHLLTPGASATLKANDETSDF

VGGIEEALALPRTQIRVFGKPKETKVGRMAVALSAGQDVEEARKTAVQAANMLKVEVN

HVQ"

CDS 1606316..1606774

/locus_tag="EFAGFIKM_01429"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSNNVEAPVLMIRECELRDAEAVTGLMREVSYP TTTNVMKERIE

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CDS 1607034..1607846

/locus_tag="EFAGFIKM_01430"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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CDS 1608136..1609008

/locus_tag="EFAGFIKM_01431"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS 1609009..1609974

/gene="lnrL_3"

/locus_tag="EFAGFIKM_01432"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94440"

/codon_start=1

/transl_table=11

/product="Linearmycin resistance ATP-binding protein LnrL"

/db_xref="COG:COG1131"

/translation="MTEQQYDSVLSVQNLKKRIGRKWIKDVTDFDVKPGEIFGFLGPN

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LEHFARMQPGVDNERIQEVVDIVRLDQRIHDKVRTYSLGMRQRLGIAQALLGRPRLLI
LDEPTNGLDPKGIKELRVFIKQLASEGMAVVFVSSHLLSEIQLLCDRVAIISAGRVLA
GGVSELIEDHSLAIWHVSPLEQGKKMLQDAGIALVGRPADVMDDTIVAGLGPNAVVA
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CDS 1609967..1610956

/locus_tag="EFAGFIKM_01433"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MSNIMPLIRNETIKMVKKKRLYIIFIVLAVLVPMTYAQMKSAE

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CDS 1611033..1613012

/gene="parE"

/locus_tag="EFAGFIKM_01434"

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/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P66939"

/codon_start=1

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/translation="MVEQIDMSAGSTGGGQGSSGYDADDIQVLEGLVAVRKRPGMYIG

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AFLNSGLRIVLKDERSGNQDEYMYEGGASQFVAFLNENKDVLDHVIHFYAEKDDIEVE

VAIQYNAGYTETLASFVNSISTRGGGTHETGFRAAYTRVMNDYARRTSMIKEKDKNLE

GNDLREGMMAVISVKMSEVEFVGQTKDQLGSASARSAVDSVVSSENIQRFLEENPQVAQ
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CDS 1613025..1615487

/gene="parC"

/locus_tag="EFAGFIKM_01435"

/EC_number="5.6.2.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q93KF4"

/codon_start=1

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DGHGNWGSQDDDPAAAMRYTEARLSPIAMEMLRDIEKRTVLFKDNFDNTAKEPVVLPS
RYPNLLVNGVSGISSGFATEIPPHNLREVIDASIAVMEKPSIELDEIMMFMKGPDPFT
GGLIMGGDGILDAYRTGKGRIYIRSKTEIENMRGGKQQIVITEIPYQVVKSRSLVTAME
NIRLEKKVEGIAEVRDESGREGLRIVVELKKEADAQGILAYLLKKTDLQVTYNFMVA
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AAIKASKNRQDAQNNLMWMFGFTERQADSILTQLYRLTNLEINSLEKELGELMKKIA
QLQSILSDSRKLIGVIRKELMEIREKYGIDRRSAIQGEVEELKVNLEVLVNAEDVFVT
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KDYVTKRSGAVAACKVGKDDEVLSVHLSTGGQDIMLITKEAMAIRFREDEVNPMGRVS
GGVRGIQLRDTDEVVSALWVEGDEGEVAVLSDLGYGKRSLLLDYAIQSRGGKGLATFE
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CDS 1615716..1616156

/locus_tag="EFAGFIKM_01436"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MYNSDFAKCWSRLTKDYKLHMDQELAPSLTEAQLAVLEVLEDHQ
KMKPSDLIPYLSTTPAAVTMLLDRMEKNDLIRNRDNQDRRIVWVSLSEKGRMETERG
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CDS 1616432..1616878

/gene="mgrA"
/locus_tag="EFAGFIKM_01437"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0C1S0"
/codon_start=1
/transl_table=11
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/translation="MTDTYEVFYIINSFRQVNQMLFRAFWNENKEELTSIQFMVLSI
LRERPSIGINEVAELCHMGSSSMSAVVERLVKGEYIVRTRSDADRRSVKLQITDKGEQ
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CDS 1616875..1618386

/gene="emrB_1"
/locus_tag="EFAGFIKM_01438"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AEJ0"
/codon_start=1
/transl_table=11
/product="Multidrug export protein EmrB"
/translation="MSTTTAAAPSSAMDNIKKGPIVAALLIGAFVAFLNQTLMNVALP
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VGARWLSVAGLAITAITTFGLSRLAIDTTYGYMMFIYTARMFGMSMLMMPIQTAGLNQ
LPQRLNAHGTA MSNTLRTVAGAIGTAILVTIMSSKLKTHLADAVAAGQVNPNDKTAMI
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CDS complement(1618499..1618843)

/gene="atl"

/locus_tag="EFAGFIKM_01439"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AFP2"

/codon_start=1

/transl_table=11

/product="DNA base-flipping protein"

/db_xref="COG:COG3695"

/translation="MTPFTKQVVAAIAAIEGKVM TYGQIAAHAGSPRAARQVVRILH

SMSRKERLPWHRV VNAKGEISIPDEHSRMMQETELISEGVEFQLNGTINLKQFGHEPD

PVFLIDPTIQPE"

CDS complement(1619037..1619768)

/locus_tag="EFAGFIKM_01440"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSEHRHDHDAIPILFEDNHLLGITKPVNVPTQEDASGDPDLLTL

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SLPAREFPWA EWPAAVYQKA FGQPQ"

CDS complement(1619771..1620634)

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/locus_tag="EFAGFIKM_01441"

/EC_number="2.1.1.264"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01858"

/codon_start=1
/transl_table=11
/product="Ribosomal RNA large subunit methyltransferase
K/L"
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NEWVRQVHGHYHRSSSGGNWDMKKPIPERWTIGYENLKFHIKPTSFKHTGLFPEQAAN
WSWMMDKISNAGRPISVLNLFAYTGGATVAAAYAGASVVHVDAAKGMVQWAKENVQLS
GLADRPVRFITDDVFKFVQREQRRGNRYDAIIMDPPSYGRGPNGETWKLEENLYPFLK
SCMTILSDNPLFMLVNSYTTGISSTVLRNMLTMTMSAQYGGDITAGEIGLPITRSGLD
LPCGILGRWES"

CDS 1620929..1621381

/locus_tag="EFAGFIKM_01442"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P26492"
/codon_start=1
/transl_table=11
/product="Flavodoxin"
/translation="MAKLLVAYASMTGNTTEEIAELIVEGITQGGHEADLKSVTDCNAS
DVLDDYDGMIGVYTWGDGELPDEFDFYEELDELDLSGKRAAVFGSGDTSYEQFCGAV
DLAAAKLQERGAEVSPLEMLKIEYSPLEQEKETCRDFGKRFAAAGLQVS"

CDS 1621414..1622193

/locus_tag="EFAGFIKM_01443"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MPVGRNDLPERLLEDYRLEEMLRSPHRFIRPEPVSEQRLPLQWR
HRVQYAVSHAVNAFYSLDPDVRKEVPVQYLLEKWWPRKTDGFESVLHYWDVKNKITDE
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PNVVEAFQHMFSAFWWEAFGKLPGMIEIYCLLEGRKIRYIPGRQSLIRSMYIRLIRD
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CDS 1622246..1622812

/locus_tag="EFAGFIKM_01444"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSTGLSQDISSSKRRAGTCEFSPLPVPQSVIRKLLDEADPSLYV
MSSEPWRFMLFAGEGRQLYLEAVRQSYPPHLADRYGDWATYQYTEAIPHLVWVAPRN
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GYGDQPALRDM DASRPASELMTVYDHLV"

CDS complement(1622834..1624291)

/locus_tag="EFAGFIKM_01445"
/EC_number="1.14.14.9"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q5SJP8"
/codon_start=1
/transl_table=11
/product="4-hydroxyphenylacetate 3-monooxygenase oxygenase
component"
/db_xref="COG:COG2368"
/translation="MPVKSGTQYRERIDAQSVPCWYKGNLITGKRSEHVAFAGLMETQ
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GRSPDYMNTAIMSFYTGADLLKELSPQYAENLKNYYAYCRDHDITLSHAFIQPYASKI
SGQLDATEDAIAAKVVDRTTEGLIISGAFMMATQAATSDEIFVYPPSPSPAPFDDENPF
AFSFAVPNDLPGISLVCRDTYAAESHTNYPLSSRYEEMDNIVIFDRVLVPHERIFFAG
SEEISSRLFSGSNFHIHAGHQVLCRYIAKTEFVLGTIQLLTDLDLNTAHVIEKTAR
VFAGLESLKALALAAEAGAIPDGRGFVLPAPKPLMAANLLFPKLYPEMIEILQLLGSS
GVIMIPQEEEFQSDIAPSLNIYLKGNDMTSHERNALFRLIWELGAGSFGGRQTQFERF
FFGNVLTVSNRLFSVYNKDQTNRQLVRDFLSNNSK"

CDS complement(1624493..1624645)

/locus_tag="EFAGFIKM_01446"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAKDVLCEVNSCRHWAQENKCNASSIYIVSHSNKEASQSAETDC
KTFEVK"

CDS 1624991..1625803

/gene="ftsH2"

/locus_tag="EFAGFIKM_01447"

/EC_number="3.4.24.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q55700"

/codon_start=1

/transl_table=11

/product="ATP-dependent zinc metalloprotease FtsH 2"

/translation="MSKINHMNRIPRAKGIDMAAFYTPKECRRKAQHIVFSAENERII
NEFITILGMKEKFREHDVSIPNKMVMFGPPGTGKTLTASHLAERLDLPLVLVRLDAII
HSHLGETGSNVRKLFYARMNPCVLFDEFDAICRTRESNDEVKEMARVVNTLLQCLD
EFDGDSILVAATNLETQLDHAIWRRFDTKMTYGMPDDSSRKLYISKLVGAFEQETRLE
DYICERLTGCSYADIEQIVLKAKRKAIASSALHKQLISDAYDEYRPRVLEC"

CDS complement(1625900..1627366)

/gene="sasA_3"

/locus_tag="EFAGFIKM_01448"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"

/codon_start=1

/transl_table=11

/product="Adaptive-response sensory-kinase SasA"

/translation="MDRQLKQKKPKRTISILSHWTLRYFLILCIGFTIIAAGALYWIR
TTSIEKSLKTAELLGLEIADRVTRENNMLRVPPDLRLVTKREKLFNTDHYFCVMILD
NNNQLIFSQPKMEQKDVHYRLSDDYLEPRNNKYAGVTVNISEGDQTLGKVVVMQSKQS
ITFGPETIWLVALILGGLILCGWFTIYLLSKKLSRPIRQVAYAAEQIRGGNYDVSLDL
NTREREINELVNSFRDMATRLQQLEEWRTLFLAGVSHSLKTPVTSIKGLVMAVRDDVV

SPQEGKEFLDIALKESERMERMVADLLDYNAMAAGSVAVRKERTDLKLLVGEIYQWK
IAYEDKMPEVQLHAPPINFFTMGDALRIQQIIVNLLNNALHATAPEQKAVFDIYLSTE
EQMLYVDVKDHGTGIAAEEQPKIFERFYRGELKKRRNRGLGLGLTYSRLLAQEQGGEL
ILVSSSPEGSMFRLSLPRWTATQEAMNTEKAYGA AVKV"

CDS complement(1627351..1628037)

/gene="srrA_3"

/locus_tag="EFAGFIKM_01449"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9L524"

/codon_start=1

/transl_table=11

/product="Transcriptional regulatory protein SrrA"

/db_xref="COG:COG0745"

/translation="MKSILIVEDEQAIARVLAAYLRKAEFEVHHAADGPTALTFLDTV

TPSLVLLDVMLPGMDGWDLLRIIREKSACPVIMLTALDDISDRLNGLNAGADDYMSKP

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GMGYQFWIAN"

CDS 1628230..1628946

/gene="yccI"

/locus_tag="EFAGFIKM_01450"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00780"

/codon_start=1

/transl_table=11

/product="Protein YccI"

/translation="MNKKAKAWLITGVA AVAVIGGGGYITNSYLGNNVEIEQVLPAS

TATSTTAVDSTGTVVANETAGAEQLNGDWSISEGSKVYFSVTTSQETVNFVEDMVTGN

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CDS 1629204..1633583

/locus_tag="EFAGFIKM_01451"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
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LEFKVWGEAEGTEPANIKGYDEIEVRTVTRSAPILPNEVKAQFQNEKSGMVPVTWDHI
DPMQYASAGEFTVTGVVYGAPPEPQLKAKVIVEGYRADYVRGVDISTLTAIEDKGGKY
VDSNGTERDLLDILKDRGVNYVRLRLWNDPQKSGGYNDKDDVIRLAERVKKKGMKILL
DFHYSDEWAHPGQQLRPKAWEGLSPEELKQAVYNYTYEVVGEMKAEGAMPDMVQIGNE
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WIPAGVGWIASEGNAWENQAMFDYDEFPANGGHSYEGRALWSLDVYKRGLSLLPADRQ
QLDAALTRAESLVQTDFTLDSWVTLAPAISTANDIYEQAYTPGGVTQADTAATAALE
RVMQQMQVITPQLDELRAKIAEARTYQQTDWSAATWAVLTKALEGAEQVLNDPRATQT
DANTAVKRLHDAIQGLSNVDKTLHQYIQQMQQTKSSYTRRSWSVLEESLQAAIQVR
DNNAVQSEVNSALSTLKQAFITNLVSLEALTGKTATASSSAGTGGNQANSPEGIDN
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SDVVVSTAPSHVLPEGTEGRYIRVTIKTGPTWVGFMFEAYGTFPADKTALQATVDAS
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GPGQPSQPSEPSQPSNPGTAPSTGNPAVTTPTPEGNPPAKGLITVKGTATGDDKYSIR
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GQTTVRVPLRSLPLIAETAGTFDIVVAKGSTDTLSTSQKAVIGNHTIVDVNLLMNNK
PLQWTNRAVEVALSNVEQPKKNDVAMVMHSISTSGEMKPVITYSKYDDKTKMTFKPLG
SGSYVIAEVEVPLNDLQNYNWALQEVQNLGKGIITGMSETRFAPQGELTRAQFLQMI
IKGIGDTRQPDPSISVPTDVKEGQWYADSVRLGMEIEIQGRADGSFGANERISREDM
AVMLNRLKVVQHDQDATNAVQGNMVFVDNAEIAAYAKEAVASMQQQLGLLNGMPDGT
APKETANRAQGAVAVARLMEQLY"

/locus_tag="EFAGFIKM_01452"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MFGFRFAKFQPSEYVMKVKNGEVQRQGVGLSFYYYEPTTSVVVL
PVSSVDVPFMFEEITADYQTVTVQGQLSYRIVDYLKITQSLNYTYNLRKNRYISDDPG
KLDQRVITIAKVLTKKHLEQMPLKEAIQSSERLASSMKREVVQSEELEKLGVELMSLS
ILAILPNKETMRALEAQAREEILRQADEALYVRRNASIEQERRVKENELNTEIAVETK
KQQIRETQLQAERSVKQKQNEMEQLQFNTAMEERKQQLIELTIANHNAEADAKAYE
IAAVMNSLQNVQPNVLQAMANMGMNSDKLIALAFQELAENAGKIGQLNISPDLLQGLM
SPTSGRDQGGRAR"

CDS 1634890..1635939

/gene="nadK"
/locus_tag="EFAGFIKM_01453"
/EC_number="2.7.1.23"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00361"
/codon_start=1
/transl_table=11
/product="NAD kinase"
/translation="MRLGRREQAEQGGKSVRQQATADDRMSEHKLILVKRRTRLEELV
VRYNTVQQAQFYIERLGADFS DYLEEDRRYRQSVQQAQQLGQLGRVQTIDREHVPNF
IFGEQDIVVVVGQDGLVANTLKYVTEQPLIGVNPDPMRWDGVLLPFTVEDLSFIVPDV
IRKQRTLKEVTLAKVELNDGQYLYGVNDLFIGRKTHVSARYEVRLGTSAEQQSSSGII
VSTGMGSTGWFKSVLAGATGIVGSAAWQNMNSEAEVATASASIHGSKQELNHFNWDAP
YLYFSVREPFPSRTTAANLVFGQIHSKQPLHIVSQMPEDGVIFSDGVEQDFLEFNSGV
EAIIGLAEKRGRLVV"

CDS 1636023..1636736

/gene="graR_1"
/locus_tag="EFAGFIKM_01454"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5HI09"

/codon_start=1

/transl_table=11

/product="Response regulator protein GraR"

/db_xref="COG:COG0745"

/translation="MQSILLVEDDAKLAGLLAAYLTRNGFQVQVTDDFRHVLDEFVEV
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FQYEVVLAKVRSQLRRAYGSYAAVQQEVKVKNGPMILYPERFVLEYDERSTELTQKEA
ILVEALMAKAGRVSREKLLEQMWEDQYFIDDNTLNVYITRVRRKLKELGAEEILETV
RGAGYRVLDLGSSAQGEGK"

CDS 1636733..1637731

/gene="graS_1"

/locus_tag="EFAGFIKM_01455"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A6Z3"

/codon_start=1

/transl_table=11

/product="Sensor histidine kinase GraS"

/translation="MRLFLKDHQMLVGFYVLQMLLVPCVYWLSGEGRPMKIVLYGMLI
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NEMGQLRTSKEQQVFMNRVWHQMKTPLSIIQLTLEDVDDTAGSIQDELDKMRKGLE
MVLHSSRLEQFEGDFRVELLSLHEVLRSSIAENRRLFIRRGITPDIRMEGELQIYSDS
KWLRFMFTQILTNAVNYSDSKSGKKVIITGYKQEERTILDIQDEGIGISSEDIHRVFN
PYFTGERGRQYHESTGMGLYLVREISARLDNRVELFSEPNEGTLVRFSWIHSKYPK"

CDS 1637917..1638687

/gene="yxdL_1"

/locus_tag="EFAGFIKM_01456"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42423"

/codon_start=1

/transl_table=11

/product="ABC transporter ATP-binding protein YxdL"
/db_xref="COG:COG1136"
/translation="MEMLQVSGLNKVYQGVQQTQALSDIHLTIKQGEFVGIMGPSGSG
KTTLLNMVSTIDEPSSGKVLINGMNPFDMMKKELAMFRRRELGFVFQDFNLLDTLTV
ENIVLPLTLDKVKLMEMESRLHRITAKLGIDHILDKRVYEISGGQRQRTAIARSMINM
PSIVLADEPTGALDSTSSQAVMESLEQMNQKEKTTIMLVTHDPLAASYCNRIVFIKDG
KLAAEVHRGDNRQTFQRIIDTSLFWGGNSHELSSVRV"

CDS 1638662..1640623

/gene="yxdM_1"
/locus_tag="EFAGFIKM_01457"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42424"
/codon_start=1
/transl_table=11
/product="ABC transporter permease protein YxdM"
/translation="MSFPQFAFNNIRNRGRAYIAFFLSSVFMVMIFFAYAVFIYHPYV
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LVILENMLIGCLSIIAGIGGGMLLSKFLMLTTRFIGMDDLFPYFPVKAILITIGAFL
LLFFCISLFTLVFIGNKRTLELLTGTNPKKEPKASWFFSLLGFALLTVGFVVLRSGL
NGGTIMTAAVTGIAGTYFFYSQLSVLIIRLLKRNKTVWQGTRLLWISEMSYKMKDNA
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EKDQAQIDRNRFRNYMEGDTLTNLEAGSMQAIVKATDVEPRFATLIYSTGVVLPDE
KYEEITQQIIGNRLSGKVLYQIPAWGHAVPDRHSSEAMVSDQLLSSADTIRSDNASSD
ENYSGLFTTRYGDFERYRQGTALFTFLGIFIGLIFSISASFLYFRLHTDLEADGRMV
HSLSKMGLSFQEMKRSSTVQIAILFFLPIGVAIITLVVVKPFLTEFGITNYTMPVLT
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CDS 1640764..1641108

/locus_tag="EFAGFIKM_01458"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MMSITSLQEVKTFSEDRFTKRVLFQQGGGVTFVLHFLPGQQLPV
HKHPGTDVILLVEGTGTLILDGKEQAVKQEDVIHCGGEVEFAFHNTGDQEVRLFVVL
NKVPAASYAKDI"

CDS complement(1641251..1641952)

/gene="ntcA"
/locus_tag="EFAGFIKM_01459"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A4U6"
/codon_start=1
/transl_table=11
/product="Global nitrogen regulator"
/translation="MSRVNKDTTAEFLQQFPIFQDLSPDELKQVEDIAISRSIQKKS
VIFSEGSEKEAVFFIRTGIVKAYKTDENGHEQIVSFLKTGDMFPHTGFFNAHPYPATAE
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FLLMLAEQHGHHMGDQVIINLPMTHQEFANSIGTTRETANRLLNQLTKENLLEVDRNQ
IIHDLQALKQQRDT"

CDS 1642130..1642852

/locus_tag="EFAGFIKM_01460"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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GAATFELLGDALNDGGIIPTAIGFTAGAVVYTLFDLLVSAKGGAGRKRSAKSGESNQS
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GKIILMWLSVLLISAIAALGGYLFLEQLPEEMGAAIGAFAGGGIIMICSTMMPEAFE
EGGPVVGLIASMGLLVSLLLDL"

CDS complement(1642984..1643685)

/gene="fnr_2"
/locus_tag="EFAGFIKM_01461"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9EXQ1"
/codon_start=1
/transl_table=11
/product="Anaerobic regulatory protein"
/db_xref="COG:COG0664"
/translation="MICTHEAKDACFSKVSLFQHLDPSEAALLISLLHTRKYNRGEV
VQEGERSDTLYVWHQGCVKLSKYNENGKEHIIRFLFPGDFFGQDSSLHQBPHAANA
EV
LEPSAICSISKHDFDQLEHDPKLAYHFLLAISKLLRETDEWNSSLSAMTTEQKIAKL
LLYFHTRNHAKHEIRLPVFKKDMALLGITPETLSRKLTMMQTQGLLQVTGNCILILQ
LEQLREKIEPPARIQ"

CDS complement(1643742..1644740)

/gene="aniA"
/locus_tag="EFAGFIKM_01462"
/EC_number="1.7.2.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q02219"
/codon_start=1
/transl_table=11
/product="Copper-containing nitrite reductase"
/db_xref="COG:COG2132"
/translation="MFSLLNVYKWSLVFAIFTATLSHCSSTDVTKPVHHDEVSSSSSS
AISQPPVDPIIRREGTTVYIEMTAQVTDVEISEGVIYNWTFNGTVPGPVLRVTEGDT
LVFTLKNKDSSLPHSMDFHAVHAAPSSKFIDVMPGEEGTFTYPTSSPGVFMYHCGTKP
VLAHIANGMYGMIIIVEPKAGYPSAHLIDREYTLVQSEWYKEHDYEAFLNGEPDYVVFN
GNDYGLVKHPLLAKVGDTVRIYVSNAGPNEVSSFHVVGTTIMDRVYTDGNPRNIQYGIQ
TVMLPASGGAVVEFTVTEEGDYAIVTHQFNHVAKGAAVLRVTKDGDHGGPAMSH"

CDS 1645020..1645496

/locus_tag="EFAGFIKM_01463"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MKRFEDEGAYKYSFYSLRRGERIDVKPCNCGGHASIDQRNGQL
GWKCYECYAQAFEEPVYQYKAKGNCAVCERWFNVEVTDEKKTSHRSTHVECPHCGSMN
REHLNYLIAYVSADLRVKYGNMPIRTASHSIPAYIKDAKNRDVWVRTLSKLQHKTG"

CDS 1645542..1646192

/locus_tag="EFAGFIKM_01464"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLRVKLTIFAILGMLMIPAYFILQTFGVFQKETVLS DYALAV
DVNGKSYGAWPLINSYAAMDKEEDNRQFYRIDVSHIQYLFNLAYQEYEVKPGGDNPY
LAGTVNIEHTDHAYVHTEKKYENANDFRTVLNLYDQDGQVIYSYDNTGKGDKQLVQSI
IHQGMSRNSGGSSEAARDPYINITALFRDKLNIDVKLTVDEEHKVVTIRMNKSEAR"

CDS 1646192..1646749

/locus_tag="EFAGFIKM_01465"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNEYGVQHGPAYLEGLIRKEADIKSDEVEWKGKLQTS DGHDKFH
IFYYGDLTEDDLITWHDSTPLLVAEHTVTGERYLLIDTAKHGYDAMLCETYSEKALH
DRPLRPYLDVEGEDIFEVELTAYYNVPWDEEFAEDVDKNGAYELITGERMHFDQVKRD
GYDAFAIRILNRKGVWTEIVQEELA"

CDS 1646795..1647529

/locus_tag="EFAGFIKM_01466"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYIVSRVLKPVPTTELDHFEQQHGISLPLSYRTWIEHYGEGTYT
GWMNVQRPDPEVLKPFVEYDFWIHTDDSPISQHQLEQCISIGSSVDGDFLAVHPEVEG
LLWLPRHDENITLWTCSETFGETLDRIYCGYYHQDKPITPLYFEPWNELRKHTFYHF"

SGTEQGSSMKELADTCKTEFKWDAVLENEYMCKMFMVSMGGYLRFNATGREVALFYE
EKNGAEEATDNEISLFLQAAHHCTAYE"

CDS 1647551..1648852

/locus_tag="EFAGFIKM_01467"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSWLKEDIAEQWRNEGKRYARDVNAFVRRSMQGEQPDESELEGD
SRSGMSTEVFQMVRQANLHGDLEMLRRELPAATWPLNEAFQASMQAVKVVGYLNEETI
VCNTGIFTENSQIYTMDQHGWQLISPYTFAGCSSDGLDYTLAGPEGIRVIRQPDRKLE
GQEIATFRWEDIQARIQSALPRIESLADCEHPERTLEGIIPMDEGRALLIHSRYGIYL
VTQDQLTLLHPDLAEIEEYELEDTQIDMGHAAVSRDGRWIAYGSQGSNHMVMMDRRLSK
TYSLYPESSYPHYAFTSDNQTVWFNACHFYNGVTIQVQLKSIAGNETKEDWPVMDEN
ARVYAAVEIEAGMVLGDAYGYLYCVNDKGEEVWRHFVGSTIYSLAVSPERSKLAVGTY
GGMLHVLDLRSKKMDEYGIGTGTLRELERYVLWRGEEPLRW"

CDS 1648906..1649307

/locus_tag="EFAGFIKM_01468"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLLKCHAFSYEDLSHPKMENGFLRSLRPFRGHLIEENFHELMEI
LQVLAPELARPSLDREVMACLWGITHMARAWAVETDGMLRSNNLISDEQVALMEQWLN
LLSYAVMILIEGGGEEEEAFWEYHQYLQEEKN"

CDS 1649329..1649934

/locus_tag="EFAGFIKM_01469"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEPNVTLYVLMDELNRLLDDEKIQDQEIRQLFEEYQQREGASEES

LDLFEKEYGVRLPGDFRAFYQRKDGSYGLHVLVSGDAETGRCTPFYLMSEEEIRETK
QYFCEVDEKLEEYSAEEISQLDPEIKPYLFHKPWIPFATIAGGSLYMLDFDPTAEG
TYGQVIMYVHDPDFVYYLTPTFTDLLSMSNRNLKMMDEITY"

CDS complement(1650026..1650370)

/locus_tag="EFAGFIKM_01470"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAYGPGSVSSPQSAGYPYPYPPPPYPYPYPYPYPPIVPVPLP

YPIGGPWWHGGYPGGGHPGGHPGHFPGGGYPGGPHGGGYPGGPHGGGPGGPGGHGGPP

GGGFHGHRRFFQW"

CDS 1650486..1651538

/locus_tag="EFAGFIKM_01471"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVAVAFHTDPRGTAYELLIDELIEKADRFMLVDRQRYEENEIPE

VARVLERLKPYLVERATMEEMMLKSGAYYSEGTYTYRCTPESGQVLKEEANRFHDWC

YPSLPDDLFCMTEDGNDYFFSVAHEHMYGMRITYKEASELMERIPGLFFELDRHKEID

HLLDDAIRHQTDKLDISLHGLSELPERIRELKHLKELTIFEQNLVSLPAGLFELTSLE

RLVITTLDLERIPAEIGKLKQLQELRIYCGSPFESAPGWRPKPQTELGLNCIPPEIGE

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PFGTHWEEVWEMKKNM"

CDS 1651689..1652486

/locus_tag="EFAGFIKM_01472"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MATSYMDYTLPTTEFTYDLSNNPLFKKDENVYINALSIKQLNTL

GNVSLLDIFLNTGNVVEPHTHQNATELVYCINGAAVVS LINPFTNELLHFPITPGQVA
NVPQGWWHYE VATADHTHLLAVFDAPVPEAIFGSDTLRLTPAKLLAYTYCLDEKKVQE
ALAPIQKTVIIGPPADCQPSTAPASNSVPNENHQPYVMPNVQPNVQPNMQPNMQPNMQPNTQ
PNNQPNMQPYVNRLPYWGTWVDPRIIHEPGCPYYRELPVNTNNQEER"

CDS complement(1653177..1654223)

/gene="ndmA"

/locus_tag="EFAGFIKM_01473"

/EC_number="1.14.13.178"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:H9N289"

/codon_start=1

/transl_table=11

/product="Methylxanthine N1-demethylase NdmA"

/translation="MITSNANRNVTSELPRGCTFTAEDWHVLSQYWYPVAQATEVTDK

PLAAQLLDVKLVLYRSNDQVVVAKDLCFHRGAPLSKGWVENGEIVCPYHGFRYNCEGK

CTVVP AHPSSKISP KKLIVYPAVERYGLIWTTLAGTEEQIPSPGWDDPDYINILPP

NFDIAGSSGRQMEGFLDVSHFAYVHTETFGDRNNTVPQYKVKREGNELLA EYWSTVS

NYGKGQDLVAPEGFQWLREFRVFPF AASLTVHFPGDDKLNILNCASPISARYTRLFC

PITRNFDKDAPIEDTIKFNLQVFEEDRE MVESQKPEDLPLDLHAEAHIPADRTSIAYR

QLLTELG LGRNYTS"

CDS 1654632..1655078

/locus_tag="EFAGFIKM_01474"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNLRTNYRVASPGAFKAMMAMEQYISGQFENKVL YELLKIRVSQ

INGCAFC LDMHAKDLMKLG DYADHILLSSVWREVAFFTDQERVMLELA EAVTRISEHG

VPLALYDKVREHFSESELVDLILAI NTINNWNRIAITTGMYPGCFN"

CDS 1655112..1656047

/locus_tag="EFAGFIKM_01475"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNSNLHANEPDVSSLDVGELYIRYKKYAFSIAYRMLGSVVEAED
IVQDCFAGIQSTSAQDIRNPKSYIARLIVNRSLLNSARNQRESYVGEWLPEPMGDS
EEANMPEETMEKKELISYAYLVMLERLSPMERAVFVLREAFRYDYSEIADWLGKTESN
CRQIFSRARRNLPERLPPIEQSDADMIAKGELLSRFTTAFLRYDVSAMLELLADQPVF
TSDGGGVVHTVMRTMNVHKGVLALLTSRRVLTRLREREWVPMCINGELQLALMKEGQL
SEVLCLELDTSGERIEGVYLVVNPKNLTSIDTSTL"

CDS complement(1656147..1657100)

/locus_tag="EFAGFIKM_01476"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRWKQPAKLGLLAMALGCTAIGAIITPSTTLAAPVPASKAVYHQ
FQTYRTEAVKSTESLVKARKYLMNHINKVGPWQATLMTLQLENMQNVKLADVDYQMYT
EHFQQAISQAHEQLGYEQKLTYGRLLEIKDPTVKKLLQEASDLGFKLETSEGLYYPI
INYEIQKFKPFVKADIAAYIDIMATESNQMTTSDGGIIISWNELIQRALEKEAFLNN
FPNSNRSAVKQGLFVDYLFYGSNTPAYDWYTDEEIRTM DPVVKQAYEKALAYREPD
TQSVLLDTMEKILLVLNQNNDELTPEVRAIIEPVQQQFARE"

CDS complement(1657341..1657997)

/locus_tag="EFAGFIKM_01477"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNPNSMNPQNAVQPTLNTNPNVTPNMNHGGHEMFDVHEILSSTI
NVLDQYMIFRTFVQSQELIGILDRQYNFILSQYNLTAECFASGQKPHQETATYMIPNM
VPPVYGLKPSAPKKPNQSLADV K DAGISGHMLGLIKSHASLLGMSCSEITNGTVRRVI
ASQIQHFIEMAYEIFMFQKNAYYQVPQLTPSDTQQMLQAYIPATGAPQMPNSNKPLH

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CDS 1658122..1658658
/locus_tag="EFAGFIKM_01478"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEETDWGVAKELFVKHYGSAIQIHREGVYADYKRWDVPEELEEQ
WIGERIQQLSSELSIMNWDVDELALIAKHRTEPSIIKEITAFASRQLKSADSMVRLV
YAERLIELIKRYESSLPMDKLRETYQLTMDLLVDVATKPLVLDPGHELQQYGLKDKRG
LNLRVEKNKEEIIRYFRN"

CDS 1658688..1659416
/locus_tag="EFAGFIKM_01479"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRKLNYIHIFILSVVTIVTLGLYYVAADWLDQRYFRFLIWNLF
LGWIPFVFSYAAYVLSVDVKWKGAAWLAVASGLLWLLFFPNSSYIVTDLVHLTARSSRY
YGGNGVDYTYWYDLSVLLMFVWTGLLLGLFSMYQLQEVIYHRIGRWASWIFVLVGCAL
GSYGVLLGRVYRLNSWDALTNRETLIELMHESVSRPSLAFCLFFGTFTTIYATLYYL
INTRSPRETKKSAGSPETDLQALR"

CDS 1659605..1660207
/gene="pbpE"
/locus_tag="EFAGFIKM_01480"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P32959"
/codon_start=1
/transl_table=11
/product="Penicillin-binding protein 4*"
/db_xref="COG:COG1680"
/translation="MLNAVELTTKVEEVMERVNFSGVVLLQQAGKTLLNMKRGYANRS
EELANQVDTRFGIASGCKIFTAVSVCQLIEAGKLSADSKLTDVLDVEFPLWDKGITIQ"

QLLHTSGIPDYFDEEVMDDFSELWKDRPVYAMRRLSDFLPMFQHLPMKFAPGERFHY

NNAGFIVLGLIVEQHSGLSFTDYVEEFIFKPCGMKNSGYF"

CDS 1660177..1660626

/locus_tag="EFAGFIKM_01481"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MWHEELRLFLTDQLPRNTALGYIDHEDGSWNTNMFSIPVKGGSD

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CDS complement(1660713..1661693)

/locus_tag="EFAGFIKM_01482"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNPSALSSKLQQIVPQLDLRSCLSVRGEIMFEHYRNQEAATDI

AKINSCTKSVLSALICIAMDKGLLPEASAPISTFFPQLTSDPDPRKPAITLEQLTMT

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GMNVAEFAERYLFDPLGIKHYEWESDPQGVHTGGFGLKMLPVDLLKFGQLFLQQGMWE

GKSLISSDLVSRSTQPFITVTPPNHGSYAWHWWVDVYPNERSDSENIAAEDDKPNLHY

YYARGFGGQYVYIVPEFELVTVLTNDKRKKEKPPLDVFPRLIAPELWKML"

CDS 1661945..1662214

/locus_tag="EFAGFIKM_01483"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGNIIEELYGNLRPEENIVPKDSEYRSINKEITASIEKFQSKL

SEDDFKQLEVLFDMMDQVHSIHSKEAFASGFKIGTLIMIESGYSS"

CDS 1662280..1662534

/locus_tag="EFAGFIKM_01484"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MFKIGNQGLFETLPDHARAIYEGDTGAVEQFIKQGMDLEEEIPL
SKYIALTSLDLALICNQPEVVKLLVERGVNLNVKNNTVIL"

CDS 1663016..1664368

/locus_tag="EFAGFIKM_01485"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKVKQISFILTFCLLANLALTPMASAGDSSNLIGFRAELKAIA
YKTYTFFEEYTDQNTGLTYDEV RHTENGIEEAKRTSPTNIAMYMMSTVSAQQLGIISK
KEAVHRLQTTINSLEKLEKWNGLFYNWYNKDDGSGVKKDWGQFISQVDNGWLSAGLIVV
GQAYEELHGETSKLVKNMNYTPLYDPEVGQFRGGYDAKGALTDHHYGMFYTEPRVGS
YIAIGKGDVPQDHWKMYRTLTPQEW DWQAQIPQGKSVKYDGVDFEGSYVYKDKKFVP
SWGGSMFEALMPGMVIEKDLGTQALGLNNQRHVELQIEYAKEKGYAAWGFSPSATPT
GYSEFAATPLGTSGYKDGATVTAHATFLALDYAPEAVRKNIKALKNFKMVGKYGFYDS
VNVETGELAKAYLALDQGMIMVSIANYLQDGVIRDYFHSDVIGQMPEELLKKEVFSIQ
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CDS 1664874..1665824

/gene="yteP_6"
/locus_tag="EFAGFIKM_01486"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:C0SPB3"
/codon_start=1
/transl_table=11
/product="putative multiple-sugar transport system
permease YteP"
/db_xref="COG:COG4209"

/translation="MKESHTVISVSPSLKKNSLGKRIWKNWELYLFMLPALLYFLVFH
YGP MYGIQIAFKNFVPSKGITGSEWVGFDHFERFFNSYFFWDLWNTFSISFYELAIG
FPLPIILALAFNEVRNGPFKKSVQTVTYAPHFISVVVMAGMIITFLSPSSGMIVRFIE
FIGLEPAQFLTDPAWFKTVYVFSGVWQSTGWGTIIYLAALSGVDPQLHEAAIMDGASR
IKRVLHINLPTILPTITIMLILNMGNILGLGFEEKILLQNSLNMEASDVISTYVYRAG
LVNAQYSFSTAVGLFNSVNVILLVTVNQIAKRTSENSLW"

CDS 1665841..1666752

/gene="dasC_1"
/locus_tag="EFAGFIKM_01487"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9K489"
/codon_start=1
/transl_table=11
/product="Diacetylchitobiose uptake system permease
protein DasC"
/db_xref="COG:COG0395"

/translation="MVTAMKESRGDKLFLISTYIYLGLSLLVLYPLIYILSASISSP
QDVNSGAMWLFPKNVTLDGYKLVFENPKIWSGYWNTIIYTVVGTLLNLAVTLPASYAL
SRSDFVGRQLFMGLILFTMFFSGGIVPTYLLVKNLGLMNSMWALILPVAASVWNIVVA
RTFFQTTIPKELQEAAHIDGCTNLKLFIRIVLPLSAPIVAVMALFYGVSHWNSYFPSL
IYLNDEAKYPLQMVLQRILVLQEMTAETTGSINGEVATAMNNKAETASLIKYGVIVV
STLPIVAIYPFLQRYFVQGVMLGSVKG"

CDS 1666791..1668410

/locus_tag="EFAGFIKM_01488"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MPTTSKPWKLLLSSALVLTLLAGCSNSNEGEANNNLGKVAVNNE
GFPIVNEPVTLSLMAPDVGIQNWENMAVLQQMQEKTGITLEYKNAPKDSFETKKNLVL
ASGDYPDILYAAGLTAEQMNYGEQDILIPLEDLIEEYAPNFKALLEENPDVRKSITA
PDGHIYSLPVVELSQHWYRNPMWYNGDFLKALNIDKLPETTEELYTYLKRVKEEDPNG

NGIADEIPISSVTPAANLRDIRTWLLGAFGIYEEEEIYVDDADKVHYTPLEEGYKEYL
TYMNRLWSEDLDDHESFSQTAEQKKAKAQNNQIALFSDWHAYMSKGGEPSTADPMFAP
VHSESVAAPAIKNRGITSGAFITQSNPAPEASIRWVDYLYSYEGAMFFNKGPEGIL
WEYTDKENRVKQYLPVPDGKEMEDYRATLTPNYGIPAPTLSDINKGLKTDFFDLWVE
QETKQKLLDKGARIPFPTLFLTVEEQTEISSLNSDLKTYVNQMEAKFITGAEPLTGWD
NYVATVKKMGGERMVEINQAAYDRWKSYPEH"

CDS 1668428..1669459

/locus_tag="EFAGFIKM_01489"

/EC_number="2.4.1.281"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00928"

/codon_start=1

/transl_table=11

/product="4-O-beta-D-mannosyl-D-glucose phosphorylase"

/translation="MQITRHPNNPIVPPGGYEWKVTVFNPAAVVIDNGKFYMIERTAG

SLTPCKNYLGLLESEDGVNFIHVKDEPIVTPDMLGFPYGSVQDPRIVKIDGTFYLNIA

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DINDRDNILFPEKIGGKYVLLRRPEEYVGEAYGTDKAAMWITYSEDLVNWEEPKLLAT

AQNLSWESRKIGGSTPPIRTDKGWLVLVYHGVDIVYRVGAMLLDLEHPEKIIARTH

FIMEPETYYEKFGFQIPNVIFPTGNVVKDGLLYIYYGVTDIAIALATVPLDELVEHIL

QEGQQQNKP"

CDS complement(1669519..1671855)

/gene="rhaR_7"

/locus_tag="EFAGFIKM_01490"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MANSALKPSLRNRFRFSWNHFKSRLLLLKYAFSYILIFLIPLTGV

TIFVYENAVKGLRVEIEQSNVNQLNQVKSTIDNRMNELQEIAGRIAYDKHLTPYMVQH

QHPYYSLEAIQALANYKASSSIAEDLLLYFHNDNSNIYSYRGLANLDVTFDSLYQFEHW

NPEELRRDLNETRQPLVRPAENVKVNSRMESMLVMLVPVKPNDPPFYGTVVYLMKESN
LTGVMDSILSDFSGSSYIFSPSGEVL TANS HGISLPQDEIENLATLGPGIHNLKMDGE
QYSVWSVQSEENGWTVYTTMPSFQFFSRVAHVQTLILIVFCITVITGIAAALLAKRQ
YHPIRDLMDRMKSGDNAPKLRNEWEWIRQTLHNYSVKIDFQEPFVRNQCMLLLLKHG
KPDDPEIEQMILSAGFRHPQGQGLYFSAILS WDDTVPDGN SCQERHLLQDILSNVCLP
GTGAQIFGVEFSVKDQFALIVSLPGDADKPIQSQLEQVIEAIQTVIREHSHLSLSIGV
GMAYRDLTRLNQSFIEAAA LEHRIIRRS GQVTYFEQLAELSPSASESFWIPRKSM LK
LEQSLKQGNESVAVQMIADTIHTIKDEPLQVHLLRCICFDLLNAFLRTASELGMNEVF
ANMPELTSFETLEELESRLLSLAADICTQVELNTKTSESTLMDDVLAYVDQQFADYTL
SLEHVALKFAISTSYLSRSFKEKTGCNFSQYIWQRRADEVMRLLENTSAPLKEIEQV
GYMDAPNFIRKFKKEIGLTPGQYRKEHALRGATT KRPV"

CDS 1672078..1673178

/locus_tag="EFAGFIKM_01491"

/EC_number="3.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q837K0"

/codon_start=1

/transl_table=11

/product="Deacetylase"

/db_xref="COG:COG3964"

/translation="MGTENVLRNLQLVDGRIMDIAIQDGIITAITPPGQAEGENELDC

SGLYVSSGWIDLHVHAVQELDPYGDDIDEIGVKQGVTTLVDAGSCGADRIGAFYTARL

QAATQVFALLNISSIGLERTDELSQLEWIDRAKVM EAAAAYPDFIVGLKARISQSVVK

DSGIQPLKLARTLSEETKLPLMVHIGSAPPAISDVLELLQSGDVITHYLNKGSNNLFH

ADGTPLQELLDAARGVHLDVGHGTSFSAFRIAEQAKVAGIALNTISTDIYRGNRMNG

PVYSMSNVLT KFLYLGYSLEEVIRAVTRSPAEWLGKPELGQIRVGQQANLTLSLEAG

EKQLEDSEGDVRVTQHYIEAKGVFANGSLITG"

CDS 1673156..1674265

/gene="dgaE"

/locus_tag="EFAGFIKM_01492"

/EC_number="4.3.1.29"

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/inference="similar to AA sequence:UniProtKB:D0ZLR3"
/codon_start=1
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SHHAVQKNMISVEEAWEVAQRRGVPLIVDAAAEENLHKYIQLSDLAIYSGSKAIEGPT
SGIVAGKKKYVEWLKVQLHGIGRSMKVGKETVFGLLQALDEYQDKADNSEREKQTLEA
LQPLDRLPGVSVRIVQDEAGRSIFRGRVQIDSSLVGVDAAKKVNDQLREGAIAVYTRDY
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CDS 1674262..1675017

/gene="dgaF"
/locus_tag="EFAGFIKM_01493"
/EC_number="4.1.2.14"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:D0ZLR2"
/codon_start=1
/transl_table=11
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/translation="MSHIQQCLYKNRAAINVLGASIGNAKDVYEAAGYVLVGVLSKN
YATSEEAVVAMTEYGQAIQDAVSIGLGAGDSRQATVVAEIAASYPGSHINQVFPVGA
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LKYYPMQGLKLEEEYRAVAQACGESGFALEPTGGIDLDNFGPILEIALEAGVPQVIPH
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CDS 1675010..1676023

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/EC_number="2.7.1.45"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q53W83"
/codon_start=1

/transl_table=11
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GKVVFDNCRPALWGTGTYVKARPHYEELLRLADLVMNEKDAKCILGIGTGEYDRIT
QMKQAIPEVAQRFGIGTVAGTHREINADHHTSLTGYYQGTFFSRKLTFPVYDRIG
AGDVFAIAIHGELQQYPQEHTVNMMAVAAMLAHTTHGDTALFTENEVLRLSDHTSD
VER"

CDS 1676034..1676756

/gene="dasR"
/locus_tag="EFAGFIKM_01495"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q8VV01"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional repressor DasR"
/db_xref="COG:COG2188"
/translation="MSLKRKQGPLYQQIQKILKDRILHGVYPLGSIIPSEPQLEKEFG
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CDS complement(1676834..1678372)

/locus_tag="EFAGFIKM_01496"
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TSAEDVAELAKLPCLTHIEMDGYTESIFSFIEDNPFINELHIIHHGQTMLDISNSHLT
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LRDF"

CDS 1678534..1679340

/locus_tag="EFAGFIKM_01497"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

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LASYSQLEQGWQSIIGQLTHPSFITNERSEVLAWNEAADTNLFNFSSMTVNERLMMRI

LFLDTALRERMHNWEEFARHSVAVFRTYYDKYTSDFEFSRIVKQLSEESVDFRTIWNL

HQVEFKQVNRVLLEPTDRADGVVYAYDIFSMNNLNSQSGIHCCIVPVAI"

CDS 1679476..1680432

/gene="iolS_1"

/locus_tag="EFAGFIKM_01498"

/EC_number="1.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P46336"

/codon_start=1

/transl_table=11

/product="Aldo-keto reductase IolS"

/db_xref="COG:COG0667"

/translation="MLKTRTLGNDKLRISALGLGVMMMPDNDESHTIQGALDAGVTM

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HAVHPITALQTEYSLWSRELEDEIMPVLHELNIGLVPYSPLGRGFLTGQIQSIDDLP

DDYRRHYPRFQGENFQKNLEVVGLIQEMAKQKGCTVSQLALAWLLGKGEHIVPIPGTR
NLERVHENLGALQVSLTDDMNQIDHISPQGIAAGGRFPGQV"

CDS 1680569..1681165

/locus_tag="EFAGFIKM_01499"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIDPILQAPNVPLAADSNAVVNYQRDSRNYVTQLFGEQLPTIAN

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KGWFHWFVAETDDVYVLTIFDQPTPDIVFGADFLAATPPEVAHRAYCLDEEAYARAVA

SIKNDAILGPPIGCDTQVSDQSTSPSKTSVSPSNKLKS"

CDS 1681373..1682053

/locus_tag="EFAGFIKM_01500"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNMSEMKTLETAMSYAPILMFDRAEPFYPDFVGISVLHQSGPSP

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RGLLKERVNVVGHVCLYSQPGKHAFSPLPVVFELLPNLYSAAGAEAGCDGLLVNELF

QDYFETNEQIDDQVERYLQTKAFVPTMEFEEYILKPEMFMTWDNLFGIIPHRIKDRLM

ELEQLYNT"

CDS 1682602..1683849

/locus_tag="EFAGFIKM_01501"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKWFGNLKTATKIISAFLIVSILAALGVYSVVTLRSTNERMQE

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VLLTNLIDLNESLAEQANIQSQVAYSQAFKVTIILVLSVLFSILIGYIISRSISKP
LMAMLGLATEVANGNLTLSKSDISSKDEVGQLAAALNRMVDNLKELINNIVMNSQSVAA
SSEQISASTQEIASTSTSQSSEAGNISELFKELSLAINSVAASAEAAELSDTVKTA
REGGLVVQTSLEGMQAVNTKMTKLEDDSRKIGDIIVIDDIAEQTNLLALNAAIEAAR
AGEQGRGFAVVADEVRLAERSG"

CDS 1683907..1684191

/locus_tag="EFAGFIKM_01502"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQAVAASVEQSSMTGQAFDQIIDMVNNSQKVNEIAAAACEEEAA

QAAEVMSSVESISASSEESAAASEETAATCQSLAHLAEELANSAAAFKTN"

CDS 1684216..1684641

/gene="cheW_1"

/locus_tag="EFAGFIKM_01503"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39802"

/codon_start=1

/transl_table=11

/product="Chemotaxis protein CheW"

/db_xref="COG:COG0835"

/translation="MSSLQKEQYIELSVGAETCAIRIEEIHEIIMLSITDIPFSRPE

IKGVVNLRGKVVCMRLNLLGMPDEPDNRATRIIVVRHQEEYIGLIVDRVNKVTTYS

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CDS 1684656..1686671

/gene="cheA_1"

/locus_tag="EFAGFIKM_01504"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29072"

/codon_start=1

/transl_table=11
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/db_xref="COG:COG0643"
/translation="MMDLSAYRDIFIEELNDQLERMDQSLLALELSPSVELVQTLFRA
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PQQLKAELSSDSDIHMLEIDPYLLESNEVAATSAPLELIS ETVQSKQSLPTVNTTGPD
EKVKAAQPTVRVSVERLDHLMNLVGELLIDQTS LADLSGSGARKESSTLIRSISGVSD
HMNRVIKELQEGVMKTRMLPIDQLFSRFPRLVRDLSQKL GKDLELVIQGGETE LDRMI
IEELSDPLIHLIRNSADHGIESAEVRAENGKPSKGRITL TSFHEENHVIRYSDDGKG
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SQIGRLNGIIDIDTEVGVGTTFTIRLPLTLAIKGLLVK VSGRVLILPMYNVAEIVRI
SPEDIQMIQGQQAILNHGRIVPFHRLCDRLNYPRTDRK SKTIPLVIVRSVDKIAAYAV
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CDS complement(1686770..1687654)

/gene="cmpR_4"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q55459"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator CmpR"
/translation="MTTNYELYKVIFYWAAKTGSLTQAAKALYITQPSVSHAIKQLEES
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LFKHYMLAYLEEFHTLYPNIKLHL SHGTTPEVITFLKEGKIDLGVRMPIVDPQLEVR
ESIQLKDCFVAGERYAQLKGKVMTLEMLLEHQLILFSRNSRVRMAITELFNSYNYTLK
PEIEVGSDLLIEFARRGLGISYVTREFISKELEEGSLFEIQLDVPLPPSHVGIMTKR
NMPISLAANRFMDLIFKS"

CDS 1687767..1689290

/gene="zwf_3"
/locus_tag="EFAGFIKM_01506"

/EC_number="1.1.1.49"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54547"
/codon_start=1
/transl_table=11
/product="Glucose-6-phosphate 1-dehydrogenase"
/db_xref="COG:COG0364"
/translation="MEPTTIVLFGATGDLAKRKIYPALYNLYLEQKLPETFSLIGLGR
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REAELGIPSNRLFYLSVGPEFFFEPIAENIQESGLGSTEGWKRLVIEKPFQGHDLQSARD
LNRKLSESFTEEEIYRIDHYLGKPMVQRLETLHQSNPIMKALWNNRYISNVQITANET
VGVEERASYDHYGAVRDMFQNHMLQLLMMMAIQLPYNSTSEKVLKKKHIMESIQPL
QKQTVGANIIRGQYAAGNIQGKPVNAYTAEPGVAENTMNDTFIAAKLQIDDFWVRGVP
FYIRTGKRMKEKSTRIVIEFKEPSGQTNVLKNKGSKPNLLVIEMSPDQSMTLQLNASD
PENKGEFKPVHIDLSPDKGDLAEAYENLIRDALLGDPTFFAHWDEVELSWAWVQPILD
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CDS 1689327..1689992

/gene="tal_2"
/locus_tag="EFAGFIKM_01507"
/EC_number="2.2.1.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P19669"
/codon_start=1
/transl_table=11
/product="Transaldolase"
/db_xref="COG:COG0176"
/translation="MKFFIDTANVEDIQKAYKIGVLSGVTTNPSLVAKEGVKFEDRIE
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YLTKKGVKTNVTLIFTVNQALLAARAGATYVSPFLGRLDDISEDGVQLVTKIAELFRT
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TVQ"

CDS 1690053..1691471

/gene="gndA_2"
/locus_tag="EFAGFIKM_01508"
/EC_number="1.1.1.44"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P80859"

/codon_start=1
/transl_table=11
/product="6-phosphogluconate dehydrogenase,
NADP(+)-dependent, decarboxylating"

/db_xref="COG:COG0362"
/translation="MSKQQIGVIGLAVMGKNLALNIESKGFSVAVFNRSPEKTNDLLK
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AYFPDTQRRSKEEEKGFRFIGAGVSGGEEGALKGPAIMPGGQESAYQLVEPILTAIS
AKVGDDACSTYIGPDGAGHYVKMVHNGIEYGDMQLIGEAYHLLKSVLNVSV EELHEIF
TEWNQGELDSYLIEITADIFSKYDSETGKPMVDVILDAAGQKGTGKWTSQSALDLGVP
LSMITESVFSRFLSAMKDERVAASKILNGPATEAFSGDKKAFIENVRKALFASKIVSY
AQGFAQMRAASDEYGWDLKYGNIAMIFRGGCIIRSQFLQNIKEAYDKDAELKNLLLD
YFQNIVESYQGAWREVIAAAVKQGIPVPGFSSALSYYDSYRTERLPANLLQAQRDYFG
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CDS 1691718..1692821

/locus_tag="EFAGFIKM_01509"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"

/translation="MFVLAGILFLVYGLLVFYIGWSGWSWMKPVVSARFRWFYIIAL
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KWAGVVTLVLLVSTLGYGIFNAYSPVVRMYNIQIDKKVEGVDKLNIVMAADMHFGLLS
GPAHAKRMVKEINALKPDLVLYPGDIIDDNLDMYLN SGIADIISEIQAPYGVYASLGN
HDKFDGPIEDLIAALEKSNMQVLYDDKIVLNDKITLIGRKDRTEKDRAEVATLMQGT
LTQPVLMMDHQP YDLDAEQNNVDLVVSGHTRGQIAPAQFITQAIYENDWG YLQKGS
MHSIVTSGFGFWGPPIRTSSRSEIVKINVT FQQ"

CDS 1693155..1694009

/gene="licT_3"

/locus_tag="EFAGFIKM_01510"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39805"

/codon_start=1

/transl_table=11

/product="Transcription antiterminator LicT"

/db_xref="COG:COG3711"

/translation="MIIKQIFNNNIVSTVDDKNQELLILGRGIGFKFKAGDEIDEERI

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FAVQRLEKGMITRNPLSWEVQHIFYKAEYDVAREALTLLKERLDIEFPKDEICNIALHF

INAEVNDISMNDVTHLMQLLQEIMNIIKYHFNVELDEDSVNYFRFITHLKYFCQRVITH

SSHDDAAEYLYEVRKNYPETFKCIGKIETFIHKNYQYDMTHSEQLYTLHLERLMKT

KRDEKSTQ"

CDS 1694142..1696061

/gene="bglF_4"

/locus_tag="EFAGFIKM_01511"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P08722"

/codon_start=1

/transl_table=11

/product="PTS system beta-glucoside-specific EIIBCA
component"

/db_xref="COG:COG1263"

/translation="MKHQETAQEIIKAVGGTNNINSVYHCVTRLRFDLKDNEKVDNGS

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GGFALAFGAKAYVLAGNGGLPGLPSLIGQTFWYSFGGMILAFIVGAIMSTIFGIKEEE
GDAEALAQFSPGASTAPAKVVSNEAATVNVDDMGDPTPTSDAVAVAPMTGKSIPLKEV
NDPTFGDELMGKGVAFVPTVGELVSPVTGTIMNVFKTKHAIVVRSDNGMELLIHVGIN
TVKLRGQYFDAHVATGARVQAGDKLLTFELAEIAKEYDITTAMVVTNTADYKQVLPVK
LGEITMGEDVLKAEI"

CDS 1696111..1697574

/gene="bglH_5"

/locus_tag="EFAGFIKM_01512"

/EC_number="3.2.1.86"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40740"

/codon_start=1

/transl_table=11

/product="Aryl-phospho-beta-D-glucosidase BglH"

/db_xref="COG:COG2723"

/translation="MINRQGFPEGFLWGGAIANQAEGGFDAGGKGWSTADMVPYFEK
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AGREVIGHFVRYAETVMNRYKDKVKYWLTNEINTTIIIEPFTGGGIIEDRVENTMQAS
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HTDVQVRGSYPTFMARYWAENGITAMEPGDEQILREHTVDFISFSYYTSLVSAVNPE
EYGVTTGGNLYSTIKNPNLERTEWGWQLDPIGLRVALKELYDRYQLPLFVVENGLGAKD
TVEADGSINDDYRIDYLRKHITQMKEAVMDGVDLMGYTNWGAIDIISASTSEMSKRYG
VIYVDQDDNGQGTLNRYKKKSFGWYQKVIASNGENLE"

CDS 1697742..1698308

/locus_tag="EFAGFIKM_01513"

/EC_number="3.1.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8CTG7"

/codon_start=1

/transl_table=11

/product="Putative 5'(3')-deoxyribonucleotidase"

/db_xref="COG:COG4502"

/translation="MKKPIIAVDMDDTICHLVKRAIYHNNLNFPTHPLRYEDMIHWDT

SHLRHPESTHDFVYGRPGLFEELELYDEYVVDENMRKLNDAYDVIVVTAAEPRTVVEKW

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RERYNFPLMSSWKEAKTYIDEVLQVVGW"

CDS complement(1698318..1699202)

/gene="btr_3"

/locus_tag="EFAGFIKM_01514"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40408"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator Btr"

/db_xref="COG:COG0614"

/translation="MNSSVQLMKSEYFLHNHLQLFVNRCSEDFVLPFHAHDFIEYSYV

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LVSQVLVMTYRQLNQEVHDEEIHSTDFEYILHYLKQHVSNRIRMSDLVRVSGWSEKQI

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GETPLAYRKKSRAQHSGQ"

CDS 1699337..1702066

/locus_tag="EFAGFIKM_01515"

/EC_number="3.2.1.40"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:T2KNB2"

/codon_start=1

/transl_table=11

/product="Alpha-L-rhamnosidase"

/translation="MFNVSHLRCEYRFNPIGLDVKSPRLSWQLQSDRRNCMQSAYQIQ

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GWVRFISIQGEAGQTVELHHAELDHEGNFYTDNLRAAKQCIRYTCKGDGAESFEPHFT
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LDVPTDCPQRDERLGWTGDAQMFVRTSSYLMNTAPFFTKWLRDLEADQGEDGGIPFFV
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QGDNPYLWNTGFHFHGDWLGLDSKPDSYVGATD TDYVATAFYAYSVS LTQKAAEALGKK
DDAEYYKQLHTNIVHAFRNEFVTPAGKIAVPTQTAHV LALQFDLLDATARTRAVDQLA
KLVKEAGNHLTTGFGVGPYLPVLS DAGLHELAYTLLFQEDYPSWLYQVTQGATTWE
HWDGIKEDGSLWSADMNSFNHYAYGAIGEWLYRYVAGIRSDEHQPGFRMVHIEPQPGP
GLDWVEASLETMYGQVSSSWHRLAEGEMEIRVHIPVNTRGTVRLPGAGA QIVLEQGKP
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CDS 1702182..1702658

/locus_tag="EFAGFIKM_01516"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS 1702633..1703172

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CDS 1703217..1704401

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CDS 1704567..1705127

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CDS 1705185..1705490

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CDS 1705715..1706554

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CDS 1706722..1708659

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CDS 1709105..1711018

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CDS 1711053..1712495

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/codon_start=1
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CDS 1712810..1713208

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/codon_start=1
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/translation="MNMDKITRTNPENMPAPVGQYTHITRIPNAELFVTSGQIGADH
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CDS complement(1713329..1714486)

/locus_tag="EFAGFIKM_01526"
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CDS 1714707..1715228

/locus_tag="EFAGFIKM_01527"

/inference="ab initio prediction:Prodigal:002006"

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CDS 1715286..1715744

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/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS 1715819..1716679

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CDS 1717082..1718287

/gene="fenF_2"
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/inference="similar to AA sequence:UniProtKB:Q9R9J2"
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CDS 1718561..1730494

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CDS 1730528..1740349

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KEITDIEIHAGKSNIGKPIPTLQTYILDKHQRIQPIGVQGELVVAGEGLARGYLNRPD
LTAEFVDHPWITEGKMYRTGDAARWLDPGNIEYLGRIDHQVKIRGYRIELGELETAL
LQIESIQEAVVIAREHKDGSKQLCAYWKGDSSTAKKIRMALSHEIPDYMIPSYFVQL
EHIPLTSNGKVDRKALPSPQEHMQKGTEYMAPQNAVEQAIVAAWEAVLGVQKVSTSDH
FFELGGDSIKCIQVSSRLLQAGYKVEMKHFFTYPTVAELSEHVTSVSTISDQGEATGQ
VMLTPVQRWFFDQNMVDTHHYNQEMMFFREKGFVRFIHSIMDKIVKQHDALRILYRQ
APEGGYEAWNREGADEEGLYSLEIVDLKTEADPASFIENKAKEIQSGMDLSHGPLICLG
LFQCAEGDHLLIAIHLLVDGVSWRILYEDIQTGQDQFLRGEEIRLPQKTTSFKQWAE
QLSTFADSPAMKQENPYWSRVEQAQLSPLPKDMDCDETIGKDSETITIHWTAVETEQL
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SFNYMGQVNQDSGQDGIKFSHYSSGPSVSENNKRPFVLNINGIVTEGRLSLSINYSSK
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GRIENVYPLTPLQKEMLYESERNPISGAYFVQIMFDMRGDLDVTSFAQSLDQLMQRHA
ILRTNFYSDFVDIPLQIVYQEKKEFFNYEVVAGTSELQRKTYVDEYIEQDKARGFDLQ

RDSLIRMSVLRTKHEEYRVIWSFHHILMDGWCMSTLSKEIFENYFAIRENRKPQVTLL
TPYSQFIEWLEQQDHQGAITYWSHYLDGYEGQTKLPGEKIKPKHERQDSRTLNCYLDD
VLIEQMKQIAEQQHVTLHTVVQTVWGVLLQQYNESNDVFGSVVSGRPPVIPGIESMI
GLFINAIPVRIQTQADESFISLMKRNQAKAVESHAYDTYSLYDIQNQTKQKQSLINHV
VVYQNFPVENRMESLGQKGETPLEIMNVGGTEHNSFDFTLIVKPHENMKIILMYNANV
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CDS 1740912..1741094

/locus_tag="EFAGFIKM_01533"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MDIAALSMAMSQASVVQSASLQVMSITKDMAQQGQQMAEMLKS

MPAPHPNLGGSLDLSV"

CDS complement(1741238..1741975)

/gene="gph_2"

/locus_tag="EFAGFIKM_01534"

/EC_number="3.1.3.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00495"

/codon_start=1

/transl_table=11

/product="Phosphoglycolate phosphatase"

/translation="MAANKESNGLGAPNDDIIQAVIFDMDGVLDSEPIYFEIERSSF

THFGARVTDEEHHTYVGVTLESMWQQVLDKHLTATLEEIYAYHQHNVMQTMLAHSNL

TAMPSVERWLSWLHEQQVPIAVASSSPRALIDLIMDKTGLGQYFEVRMTGEEVTNGKP

APDIFLTTAEMIGASPSNCLVIEDSRNGVQAASAGMRCIGYRNPGSGNQDLSKADLQ

ISSYDELWTLKDTLPFEGRLPSLSKFR"

CDS complement(1742047..1743096)

/locus_tag="EFAGFIKM_01535"

/EC_number="1.1.1.407"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A9CES3"

/codon_start=1

/transl_table=11

/product="D-altritol 5-dehydrogenase"

/db_xref="COG:COG1063"

/translation="MLALVYKSAWDVALED RPVPEITRDNQVLVRIRATGVC GTDLGI

VSGKYHAVPSVILGHESAGEVMDVGS AVTTLQPGDRVIDPTY YCGQCDMCR TGRQNH

CTHKS VTETGVSADGTFTDYYVTEDRFLYKLKEHVS YEEATLTEPLSCMLTG INQIHL

LPNFR TIILGAGPIGILYSYALASKGVTGCLVDISEERLAIAGSIAPDRWEVHSSFEN

AIESL SPATQQVDMIVDTTG VVG TQVLSQLASGGY LMLVGLRDGNTS FNPKEV VDRSL

KIIGS IDSLGTFATAHYMIEQGIIPAKKIITHSFPLEDYEEAFRTLGC DIQGRTLQAS

SHAIKVVLQSSGSSF"

CDS complement(1743366..1744604)

/gene="dat_1"

/locus_tag="EFAGFIKM_01536"

/EC_number="2.6.1.76"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P44951"

/codon_start=1

/transl_table=11

/product="Diaminobutyrate--2-oxoglutarate

aminotransferase"

/db_xref="COG:COG0160"

/translation="MQTLTNNRFIAGKG IKLIDDSGVEYLDGVSGTFNL SLGYNHPHV

VSKIQE QVGNLTHMSSSFTEPYVNEVLDH LIEYAPNDINAGW MRDITG STANECATKI

AQKYTES DIIISLYLSHHGQTQFATGISGNAFR RKRFPNSAVANAVHVPAPYCYRC PF

KSSNGDCDYQCVEAISDAIEYASSGSVACMIIEPILGN GGNIIPPAGYFKRLRKL CDE

YNIIIADEVQTGIGRTGTMFAS ELFDIQPDMITLAKGLGGIGVPVAAVLMQSRLNVL

EKHEHSFTSGSNLISVTA AKSTLEV VSEPGFLDAVKRKGEILGELLQELAMKYP SIGE

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TEDELVEIVERLDSVLASVH"

CDS complement(1744694..1745902)

/gene="glcP_1"
/locus_tag="EFAGFIKM_01537"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07563"
/codon_start=1
/transl_table=11
/product="Glucose/mannose transporter GlcP"
/db_xref="COG:COG0738"
/translation="MKRIFALSCGFYLLIGISSVVLGALLPVLLSHYERGYSDDGGFLL
FLQFLGFLVGVIVAPALTARIGRKAMLTALICIVAAYIVLGFLPSWSVLLLLTIIVG
FGSGIIEPSVGAFTIEFTENQKAVAMSKLDVFFALGALLIPAVAALFIWMDLWHLTFY
TVAVLSMVLMLLWITMPRPAALYLEQAGENTVAHAAGKAQYSRHLGLLTIFVIFFFI
YMGLELGLMNFLPSILVERLHLQESVASLSVSILWIAMIIGRLFSGKIAEAVNYMPFL
IWSTVGTLLFTVAMVFVTGQWATYVLIFGTGLFMSGFLFCIALVYANVLIPGMTERTTS
ILIASGGIGGAILQYVTGWSMSTGPVVNTIWILAGFCLLLLLTLMVSHLWTVKNNAVR
TALAQHSKEM"

CDS complement(1746247..1746879)

/locus_tag="EFAGFIKM_01538"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MYKVTRFTVDPDNPYQHSGMWIGGETAYVSDWPLNPEGQPLLHL
FSINCNSLSQQVHIPSLPQDKYISVFSTYSASEYFLDQVYTGDELEWNNENILAGCTY
VSVSSHPLTSVCPVPPIPLSGVRLIEMELDDQEFPAFSFFSPTLPNGVKGIDHLLLEEH
QLVCQIYSGDFPDYPYRDILGLPDANGYLFLRRGPASAHAPFDGIFVQTA"

CDS 1747084..1747785

/gene="rluF_1"
/locus_tag="EFAGFIKM_01539"
/EC_number="5.4.99.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P32684"

/codon_start=1
/transl_table=11
/product="Dual-specificity RNA pseudouridine synthase
RluF"
/db_xref="COG:COG1187"
/translation="MLINKYISETGFCSRRETNRLIAAGRITINGRVCEKGAEVEPHD
VVLIDGNQIPRNDSEPVYIALNKPIGIVCTAAEHVKGNIIQYMNYP SRIFAIGRLDKA
SEGLILLTNDGGIVNKM MRSEHNHDKKEYVVTVDKPITDEFVKSMSEGVEILDVVTKPC
EVYRQSDKVFRIILTQGLNLQIRRMCKALGYRVLKL ERVRIMNITLDQLERGQWRHLE
QEELEILLSQLNEIK"

CDS complement(1747856..1748794)

/locus_tag="EFAGFIKM_01540"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTSHLGHQNSKASTGHLLALFTILIWGTTFVSTKVLLIDFTPVE
ILFFRFLIGYLVLLLIYPRSLRIASFREEWLFIGAGLCGVTLYFLIENIALVYTASN
VGVIVSIAPFFTAVLAHFFLDGEKLT RRFIIGFGIALSGILLIALNGSFILQLNPIGD
LLAFIAPAVWAIYSVL MRKIGQLRYHTISATRKVFFYGLIFMLPALFLFEFHWNLGRF
TNMTNLSNFLYLGLGASALCFVTWNRAVNLLGAIKTSVYIYLPVITVVS SVLILQEQ
ITWVIVLGAFTLFGSYISEQKGHKHNNKNTNPHSG"

CDS complement(1748791..1749642)

/gene="rhaS_9"
/locus_tag="EFAGFIKM_01541"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P09377"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaS"
/translation="MTREVRTVVFDTDLQLEAYQFEGIMQKFPNHFHDYYVIGFIEQG
KRHLLCNNEEYILNSGDMIVFNPHDPHACEQVDGRTL DYRCINVQPEVMREYAREITG"

QAYLPRFTSPVLYQSELVGSLEYELHQMILEEQSDFCKEELLLLLLDQLLRDYSDAEPP
VSTQDVTLEIRRICDYIEAHYMESISLNELDLTEMSKYHLLRLFTRQKGISPYRYLE
TIRINQAKRILLEQGLLPIEVAAQTGFSDQSHFTNFFKKLIGLTPKQYRRIFNHDSELK
RTTTNIV"

CDS complement(1749868..1750983)

/locus_tag="EFAGFIKM_01542"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P32382"

/codon_start=1

/transl_table=11

/product="NADH oxidase"

/translation="MSNQQHNVISTELLFPYTVKKLTSSRIVMSPMARAFSPDGVP

GPDVAAAYRRRAEHGVGLIITEGATIEHPSASSEPRIPHMYGEAALQGWAEEVVEQVHE

VGGKIFPQILHMGIVRPSGSQPHPEAESLSPSGVDMEGTQVGAPMTEAEIATVIQAYA

DAAANAQSIGFDGIELHGAHGFLIDQFFWKTTNRRTDRYGGDLQKRTQFAVELVMAVR

AAVGPDFPIAMRISQWKMNQYQARLFDTPLEQLFLRLLDAGVDIFHCSTRRFWEPE

FEGSELGFAGWVRKLSRQTTITVGSVGMPDEPEAAADKTTHPGMGELMKRYEQQEFDL

VAVGRALLGDPAAWAAKIRDGRISEIQAFTPEALATLH"

CDS 1751207..1751788

/locus_tag="EFAGFIKM_01543"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSGVLSPNSNDPRVIRTRQLILDAFLNQLNLKNFNSITIQNITE

QATINRATFYAHFQDKYALLEALLSDAFMEYVTKRVPDARLSAETIQQILFSLCDYH

VSSNGCIKKYETVAPIIEENIKTQLEQFLLELMKSVAGDVPPTLKITATMLSWSIYG

MTYRWNIIEGGQESPAELANRVVPYMMGGLELLN"

CDS 1751843..1752142

/locus_tag="EFAGFIKM_01544"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MFEHLVVFKFNDKTTLAKQKEWVDQLLALQEQIPGIVALTAGIN
ATEETDRIQGYTIGLRVTFEDQEALRAYGPHSAHQAFVASLDGWVEDVIVADYAI"

CDS 1752188..1752967

/locus_tag="EFAGFIKM_01545"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MCLILFAYNMHPKYPLILGSNRDEFYHRPTAQAHYWEDHPHILA
GRDLSKMGTWMGVTKGGRLAAVTNYRDPNEEIHAKGSRGDLVADFLKGTSTPEQYMQH
AEQSRNDYPGYNLLVGDPDDLYYYYSNVGNVVMKLKPGIYGISNHLINTDWPKVKRGKE
GLEKIIHGEDESTLTEQILGLLQMADPSVDELLPHTGVPLEWERFLSPIFVKSEKFDY
GTRASSVVLNREEVFFTERVHQNGEVMEQRFNIKPLNSTS"

CDS 1753281..1754597

/locus_tag="EFAGFIKM_01546"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A0A2A5JY22"
/codon_start=1
/transl_table=11
/product="Nucleobase transporter PlUacP"
/translation="MKEAKKMRVFSLGIQHVLAMYAGAILVPLLVGRALNLTAEQLAY
LVSIDLLTCGIATWLQARKGKYLIGLPAVLGSSFVAVTPMIAIGSQYGIPAIYGSII
AAGLFIVIFAVFFSKIVKLFPPVVIGTVVTIIGLALIPTGIKNMAGGANSENFGSLDN
LALSFGVLLFILILNRYARGFVKSLAVLLGIIVGTLIAAIMGKVNFAVQSEASWFHLP
QPFYFGWPTFEIGPIITMIIVGTVVIESTGVFMALSKICDQPINEKDLARGYRAEGL
AFVLGGIFNAFPYNTFAQNVGLVQLSKVKTTNVVVAAGGILVFLGLIPKVAAFATIIP
SAVLGGATVVLFGMVVSSGIKMLQNVDFGKQSNLLIVACSVSLGLGVTAVPDLFAQLP
QSIRIIVSDGIITGSLSAILLNVFFNLALKKESLPIQPVQAQEAHT"

CDS 1754911..1756380

/gene="selO"
/locus_tag="EFAGFIKM_01547"
/EC_number="2.7.7.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P77649"
/codon_start=1
/transl_table=11
/product="Protein adenylyltransferase SelO"
/db_xref="COG:COG0397"
/translation="MQQETLNKGWNLKNSYARLPQPFFTSQGAVPVESPKLIIFNRLL
ASSLGLDVESLDSDEGAEIFAGNLIPEGAEP AQAYAGHQFGNFMMLGDGRALLLGEQ
ITPQGERVDIQLKGSGRTPYSRGGDGRAAVGPMLREYIISEAMYALGIPTRSLAVVS
TGENIIRETERPGAILTRVASSHIRVATFQYAARWGSIDDLRALADYTLHRHFPDVAQ
AENRYLLLLQEVIKRQAALIAQWQRVGFHGMNTDNMAISGETIDYGPCAFMDAYNP
STVFSSIDRQGRYAYGNQPYIAGWNLARFAETLLPLLHEDEEQAVQLAQDAIAQFSEL
YHHHWLQGMRAKLGLLDEEADEALIKDLLELM EKHSADYTNTFLALTFDTLEGTALF
GTPEFAEWNERWQARLDRQQGAKKVSQELMRTNNPAVIPRNRHVEEALEQAENHGDLS
VMQKLLAVLSDPFAHSPEQAEYAELPAQCNTSYQTFCGT"

CDS 1756409..1756915

/locus_tag="EFAGFIKM_01548"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGSFFIFSCHRRYFIEAGAFMSNMLSKQQLADILLQLEHTSS
PREQM QNYVNRLFDTFKWDGVPYVESRKDAYIVRIYERGLVSLEKRVKQPDEVIYWLL
EDIIFTATHVGLLERHGVDNKEMHLNYTNEVMKDLNRGVLEAFQQIGNPYLHWHQTKG
RQELEGMA"

CDS 1756936..1757385

/locus_tag="EFAGFIKM_01549"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSEQDINDVWYDYAVLFVEKKNESEQGWASLTSNEQDIAALWLL
EADVFNNGGFIQFFCNWGEEVYRYALRALHIIDATQVVEIITSAYGCIEHLKEDERLTE
LWDIPKFLTKEQEQQLDALDQQFWNNEDQIAEKAYGYHKGKLNMMII"

CDS 1757828..1759093

/gene="tyrS1"

/locus_tag="EFAGFIKM_01550"

/EC_number="6.1.1.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P22326"

/codon_start=1

/transl_table=11

/product="Tyrosine--tRNA ligase 1"

/db_xref="COG:COG0162"

/translation="MMNIIDELQWRDAINQQTDTTEGLRELTETKISISLYCGVDPTGDS
MHIGHLIPFMMLKRFQLAGHRPVILIGGATGTIGDPSGRQAERSLQTMEQVQENVDAL
TTQMKKLFVTDGDNQVRMVNNYDWTHKINVIEFLRDYGKNFNLNTMLAKDVVASRLEG
GISFTEFSYQILQSLDYHLFQNEVDVQLQIGGSDQWGNITSGLDLIRKKEGSEAKAYG
LTIPLMLKSDGTKFGKTAGGAIWLDPNKTPFEFYQFWANTDDRDKYLYFTFLGK
EQIEALAEKVETEPHRRQAQKALAEEMTKFVHGEEMLEQAKRITAALFSGDIRSLTAD
EIEQGFKEMPFETDGEAKNIVDWLVDLGLPSKRQAREDVTKGAISMNGEKITELEF
TVSAEHAIGGKFIIIRKGKKNYSLVKLQS"

CDS complement(1759252..1759530)

/locus_tag="EFAGFIKM_01551"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVLSDMEIVNAICIHMAERKGVPTDNNVELSWEEDTGYSAEVW
IQGRSQYLVESNMIEAILRYLHSEYNIRAYRENVRLDLDEEITAVNQ"

CDS complement(1759536..1760003)

/locus_tag="EFAGFIKM_01552"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMVFMAFTLLFATVGVTPDSADARRGGGFKSGTKSYSNTPKKS

DSNVKSNTNNSSNGAATTNRGGFFGGGGGFMKGMMMLGGLAGMMFGGLFGGMGALGN

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CDS complement(1760132..1760698)

/locus_tag="EFAGFIKM_01553"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNILSYGLLGLLTREESSGYDMLKIQPHWQAKHSQIYPLLSKM

ENDELLASRWVQQSDKPKKMYAVTEKGIEKLEWMITPVTAPVTRDEFNLRLCVGI

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GLEWCHWVTQLLDGQAAIQDPSPSVSEI"

CDS complement(1760872..1761447)

/locus_tag="EFAGFIKM_01554"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNNIQEILTYNKSFVETKEYEKYTAGKFPTKKMVIITCMDTRLV

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SLHAETMIGHMVERGVSEEVMTTLENSGIRLQKWLRGFDSVEEGVKHTVEVIKKHPLL

PPNVPVHGMVIDSATGELDLVAEGYGQQASL"

CDS 1761797..1763311

/gene="ypwA"

/locus_tag="EFAGFIKM_01555"

/EC_number="3.4.17.19"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P50848"

/codon_start=1

/transl_table=11

/product="Carboxypeptidase 1"

/db_xref="COG:COG2317"

/translation="MDKQTQEHLESFRNLARKIKSYHEAIGLLHWDLRTGAPKKGVPT
RSETLGMLSTEAFKLQTSADMKTYLDALTPVVLEQLEDIDRRLVEDCKKEYDRSQSV
PPEKVQAYTVLTAKSETAWEDAKHNSDFAGFSPYLTDIVKLKQEFIDYWGVKDTTRYDT
LLDMYEPDLTVEKVDAVFARLKARLVPLQEKINASENKPNTTEFLNQLFDTKQKEKFSL
FILEQMGYDFEAGRLDESVHPFATGLNPGDVRITTHYLQDDVASAVFSSLHEGGHALY
EQNIDDSLAGTLLAEGTSMGIHESQSRLWENMIGRSLPFWTRYKDLQQHFPQLSEVE
LEDFYRAINRVESSLIRIEADELTYNLHIIIRYEIEKMLFNDGLEVKDLPETWNAKYK
EYLGIMPTNDGDGVLQDVHWSGGDFGYFASYSLGNMYAAQILHLRKMPEFDTLIAE
GNLIPIKEWLTDKIYRYGRSRTPSELIVAITGEELNPDYLADYLEAKYAEIYKL"

CDS 1763472..1764476

/locus_tag="EFAGFIKM_01556"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKYTPWFVRGIVILLIIIVALTSCNKEENEAKITIGEVTRSVFY
APEYVAVAQGFEEQGLEVDIQTAGGDKTMAALLAGSVDIALVGAETSIYVYQQGAE
DPVINFAQLTQTDGTLFARNTEGSFDWEQLRDSTFLGQRKGGMPQMAGEFALNKHGI
DPQSDLELIQNVDFANIASAFASGTGDYVQLFEPQASIFEQEGRGKVVASFTEGGLL
PYTVFMTKQSYLNDNKDIVQKFTNGLHKAQAWVDSHTAEEIAEVISPFFKDIDPAILV
SSVNRYKEQGSYATDPIIDEEWNNLLDVMSAAGELKERVDLNAIVDNAHAEATKSK
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CDS 1764506..1765300

/gene="ssuB_1"

/locus_tag="EFAGFIKM_01557"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P97027"

/codon_start=1

/transl_table=11

/product="Aliphatic sulfonates import ATP-binding protein

SsuB"

/db_xref="COG:COG1116"

/translation="MPESSEVIRLEGISQVYVSEREASLVLEDLSLEIQKGEFVSLVG
PSGCGKTTLLSIIAGLLTPTRGEVKVKGKLVGGPSAQIGYMLQQDYLPWRTILDNAL
IGLELTGRLDERSRERVRELLVSMGLAGTENQYPSELSSGGMQRVALVRTLATDPGIL
LLDEPFSALDYQTKLQLEDLVSDTLKQFGKTSVLVTHDLSEAIASDRVIVLDRNPGR
IRREFIIPDGIRKSQPFHAREQEGFNALFQALWSELDQSGGGGEEDA"

CDS 1765297..1766130

/gene="ssuC_1"

/locus_tag="EFAGFIKM_01558"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40401"

/codon_start=1

/transl_table=11

/product="Putative aliphatic sulfonates transport permease

protein SsuC"

/db_xref="COG:COG0600"

/translation="MNPMNPKQEKRDEWMGQLHRNHIQQVARWRHQVLAVQLSMLVCM
FLLWEVAGRLRWIDVLLFSYPSKVFAQIGKDIASGELWAHVGVTVGETAVGFLLGTLV
GTLLAVLIWWSPFLSKVLDPYMVVFNSMPKVALGPFIIVMFGAGFTAIVMTLSITVI
ITTLVVYNSFNEVDPNYIKVIRTFGGDRSEIFTKVLPASFPAIVSTLKVNVGMAWVG
VIVGEFLVAKQGLGYLIYGFQVFNFTLVLSLLIIAAVATAMYQLVVYAERKMLAGR
R"

CDS 1766479..1767456

/locus_tag="EFAGFIKM_01559"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MGFRVIKTAIAALMAVLIADWCRLPGPTSAGLLAILGVDVTRKR
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VVFRVFGGGEMDVHVVLVQIALLLIGLGSAMAVNLAYMPAADPQMLRIRKRIDELFSK
IFKEFAATLRNPNEAWAGRELIEADKAILGGIDAAKRSLENQVIHPNEEWSVYFYMRK
TQLDSIQHMMHLVSQIQKMPHAEMVSELDQLSQDVLTESYTGRTKLLADVQEEFK
RMELPDTRREEFEIRSAILQLCRELALYLKVAKKDKAPSPISDRSQSTNE"

CDS 1767532..1768092

/locus_tag="EFAGFIKM_01560"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSLSHKHQCREITKAICGKGRKFSTVTHTVTPNGPTSILGAW
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TSTVEVSADATQEPSCVEATVSAGGSSVIIRVEREFAVELVAETKVCVKVCTDGC GDY
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CDS 1768294..1769547

/locus_tag="EFAGFIKM_01561"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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ILGMDPEFLLVQMPESKIVPASKFLERTGMAGCDSVTIGGRRIYPVAELRPAPSSEPR
ELLAHLMRAFAAASRSISDHSLIWQAGGMPQRGLPLGGHIHFSGVNLTGELLRALDNY
LALPLAFLQDPRGSGRRPRYGALGDFRLKSYGGFEYRTLPSFLVSPLVAKGVVALAGL
IASGYTQLRQRPLAKAEVHAAFYEGKREVIKEHIPTLVDDLKRLDGYARYERYASPLI
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CDS 1769751..1772552

/gene="mutS"

/locus_tag="EFAGFIKM_01562"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A1Y0"

/codon_start=1

/transl_table=11

/product="DNA mismatch repair protein MutS"

/db_xref="COG:COG0249"

/translation="MAQYTPMIQQYLQVKAEAQDAFLFFRLGDFYELFFEDAINASRE
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ATGIRSLKIGYNKVFYGYIEITKSNLSALPEGRYERKQTLANAERYITPELKEKETLI
LEAQDKMVDIEYGLFAELRERLNKEIARLQKLAEQVAEIDVYQSFVISAERNFVRPT
LTDGYDLVVEEGRHPVVEAVMRDGAFIANHTAMTKEEARILLITGPNMAGKSTYMRQV
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QVAVGSEYIGNEKQEGLKLKGGEFRHTDSAPLIREHEIEESAETPSIEDSVGKQHA
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CDS 1772574..1774790

/gene="mutL"

/locus_tag="EFAGFIKM_01563"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00149"

/codon_start=1

/transl_table=11
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QGLYLIDQHAAHERVNYEYEEYKFGNPAQASQELLLPITLEFTPSETEKLKTRLAWFE
QSGVYLEHFGGQTFRVRSHPFWFPGDEKDIEEMSEWVLSERSIDVAKMREAASIMC
SCKASIKANQKLTQAEVLIQRLGSCRQPYTCPHGRPIVISFSTYDLEKLFKRVM"

CDS 1774808..1775593

/gene="rsmJ"
/locus_tag="EFAGFIKM_01564"
/EC_number="2.1.1.242"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01523"
/codon_start=1
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/translation="MYITTGEKEAALLVERARNLAETTGGTYVRRNKMSLPMIEHYE
AEEVLVVLQGKVRLFRKDSPLEFHPSMGFVRAKRILRGEPDPLLEAGAVNEGDTIID
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HHANHLELLRSMPDRSCDTVYFDPMFREPMMDSSAIQPLRDYANAHALDEQSIMEARR
VARKRVMKEKRGSAEFDRLGFEILDRANAKTLYGVINVESGS"

CDS 1775574..1776530

/gene="miaA"
/locus_tag="EFAGFIKM_01565"

/EC_number="2.5.1.75"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9KAC3"
/codon_start=1
/transl_table=11
/product="tRNA dimethylallyltransferase"
/db_xref="COG:COG0324"
/translation="MLKVEVKPKPKLLVLVGPTAVGKTRMSIELAQAFNCEIISGDSM
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FIVGGTGLYVESVCYGFQFSDSGSDEAFREEQFSYAE LNQAQALHDRLREVPVSADR
LHPNDQRRIVRALEIHHLTG EKWSDQLAVQKKESPYDLLIVGLRMDRQKLYARVEERI
DLMIEQGLVDEVKFLLE RGVARGHISMQGLGYKEIAAFLQGEVSWEA AVEWLKRDTRR
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CDS 1776904..1777146

/gene="hfq"
/locus_tag="EFAGFIKM_01566"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31796"
/codon_start=1
/transl_table=11
/product="RNA-binding protein Hfq"
/db_xref="COG:COG1923"
/translation="MNKSINIQDTFLNQLRKENIPATVYLTNGFQIRGTIKAFDNFTI
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CDS 1777317..1779971

/gene="mtgA_2"
/locus_tag="EFAGFIKM_01567"
/EC_number="2.4.1.129"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00766"
/codon_start=1
/transl_table=11

/product="Biosynthetic peptidoglycan transglycosylase"
/translation="MPNDPLSRNRRNNNNKSPKKAKPKTSKKKKITGKRVGWTLFFT
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MFLSRDKTFFRKATEVSIAMALERKYTKDEILTMYLNRIFFGHQRYGIKAASEFYFGV
TDLKRLKLWQIATLAAMPKGPSAYNPVSNPNSKARRGVVLQLMYEQGYITKAEMDEA
KEINYNYKRPEKDRKYQGFIDYVLEAERVTKGTEDDLNIGGYKIYTTMDAQAAQTAME
TAFTDDSLFEASKDDQVQVQGSVMIMNHENGSLVALLGGRDYQTKGYSRVTSRRQPGS
AFKPIVSYPAALESNGYSANSSLSNAKQCFGNYPGNLHGYSSTISMTEAITKSENIP
AVWLLDKIGVNTGINFAKSVGIQLTDEDKNLAIALGGLSKGTNTLEMAQAYSANLG
EYRQAYSIKEIKDSAGKTTYKHDNSDTRVMSEQNAYQLTQMLQNVVNDGTGRSARLD
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FFAKVMGDALKGVVPVKQFKAPAGGQAPPPVEEPEKPVLSVSGLSGSYDPNAQTVSLSW
TGTGDASTQYRIYRKETSEAQFTHLIDAIGATNAQDLSALPGLTYEYYVTAYDLASGL
ETDPSNTISLMIEAQEVPPEEPDPGIDPGTEIDPEQPGTENPDNGTPDNGNSNGNNGN
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CDS 1780260..1780823

/locus_tag="EFAGFIKM_01568"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKRKFGDRANWRRITNRQFTCRFVQSKIFTGYITLYTIQDLKEP
LWKTYGGSTFCIADKGYSWLQYYPKGEHFVVTAMFDDQERIVEWYIDTCRSQGIDTQG
VPWFDDLYLDVVLKDGDEVLLDEDELEDALSRKHITTGDYDLANKTAKELLHAIDAH
VFPYFQLSLKHRPSLFENGFEFRKNIQI"

CDS 1780934..1781905

/gene="spoVK"
/locus_tag="EFAGFIKM_01569"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P27643"

/codon_start=1
/transl_table=11
/product="Stage V sporulation protein K"
/db_xref="COG:COG0464"
/translation="MNGRVMAAGEQPGGRPSRQINIVLRNQEPQMLVKDEAAAVQAAK
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GNPGTGKTTVARIVAKLFQKMGVLSKGHLIEVERADLVGEYIGHTAQKTRDLVKKALG
GILFIDEAYSLARGGEKDFGKEAIDTLVKSMEDNKNQFILLAGYSDEIDFFLQTNPG
LPSRFPIQVEFPDYSIDQLIQISEIMAKERDYILMPQTILKLKQHLLQEKNDLHAFS
NARYVRNAIERSIRHQAVRLLEQYSEGSPGKLELMTIRTEDLNFERK"

CDS 1782030..1783316

/gene="hflX"
/locus_tag="EFAGFIKM_01570"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P25519"
/codon_start=1
/transl_table=11
/product="GTPase HflX"
/db_xref="COG:COG2262"
/translation="MTNGTHDMDVMKKDRAVLVSLVTDDVKRTGINPEYSLEELVKLA
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GTRGPGESKLETDRRHIRGRIDDLKRHLEELTRHRKLHRERRRKTGIVQVALVGYTNA
GKSTLLKQLTAADVYIQDQLFATLDPTSRTMELPSGKEIVLTDTVGFIQNLPHDLIAA
FRATLEEVDNEADLILHVVDASSAMREDQMRTVNTILQELGSGDKPQLVLYNKKDACTP
EQLEMLPLDKDHIKVSALDSEDLLKIREFIQTTELTGDTKRFRIPAERGDLTSLVLYKIG
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CDS 1783400..1784653

/locus_tag="EFAGFIKM_01571"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MVSFDSEISELQRQVDRQIEGQLQQIDRITDHNQWKVINAFQQR
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PATKVIQIQRSGYDWRSSFCVAEIADMVTRVKALKEDVIVFVDNCYGEFTEEREPT
VGVDLMAGSLIKNPGGGIAETGGYICGKEQYVQLAAYRLTAPGIGGEVGAMLGTT
RSIYQGLYMAPTIVGQAIKGSTFAAAMFAESGFVTKPAWNEARTDLIAVKFSSAEHLIAF
VQGIQRAAAVD SHVPEP WDM PGYEHVIMAAGTFIQGGSLELSADAPIREPIGYMQ
GGLTYSHVKYGVLMALQTMKDRKLL"

CDS 1784730..1785149

/gene="glnR"
/locus_tag="EFAGFIKM_01572"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37582"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator GlnR"
/db_xref="COG:COG0789"
/translation="MNMGDEIRRNMALFPIGIVMKLTDLSARQIRYYEQHSLIVPART
SGNQRLFSFNDVERLLEIKALIEKGVNIAGIKQVMNPVSKESSEATVITPDTEVKRRE
LSDTQLHRLKQQLVSGKRPGQVSLIQGELSRFFNKN"

CDS 1785279..1786607

/gene="glnA_1"
/locus_tag="EFAGFIKM_01573"
/EC_number="6.3.1.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P19064"
/codon_start=1
/transl_table=11
/product="Glutamine synthetase"
/db_xref="COG:COG0174"
/translation="MSYTKEDILRISKEENVRFIRLQFTDLLGAIKNVEIPVSQLTKA"

LDNKMMFDGSSIEGYVRIEESDMYLYPDLDLWIFPWWAENRVARLICDVYLPDGNPF
PGDPRGILKRNLKEAQDMGFTSFNVGPEPEFFLTKDEKGNPTNELNDQGGYFDLAPT
DLGENCRRDIVITLEEMGFEIEASHHEVAPGQHEIDFKYADALKAADQIQTFKLWKT
IARQHGLHATFMPKPLFGMNGSGMHNCNQLFKGNENAFVDESDELGLSKTARHFMAGT
LKHARAFAAITNPTVNSYKRLVPGYEAPCYVAWSASNRSPMIRIPASRGLSTRVEVRN
PDPAANPYLALSVELLKAGLDGIKRELSLPAPIDRNIYIMSEEERVEEGIPSLPADLKE
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CDS 1787198..1788499

/gene="aldH1_1"

/locus_tag="EFAGFIKM_01574"

/EC_number="1.2.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2FWX9"

/codon_start=1

/transl_table=11

/product="4,4'-diaponeurosporen-aldehyde dehydrogenase"

/db_xref="COG:COG1012"

/translation="MDQAKQLVTEQRTFFYTGGQTKNIDYRINALQQLRKGIEKYQQRI

QDALRADLNKSEAEAYGSEIRIVLGELDFALEHLQEWAAPKQVPTNSAMPDGVSTIYP

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EYIVVMEGEVEASTALLKEKFDYIFFTGSTGVGRIVMKAAAHLTPVTLELGGKSPAI

VHSDADLKLVAQRIVRGKFLNAGQTCVAPDYLLVHEQVHDELIDMIGAEIKDKFGDDV

LKNADFPHIVNARNFDRLSKFLTDGKTLIGGRSVREQLLIEPTVLGDVNWESAVMQEE

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CDS complement(1788604..1789230)

/gene="lexA"

/locus_tag="EFAGFIKM_01575"

/EC_number="3.4.21.88"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P31080"

/codon_start=1

/transl_table=11
/product="LexA repressor"
/db_xref="COG:COG1974"
/translation="MSKISSRQQAILEFIRNEVRLKGYPSPVREIGEAVGLASSSTVH
GHLDRLLEKKGLIRRDPTKPRAIELLSQEESEHSHQFAHSVARIPVVGKVTAGVPITAT
ENIEDYFPLPTHYVGEQKVFMLSVVGDSMVEAGIVNGDYVIVRQQQTADNGDIWVAMT
EDDEATVKTFYKEKDHIRLQPENATFEPLRLKHVSILGKVIGLFRDIH"

CDS 1789528..1789905

/gene="yneA_1"
/locus_tag="EFAGFIKM_01576"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_02014"
/codon_start=1
/transl_table=11
/product="Cell division suppressor protein YneA"
/translation="MRYSTYQSIYEPMNSELVKSNIKNYKKVLARFKISSWMLKVAIT
SMIIFIGCSTVLTVFAGNENDVLPGGKIAVSQGETLWSISLEHKPTNMDTRIYIEAIK
KVNQLHTTSIQVGQVLALPQFAE"

CDS 1790001..1790210

/locus_tag="EFAGFIKM_01577"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDIDSLVARINELARKQKSTGLSEEELAERAELREIYLSNIRSN
FRQQLDTIEIVDDENDKGHQGKCLKH"

CDS 1790336..1790845

/locus_tag="EFAGFIKM_01578"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MSRSFERTVKKNSKQLNQQRKKSGQPITGTPGEEVFKGRSLLFP
IFLIGLAFLYLFMSTFLVQAPMTTWDWVTMLLYVFLAVIFMLRRPYIKISSNRIITTK
GNRERSIGVDDIVKFRIEPTGVVIEHNSRGKRWWFTKLLNRYDTDAIAERLLKFAKAH
QITVETVEK"

CDS 1790865..1791665

/gene="gph_3"

/locus_tag="EFAGFIKM_01579"

/EC_number="3.1.3.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00495"

/codon_start=1

/transl_table=11

/product="Phosphoglycolate phosphatase"

/translation="MIGMALKAILFDLDDTLLWDERSVREAFHETCLIAAQETGVKPE
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ESWRRGLLKLGDREDLAEQLAAQFGVERRSRPHVYEETMDTLRQLQGKYKLLLLTNG
CPALQKEKLDGVPELTPFFDEIIISGNFGKGKPDPSIFEHALSKLGVKPEESMMVGDK
LTTDIRGALSSGIQSVWINREHKTNNETYAPDHEITHLSELNQLIANF"

CDS 1792222..1793184

/gene="yteP_7"

/locus_tag="EFAGFIKM_01580"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system
permease YteP"

/db_xref="COG:COG4209"

/translation="MESETAKTTLTMTSLRKESRLRTAATLFRKDWQLYSLILPIY
LLIFKYGPMIGNVIAFRRFVPGGSIFGETWVGLRYFKMFIEDPTFWRVFGNTLMLGGL
ALLFTFPVPIIFALMLNEVKSKRFKKFVQTASYLPHFLSIVIVAGMILQLTAVNGSIN
GLVAFFTGDNIIPFMQRAEWFRTIYITSEVWQGMGWGAILYLAALTTIDDSLYEAARID

GANRWKQTIHVTLPGLPTIVTLLILNMGNFLAVGFEEKILLYNPLIYETSDVISTYL

YRVGLESSNFSYATAIGLFEGLILVFSVNAISRRLTQRSLW"

CDS 1793197..1794069

/gene="ycjP_1"

/locus_tag="EFAGFIKM_01581"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77716"

/codon_start=1

/transl_table=11

/product="Inner membrane ABC transporter permease protein

YcjP"

/db_xref="COG:COG0395"

/translation="MQESRSYKVKVFNVIFLLFVVFITLYPFLNVVAQSFSSSESYIN

SGKVSFLPRGFNVETYKTISRDSMFWTNYKNTIYTVVGTLSMFMTTIFAYALSKKR

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ENMPEELEEAASIDGLNTYGILLRIILPLSKAVMATMVLFYAVGHWNSWFPAFLYLDK

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RYFVTGIMLGSVKQ"

CDS 1794208..1795842

/gene="lipO_4"

/locus_tag="EFAGFIKM_01582"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37966"

/codon_start=1

/transl_table=11

/product="Lipoprotein LipO"

/db_xref="COG:COG1653"

/translation="MNQKPRKFVGKMLLASMMTVVLAACSSGTGAGGDVTEVQTKAAM

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LEGLRQEDGKYVLPGLHEEVWPDYTLVVRTDVFEENNIAIPTTWDELYDAAKKLKEI

YPDSIPFSDRFQFNSTLNIAATGFGTKAGWGFGNGLTYKEDQDEFVYTATTPEYKEML

TYFNKLVSEGLLDKESFTQDDDQAVQKFVSGKSFMINGNSQTVVLHRNDMNKTLGEGK
YSVAKITVPGGPKGQLMSGSRLENGVMISGKIQKSENFKAIMQFVDWLYYSDEGQEFA
KWGVEGETFTKEGGKRKLVEDVNYNGLNPKGTKDLRIDFGFSGGVFAYGGTTDLLQSM
FSEEELKFQQDMKDTKEVIPAEPPIPYSSDRERVTLSTPLKDYSQNTLKFILGER
DLSEFDTFAKELESQGLSNYLKLANDTYKAYKENKQ"

CDS 1795947..1796621

/gene="rspR_1"

/locus_tag="EFAGFIKM_01583"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ACM2"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional repressor RspR"

/db_xref="COG:COG1802"

/translation="MSLNQKIRGSTRAYSYNLLKERILHLELKPGTKISEKEIADELQ

VSRTPVREAFMKLAEEELLDIIPQSGTIVSHINLEHVEEGRFMREKMEKEIVTLACVS

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YPHYFI"

CDS complement(1796718..1797263)

/gene="mtnD"

/locus_tag="EFAGFIKM_01584"

/EC_number="1.13.11.54"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81MI9"

/codon_start=1

/transl_table=11

/product="Acireductone dioxygenase"

/db_xref="COG:COG1791"

/translation="MAEIVIRNTNERITGDENVRNFLNKYEVLVEKWDASKLNTDLQN

NFGLTDEQKTEVLETYDYEIRDLAARRGYQIWDVITLSEQTPDIEEKLAKFEEIHHA

EDEIRAIVAGKGIFVIKATDDVGYFNVELSPGDVISVPENTPHFFTLMENKQIIAVRL

FIEKDGWIADPYPDPTFIKQA"

CDS 1797512..1800883

/gene="methH"

/locus_tag="EFAGFIKM_01585"

/EC_number="2.1.1.13"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O33259"

/codon_start=1

/transl_table=11

/product="Methionine synthase"

/db_xref="COG:COG0646"

/translation="MIQQVDLTGEDFGGEDLDGCNEMLVLTRPELIQRIHEEYLEAGA

DLIETNTFGATSVVLAEYDIQDRAREINLEAARIAKA AVDRFSTPESPRYVVGAMGPT

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SGVTLPMLISGTIEPMGTTLAGQNIESFYISLEHLNPISVGLNCATGPEFMRDHIRSL

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CDS 1800961..1801899

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/EC_number="3.1.26.11"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54548"
/codon_start=1
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/db_xref="COG:COG1234"
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AKLAEYGLKPGPLFGRLKRGETITLDNGDSL RPEDVLGAPKRGMVITILGDTRPCDNV
QPLSVNADVLVHEATFMHDLADTAHEYHSTSKQAEEAARAANVGQLIMTHFSSRYKD
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CDS 1802256..1803065

/gene="yutF"
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/EC_number="3.1.3.-"
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/inference="similar to AA sequence:UniProtKB:O32125"
/codon_start=1
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/product="Acid sugar phosphatase"
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CDS 1803072..1803893

/gene="mutM_1"

/locus_tag="EFAGFIKM_01588"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42371"
/codon_start=1
/transl_table=11
/product="Formamidopyrimidine-DNA glycosylase"
/db_xref="COG:COG0266"
/translation="MPELPEMENYRTLLSEKILDLPITGVVINRDKTINTEPDLFINE
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ILFFIGLRLGYIHLLTSKETEEAMSDLGPEPLDRMNVERFASLLKGRRGTLKTTLVN
QHIIAGIGNCYSDEIAFAAGLRPSSKTQNIATSPELTERLFHSMQSVLREAASEGGYM
EMPLMQGDTKTGSFDEQCRVYDREGETCPRCGGTIERVEITGKKAFFCPKCQHEA"

CDS 1803961..1804731

/gene="nfo_1"
/locus_tag="EFAGFIKM_01589"
/EC_number="3.1.21.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9WYJ7"
/codon_start=1
/transl_table=11
/product="putative endonuclease 4"
/db_xref="COG:COG0648"
/translation="MGATAFQYFPKNPRSLGLKSLDLKDTEQCRDWCEQQGLASIAHS
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FASGLWSSGNEAAMLDKGRMLGYWDNVAHVHFNDSKYASGLCKDRHARIGQGYIGNES
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CDS 1804751..1805089

/locus_tag="EFAGFIKM_01590"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHVFLDDYRACPKGFVLATNAEECLMLLREGDVDILSLDYELGP
DSPNGGEVAASIVREGLFPREIYLHTSSMFGKRQMYEMLYSNKPDSVTIHNGPMTGEV
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CDS 1805089..1805406

/locus_tag="EFAGFIKM_01591"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKPITSKMLMRSVWEGMPQAVFIYTPLCGTCTAARRMLEVVEHM
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VLK"

CDS 1805403..1806182

/gene="ylmA_1"

/locus_tag="EFAGFIKM_01592"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31723"

/codon_start=1

/transl_table=11

/product="putative ABC transporter ATP-binding protein

YlmA"

/db_xref="COG:COG1119"

/translation="MSIISMEHVSLRREENQILDNVHLRIEQGEHWWILGRNGSGKTT
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GAYAFLRFYQTIPDEVKAKAMSLDDMGFANLANNPLGTLSSQGERKKVMLARSLMAEP
KLLIMDEPCAGLDLYEREKMLAEIDRLRQRNITVVVYVTHHVEEIVPLFTHVALIRDGR
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CDS 1806189..1807238

/gene="rlmM"

/locus_tag="EFAGFIKM_01593"
/EC_number="2.1.1.186"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01551"
/codon_start=1
/transl_table=11
/product="Ribosomal RNA large subunit methyltransferase M"
/translation="MSTQSSWEEGNFSRFICTANHGFAPYAEELRRTFGAVKSTVLV
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ELNGASVVLQVRKTEGAFWQENAASLKQLLTEKLDLGCEWVVRDAEYVISVFATNDM
LYAGISRPEQNLSDWSGGAVRFQKEDGQISRAKFKLLEAEQTFGIDFTSFHKALDIGA
APGGWTSFLLERGLEVTAVDPAKMDATLLASPKLTLKKNAGDVRFREGEFDLLVCDM
SWSPKLMSRLVSDLLYSLQPGGTAIVTVKLLHKKPLAMIKDVIDTFERSRMQIQRSKQ
LFHNREEITLYMVKY"

CDS 1807466..1808944

/gene="pknD_2"
/locus_tag="EFAGFIKM_01594"
/EC_number="2.7.11.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01957"
/codon_start=1
/transl_table=11
/product="Serine/threonine-protein kinase PknD"
/translation="MRHPARLERGSLLGGRYRIVSILGTGGMSHVYEAEDLKLPGKIW
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FGIARSYKRQSAEDTVKLGTAGFAAPEQYGGSGQTDARSDLYGLGALLLYLMTSGAYTE
WIQGVESSIRSDVPRTYIPVARRLLRYNAEERFQSADEVKELLRIPGGTTPGGDTTM
TLNGGTRVIALTGASSGVGVTHTAIAISHYLERQNFKVAVIEMSPRSQSFARIQQIAH
AGKPVPAGRQFAVDGVHYWKQSGRADILSLLGGSYQFIVMDLGSGQDQNRLEEFLRAD
LPVIGSGAEWRQAEIGAFVRSHHRYPREKWIYCLPLAASEAVQRIRKALDTSSVYGL
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CDS 1808969..1809988

/locus_tag="EFAGFIKM_01595"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKLRKQSRQLIYAGLIGAGAVGLVFGGYVIYNVKTMGDVRS
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SSTKQMEGQVAKIELKKGTATTEMVYEDTPAPPDLRNRELQVLLPSSLVKGDIIDV
RIQFPTGQDYVLLSKKKVERLNAATLWITMTEEEILSLSSAIVDAYLHKASIYALTYV
EPQFQTPAIATYPANSEVLKLESDPNIVRRAEQELSRQVRSSLESSLAASMTAPSKG
VEQDVAQSSVTYNSRPSSNNPATSDGVMWNDGSGNGAGANSVNDPADASQTEQQSL
LTGGE"

CDS 1810064..1810777

/locus_tag="EFAGFIKM_01596"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHTWIFAGLCEKNDLMLYLCKILASTGNKVLLVDGTLQQKYGYG
VGDSQQSLRITEFEGFDIACHFVTSAAVENHLEVNGERLDSYDYVLYDMETSHFASRN
LWLTADVRVWVSDYERYNLERGKGWLKRLLEEQSLPGELSFQRLLINGVDCKLEARYL
WAYLEGSPFVWTGESLVPWDELTA AVKLENEHHRRVHLGPLSRNYKKS LCRVVEQLT
GWESVRSRRAMKEAERMRA"

CDS 1810774..1811604

/locus_tag="EFAGFIKM_01597"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTITFWSPFAGTGCTSSTLISAYAMALHYRTRVLLVNAGLAGT
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GRIDEMERSPQEHGETVKRLNVANEYYDLVLLDADHAGVDSQLKLQQADYVWINLDQ
NMRNLELFFEEILPERMNNKNIHVINKYDLHSRATLSNIRRQFRYKGTISAIPYTTG
YLDAMNRRDVARYLQLESLTEDKDIRKGSFAASMSELARLIMDGAGMRTVLKRLERGA
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CDS 1811612..1813438

/locus_tag="EFAGFIKM_01598"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLWNTIWISLILLCMTYIWFKYRTFLREKNARVPEQESFTIDM

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CDS 1813428..1815494

/locus_tag="EFAGFIKM_01599"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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VRHRYHQHGMVEEALYEAAGTGEAAEQVRLIYEALTSPDPNEALERYYEAPNRFL

KGFAGVSYMVMEFGDKDRAQGSYILKGLGNLTQEIHLEILRRDKLDYLLKGLNIIALA

PVLFTAPIERWARVSFPTMDEFYRSKIGFVTKISIVVIIIILAYLLLQRLQQYDETRYR
SGHKHSWLDQFLYRQTFIRKLAMLFASKPGSAQYSQTIRLMRESSSELKYEWLAIIRRV
MLFAGCLVLTMVCILLHQVERSHILYDPIRDDRMMFGAMAEADLRKAEEKTALDQSVL
ESVEMNRGATYEEVSKALQQLSPVQLDHDQTNETITRIMQKLEVYNKQYVRWWEMIIA
ILMGAAGYYMPVWLMLFQRKMRRLLDMRHEIYQFQTVISILREMDRMSVEEILEWLNRF
AVIFKRPLQKCLLHFEHGPALALEQLKEEAGLPEFQRLVDKLQLALGKISIREAFDDL
ESMMAFYFEQRKQEYSKMIDVKASWGRTIGFTPMYALIFLYLVIPLVGMSFLQMNIYY
EQIQKL"

CDS 1815557..1816042

/locus_tag="EFAGFIKM_01600"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNNASSALKVAAGIFLTIALITIVLLFISAQEATKTAQNNFAD

IQTELSQAFTVYDGTISGSQVTNALRKYADKDQFGIQVITGKNKAGQWYGNQLNIS

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CDS 1816059..1816457

/locus_tag="EFAGFIKM_01601"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSRNTQHLMFLCTAVVLFVTACLYGQQNVKILSAALNDRVQTTA

GMEGRLLTTLHTTNLYQYSGAGVLHTRVQMTGTGIPVEVDGTSYVIDPLVSKTATIPV

QLDATYRPEFIRNETGELLKIVFWKEASVN"

CDS 1816454..1817005

/locus_tag="EFAGFIKM_01602"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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FVDAVRTKGYISPRMLADFEELAQGTGNVYDVSMEHLHKKYVPHYIDPMDNNSFNGTY
EVVQDGYAAQIRERLFPSSGVIPVDDPGRRYTLTTGDFFTVTLQNTNRTPSMLIREW
LSGTVQASAVFVTYGGMVLNEDY"

CDS 1816992..1817975

/locus_tag="EFAGFIKM_01603"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKITELSIVFVLIFPLFWIISLHTQDAEEAQYLGQRYRSALQT
AVMDAGAVMHQNEKQNDEAGYDSTKFVKADKELALLTFTQTMALNMGIQNDPAAIRNM
FNYIPAVVILDYDGYMLSTETELTGNREDSLRQVWGPKKPYTSDSNGNSINFTLDD
YVYAFDASAGKWIEGFQKELASSTQIPLLQNTSVFEQVRQSRIVTAVQDDLADVNRH
NEFARKNGISYFTMPLIAQEDWYNSINDTGIMAFIQGIGVGDQKINNYAIGGGRLVK
KTAIVGGVDPLTGIKYYPSTCGNGYRAEEVFTDARQAAQGYFEYKCSNR"

CDS 1818114..1819664

/gene="ybiT_1"
/locus_tag="EFAGFIKM_01604"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A9U3"
/codon_start=1
/transl_table=11
/product="putative ABC transporter ATP-binding protein
YbiT"
/db_xref="COG:COG0488"
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NITDQMADADPDKLEQLLEEMGDIQEQLQGDYFYLIDVKVEEMANGLGLSAIGLDRDV
AALSGGQRTKVLLAKLLLEKPTALLLDEPTNYLDVEHIEWLSRYLKDYPHAFLISHD
TEFMNEVVNVIYHLEFAKLTRYAANYNKFLEMADMNKAQHIDAYEKQQEYIKKQEDFI

QRNKARASTSGRAKSREKQLDRIDERIDRPDEAAKPTFKFKDARASSKTVFEGIDFEIG
YTYPLLPKMTMTIERGEKIAIVGCNGVGKSTLLKILGRISPLSGKTFLGDYLETAYF
EQEVRAGNITPIEDVWNEFSHLTQNEVRGHLARCGLKNEHITRPLNMLSGGEQAKVRL
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VEEWSEKN"

CDS 1820075..1820737

/gene="tenI"

/locus_tag="EFAGFIKM_01605"

/EC_number="5.3.99.10"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P25053"

/codon_start=1

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/product="Thiazole tautomerase"

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AVISNVQRLRLGVSVHSIDEAKIAEERGADYLFFGHVYSTNSKPDLEPRGLYALAEVC
SGVSIPVMAIGGIEPGNIHAIRSAGSQGVAVISNVWASDSPDRAAESLRQAIVATESL
SR"

CDS 1820755..1821927

/gene="thiO_1"

/locus_tag="EFAGFIKM_01606"

/EC_number="1.4.3.19"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31616"

/codon_start=1

/transl_table=11

/product="Glycine oxidase"

/db_xref="COG:COG0665"

/translation="MKKIITDRPDKIYAETIIVGGGVGCAIAYELASRGQDVLLER
SAIAGGTSCAAAGMLAADSEDFAHPLMAKLARQSRQLLIEQQVLMATLSEVETGLQRQ

GFLTPFCSSYSELSSYKDNRKSALESASADEVWWDRSVVQQEASWLNRTYGAYRPPYES
EILPVHLTKAYAESAQALGARVMEDIQNIRVQANEHGVQGITT SIGEMRCKHVIIAAG
LQSEELMRHVNLSLPVWSVKGEIAAVQFSDEHAGYRPDRTVYAEDIYIVPKANGEVWL
GATSLPGRTDLTVSVQGVQKLLTAATHWVPGMKEAQFIRAWAGVRPATPDGLPYIGAC
KSIPGLFAAFGHYRNGILLSAITGRLIAELLAGKSSEELGIEALSPERLNRKGVVQ"

CDS 1821924..1822127

/gene="thiS"

/locus_tag="EFAGFIKM_01607"

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/inference="similar to AA sequence:UniProtKB:O31617"

/codon_start=1

/transl_table=11

/product="Sulfur carrier protein ThiS"

/db_xref="COG:COG2104"

/translation="MNIIVNGQRMEIEDRLNRVDKLLQSFDLQVKTVVVELNKHILTR
EYHETTALREGDRIEIVHFVGGG"

CDS 1822127..1822897

/gene="thiG"

/locus_tag="EFAGFIKM_01608"

/EC_number="2.8.1.10"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31618"

/codon_start=1

/transl_table=11

/product="Thiazole synthase"

/db_xref="COG:COG2022"

/translation="MMLNIGKYTFESRLLLTGKFSDELVSQAVEASETEVLTFVR
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DGMTLLPDPIETYKACEILLEKGFTVLPYISDDVILAKRLQLLGVHAVMPGASPIGAG
RGIINPYNLEIIIEQAVVPVIVDAGLRSPKDAAYAMELGADGVLLNTAVSGSGDPVSM
AKAMRLGVEAGRLAYEAGMIPVKRYAAASSPVEGMVHT"

CDS 1822894..1823943

/locus_tag="EFAGFIKM_01609"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTDQLTSSEQADRYSRQERYAPLGKEGQARLKGSRLVIVGAGAL
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ANALRRKLLSFDVWRNEYISINVDGAKKQDCPSCSDTATYPYLSASNLEKTDVLCGRD
TVQIRPARRMNLDLQHTADRLDRLQEGKVESNPFLVSFTTGVYRMVIFQDGRVLVHGT
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CDS 1824153..1824767

/locus_tag="EFAGFIKM_01610"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEWSELNQSVESLLHINLIILVDREEGTKHCGQDQKLELKRWL
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YEYAMDTNVVDVYIKHLRVKVDKGRSVKLIHTVRGIGYMLHDRN"

CDS complement(1824876..1825376)

/locus_tag="EFAGFIKM_01611"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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ANLRVGDLVFFSSGSRSTGSNVTHVGVYAGNGKILHTYGSPGVTLSDLDSTWKRITYV
KARRVL"

CDS complement(1825673..1826314)

/gene="thiN"

/locus_tag="EFAGFIKM_01612"

/EC_number="2.7.6.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34664"

/codon_start=1

/transl_table=11

/product="Thiamine pyrophosphokinase"

/db_xref="COG:COG1564"

/translation="MTVKRIVFTGGNLSVELLQEIREDDMIIAADRGALFLIEHGIQ
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HEVTGITLDGFMYPDQATIRMGQSLGVSQQLLGSSGTVTIDSGLLLIQSKD"

CDS 1826497..1827198

/locus_tag="EFAGFIKM_01613"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDLHIFEVFSIIGTIAFAMSGAFVAMEEEYDILGVLVLGLVTAF
GGGIIRNVLIGIPVTTLWSQGSLIMLALVSVAIAFILPLKWISHWKRTEALFDAIGLA
AFAIQGALYAANMGHPISAVIVAAVMTGIGGGVIRDVLAGRKPLVLRDEIYAVWAMTA
GFVIGMGWLTNAGLLFCFAAVVFFRMCSVHYKWKLPRRSLVPSETGNVSPQPESIVP
QPTSSVLQGTLSKGD"

CDS 1827200..1827676

/gene="yfkJ"

/locus_tag="EFAGFIKM_01614"

/EC_number="3.1.3.48"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O35016"

/codon_start=1

/transl_table=11
/product="Low molecular weight
protein-tyrosine-phosphatase YfkJ"
/db_xref="COG:COG0394"
/translation="MINVLFVCLGNICRSPMAEAVLRHKVLEKGLEHQIRVDSAGTGD
WHVGKPPHEGTRKLLDSYQISYANMAARQFASEDFTQFDYIVCMDNSNADNVRNVP GG
AEADIIKFMDMLPEEKLREVPDPYYTGNFEEVYELVNVGCDVLLSKIEAEHSLPKK"

CDS complement(1827835..1828569)

/gene="ybbA"
/locus_tag="EFAGFIKM_01615"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P55192"
/codon_start=1
/transl_table=11
/product="putative protein YbbA"
/db_xref="COG:COG2819"
/translation="MTDSRYLKRTIVKEEIESRYLGKRTLRIYLP PGYNELLSYPVV
YCQDGEEFFNFGRIATTANQIILDEGAEPFIIVGVQVDVSVRTKEYAPFGDRFKTYTA
CFAEEIIPYIEEKYPVRPSPQERILAGDSLGGSVSLHLALLYPDLFTRVISMSGAFYS
ASQEIYAAAEDLSWLSIWMIVGLQETD FEADTGTYDFVQLNRDTRELLEKRGALVSYQ
EKDGKHQWGFQWQKELPEALLYFLQER"

CDS 1828826..1829893

/gene="pdhA"
/locus_tag="EFAGFIKM_01616"
/EC_number="1.2.4.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P21873"
/codon_start=1
/transl_table=11
/product="Pyruvate dehydrogenase E1 component subunit
alpha"
/translation="MSKVPYEVYTEDVEALSVLSPDGEIVNKMMP T LSDDQLKEIMY

RMVFTRTWDDRAVNLGRQGRLGFYAPVSGQEATMVGSEFAIEKEDFVCPGYRDIPQLV
WHGLPLYQAFLYSRGHQHGGQIPDGVNVLMPPQIIIGAQILHAMGIAMGYKLKKQKQVW
ITYTGDGGSSEGDYFEGLNAGVYKLPVIFVQNNGYAITTPFAKQTAALSIAHKAVA
AGIKGVKVDGMDIFAVIKAVQEAERGRNGEGATLIEAVTYRFRPHSLSDDASKYRTK
EEEEAWSAKDPIARFAKYLEKKGLWTEEDTARVKEEAKAKVNNEIKKAEKTEKMTISG
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CDS 1829995..1830972

/gene="pdhB"

/locus_tag="EFAGFIKM_01617"

/EC_number="1.2.4.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P21874"

/codon_start=1

/transl_table=11

/product="Pyruvate dehydrogenase E1 component subunit
beta"

/translation="MAQMNMKEAIRDALRVELKRDPNVLLFGEDVGNVGGVFRVTEGL
QKEFGGEERVFDTPLAESAIGGLAVGLGVQGFRPVAEIQFVGFI FEALDQM VVQAARMR
FRSGGKYNSPIVFRTPFGGGVKAAELHTDSLEGLLTQTPGIKVVVPSNPYDAKGLMIA
SIRDNDPVFFMEHLNLYHAFRAEVPEEDYVVELGKANVVREGSDVTIITYGMMVHTSV
KAAEELEKQGIKVEIDLRTVSPIDIDTIVASIKKTNRIVVQEAQKSAGVAAEVIAQ
INEKAILHLEAPVLRVAGPDTVYPFAQIEDSWLPNPARIVA AVNKV VNF"

CDS 1831149..1832465

/gene="pdhC_2"

/locus_tag="EFAGFIKM_01618"

/EC_number="2.3.1.12"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P21883"

/codon_start=1

/transl_table=11

/product="Dihydrolipoyllysine-residue acetyltransferase
component of pyruvate dehydrogenase complex"

/db_xref="COG:COG0508"

/translation="MAKFEYKFPELGEGLHEGEIIMHIKVGDKVTDDDIIMEVQNDK
AVVEVPCPVNGTVTEVFAKDGQVCHVGEVVAIIDAEGELPEQDDAPAGDQGEQEKDAA
QGGADTSGSSAAASSTDAAKEGGNNSVPAVPAKDVLATPSVRKFAREQGV DIAQVNGT
GNNGKVTKEDEVESFKNGGGSSAAASSEAPAQEEKSAAPAAADQYLEEERV PFKGIRK
AISNAMVKSAYTAPHVTIMDEVDTVTELVAFRTRMKPIAEKKGTKV TYLPFIVKALVAA
SRQFPALNAMIDEEANEIVYKKYYNIGIATDTDNGLIVPIKDADRKSIWMIADSIRD
LAARGREGKLSANEMRGSTISISNIGSAGGMFFTP IINFPEVAILGTGRISEKAVIKN
GEVVAAPVMALSLSFDHRIIDGATAQNF MN YIKQLLANPELLVMEV"

CDS 1832469..1833884

/gene="pdhD"

/locus_tag="EFAGFIKM_01619"

/EC_number="1.8.1.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P11959"

/codon_start=1

/transl_table=11

/product="Dihydrolipoyl dehydrogenase"

/translation="MVVG DASLNIDTLVIGAGPGGYVAAIRAAQLGQSVLIVDKSELG
GVCLNRGCIPSKALISAAHQYESALHGEAFGISAENVKVD FSKTQEFKNGVVKMTGG
VAGLLKGNKVEVFNGECMFINENEARVFNDHESPRYKFKNAIIATGSRPIELKPF PFG
GRILSSTEALNLPEVPKSMIVIGGGYIG AELGQMYSKFGAKVTIIEGLDTVLP GFDDK
MTSLVAKNMKKTGIEIVTGAKAESAEQTDKDVTVKYSVNGESKEVTADYLLVTVGRRP
NTDGELGLDMIGVDVDERGFVKVDHQGRTSIPHIFAIGDIVSGLALAHKASYEGKVAA
EAIAGQPSVVDYKCMPAVVFTDPECSSVGYTEKEAKEKGYKV KAGKFPYAGNGRAVSL
NHAEGFVKIVADEESGLVLG CQIVGLEASNLIAELGLAIEMGATLEDLALTIHAHPTL
GEIVMEAAELVMGHP IHIISR"

CDS 1834362..1835156

/gene="thyA"

/locus_tag="EFAGFIKM_01620"

/EC_number="2.1.1.45"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A884"
/codon_start=1
/transl_table=11
/product="Thymidylate synthase"
/db_xref="COG:COG0207"
/translation="MKNYLDLLQDILNNGVHKGDRTGTGTQSVFGRQLRYDLSEGFPL
VTTKRIHLKSVIHELLWFLSGDTNISYLKENGVKIWDDWADENGDLGPVYGSQWRTWE
APNGDKIDQIAAVIDSIKNNPDSRRHLVSAWNVAEINNMLPPCHFAFQFYVAEGKLS
CMLTMRSDTFLGLPFNIASYALLTHMIAQQCDLEVGDFIWSGGDVHIYSNHVDQVKT
QLEREPYALPKLVIKRPDSIFDYKFEDFEFENYQHHPGIKAPIAV"

CDS 1835207..1835695

/gene="dfrA"
/locus_tag="EFAGFIKM_01621"
/EC_number="1.5.1.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P11045"
/codon_start=1
/transl_table=11
/product="Dihydrofolate reductase"
/db_xref="COG:COG0262"
/translation="MSIELVWAMGENGVIGLNNSIPWRLPKDMAFFKQRTLNKTIIMG
RNTWESFGGSPLPQRRNIVTRDLNYKVEQAEIVHTIEEGLSVTKGEELCVIGGSQVY
REFLPLADRLVVTKIHKNFEGDTFFPEVDWSEWELIEQIEGEQDEKNVYAYTFEFYER
KR"

CDS 1836312..1837799

/gene="gltB_1"
/locus_tag="EFAGFIKM_01622"
/EC_number="1.4.1.13"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34399"
/codon_start=1
/transl_table=11

/product="Glutamate synthase [NADPH] small chain"
/db_xref="COG:COG0493"
/translation="MSTPTGFMEYKRQLPTDREPAERIKDWEEFHKHMAEEELRTQGA
RCMDCGTPYCHTGMIGGTSGCPVHNLIPEWNNLVYRGLWREALERLHKTNNFPEFT
GRVCPAPCEGSCTVGLIGQPVTIKTIEEAIIIEKGFEEGWVVPQPPEKRTGKRVAVVG
GPAGLATAAQLNKAGHSVTYERSDRVGGLLMYGIPTMKLDKNVQRRVDLLEAEGIQ
FITNTEIGKDIAAQQVLVEYDAVVLCCGATKREFNIEGSDLKGVHYAMDFLNGSIKS
YLDNLEDGQYLSAKDKDIIVIGGGDTGSDCVATSLRHGCRTITQFGTHTQAPMERDR
INNPWPQFPNVYTLDYAQEEAKALFGQDPREFSIMTTKFVGDDDEGNLKLHTVQIERI
VDETGRKIYQPIPGTERVFPAQMAMIAIGFDGPEQTLVEQLGLATDRRTNVKARYGKY
NTNVDKVFAAGDMRRGQSLVWVWAINEGREAAAREVDKYLGMASVLV"

CDS 1838031..1838522

/gene="fur_2"
/locus_tag="EFAGFIKM_01623"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54574"
/codon_start=1
/transl_table=11
/product="Ferric uptake regulation protein"
/db_xref="COG:COG0735"
/translation="MASNRDKSISEQIFHIKNQLVEKGYKLTQQREVTVRVLLEHEKD
HFSAAEEVFLLVKEQFPEIGLATVYRTLELLSDLQVVEKINFGDGAARFDLRSTDGSHH
HHHLICTECGKVEEIMEDGLLRLEQQIERQYGFVTDHRLDFQGVCKEQRQKHVLKEQ
AAG"

CDS 1838648..1840987

/gene="topB_1"
/locus_tag="EFAGFIKM_01624"
/EC_number="5.6.2.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P14294"
/codon_start=1
/transl_table=11

/product="DNA topoisomerase 3"
/db_xref="COG:COG0550"
/translation="MKTLVIAEKPDMGRTIAAVIEPKAKNNRTYLEGEHYIITWAIGH
LLGLAEPDAYDTKYKRWNIADLPIIPDQFKIVPNPRTKDQLKMIGELAKRASAIVNAC
DAGREGQYIFALIQQQLKLRQPVKRLWISDLTAESIRRGFDGLKDASEFENLTHAARA
RSEADWLIGMNASRAFTTRHNALLSVGRVQTPVLALIYDREIEIEAFQSQTIFYEVAAW
FRQEGVEYRGLRQGDKLTDAAEAAEIAASVKGKTGQITKYEAKQTKEYPYRLYDLTLL
QREANAKFGYGAKKTLDAQALYEKHKVISYPRTNSNYVTEQNIEGMHKTLLNLLKNGT
YSELAQGAKPELVHKNNKGVCNPSRVEDHHAILPTLKRPGTLSKDEQNIYDLIVRRFL
SHFYPPAEYKQHTVLTEVEKHQFKTSVKELLSLGWKVVLGSGDQEQGGAGKKKTKKNG
NEEEEEAEWTDKAFSVQPELPVQCTKSEFKEKATQPPKSYTEGTLLKAMESAGKQIEN
EELRDAMKD SGLGTPATRAATIERLKNVG YITLQGKKMQLTLKGRTAIELIRRAGVDL
LTSPEMTGQWERRLYQISKGEAGQDKFMENVKKFTLSIIEKVRVQAPAPADAFGEDSR
AGRGKGGKARTQAGNTRTSAKTASGGSTVKTSRQATASSSRVGS GKSTATKAPSSTAS
PTGVRELLAPCPSPGCTGQIIEGKKGYGCSRFKEGCSFVWKEYAGKKITSTMLKSLI
EKGSTQVLSFKRKDGSTVKARIILQDVVTGKLSGEKQDA"

CDS complement(1841023..1841787)

/locus_tag="EFAGFIKM_01625"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKIMKQHILFDLDDTLVYCNKYFNLILGEFFENMQEWFDGHSLT
TQEIREKQLEIDVTGVNKLGFASHHFPQSLIDTYRYFSGKFARLTSPREESYLSKLGM
SVYDQEV EYPH MVETLENLKSAGHS LYTGGETVIQQRKIDQMKLSAYFDDRIYIR
QHKNVEALEGILSNGPFDRRATWMIGNSLRTDIMPAVKAGIHSIYIKQPNEWQYNIVE
LQPNPETS MYTITALEEVPKVIHENIQQQQKRTL G"

CDS complement(1841837..1842757)

/locus_tag="EFAGFIKM_01626"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MAYHVKIDVSPİYEMLN SFLVYVTKKWIQHLDIGPEWILEVEGK
LSSNVRAALAPAATWPFDDFDVLF AWAAYQNDTSEN RDFLDMLAGMTAEDLFARVSPL
LPALTIEESTRIRNSYVPLRLWDEHYCQNMSEDQRVWLEEDAEEKRILLDKMGSELL
IEYATAGVLVEPMPGLNEVILFPTVHNRPINMYCFYEGMMIMQYPVDAPEENEDQPPT
CLLRFTHALADPERLRLRLRYVSDEPKSLAEMCEELGKDEDTVKDQVMALRIAGLLRTH
LLGSRKEKYSIRPDGVSELNMFLESYIRI"

CDS 1843062..1844252

/gene="ycaD_1"
/locus_tag="EFAGIKM_01627"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01149"
/codon_start=1
/transl_table=11
/product="putative MFS-type transporter YcaD"
/translation="MSSITRPKLSHSTANYLILITVIVVAGISQGLLLPVLSIFLEQK
GVSPGLNGLNAAALYIGSFAMTLVAERLLGALGFKKLIVGGLILVMAPLILFPYLPDI
KIWFILRLIVGIGDSALHYAAQLWVLLVTAPEKRGYISLYGMSYGLGFSIGPLGIKL
LGFGDAVPFWVLFVCIAAVLILVLMKLPDTKPEKAEHGQLPERRFRRSLAWAWYALLP
ALLYGYMEAGMNSNFPVYGLRIGFDTSQISSLLPFIGIGGLFLQLPLGMLSDRYGRKK
ILMFAGISGGIIFMLVPVVGTHFWWTLVLLTIAGGLVGSFFSLGLAYAADILPKVLLP
AANVVASFHFTIGSIIGPNLGGQMINWITPGSMFTLLGILYLLFGVAGILFRRKPEFE
SVLK"

CDS 1844336..1845061

/gene="glnQ_1"
/locus_tag="EFAGIKM_01628"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P10346"
/codon_start=1
/transl_table=11
/product="Glutamine transport ATP-binding protein GlnQ"
/db_xref="COG:COG1126"

/translation="MIRVENLSKSVGDRVPVLRDIRFDMQQGEMIAVVGSSGSGKSM
LLKCLAMMEKWDSGRFTVDGAEILKEGWSGKRRIKREWAYLEQNPELFPRTALKNVL
IGRSGQTPVWRMTGMVRSDDYMGAMDYLEGLGLLDKAHQIAEKLSGGGEKQRVAIARA
LAHGAKVVLADEPVIGLDPHTADSVLETLRKLCEEERATVIAVLPIELAEKHATRIWG
LAEGKIAFDIRGRRLTQQEKNQI"

CDS 1845135..1846403

/locus_tag="EFAGFIKM_01629"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLGSVLSGCTVISDPKGLMRKPMSTDEKLYNVVQVKLPPEST
LIRPKDMNNTSMIRVEDLNGDGTREAI VFYETPNENVRIHGMILEEQGGTWVKKLTFD
VPGNELQSFKVLDTNDGNPDII LGVSLQEQA LTA SYKGGALEQVLGGVPYNQYII
DDAQGNTLDLSGDGKSDFVIISLNNSGFATIALYQYEDGSFKEVDRVQTDYTVKEVYN
ALGGEIAKGQMGI VLDAELDDRSSF SQIMYVKDNKLVNAFKSPDQTYRDDKILSGDVD
NDGIIEFGLKETPKGWEHYVFD SRLWFYTYQWDGKDSKKFVSFQFRDDADLFHLNLK
PEWYGKITIDTKSEKEYIRFKMIDTDETVAEIKYFTLSKWEQEGKGSWKEITRTKDR
VIASRVAQSEAGKDALSNTSQLNRKGELNE"

CDS 1846396..1847094

/gene="phoP_1"

/locus_tag="EFAGFIKM_01630"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P13792"

/codon_start=1

/transl_table=11

/product="Alkaline phosphatase synthesis transcriptional
regulatory protein PhoP"

/db_xref="COG:COG0745"

/translation="MSKVLILEDEESIRSFIVINLKRNGFEVLEAGDGHEALRILQTV
PDIDLALLDVMVPGIDGFEVCRRIRETNERLGIIFLTAKVQE QDKVYALSVGADDHVS
KPFSPTELIARIQSLLRRVNVHRETA AKVTFQSGPFSLDLISKQFKKQNEAIELTPTE

FSLIQFFLEKENTPLSRDVLDDHVWGKEYMGDPKIVDVNIRRLRQKIENNPSEPEYLQ

TVWGHGYKWKGREQ"

CDS 1847091..1848590

/gene="rscC_4"

/locus_tag="EFAGFIKM_01631"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00979"

/codon_start=1

/transl_table=11

/product="Sensor histidine kinase RcsC"

/translation="MIKKGITRQIVLHYFFVFLALLLVEFVFM LAVQRYYYESIYNT

ISTHISNSKDFFEPIARENTTEDGNNLSRLLVNLALSNTLEILDN GRVLASSTAFE

SDRAVLQTS DIMQALNGDMGRWIGRQPGTGESVMAVSHKFDLGGENTYVIRYLT SLED

VNSKLLNMGLLAAAVGVGVLAIVLIISIGMANSIVRPINNITAVSAQMARGRLDVRVK

GNYPKHELGE LASTLNFMAHEIVRSNQIKDDFISSISHELRTPLTSIKGWSETLD SGGY

DPEETRIGMG IISKETERLIGLVEEMLDFS KLQQNQM KLVKGTVNIREIVQETMLNVW

AKAEQKQVHLKLETD ETRAYNVHGDGNRLKQVFLNVVDNAIKFSHENS WIFLSVKEEN

GQIIAAVQDTGIGISEEHLIKVRDRFFQVNHQNGGTGLGLAITQELVELHEGTITMQS

ELGSGTTVTVTLP AVAEEMGP EESVTASGDAEVT DERTASDAKSDLEKS"

CDS complement(1848714..1849940)

/gene="glgC_1"

/locus_tag="EFAGFIKM_01632"

/EC_number="2.7.7.27"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39122"

/codon_start=1

/transl_table=11

/product="Glucose-1-phosphate adenylyltransferase"

/db_xref="COG:COG0448"

/translation="MFNKDCIAMLLAGGEGKRLAPLTSSLAKPAVPFGG HYRIIDFPL

SNCVNSGIDTVGVLTQYQAESLHDHIGGGEPWGHGNSSEAGISLLPSYHTGNDEYLGT

ADAIYKNIDYIDQQNPENVLILSGDHIYHMNYRDMLEAHQANNAAATISVMEVPWDEA
HRFGIMAADADLRVTEFAEKPAEPKSNLASMGIIYMFKWDYDKRHLQDAANPESSHDF
GKDVIPQMLNENNPLFVYNFNGYWKDVGTVKSLLWDAHMDLLHNEEDWSLQKENWPMFT
RDWRSKPSAYKARHTKIEHVTSMIHDSCAIEGRSERSVIFCGAEVKGKSEVKDSVVMF
NARIGRGVHIERAII GEGAIKDGAIVKGTADEIVVVGPNIVSAKPAVRTQPVRMLK
EVEKSGRLRAGELSS"

CDS 1850134..1852140

/gene="glgB"

/locus_tag="EFAGFIKM_01633"

/EC_number="2.4.1.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P30538"

/codon_start=1

/transl_table=11

/product="1,4-alpha-glucan branching enzyme GlgB"

/translation="MAIQPLAHPDILPEHIYLFHEGNLHHSYRMLGAQPETCDGLQGY
RFTVWAPNAVEVGLAMDRNEWKGEKEPLYKIPESGFWSRFFPEISEGTLYKFRILTED
GTELLKADPYAFQAEVRPQTASVTSSIEGYKWNDGAWRRKQRAMYNKPLHIYEMHMG
WKRKEDGSLYSYREMA DLLVPYLLEMKYTHVEMMPLSEHPYDL SWGYQNTGFYAPTSR
YGHPKDLMYLVDTLHQAGIGVLLDWVPAHFAKDAHGLRMFDGTPLYEYADPMLAEKPG
WGTL SFDYSKPEIRSFLISNALYWMEMYHFDGLRVD AVTSMIRLDFEKQPGQYRTNDE
GGLENKEAVAFLQQLNETVFKYFPYALMMAEESSAWPMVTL PVDEGGLGFNYKWNMGW
MNDTLDYMESDFHERPSKHLLTFPVVYSFAENYVLPLSHDEVVHGKKSLLDKMPGT
EQKFAGMRAFLGYFMTFPGKKLLFMGGDFGQFIEWKDEDQLDWFLLDYDSHRNLHKFE
RELSNLYLSEKALWELDHSLDGYEWITPDDQDQSVISYVRKGKKPADTLLVLINFQPV
KRERYRIGVMRPGMYTEVLNSDHSVYGGSGITNDMQLPTEKIPFHGHPSLELVLPPL
SIVILKKNTRRKTDSPASITSVSSKTKNKNESNTLKPKRRTKA"

CDS 1852137..1853579

/gene="glgA"

/locus_tag="EFAGFIKM_01634"

/EC_number="2.4.1.21"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39125"

/codon_start=1

/transl_table=11

/product="Glycogen synthase"

/db_xref="COG:COG0297"

/translation="MNILFAAAEVHPFIKTGGLADVIGALPFALKKSGADVRVIMPKY

KGIPAEEKDALQPVITTDVPLGWRRPYCGIEMLVHDGIPVYFVDNEYFGRDGVYGYM

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TIHNLLYQGVFPHELFSEILELDDRYFTVDGAEEYGNVNFLLKAGIVYADHVTTVSPTY

AQEVQTSYYGYGLDGLLSSLGDRFSGIVNGIDTKSYNPATDTKIPVKYRTSLSKKTEN

KIELQKELGLPVRPDVPLMVMVTRLVDSKGLDLVCRILDELLYDDIQFAVLGTGEQS

YEHWFREAANRYPLKMSAQITFNDGLSRRFYAGSDIFLMPSRFEPGISQLLALRYGS

VPLVRETGGLNDTVQAYNEFTGEGNGFSFTSFNAHDMMNITIRRAEEIYKQPEHWKKIV

KNAMGGEYSWNVSAEEYMDIYRRITLDPVN"

CDS complement(1853721..1855487)

/locus_tag="EFAGFIKM_01635"

/EC_number="3.2.1.54"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q08341"

/codon_start=1

/transl_table=11

/product="Cyclomaltodextrinase"

/translation="MLLEAMYHVPRDKWAYAYNSSTIHLRVRTKRNDVQYVTALTGDK

YDWNGTYKEIQLEKAASDNMFDYWEAAVKPQFKRLTYIFRITAGSEDVFLADNGIHYE

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ELDNFYGGDLQGVLDHLYDLTELGVNAIYFTPLFQANSYHKYDTIDYKKVDPHFGDNA

LLKQLTEECHRLGIRVMLDAVFNHCSEDFPPFQDVLQNGKNSKYADWFHINEYPVQIK

DGIPTYDTFGFYGNMPKFNTANPEVKAYLLDVAEYWIKEIKLDGWRLDVANEVDNHFV

RDFRKVVKAANPEAYIVGEVWSDSLTWLMGDQFDSVMNYPFADKVLQFFCGSMDGYNF

ANEMGSLIMRYPQQTNEVIFNMLCSHDTPRLLTRLGEDKRRLLKLSVVFLFTYIGTPCI

FYGDEVGISGDADPDCRKCMEWDPKQDRELYDFYRLMIDLRKSNEALRKGRFRFLKA

DHNDPCIVYERVDDNLHFTVWMNNTPQDRTLSPMETKDWKDALTEEPVFPTEGMMNI

KLDPYGYRILYRQLDPATILHN"

CDS complement(1855755..1856930)

/gene="abgB_2"

/locus_tag="EFAGFIKM_01636"

/EC_number="3.5.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P76052"

/codon_start=1

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/product="p-aminobenzoyl-glutamate hydrolase subunit B"

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KSGSSLAIDAVQFEFHGRSSHAAASPHEGINALDAVIQTFNGINAFRQQVKSTVRIHG

VINNGGQAANIIPDYASAQFYVRAATRKE LNILTERVIQIAEGSALQTGCKLVTSNYE

TSYDEMVTNEAFSAAFSQNLME LGIPQEEIVSGNDHGSMDIGNVSLKCPAIHPYIRVV

DEVHTLHSIAFRDLALQERALDGMILGAKALATTAYDVLSQPELLQTIRTEFEQAIR"

CDS 1857114..1858577

/gene="mltF_1"

/locus_tag="EFAGFIKM_01637"

/EC_number="4.2.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_02016"

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ADFAPYEFHKVINGKDEIVGFDIEIAKEIAKDLGAELVIEDMGFDGLLPSLQSGRVDL

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TIGQSIPGAKLTALDKISDIVLQLQTKRIDAAIVEDTVAAGYLDDIIGLAAAVPDEEQ

AEEAIGIRKGNTPELLATVNGTLERLKSEDKINQMVT DASLLMADKANKSQNIFQVFEW

YKSFYATGVGYTL LLSALGVIFGVIIGLIICL FRLHDAAILRWIGTAYVEVIRGTPML
VQLMIIYYGFSLSFGINFTALQAGIITLSINSGAYLAEIFRAGIQGVDRGQLEAARSL
GMGRGAAMRYIILPQAFKAVLPAIGNEFITIIKESSIISVIGMVDIMYQASVVKNTY
QGLSPFLIAAAIYFVMTFILSKLLGRLERKLSASDRR"

CDS 1858558..1859286

/gene="artM_1"

/locus_tag="EFAGFIKM_01638"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54537"

/codon_start=1

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/product="Arginine transport ATP-binding protein ArtM"

/db_xref="COG:COG1126"

/translation="MQVIDVRQLHKS YGNNDVLKGINVTIGKGEV VVVIGPSGSGKST

FLRCLNLLEQPTS GEIDFEGVSITDPKHNINATREKMGMVFQHFNLFPHKTVEQNITI

APIKVKKQSNQEAEKIAADLLNTVGLYDKKDTFPNQLSGGQKQRIAIARALAMQPHVM

LFDEPTSALDPEMVGEVLDVMKRLAEGGMTMVIVTHEMGFAREVGDRI LFM DGGVIVE

EGTPDEVFGAPKNSRTRDFLAKVL"

CDS 1859704..1860378

/gene="yocH"

/locus_tag="EFAGFIKM_01639"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34669"

/codon_start=1

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/db_xref="COG:COG1388"

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KQYGVALNTMVKANNDISAYNIYGG LKIKIPGKANNVAAAAATESKSQAKTVTTASLD

VNADNKVVQAWGKTFDYSKAVNVKATAYSADPSENGGWGAVDYFGNDLELGTI AVDPS

VIPLGTKVLVTGHSHPLPKQAFVATARDVGGAIKGHRIDIFIPGSKQSVSSFGFQDI

ELYILK"

CDS complement(1860486..1861277)

/locus_tag="EFAGFIKM_01640"

/EC_number="3.5.1.104"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81EK9"

/codon_start=1

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/db_xref="COG:COG0726"

/translation="MRVRLIMLMVIVIFLGGYHAPVSSRDVSSPPSESVSGSDSTEEE
 QLTLGQLRQKYADTFKTNGPSTKKVALTFDDVPDPRFTPQVLDVLKKYNVRATFFIVG
 SRAEKHPDLVKRIVKEGHMVGNHSHYNHPEFSKLSMNAFRKQILHTGDIIRRLAGYTPK
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CDS 1861431..1861772

/locus_tag="EFAGFIKM_01641"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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 SGTTVHIPGHKEQELCERLARKAALQLKVTVIMGIHFDSITRMQIDEIVQTAERLM
 EDHLNKDKRSS"

CDS 1861884..1862555

/gene="liaH_3"

/locus_tag="EFAGFIKM_01642"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32201"

/codon_start=1

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/product="Protein LiaH"

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/translation="MSIFKRLRDLTMSNVNAIIDKAEDPIKMTDQYIRDMQEDLEDAE
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EYKTSYDQNKASADNLRGKLDEMQRKQLTQMKNKRETLVARYNAAKAQTEINKALNGFG
SDTASAGMKRMEEKMMQMEAQAEASNEMSSKGKSLDDEFELGKDQAVEDELAALMKQ
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CDS 1862651..1863052

/locus_tag="EFAGFIKM_01643"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

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/translation="MDLNILAMLVWTGSGSVLLFVLMYVDSLFTKYKDFAEVKAGNMA
VTRMVMKLFAGGYVLATSISTAGHLGEALLVSVVSFIILLILESVVHFMIRKWANLD
LDTGIQQGKTGYGLFSGALHIVGALIIAACL"

CDS 1863076..1863582

/locus_tag="EFAGFIKM_01644"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSVWKRIKGILTKPEPPQAEKTMLQLAPGDICEVSLVTYEVVGR
VQNRARNVAVLTLQDGTAFRYLHIEERELTRYALYTPIDGRLDAPDEVPTLLDLDGRA
YHLEEEYGGMVSTAGRTPYGGAGEQLVWQYQSDDNMLLRVEWQDRRFTLYEGESILPA
DIKVIRSS"

CDS 1863594..1864334

/locus_tag="EFAGFIKM_01645"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKRLAHGLKLMLVLSLVMSLLSACGAAPSVQDTPLESVNGSG
NSTSYVYRASDRTVPEVAQELSDQRQPDQISAENTERMFLVYQDEYYHLQQDPNKPED"

TLVEVDSKEYVRQNYDSSFLQGYLTATLIGNLFDSFGGRGYGNRYGYTNKD TYKPSAG
SYRAPTSNDKKLAPPITVDRKGTITRRGSDKDSSVGSGGGLFN RNKDQSKGTIDRNKS
SGGLFDSPKKS YKKPKTRVGGGRIKRRR"

CDS complement(1864447..1864737)

/locus_tag="EFAGFIKM_01646"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKRCELCGREPVNTTVHHLTPKEMGGTFLPTANLCIPCHKQIH

SLYTNCDIVTLGLTDLQSLRQDERMIPFIRWIRKQPATTIPRVKSNHVRKS"

CDS 1864932..1866227

/gene="moeA"

/locus_tag="EFAGFIKM_01647"

/EC_number="2.10.1.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P99139"

/codon_start=1

/transl_table=11

/product="Molybdopterin molybdenumtransferase"

/translation="MKMNSHSHDMTTAKFNRTAVQVPDAQAQAARVTVGSIEKVHLE

SAHGRTLAETIQAPHPYPFFRRSGMDGF AISTDTIDASSDHQVWFRVIDEIPCGYTS

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LEVQEGQQLLEAGTIIRAGEQSVLATFGIAEVPVFQRPKVAIFATGTELLDVDEPLQP

GRIRNSNSYMLRSLVVEAGGEPVMYGS IADDVNTARAKLEEIQDNDIVVTTGGVSVG

DYDIMGELVLEEHVEMLFNKVTMRPGSVTTAAIYKDKLLFALSGNPGACFVGFGFLFVR

PTIRSMQADAHPYMEEWTAILEEEYTKVNNFTRFVRGTTEIRNGMVYAIPAAARVDES

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CDS 1866234..1866794

/locus_tag="EFAGFIKM_01648"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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HDGHDHFEMDQEGTDSYQFGEAGASAVVVMSEKRTAIMERQATKLEDMLSYSYSGYDWI
VVEGFKDASYPKFVMVREEKDLTLIDQLKGVVGMISWLPSEQFIERSTVSRDITWYSV
HVTEDIAKALLAMVESECRQNGEVES"

CDS complement(1867013..1868104)

/gene="xerS_1"
/locus_tag="EFAGFIKM_01649"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A2RKP9"
/codon_start=1
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/product="Tyrosine recombinase XerS"
/db_xref="COG:COG0582"
/translation="MTNVQKEIDRRKLDDKLPSMPWFVQQFMDYKLPDLSPSTLLEYL
RDYEAFFGWLRAEGLSEASSNKEVTLTEVLRLMDSVTAYRLFLTTRKREGTNSRITVS
RKLSSLRSLFHLYLSQIAEDEDYPLLKRNIMAKIEIKRTHKPKDTAAKLGKILEEEE
LLEFIGYILEGYAVDMEKNKQALYSHELNERDACIASLILNSGLRVSEVVNLNVDDL
DLNNKLLYVYRKGNNDETYKTPVYFREQAKDELATYMNLRQSRYPKREKGLFIALR
NGDSEGSRMKRAIQAMIMKYAKRFGKPFLTVHKLRLHSFATDYQLQNDIYKTKEQLGH
ASTETTEIYAHLTDKTMSEAIERRTEDGM"

CDS 1868298..1868786

/locus_tag="EFAGFIKM_01650"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MNMKIELVPQERSQVIRHLMQFYLYDFTKYLNIDVDSNGIFPEY
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GTRAAYELFKRFPGRWKVTQVRNNVIAQAFWRKIIGDYTGGRFREKFHPELGNPSQYF
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CDS 1868950..1869723

/gene="gno"

/locus_tag="EFAGFIKM_01651"

/EC_number="1.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P50199"

/codon_start=1

/transl_table=11

/product="Gluconate 5-dehydrogenase"

/translation="MNVPTFHLDGQTALVTGAGRGIGKAIAIGLAQSGSDVVLVSRTM

KEIEETAAYIYEQTGRKALALTADVTSKEQMEETFQEAISEMGLDILVNNAGMNIRT

PALEVTDEQWETIMQTNLKSFAFFASQLAGQHMKERGTGKIINISSVGGHTALRTGVVY

GATKAALIHMTKVLALEWGKYGIRVNSVGPWYFRTPLTEKLLDDPQYLQEIVSRTPLQ

RVGELEEVVGPVFLASDAAGYITGQTLLVDGGMSIYGF"

CDS 1869852..1870745

/locus_tag="EFAGFIKM_01652"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="METRKYGNTGMNVSTLGFGGAEIGKNVSKTDVATLLNSALDAGL

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FDSLETSLNIADQEAIDLTLPEARKRNMGVIAKRPIANAAWTYDTLSEEAYPFIYWKR

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LYDEIRARWKEIAGADWTGRT"

CDS 1871367..1872713

/gene="gabP"

/locus_tag="EFAGFIKM_01653"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P46349"

/codon_start=1

/transl_table=11
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/db_xref="COG:COG1113"
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ISVLILLVLAAAGTYFVFGALAQMTADDPKEGAFRTYAGEAYGPWAGFGSGWMYWFSE
MLIMGSSLTALGLFSQFWFPKFLWAFVAIYAAIGLFIAALGAKGLTKTENILAVIKL
AATVAFIAIAGAACLGWLPVKVTPEQLKNEWFPHGGKGVWTGFIYAFFAFAGIEVMGL
MAANLKEPKDAVKSGRVMLLSVSTLYVISIALILLVPSAQLTPDESPLVKAMSTIGF
TVVVHILNGILIIAGFSTMVASLYAITSMLVCLAEDGDAPKLFTKTWGGKDMPLQALC
CTAAGLVLSTLMALWMPKSLFEYVTTAGSLVLMYTWLLICITYIKMKPVKWNRIKVV
IAIVLIVAAVAGTAMEKASRTGLLASVGLLVFLGIITYVVHKVRGSKTPQSAPSKP"

CDS complement(1872770..1873531)

/locus_tag="EFAGFIKM_01654"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MAELYSADEINTLFERLPSWQQDAYSQFADMIADENNTYPCVPG
RMGFLSGHLRYGFTCDPRSEHAAEDMADLLRQYGPVSRDTGHYASMVICETPSDLKD
HTTVEQYQTLFWQMLNRVSSHDEPWPEHISTDPHDSSWEFCFGGEPYFCFCATPAHE
LRASRHFPYLMFAFQPRWVFESINDNTPLGRKMKTILIRKRLAAYDAVPAHPSLMWYGQ
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CDS complement(1873614..1874240)

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/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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MFADLVYMLLIYFGVAHFLDTPFMRSFLWSFGSFILIYTGVELSKLKQGIQGTSTAE
ATVRKSFISGFLMALSNNILFWLGIYGSILATTVKHTDMAHLLLYSSGIFIGILVW
DVIMAGMASRFHKHSSENVLRWISIISGICLIGFGLYFGYEAVRSIFF"

CDS complement(1874357..1874974)
/locus_tag="EFAGFIKM_01656"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MNSTESHKQSIHIPAKTGYALKVKKGSLIRITDLEGQQVVDFA
YDAQNINNRLDPGVTL DVL RNYRIKPGQCLYSNRYKPLISISETVGIHDFFN SACRP
EMYEVL YDKKDHPSCYDNLNTALEPFGISPPDQHYPFNLFMNSVVDGEGKIDVIAPES
CAGDYVEMEALMDLIIGLSACPCEESSCNGYHCTPIQLDVESPAV"

CDS complement(1875123..1876616)
/gene="nylA"
/locus_tag="EFAGFIKM_01657"
/EC_number="3.5.2.12"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P13398"
/codon_start=1
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/product="6-aminohexanoate-cyclic-dimer hydrolase"
/translation="MSSF SYTSYDAVGLAELIRSREVSPVEMVEAAFARLEEVNPQLN
AVIRTYENRARVEAGLVRPGEQPFAGVPLLLKDISQSLEGEFLTSGSRLFSEHRALRN
SNFVTRLRDAGFIFIGHTNTPEFGLKNITEPRLHGPTRNPWNINHSPGGSSGAAAAV
ASGIVPLAGASDGGGSIRIPASFGLFGLKPTRGRTPVGPVGRQWQGASIDFALSRS
VRDSAALLDTLQVIQPEAAFHAPLFPGSYLADMSYPHQ RKLKIAYTTDSPVGTPVSAE
AKESVYKLV RWLEDQGHVVEEKLSPVNGVRLMENYYMMNSGEMAAMISSMERSMGRAL
TSDDMEIESWVLA EAGKKVSAAEFVHSLAEWDVAAAQMSTL FERYDFYVTPVNAFPAP
KIGELTPHDEQIRNLMRISELDKTQQQLIYEMFEPSTLYTPFTQLANLTGQPAISVPL
HMTPEGLPMGVQVMATKGREDWLLHLAGQLEQSDLWIGMRGNPLFPA"

CDS complement(1876934..1877914)
/gene="impX"
/locus_tag="EFAGFIKM_01658"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:D5RAW5"

/codon_start=1

/transl_table=11

/product="Riboflavin transporter ImpX"

/translation="MEKTSATSTVYRKERSNTGFWLVVLGAALWGVDPFRILLNTM

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THNDPNTVLLLQKMQLFAIVLAKLLLKETLPRRFGGLFFIALAGTYLLTFGFTLPLG

NWDNWIHAGSLLSLGAAALWGGSTVMGRMLGQARYETVTSRFRVVALPLLIFMTWNE

GAAWTFPSGTGEQTAVILNILGQALLPGLLSLLLYKGLSSTKASVATLAELSFP MAG

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CDS complement(1878297..1878797)

/locus_tag="EFAGFIKM_01659"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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SGGLSIWQLVNHMYYYNHRLLCRMQGKEPTLPAVDSNEYTFGNPGDATDAAGWNTLLQ

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SWKIVF"

CDS 1878941..1879492

/locus_tag="EFAGFIKM_01660"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDRLWTDVFNSDYHDWRGGDRSEDRLGKASWQQDFLERWQLNAS

VPASPEDELSMTNFRNELLALGVRVSSGASLTDIEKQWLNGVMEAGHVRRILTIDQE

LKLQLVAVEAHWHQVMAEVAADFATTLVEGEGRRIRICDNSDCRWMFYDDTRSRTQKY

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CDS 1879613..1880983

/locus_tag="EFAGFIKM_01661"

/EC_number="3.5.4.32"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9I6Z0"

/codon_start=1

/transl_table=11

/product="8-oxoguanine deaminase"

/db_xref="COG:COG0402"

/translation="MRTSYLLKNGCVLSMDAKIGQYKRADVLIQDSLIMAIQPDLDIP
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NRDSQLTYSNNDVRRVKERYFSSRDQLITYGLAIRGPEFSHWDTTVKEIELAQELDAI
CSMHAGFGSWGSDRSISHLYEAGLLSPRVNIVHGNTMGMDKEYKMLADSGASLSVTPE
VEMMMGHGYPATGYFLEHGGTPTLGVDVVTSTGGDMFSQMKFALQAERSRANEQLLQQ
GEMPGELNLQSSQVLRFATSAGAQAQGLEQKVGTLPKGKADLIMIRTTDLNMFPVHD
PIGAVVQFANPSNVDTVFVAGRLVKREGKLLNVDLDAIRHTAMQSKDYLLTQYRMSDA
ERITFS"

CDS 1881503..1882939

/gene="yhdG"

/locus_tag="EFAGFIKM_01662"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07576"

/codon_start=1

/transl_table=11

/product="putative amino acid permease YhdG"

/db_xref="COG:COG0531"

/translation="MRENKQRSSLFRKKPIASEGNNSSALKRALGPLDLTTLGVGAIL
GTGIFVLTGVAAATYAGPGLVLSFLLAGIICAFALCYSEFASSIPASGSAYTYSYTA
FGEVIAWVLGWDLILEYGFASAAVASGWSGYFQTLLSGFGLLELPHALTSAFSLEKGT
FDITAAVITLIITFLLTRGVKEAARANGIMVAIKIIVVLIFIGVGVFYVEPTNWQPFL
PFGISGVTAGAAATVFFAYIGFDAVSTAAEEVKQPQRDLPIGIIASLAICTVLYIVVSL
ILTGIVPYNMLNVSDPVAFAFEFVQLKGLSWIVSLGAIAGITTVLLVMYGYQTRLLYS
MSRDGLLSPVFSKVSQKSGKSTPAVGTWVAGIIVALFSGFISLGHLELTNIGTLFAFAV

VSLGIIVLRKNNPDLKRGFRVPLVPLIPILSALGCVYLMTRLAALTWITFFAWLIIGL

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CDS 1883198..1884277

/locus_tag="EFAGFIKM_01663"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNTPLHTNSDHQNAAFGFALADSSVLAEQLIVSQSGGAGDLQL

DIDPQRFLKDGRKVSIAQQLDSPVNRQDANIYGQELAYVQYAVNLKPDSTISIASI

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PAEAASLSSPSQAVWSRNHHVFDSYGRGGFILADLPRLAERVEELMGLGNHNLIEQFA

EGDLSNTLLEEGMMAIAWGVTPWCYSLYSAPDEQSARILAVDKLGDEPERKGIYRLDP

SIQQLSIVPANELAYWPACVQNDWPVIDVAGEGETLHMDLYTQICESVNGLHENPLPS

FVLTRSQGKPEAILPLINVVIVHEA"

CDS 1884553..1885473

/gene="xerC_1"

/locus_tag="EFAGFIKM_01664"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A8P6"

/codon_start=1

/transl_table=11

/product="Tyrosine recombinase XerC"

/db_xref="COG:COG4973"

/translation="MMTEEIQEQYADELEAFHIWMKDAGYTGHTVKS YTRDVVEFLIS

IQGKSLEQVKKLHVLSFLSRARERGVSDATRNRKHA AVNCFYKSLIELELLTNNPAFG

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DYNAERRTLDFVGKGRKWRS LPVPETVANVLSQAMAERLDPWRPKEEALFVSQKGKRL

SIRSIQLISTETFERFQQESPVNQRQNYSSHKL RHSFATMMLRRGADLRTVQELLGHA

SIQTTTVYTHVTSREKEEAMALLDVKLPTY"

CDS complement(1885747..1886676)

/gene="ldh1"

/locus_tag="EFAGFIKM_01665"

/EC_number="1.1.1.27"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P14561"

/codon_start=1

/transl_table=11

/product="L-lactate dehydrogenase 1"

/translation="MTNSAALKPSRVVIVGMGAVGTTTGYTLMLRQRSSSELVFVDVNH
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SIFKDIIRITEVNSHGILLIATNPVDILSYTSWKQSGWPASRVIGSGTLLDSARFRY
LIGKNKGIDPRSIHAHIIIGEHGDSEVPVWSLANVAGTDLELDEETQQDIFDRTKNAAY
EIINAKGATSYAIALALDRIVAAILGNEGSVLNVSTYLEDYNGVSDVYLGVPVVDNRN
GVREILPLPLNETEKVAFQASANKLKEQIAGLE"

CDS 1886975..1888291

/gene="hcf136_1"

/locus_tag="EFAGFIKM_01666"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01348"

/codon_start=1

/transl_table=11

/product="Ycf48-like protein"

/translation="MRACILDERGGTHLRLQWIKIAQTALLSIGIAAVLAACTDSDQP
PVAEPPQQQEDAGNTGQTLTVPPVNSTESADMAKYQIQTRLTDFQLLNDNGGLAWGV
TRNALRLYYTQDQGKTWTNISPSENVQFPANPKYGQSIYFVDRAHWIVREGMGGTD
MVLRTNNGGVTWSLSSLSKTDKVTAFVSPEKGWILTTVDTAIGKQEKKLYFTEDGG
ITWNRMSSSNEDGKQEAEEISKRGYTTGMTFSDPKHGFLEFGTPKLYVTSDGGEN
WDTGPSFFDRNKFNGCGNFSVSSPQFFGREAQSAWMSMSCSKGESTTFNGFFTTDGGK
SWKLSNFTLNKQTGANRNLSPVFLNASEGWAMQKGITYHTKDAGKTWSALPASSVLEK
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CDS 1888438..1888647

/locus_tag="EFAGFIKM_01667"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
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/translation="MRTNGQTQFTQADELTRYMLQLCYTCDDANRCTTEEAVKACMAE
HAQADQPEPAEGGEVTRGFMDLMYA"

CDS 1888878..1889351

/locus_tag="EFAGFIKM_01668"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:ISfinder:ISDha13"
/codon_start=1
/transl_table=11
/product="IS200/IS605 family transposase ISDha13"
/translation="MANKSYSLAHTKWMCKYHIVFTPKYRRKEIYNQVRKDLIEIFKR
LCKYKGVEIIEGHMMPDHVHMLVAIPPKIAVSTFMGYLKGKSSLMIFEKHAQLKYKYG
NRKFWAEGYYVSTVGLNEATVRKYIREQEHDQALDKLSVKEYEDPFSSNRSKKK"

CDS 1889627..1890049

/locus_tag="EFAGFIKM_01669"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTTFLDARTSQNASLANSIAIPITVLNTPQLFGQIGLQTAGAGA
NPRVQFKGTVSVQLPLALVGITITIVRGTLSTDPVIYSATSTFGLSVLAPQIITFSAD
DFNPPITPQLTYTAFVSSNLLGTVRVGPENFDGLVVSD"

CDS 1890667..1892460

/gene="dap_2"
/locus_tag="EFAGFIKM_01670"
/EC_number="3.4.11.19"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01960"
/codon_start=1
/transl_table=11

/product="D-aminopeptidase"
/translation="MKINQRYYYVYKAITCFLSLALIIMTCAVPVNAEVGNVETTPSR
IALSSLEETIDSYVATNQNTAAVSVVAIKNGETIVNKAYGYADFELQRKADTSTVFE
WGSTSKLLVWTSVMQLVEQGKLDLTDIQNYLPEGFLKKLEYDAPITLLNLMHHNAGW
EDRLIDLWYSSESDELGEALQKFEPQIDKPGSVVAYSNYGTAMAAAYIVELQSGQP
FYKYVNEHIFKPLNMKDTSIHPSQYDNLNVLKRRNEIQGYTTRLKLIPKNRAYISLFP
AGGAMGTAEDAARFLAALMPVDRSNLLFENNDTLDEMLSTSLYDGTSTPRIAHGFFE
VEYWVPALEHAGSTAGFTSKFVFDPESNFGFVMTNQSNEMAYNVGLVQKVFGSSFST
NSVESESGGYLPARRVVSGFTKAYSMLSLQKYTTFDLSNFASVVERNGTVEKVSISY
NDFLPVSNTINLIKASFIALAVAILLSLRAIIGYFIRLSKYKLKNWERPGTGFDKYH
IVINIASMVLILNTILLFMRALGFSPYSSLRIHLILNLVYVILAVAYLVLLFYKLLKR
SYSKKQKAVYIMSGMSAFLFAAFIMGWDLYF"

CDS 1892518..1893297

/locus_tag="EFAGFIKM_01671"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNIQDLPIEIKEHIGEVQKITFPKQGHTSTVAILDTFDQKYIHK
KTENDLYNEWLSDEYKVLQYLYHTGLPVPKAYSFHIEDTSRWLLMDYIDGISLREFLS
KMPDLQSKEKAIFNFGCLCKKIHECSCPVELLNNNTPWLDTMLNKAEYNLTHFAVDGS
EELLQQLKEGRPKPIENTFIHGDFITDNLVNDCNIVGVIDWAGATYGDPRYDVALAI
RPKHNAFDNERDREIFYNGYGKLKITDEEYNYEDGIYNFF"

CDS 1893355..1893780

/locus_tag="EFAGFIKM_01672"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSPPKHILSAAAVINEQNELLIRGPRRGWEMPGGQVEEGESL
SQAARETKEESGIDIEIKFCGIFQNIENSICNTLFLAKPIGGELTTSLESLESGFF
PIEEAILKVEWKNFRERIEYCLKPEMQPFCIEFSDKNNI"

CDS 1893900..1894970

/locus_tag="EFAGFIKM_01673"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSSGKKSKRLDTVRSLVHEMLLEESNNKEGMLVHLYGVSNFASM
LAMKRVQDSEITAIALGLLHGFYFYKTGIEDFPGPNSADAVRPILRSAEIFTTDELSII
LKSIFYQEDTHLVHGPYEEVIKDAILFQIYFQNPNNRNLKAEISRIQNVFTELGISKE
NIKADVNNVNVQTVHINTEERRSKLADLAETLARQNIIGTSGDQRYQEICRYWPDSDIC
KVLEANWCAAFVYHCCMKVGIKLPIRYPNRMRLAGVGAWLDWAQLAETEFFYQDMQE
GFEPERGDIVIYEKLLTDNSHDHIGIVLACDGDQLLVAEGNTDNKNYSSVLYRERGHG
ILGYIRVDESYQFNFQGEYRPT"

CDS 1895066..1895488

/locus_tag="EFAGFIKM_01674"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRVDVVYSLTNPSKSKVLAVRNVGRSSWSLPGGAVEADESWE
QAAIREAKEETGLDVGVGIVAINNECKFEEIKEHAIFITFRAEIVGGREEISRPDEIF
EIAWLDITQADELMPYYKNGFKSLLNGNEITYFNEGK"

CDS 1895523..1896269

/locus_tag="EFAGFIKM_01675"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKHSVYETNSFYWDTKGNDFLSAIVLPNYGAFISEEKHQLFGD
VSGLKMLEVGCNGQSLQYHGDRKAGELWGMDISQKQIEKTQQHLRTYGISATLICSP
MEEECGIPTNYFDAVYSIAGWTTDLEGTFSRIASYLEKDGIFIFSWSHPIHRCVVE
ENDRFVFNKPYSDESCYAVSPDFCHGELTLADRQLSTYINALAKAGFVIEQMIEESDE

DIMQLHNNSDSLLKRAKMLPVSFVIKARKR"

CDS 1896403..1896897

/locus_tag="EFAGFIKM_01676"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRRLLPLFVVTGASGTGKTTISLVRKQLPEFDVFDMDIIDNV
DW
QVAKENWLRIAYNISLSGRGTVLCGTMVPENIASSDYIDRFDRILYMNLHCDDVTRET
RLRARGWDVNLIEDHKSFANWLLQNSITAFDPPMQTIDTTELTAAGVAEQIKEWVLKN
WCEE"

CDS 1896941..1897483

/gene="ydaF_2"

/locus_tag="EFAGFIKM_01677"

/EC_number="2.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P96579"

/codon_start=1

/transl_table=11

/product="Putative ribosomal N-acetyltransferase YdaF"

/db_xref="COG:COG1670"

/translation="MLPFQVNESIVLKLQSRDRDELYALIDENRKYLRAWLLWVDKR
QSPSDLDSVIEVWTHNYEEKNGFDSGIWFNEQLVGMLGLHYIDWNNRATSIGYFLAES
AQGKGIITKSIEQLLKYL FNELKLN RVIIQCAENNFKSRVIEKIGFSNEGTSREAQW
VYDHYENIVTYSLLSSEWHT"

CDS 1897526..1898119

/locus_tag="EFAGFIKM_01678"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFLNVLLWLIIILWVISLYFSFPKKDRMYTVNVPSTYYIQSSNRL

DIQKNYECAAFSSAFVLRHFGLESKGTKLYETYPKLLDGTVPKAVVFFRKLGYQA
MYLRGNVNTLKKQISQGVPIVLFIRVHPKQRYLHFVPVVGYDETHFYLAESLDHKINC
DEEYYNRKTSINELNMLWRSWLPFSQNSYIVIHMPMQI"

CDS 1898436..1899512

/locus_tag="EFAGFIKM_01679"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSYSEVKKRMKRKKATFHPCKVKRKERRLKVVKKFVQVKCPPPE

VNISTPTVVGPTGPQGIQGVQGIQGIQIPGKQGVGPPGAQGPAGGPPGPQGPQGQPGPA

GAIGSQGPVGPAGPMGAQGIPGEAGAVGPQGPQGNPGPAGAIGPQGFPGPPTGATGPAG

ATGVIGTTGVAGPAGTTGVTGTTGVAGPAGATGVTGTTGVTGPAGATGVTGATGAAGG

VLGFADFFALMPPDNAATVAPGADVNFQDGPTSGTTISRTGPSSFNLAAIGTYLVMF

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ALMTPLAGGTRPVSAHLVITQIA"

CDS 1899766..1900335

/locus_tag="EFAGFIKM_01680"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKNGHWRKITWVVAALLLIMITACGNSKFNPNEFSEQDLAVTKT

DSEDKITYGMSQEEAEKILGEGTSTGVGQSYQYNNGITIGYRDAKVVSILNKDSKGY

FKTAREAEAGMTHQEILDLYGKEHVLVESERNIDYAYHIQKETFLDEKSLQAEKDDLA

IYRASFMLTKEGQVNQVILSDQRFATTFK"

CDS 1900544..1900936

/locus_tag="EFAGFIKM_01681"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGIESSWMFDLFGTVFPVVFVLIIGIVLLSMGKEVWRWGRNNSE
PLLTVPSTRITSRRMKMSQSQSEPGSTARTLYYVTFEVESGDRLEFKVNGEEYGLCAEG
DEGRLSFKGTRYVGFERYNRVYSERLRG"

CDS 1901084..1901833

/gene="gdhIV"
/locus_tag="EFAGFIKM_01682"
/EC_number="1.1.1.47"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39485"
/codon_start=1
/transl_table=11
/product="Glucose 1-dehydrogenase 4"
/db_xref="COG:COG1028"

/translation="MSFTDQVVVVGTGAAQGIGRSVAEAYAVAGAKVVLADYKEAEGAA
AAASIRNEGGEAIFVQC DVRSEQDITNLFRTTVEEFKQIDVLVNNAGLAKWKSPYELT
LEEWDDVLNTNVRSCFLASREAAKHMKSNEHGGAIINMASTRALMSEPDEAYAAASKG
AIVALTHALAVSLGKDQIRVNCISPGWIETGDVEKLLKKEDHEQHPSGRVGVPSDISRA
CLYLSDPSNTFVTGTNLVIDGGMTRKMIYED"

CDS 1901978..1903723

/locus_tag="EFAGFIKM_01683"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MFGKQSRKVFWLLLLIGGMIMIGNESPAEADGADIRAAWVWQAQ
SVSNGDELLANAANKHINRLYVNVDLTSLKEVYQTFIAKASRAGIAVEALGGDPSWAL
SGREGPMLRLASWVSDYNQAAEPNEQFDAIHLDIKPYVLPWKEDAKPLVQSWVANMN
LLFEQVRQDGAVTVNIDLFWLDSYTVTGNRVSEADNEPLSRWFIEQVEHVTLLAYR
DNAQGNNGIIRLIEQEMNWADASNVSVTVGLNTKMPGEEFTSFAGKGAAQLESVIEE
VASAFSEHNSYAGSAVHDIVYWGQLEPSELPSPENPSNQPEIRGTIWEATQVTNDGG
EHILAFAREQNINWLYVRLDLDPYSSYRSFVKRAKAQGIEIHAMGGHPIWGKKENRP
RIKRLIDYVKNYNAESEPDERFEGIHLDIEPYTLPEWENSRTLLTEWAANITFFQEE

TKKDSLETSA DLAVWLDSFALPGKDTSVAEFMIRTL DHVSLMAFRNNAEGSNGIAAI
VSQEMEIADRFGKRLMISVEMKQNH EGP HISFY EKGA AEMELQLAKLPDLLAEYQAYQ
GNIVHAYDYWIEAKP"

CDS 1903689..1904306

/locus_tag="EFAGFIKM_01684"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPMIIGLKPSLKQASIIRNELLRDFTLGEVPGFFLWKKDGIVSP

NGLLHNTMYGDEQLKQGRKQTM AVIKANSE DVKLLARLMRAEAE GDGEQGM LLVGNVS

VNRVLVDCLDFKDIRDINRMVFQNP GGYESTQ KGYFYQRARQSEIRLAQRVINGERFW

PASNSLWFFRPVAECPATWYDQ QNTGRFKAHCFFSPSGEDCPEVY"

CDS 1904325..1904840

/locus_tag="EFAGFIKM_01685"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MINQPYQPTTQTLGQQANSVMGQQANSQVQGTSYKIGNGMPAMS

PTPGMVSPSSTSVPLVSSGSPMTPTGAVITTTAPQFEQSYIENILRLNLGKFGTFYM

TYEGNKEWNARIFQGIIEAAGRDHIIISDPKTGRRIMLLMVNFDYATFDEPLLYQYPG

VVGNYPQAPSR"

CDS 1905067..1906650

/locus_tag="EFAGFIKM_01686"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNSWIEGAMKGETEAYAQLMSQYRGMALAVAYNRLGDTFWAEDV

VQEAFTAEFGNLSKLEAPEAFPGWFKVIVERQCYRWLRRKQHTMIPVQELDHVFHEED

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KRLFDARSKLKRSMPVRDLVSVFSDLYEGGKGLLHIMNGDHAANRLRESGIQGDILVW
RELYTFGPVAKEMGDTKERQNRASVLEQQLGIPQAEYLKIKELERKLHSFQQYKEIVL
WFEYDLYDQTMLSYLLHYFKGQALQNTKLNLLCIDSYPEIEHFRGLGQLTSTQIERLS
GSWHVIEKNELQAGAQFWEAYTSTDFRHHLDDLQADTSALPFAKAAFKAHL SRLPSVS
NGLGLIEQATLETIRAGVEHPYPLFREVGDKLHILGMDLEYWAHLKRMTEGPHALLQ
MSGATTFPNFKQHDEKFRDGVLSLTALGIQVLNGEVDWALLKQDEFWIGGLHNESGER
AKWRWNPASETLVEIESTS"

CDS 1907026..1908342

/locus_tag="EFAGFIKM_01687"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WFP3"

/note="UPF0053 protein Rv1842c"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSDPLPSILNLVIIGLLVLMNGFFVSAEFAMVKVRGSRIEALVE

TGNKNAIYASNIVRNLDAYLSACQLGITLASLGLGWLGEPAIAHLLPEMFTAFGLGPV

YVHGISIAIAFVIITLHIVLGELAPKTMAIRKSETITLWSAALLTFFYKLMYPFIWA

LNGMANGLLRLFRMAPASEMDSAHSSEDEIRILMKESNKSGLIDNTELALVDNIFDFTD

TTAREIMIPRTEMICLNANESMLENLEIASESMRTRYPVYNGDKDHIIGFIHIKDLMR

SQLTDTISVIRPILAVPDTTLISDLLKRMQRSKTQIAILIDEYGGTSGLVTLEDIMEE

IVGEIQDEFDHERPVIEQVDEMEYSIDGLMLIEEVSERFGLEMDRADYDTIGGWLYSR

VDAIPPEVGQSVEYGGYVFIQETEHKRISRVNVIKLELLVEEEGA"

CDS complement(1908412..1909062)

/locus_tag="EFAGFIKM_01688"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKFQFKSRRHRHSSNPNELHIEVSGSFKRWLVILVSALTAGTL

IYFLATARESWISMGIDRYVLPFMIWGLVLSPILAFLFKQSGRTL SHVKFLRVFGIA

FCLLPLVLLFYVLPVTLGMVNDHLTQFKKNPVLSTTKVGDYNSYEVTFVDTMPYAIIT

IKTPTTTQSTRKKLNIQYDLAPGENAYVTYKRISIENCLVTENRYADIVIHAPKES"

CDS 1909295..1909807

/locus_tag="EFAGFIKM_01689"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRKMKTSAASMLKITLVALLMVPTILAIPTSEPAVASPMINVS

SGALTAPPPPEPSIHSLATTRELGHYQAVGAVIPGGGLSAIVNTKTMTYTAMKTLVS

DYRLERWTGTAWVTFKTNSNNATNTNLLNATSDWTVMPGYYYRVTSIHTAYDGSTTDT

SKHVSGTVLF"

CDS complement(1909810..1910772)

/locus_tag="EFAGFIKM_01690"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEALSKGKSDKNVERFDSELEDEYFDAAFDLAFDEAFHQAVSAP

SASHTESMQQSWQKVNREINRIGLRKKRIRTLRLSVVVAASVTIGAVIFSLPSGTQAV

SPFVQSIKDWGNGMKSIVIEDRTTHLGADPSTAKTPPPPETSLDDILKVQEEEEALNTP

SYELSSHLFRPVLVTEEIARDGFMGDFLLSKAIPERFNKVKFELVIDTENPVNPDDYY

ESTQMRVQYTSEGKSIEDIIQFDYVHVMPGEKIEGAMLRDMSTVKLADGSEALMYIG

PPYNSFQWMMGSNNMSLFGTLSEEEMTAIANDFQEQKFPGSTRR"

CDS complement(1910741..1911331)

/gene="algU_3"

/locus_tag="EFAGFIKM_01691"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q06198"

/codon_start=1

/transl_table=11

/product="RNA polymerase sigma-H factor"

/db_xref="COG:COG1595"

/translation="MANRLQLLLASDFHNLGSALQEEVYYEYNNMVHGLIVYIIKERA
AAEDIIQEAFIKIKNKPIFEDEVKLKAWLKVVTRNTAINYLKKNKNNRNQLDTSVF
IDMETMNQTAASVESMVETQMMEESIEYYLRQLKPEYRVLVELRWKKGLSYREMAELL
DTSEDIVKQRLFRARGSIKKKLHKEWGGSSIEQRQVR"

CDS complement(1911578..1912810)

/locus_tag="EFAGFIKM_01692"

/EC_number="3.4.11.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P24828"

/codon_start=1

/transl_table=11

/product="Aminopeptidase 2"

/translation="MLSFEQKLDRYAELAVKVGANVQPGQVFVISAMIDTAEFVRLLV
RKGYEAGAKQVIVKYGDETVNRLRFEMAPEESFQEPKWHAAELEELAANNAFLTVL
SSSPDLMKGIDPERISTHQRTNGQAMAKYRQYQQADKMSWTGVACPSPDWAAKVFPDL
PAAEQVSQLWEAIFAARADLEDPAVAWEQHIERLETKAVALNNKKYQALHFLSLGTD
LTVELPEGHIWAQAGSVNEQGTPFVANIPTEEVFTAPAKHGVNGKVSSTKPLSYGGS
IDRFSLTFENGRIIDFHAEEGQDTLERLISMDEGSHYLGEVALVPFHSPISESGILYY
TTLYDENASCHLAIGSSYAFNIEGGKTMSPEELAARGMNTSITHVDFMMGSPETDIYG
ITANGEREAIFLKGDWAF"

CDS complement(1912901..1914133)

/locus_tag="EFAGFIKM_01693"

/EC_number="3.4.11.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P24828"

/codon_start=1

/transl_table=11

/product="Aminopeptidase 2"

/translation="MNNFETNLQQAELAVQGVNVHVGQTLVVNAPISAAHFVRLIV
KAAYGKGAKLVKVNWSDETVTRLHYDLAPDEAFSIEPKWFAAEMTELVEEGAAILHVI
AENPDLLNGVAQERIITSQKVRGKALEKYRSYQMADKFSWSIVAVPSPEWAAKVFPDL
PEAQQVDRLWDVIFKTVRIGEQDAVAEWKTHLQNLDSRADLLNNKKYKKLHYTAPGTD

LTIELPEGHIWVSGGSVNEQGHVFIANMPTEEVFTAPLKTGVNGTVRSTKPLSYGGNL
IDGFSLTFENGRIVDYTADQGLDALKNLIEMDEGAHYLGEVALVPHQSPISDTNILFY
NTLFDENASNHLAIGNAYAFCLGEGKTSKEELIERGMNSSLTHVDFMIGSGEMNIHG
VTSEGAEPIFLQGNWAY"

CDS 1914384..1914650

/locus_tag="EFAGFIKM_01694"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNIEIISAEMRREGEKGYVGNTVYRTEGEKSVYEITFMSKNGKD

WDYSLHFTEQSGDEEELLRMDELLENDDLYNQLLDAALEAFPA"

CDS 1914831..1915640

/gene="yflN_1"

/locus_tag="EFAGFIKM_01695"

/EC_number="3.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34409"

/codon_start=1

/transl_table=11

/product="putative metallo-hydrolase YflN"

/db_xref="COG:COG0491"

/translation="MASDNLITEGLTGLEEVAPDILSLRTL FVN VVFIGVPGSRNWWL

VDTGMARFTDHIVQLATERFQGPPSAILTHGHFDHVGTVIELEQFWGVPVYAHPLEI

PYLTGLKDYPADPSVGGGLMSRLSFAYPNEAINLDDRIFSLPKDHSVPGLSGWEVWH

TPGHTPGHVSLFREADRLLIAGDAITVKQESLWSVLLQDKQLHGPPSYFTTDWQAAH

QSVQHIRHLEPKLAITGHGHALSGDMLSESLKRLDLDFEESTVPDHGKYVD"

CDS 1915835..1916845

/gene="galM_2"

/locus_tag="EFAGFIKM_01696"

/EC_number="5.1.3.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39840"

/codon_start=1

/transl_table=11

/product="Aldose 1-epimerase"

/db_xref="COG:COG2017"

/translation="MTQQNAAFEEQFGGIPAVWLRFNQFEAAVIPSVGANLVAFRDTE
KGFRYLREPNQDQMDEFMAAPAVYGIPILSPPNRYEDGRFPWNGKVYQLPVNEPATGN
HLHGFLHDAEWKVEGYGSDQLESYVLLSQDVKEGHTFHQYLPFTFTVTLRYSLSQGL
QQQLIVRNNGTEYMPNLF AFHTAIAVPFAPDSQASDYTAKVTIGQRRELNERSLPTGQ
FQPLTPEEEQLKKDGVSPFFAAMDNHYAEPQNGRNYMELTDNRTGDKLVYDVGTSYK
HWMIWNNNMGGEFFCPEPQMNLVNAPNVEGIPAEIEGLIGLEPGELFEQSSRLYPIAS
QK"

CDS 1916978..1918366

/gene="fumC"

/locus_tag="EFAGFIKM_01697"

/EC_number="4.2.1.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P64173"

/codon_start=1

/transl_table=11

/product="Fumarate hydratase class II"

/translation="MEYRIERDTLGEMKVPADRLWGAQTQRSKENFPIGNEHMPMEVI
RALAILKKSAAASNHLKGLSAAKSDAIYAADEIIAGRIDDHFPLVWQTGSGTQSN
MNVNEVIANLGNQLLEQKGKEERLHPNDDVNMSQSSNDTFPTALHVAGVLAVEDQLLP
AIAVLKATFADKSEAFKDIKIGRTHLQDATPITLGQEISGWEAMLGKSERMIRESVQ
YLKELAIGGTAVGTGINAHPDFGDFTAKEIGKHTGKDFVSAPNKFHALTSHDEVVYAH
GAVKALAADLMKIANDVRWLASGPRSGLG EIRIPENEPGSSIMPGKVNPTQSEAITMV
VTQVMGNDA AIGFAASQGNFELNVFKPVIINFLQSVQLLADSI AFNDKCAVGIEPN
LDQIEHNLNNSLMLVTALNPHIGYENAAKIAKLAHKEGLSLKQATLQTGLLTEEQFDQ
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CDS 1918543..1921287

/gene="rcsC_5"

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/EC_number="2.7.13.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00979"
/codon_start=1
/transl_table=11
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/translation="MSKTRRFTIRSKILLGYLVVVLLFGAVLLVLT AQINVLQKENDF
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SQLTTFRNTEIALTEARVTELARRSSTLLTIMYTLWGIIAALSIAAAIVISGNIVKTL
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APGEGLVGQSAVEKRVLRMNDLPQNYIRISSGLGYTSATSLTVVPVLFEGRTIAVIEL
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ILRNLLSNAFKFTSEGEVALTISKMSLAHPELKDQETDVIAFSVSDTGIGIADNKL VQ
IFDAFKQADGATARKYGGTGLGLSISQSLANLLGGSISATSREGQGSVFTLFLPLRRD
EPETMNASRLFLNEVATTPEINKLP SMTSGQSDVLLT PLEEALLSGRQVLVVD DDIR
NVYALANALEQYGMNVISAQNGYECLELLERGGVKPDIIMMDIMPELDGYETTRQIR
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CDS 1921715..1923337

/gene="pucR_2"
/locus_tag="EFAGFIKM_01699"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32138"
/codon_start=1
/transl_table=11
/product="Purine catabolism regulatory protein"

/db_xref="COG:COG2508"

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DEEYGSLLVFTDSALSLRAEEELFQQAADVLA FYMDMTYREHINPTVQDEMRTLTSQY

LDNKMTVQELTTLSENKGVHLFQGT YQCVLITLEPTLFAEGKLLKQIHRELQYNPLMQ

FTASQHFQIEDGILSIYTCPTGRDYGEELSSFLLSRFGDVLA AQEAKGAPAPRFWISK

MKHEPKSLREAYQECLDTRQLARRFGMKDRALQFEMLEFAYVFQHVPDNIMENYCNKV

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CDS 1923576..1925081

/gene="uao"

/locus_tag="EFAGFIKM_01700"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q45697"

/codon_start=1

/transl_table=11

/product="Uric acid degradation bifunctional protein"

/translation="MSDLIKLVNNWSITQFVHTFGGLFEESPWVAERAGLSRPFDSFE

QMMKVMKNEVQASDDQVKLQLLRNHPDLGARISMSSNSVQEQAGAGLDSLSQEQYNEL

QQLNKVYTSQFGFPFILAVKGHTASSILESMRQRHRRGREEEFETALKEVFKIAGIRL

EQWLAQIGHEHEFVSKPAAVQQRTMYYGKGDVW MYRSYAKPLTGIQSIPESPFIGRSN

ILFGLNIKVAVQGDEFLPSFAEGDNSLVVATDSMKNFILKHAADYTGATVEGFLALVS

RRFLETYPQMSKVQMTADQIPFEDIPIGLEGSYRPSALVFRYSQNDRATAAVEAERSG

DSIELSNHFSGVADLRLIKVKGSEFAGFMQDEYTTLPETWDRPLFIFLNINWRYEDPR

DGMDDQRGRYVAAEQVRDLAAAVFHECRSASIQH LIYQIGRLLSRFEQLSEVSFESN

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CDS 1925081..1925458

/gene="pucM"

/locus_tag="EFAGFIKM_01701"

/EC_number="3.5.2.17"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32142"

/codon_start=1

/transl_table=11

/product="5-hydroxyisourate hydrolase"

/db_xref="COG:COG2351"

/translation="MALSDGQITTHVLDTSGVPAAGVQIELYTLKRDGEQESKTKVA
ESVTNADGRLDAPLLDGGKLEPAIYELQFHVESYYAQRSLEELGQALWTIVPIRFAVS
DASRHYHIPLLIAPGGYSTYRGS"

CDS 1925502..1926905

/gene="allB_1"

/locus_tag="EFAGFIKM_01702"

/EC_number="3.5.2.5"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32137"

/codon_start=1

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/product="Allantoinase"

/db_xref="COG:COG0044"

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TRPEAWKMKMKAAADQSYVDYAFWGGLVPGNREELAPLAGLGAAGFKAFMSEPGGDGE
DIFARADDHTLLDGMNEIATLNRVLALHAEDGEIVAELGAKSIAAGKNEPMDYIRSRP
VEAEVVAVARALQYGKQTGCALHFVHISTREALDMIAEAKRRGQDVTSETCPHYLTLI
DQDVVRLGAVAKCAPPLRSSSEQQLWDALTSLIDVIASDHSPCPPSMKQSDNFFEI
WGGISGAQSTLLIMLEDGHLQRNIDLPLLGRVLSLQPARRLGLENKGEIAIGKDADLV
LIDWEKSTSLNTEDLLYTHKQSPYVGRTFNCQIADVFCRGQRVYNSESGLSVPVPLGQH
ITAYSSSPIEAGTEETP"

CDS 1926902..1928209

/gene="pucF"

/locus_tag="EFAGFIKM_01703"

/EC_number="3.5.3.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32149"

/codon_start=1

/transl_table=11

/product="Allantoate amidohydrolase"

/db_xref="COG:COG0624"

/translation="MTESGVYRSSGTNNAPLPLPDVEQVELQAMLDWLSTYGADTQGG
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GSHIDTVVYGGKYDGAYGVVAGVLALEYLQKHFGAPKRTLQVVSLEEEGSRFPFAYW
GSRGITGITSLEDVEHLKDQDGVTFQAIRDAFGPD SAYRPAAKNYGAFIELHIEQG
QVLERLGHSIGVSDIVGQKRFSITVSGEANHAGTTPMSWRKDALAGAAEMIAAVRNI
ALEAGEPLVATVGRITADPGVGNVVAARAVFSLDIRHIRQESIDRCWQDMLQAFSRIA
AEQQLGLDWEEHLSVTPIPMNAEMISDIQDTCEQELLSYWLMPSGAGHDSQIFQPACP
TAMIFVPSQDGISHNPLEYTAEADLMHGFRVLVRLLYKYGYS"

CDS 1928216..1929457

/gene="pucG"

/locus_tag="EFAGFIKM_01704"

/EC_number="2.6.1.112"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32148"

/codon_start=1

/transl_table=11

/product="(S)-ureidoglycine--glyoxylate transaminase"

/db_xref="COG:COG0075"

/translation="MSNYKELSPSLRTIMTPGPVEVDPRVLRALSFILGQFDPEFTS
LMNETMAMLRRELYMTDNEWCPVDGTSRSGIEAVLVSLIQPGDKVLVPIYGRFGHLLV
EISERCGAEVVFETEWGTVFDPEEVIKAIHTHKPSLVAMVHGETSTGQMQLAEIGK
ACRDL DILLVDAVATIGGTPVETDAWHLDVAMGGTQKCLSVPSGMAPLTYNRVEQK
LMSRKTVERGLRDATSARAEGRTIASNYFDLSQLQDYWSSARLNHHTEATSMYGLHE
GLRILLQEGLEARFQRHLVNERALVAGIQGMGLQLYGDMSSKLPVVTCTIPEGIDGE
SVRSMLLNDFSIEIASSFGPLKGQIWRIGTMGFSCQRKNVLHVLGALEAVLLRHRHVL
PAGEAVQAALDVYAGKEGALC"

CDS 1929451..1931046

/gene="ywrD_1"

/locus_tag="EFAGFIKM_01705"

/EC_number="2.3.2.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O05218"

/codon_start=1

/transl_table=11

/product="Glutathione hydrolase-like YwrD proenzyme"

/db_xref="COG:COG0405"

/translation="MLNQMPISREVMVTSPHYLASAVGSSILQQGGNAYDAAVAVSAA

LGVVYPHMTGLGGDAFFLIHDGASGEITAYNGSGRSAAGIHADTFKAMGMNAIPQRGV

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GHTPLRAVFAPLGTLLQEGELLIQPDLAASIRLIQTEGRDTFYTGELADRLTSAIRED

GGMLAPADFAGHRGEWVNPVSTGYRGYEVHQMPPNSQGFSMLMMLNMLEHTDLSSVAR

TSPEFYHLMAEVVKKAFRDRDRYLTDPDFRDIPLDLLLSKSYGDQLWNEIQSAPPVAQ

PFLSKTIGQDTAYAAVVDSEGNVSVFIQSLYDFGAAYVPGDTGVIMQNRGAFFSLDP

RDANVLEPNKRSFHTLMPGLVTRDGKPYMLVGTQGGEGQPQTQLSVLTGVLDYGLNIQ

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CDS 1931142..1932464

/gene="triA"

/locus_tag="EFAGFIKM_01706"

/EC_number="3.5.4.45"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9EYU0"

/codon_start=1

/transl_table=11

/product="Melamine deaminase"

/translation="MGTILLKGAQLVTMNAAAAEVEFIGDLLIEDNKIKEIAAHIDVQAD

QVIDARGKVLLPGFIQTHIHLQCQLFRGRADDLELMDWLRQRIWPLEAAHDEESVYYS

AMLGLGELISSGTTTILDMETVHHTDSAFQAMAQSGIRVISGKVMMDHGDEVPEPLRE

DTATSLQQSVDLLEKWNGFGGGRIQYAF CPRFVVSCTEELLVEVRDLSNKYHVKVHTH
ASENRGEIELVEHERGMRNIVYLDHIGLATPRLVLAHCVWLSEEEKEIIRKRGVKVTH
CPGSNMKLSSGVADIPDLLNRQIAVGIGADGAACNNNLD MFQEMRLTALMQIPHGPT
VMDARTVLRMATMGGAEVLGMSKEIGSLEVGKKADM LLLDLDDFHTYPSYETDVYSRV
VYSATRSCVDTVIIDGSIVLKNRKIQTIDRGIVLRES DKSIARLMKRI"

CDS 1932507..1933787

/locus_tag="EFAGFIKM_01707"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEMHDLCAIAARETRCVLATAIKVEGHAYRKQGVSM LLTEDGKM
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CGELRYTLQKMHECFQSGVTTALTRTFQDDYTRVQYGCKRIEPKGTRRQPILRPSLVP
PHDRVANYNPSSLQVDVQHSSGNIKHEYSASKQHSPDIPRLTLVPEMVIATSNESHSS
HLSGDSQHISDTDAEIPTNDGISTNPWDL PQQLTSLYTPKPRLIIGAGNDVIPVARL
AQSAGFRVVADWRESLCTSERFPETELVLGFPCEIMPQLNVNNGDYLILMSHNFPRE
RELLEMVVDCEYAYLGIMGSKTRTARLLDGLPPLKYVHSPVGLSIGADGPEQIAISIA
AELIACKHKVSSLSELQKGSVAHANDGHSSGSR"

CDS 1933753..1934400

/gene="pucB"

/locus_tag="EFAGFIKM_01708"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32146"

/codon_start=1

/transl_table=11

/product="Purine catabolism protein PucB"

/db_xref="COG:COG2068"

/translation="MRMTGIVLAAGKSRRLGRDKLSVVM PDGRSLAAWSLEAALNSEL
DQVVCVVKPEDSLTWLPVKWFDSAAYAYHPTARLRIVVCADYACGMANSLHSGVLSAM
EYKPEGILMLLGDQPLLQAQDINRVTTALATHKLSDYVAATDGEGGKPPVAFRSHMFG
PLLSLHGDEGARKIMRSANYSGVHVPLSETSFWDADTEPELERILSHVYESQQT D"

CDS 1934691..1935608

/gene="pucC"

/locus_tag="EFAGFIKM_01709"

/EC_number="1.17.1.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32145"

/codon_start=1

/transl_table=11

/product="putative xanthine dehydrogenase subunit C"

/db_xref="COG:COG1319"

/translation="MVTPAYGSGALPSVWQPENLQELQTLRSRLKGICCF TAGGTLLR

TQWEGGLIPAPEHMSLVRIPEMSGISIRGDEIVIGAMNRLKECASDDVLLQQLPILQ

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GRDGSRNPGDVLISIHIPRPSSLVDVDDEQRHAAREVSFYRKLGRRETFSASLTV A

LYGEIDLDNRWTKIAIAAGGGSGMAIRLLESERQLLGSEATVMQAANLAATVVDEFTT

YGDAFATEQYRKQTAGNMLGAGLWEALHE"

CDS 1935642..1938167

/locus_tag="EFAGFIKM_01710"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLLN RKQSGKRWHLRPDGTPKVTGQLQYL TDM TLPDMIHGRVLR

SEYPHARILSIDTSEAEALEGVYAVLT SKDVPGLNRFGIATPDQPVFCEDIVRYVGDA

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RGDAKQAFATCDHIVTETYYTPRQMHAYMETEGGLFVPDEEGRLNVYAATQHGYKDRM

QLARIIGCPEEDIRVVSSPIGGSFGGKDELNVQPYGALLALRCGRPVKMHNSRKESVR

AGLKRHPMKIEMQTGMSREGIIQAHRVRITADTGAYATLGAPVLNFCTEHCLGPYAIP

NVDVEGVSVYTNNGLSGEFRGFGGNQAIFAMEGQMDRLAAIMNMDPWEFRRRRNMREKN

DPGPLNQ RILVTDGLSQVWEAVDRSELWQRHQSP PADPALPPWIKRGVGAAIAMHGAG

LGYGIPDPAGGRSLNNEGKIEVAFSYEEFGQGLIATLEIMLGDLFQCSTSDLSIIIG

DTDRVPHSGSSTASRSTTMAWMALQRLQTPFRSHVLTVASALSGVPADELVTGPGGVW

RKDQLPAGSSEAETDLQRTGKSEKEIVLALEDVNQTSEEAGKLEKAKEYELAENVAGG
TESDQTVEIHLGASPYLAKEGVSSGLLISYAELATQGEADEWIFDTKFDYPTTPDNVV
GGHYLYTAAVAEEVNTLTGETKLLDTRHVVAAGPVINPMGYIGQIEGGSVMALGF
TLTEDAVMQDSRYVTTNLDTYLIPTIQDIHTNLEVEAIEDLPEGDAFGPRGIGEIGSV
ALAPAITAAIHQATGVWVNRLPVPREQLVRPLNVPLQEGVSPS"

CDS 1938164..1938682

/gene="pucE"

/locus_tag="EFAGFIKM_01711"

/EC_number="1.17.1.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32143"

/codon_start=1

/transl_table=11

/product="putative xanthine dehydrogenase subunit E"

/db_xref="COG:COG2080"

/translation="MSKPLENHWTAVVNGEQKYLEIAQTTRLVDVLRTHLQLTGTKVS
CEVGRCGACMVLMDGEPVNSCLIMAYQCEGSDIMTIEGLHGEEKGTLHPQQAFVEEG
GFQCGYCTPGMVISTKALLDAHPEPSQEQIETGLCGNLCRCTGYGGIIRAVRKAGERC
VVKETSAEETVS"

CDS 1939049..1941628

/locus_tag="EFAGFIKM_01712"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKNLLKKATAMMLALALLGLMTAPVHADTPLFTIESEDAQLTP
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QNLIVNGVTKGAYMLPYTTAWSDFDFGFHKLNQGANTIELKAGWGFAYFDTFTVDHAD
LDPLNVQPVLTDPEATPETQILMNYLTEVYGNNIISGQQEIYGGGNDGDSELEFEWIH
ELTGKYP AIRGFDLMNYPYLGWEDGTTDRMIDWVNNREGIATASWHINVPRNFNTYE
LGDFVDWKEATYKPTETNFNTANAVIPGTKEYQYVMMTIEDLAEQLLILQDNDVPVLF
RPYHEAEGNGGLNGEGAWFWWASAGAEVYKELWDLTYELTETYGLHNLIWYNSYVY

STSPAWYPGDDQVDLVGYDKYNTIYNRYDGLSGVPNEDAITSFYKLVELTNGTKMVA
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NLKVNNPNPSASITPGNVEFDKYTPNQSDKTVTVNANGNTLTALRAGNNALTTTDDYT
LNGSTLLLKKAYLATLPVGEHSIVLDFNQGDVPVLKVKIVDSTPGTNAVISPVHATFD
KATNPAQDITVSLTLNGRQLTSITKGDVTLVSGQNYTASSSAVVLNKSYLATLPLGQN
VLTFHFNGGNDVLTVNVDSTVTPAGDLTIQSFNGNTSASTNGVSPKFKLINSNGNS
AIPLSDVKLRYYYTIDGEDAQSFWSWASMGSANVTSNFVKLATPVAGADHYLEVGFT
SAAGSLNAGQSAEVQTRFSKNNWTNYTQTNDYSFKASGSQFADHDKVTGYVNGQLVWG
IEP"

CDS complement(1941711..1942355)

/locus_tag="EFAGFIKM_01713"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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FLLSGPIGLGTLITVCCAGVLLQFIMGHTKKIIDRILTDMDISSHTKSEKEHSV"

CDS 1942480..1942998

/gene="paiA"

/locus_tag="EFAGFIKM_01714"

/EC_number="2.3.1.57"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P21340"

/codon_start=1

/transl_table=11

/product="Spermidine/spermine N(1)-acetyltransferase"

/db_xref="COG:COG0454"

/translation="MTIRIEICTIEHVCELQEISYETFNETFKAQNSPENMKAYLEKA

FNREQLETELSMADSQFLFIYVNNQVAGYMKVNINDTQTENMGLESLEIERVYIKKEF

QKHGLGKVLLYKAIEMAKEHHKTNIWLGVWEKNENAIIFYEKMGFVQTGAHAFYMGDE

EQIDFIMKKTIL"

CDS 1943689..1944765

/gene="glpX"

/locus_tag="EFAGFIKM_01715"

/EC_number="3.1.3.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q03224"

/codon_start=1

/transl_table=11

/product="Fructose-1,6-bisphosphatase class 2"

/db_xref="COG:COG1494"

/translation="MERELALEIVRVTELAALASAPWMGRGDKNSADEAATLAMRAMF
DSVSIRGTVVIGEGEMDEAPMLYIGEEVGNAEGPEVDVAVDPLEGTEIVAKGLNNALS
VIAVAGKGNLLHAPDMYMEKLAVGPALVGKVSIEDPVEVTLEKAAAALNKNISDLTVM
ILDRVRRHESTIKTLRKVGVRIFLSDGDVAGAMAPAFPEAGIDLYVGS GGAP EGV LAA
AALSCLGGEIQGRLMPANADEFQRCLQMGIDNPYKVLTMQDMIGTEDVIFAATGVTPG
EILGGVRYLADDRAETDSIVMRAKTKTIRFIRSQHFLPNKEVLHKVRQLQSTPEPSDR
IHAKTMEQAEFSQSSVDLGVTTL"

CDS 1945045..1946094

/gene="degA_3"

/locus_tag="EFAGFIKM_01716"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37947"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator DegA"

/db_xref="COG:COG1609"

/translation="MASRKEVADLAGVSEATVSRVLNGVGPIKEETRRKVLEASEQLG
YVPSALARSFARSKSGNLGVVLPYVPKAHLFSAYFFSEMLSGIGSKARDNSMDLLVMF
RTPGEVMNYTDLFRRQKVDACIILGARD DHEELAAMQQLHQEGHPFCVMNQHFEGQSF
TEVDADHVEGSRLAIRHLTDQGYRKIAFLNGPDSYSNSQERM EGVRLGLQEAGMELDP
SLLLKGNYSRRSGIEAAAIVADRLHEIDAVFAANDRMAIGVMHGLRERGIRPADFPAP

VGYYDDSDAAEMAVPPLSSVRVPFFAMGELAVSKLMHGSGVDTHKANNSVVAVTESARA
LLPTELIIRASSIRQ"

CDS 1946149..1947321

/gene="iolG_2"

/locus_tag="EFAGFIKM_01717"

/EC_number="1.1.1.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9WYP5"

/codon_start=1

/transl_table=11

/product="Myo-inositol 2-dehydrogenase"

/db_xref="COG:COG0673"

/translation="MSNRLRVGMVGYKFMGKAHSNAYRSLPMFFPSAPLQPEMSVICG

RNEQGVQEAANQFGWSESVTDWRELVKRDDIDLIDINAPSDAHKEIALEARQGKHLF

CEKPLALSLADSREMLQAAEDAGVAHMGVFNRYRSPAVQLAKDLVESGRLGKIYHFRA

FFLQDWIMDPSFPLVWRLQKEVAGSGSHGDLGAHLIDLARFLVGEFQEVIGMSETFIK

ERPLAAEMTGLSAKGSSNADAPMG EVTVDATLFLARFAGGALGSFEATRFAAGHRST

NSFEINGSLGSRVDFDFERMNELEVYFTKDEEDVQGFRRVLATDPAHKYAEAWWPAGHT

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CDS 1947392..1948117

/locus_tag="EFAGFIKM_01718"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKALIVWGGWDGHEPEQVAAIFERILKEEQFEVEVSNTLESYA

DAEKLLGLDLIVPLWTMGQIEQELVNNVSAAVQSGVGLAGLHGGMCDAFRNNVDWQFM

TGGQWVAHPGNDGVEYMVNMKRGSSPLLDHIEDFQVKSEQYYLHVDPAVEVLATTRFP

VVAGPHAANGPVDMPVWVTKRWGAGRVFYNSLGHHADIVDMKPVTEM MRSGFKWTAAG

KELAKSRVSSATEVYTG MADNQN"

CDS 1948214..1949320

/gene="iolG_3"

/locus_tag="EFAGFIKM_01719"

/EC_number="1.1.1.369"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01671"

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3-dehydrogenase"

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AAAYNVPNVYSVDEILADPEIELIINLTIPSVHADVCLRALESGKHVYVEKPLAVTRE
EGQAVLETAKRKGLLVGCAPETFFGSGIQTSLQLVEEGVIGKPVAATAFMMSRGHEHW
HPDPEFYASGGGPMFDMGPYYLTALVQLMGPIKSIAGMTGKAMEERTITSEKKRGQT
VPVEIPHTHTGLLQFEQGAIGTLITSFDVFGGSALPPIEYGTHGTLQVPDPNTFGGP
VRYRLLGEHEWTEVPLLPGYQENTRGIGVADMAYAAHSGRAHRASGELAYHVLEAMWA
FHDSSDEQTFYQMKSSCQRPAALPVDLPLYTLDK"

CDS complement(1949489..1950307)

/locus_tag="EFAGFIKM_01720"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MKTNLTYKVPKTLNKGTFNGYHTLNPYTGCAFGCSYCYVR
QMPVSLFRKEDWGSWVDVKQEASRVFAKELQRALTKGKVTLFMSSSTDYQPAEYKEC
ITRSLLETMVQHPPDFVLVQTRSPVTRDIDLLQQLGDRVRVSMTVETDLDDMRKHFS
PSAPPIAGRLRALEQLRDAGIPTQVAIAPVLPSSSEQFAAILRPLVQRCIDDYFMGDG
SEGKRTRRLGMESLYQQVGMHWHYHPDAYQTVVQRMKDCFAEDEIWISQAGFEP"

CDS complement(1950304..1950888)

/gene="adaA"

/locus_tag="EFAGFIKM_01721"

/EC_number="2.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P19219"

/codon_start=1
/transl_table=11
/product="Bifunctional transcriptional activator/DNA
repair enzyme AdaA"
/db_xref="COG:COG2169"
/translation="MESPDQDRILPKSIDEKYWHAIINNDNSYDGTFFYGVQTTGIFC
RPSCKSRAPKAENVLIFQHVEEALARKFRPCKRCKPTGERVPDQEWIYGITDYIEHHY
AEPLSLEVLATVSHGSPYHLHRVFKRITGRTPVQYIQDKRITEARKLLEHTGLTVTDI
GRHVGIPNSAYFITVFRKHTGLTPAHYRERHENL"

CDS 1951081..1952061

/gene="iolU_1"
/locus_tag="EFAGFIKM_01722"
/EC_number="1.1.1.371"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O05265"

/codon_start=1
/transl_table=11
/product="scyllo-inositol 2-dehydrogenase (NADP(+)) IolU"
/db_xref="COG:COG0673"
/translation="MVRFGVVGTNWITERLLEAAAQVEGFKLTAVYSRTEDKANAFAD
KYDVEHRFTDLEKLAASDVIDAVIATPNTVHAEQAELFLRNGKHVLCCKPLAANSAE
VRSMIDTARKHQVLLMEAMKSTLVPQFKMVQKSLHKIGPVRKYVAGYSQYSSRYDKYK
EGIVLNAFKPELANGALMDLGVYCLYPLITLFGEPNRVQSQAMMLESVDGQGSVLLD
YDGMDAVVITYSKISNSHLPSEIMGELGSIIDKIGSPEHAEIRYNDGTVEQLTVEQNH
PAMYYEVEEFVNLVQQGQKESDMNTYERSYVTMQVMDQIRKQIGLVFPND"

CDS 1952107..1952862

/locus_tag="EFAGFIKM_01723"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSNNGERQKNSREDQQSNESGGLELTQIVFIGRTFEEYMKMFNL"

TVEDLTGKSILDCPGGACSFSSQARKLGANPMAVDMAYKYEIDELEVKGFDIEHTMK
QMEPVQSIYVWDQFGSIQGLKEERTRAITDCVADMRMFPDRYVTSVLPDLPFADSEQFD
LTLSAHFLFTYADRLDVDFHVVTVMELLRVSKREVRIPTVDLSGERYKHMDCLKLIL
EELGYTVSEEPSYEFQRNAHTMLQIVKHNRTTR"

CDS 1952875..1953768

/locus_tag="EFAGFIKM_01724"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MNKVLILGGTRFFGKRLVDHLLWEGKSQITVATRGKTDVDFGPE
VNRIKMDREDPESLAQVAQTDMWVVDNICYSPDAAKAACDAFAGRTKRYVLTSTLS
VYGDPRPGFKETDFDPYTYPLQYGSAEDFSYGEGKRLAEAVFFQEADFPVAMRIPIV
LGIDDYTRRLHFHIEHVQKGKPIGMPNPNAEIGFINSTEAAARFLAWLGHSSNTGPNVA
ASKGAILTSAMIHLIETVTGMQSQILTETVKEDMSPFGIEQSWTMETTKAEQAGYTFE
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CDS complement(1954003..1955019)

/gene="degA_4"

/locus_tag="EFAGFIKM_01725"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37947"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator DegA"

/db_xref="COG:COG1609"

/translation="MITIYDIAKKANVSAMTVSKVINHTGRISSATRERVQQVIDELG
YIPNSNARSLVLQRTQMLSLITDITNPFYTTLARGAEDAAHLRGYRLLFGNSDEDYN
KEKDYVDAILSTRVDGVLYAPAGDRSLPHLKQLQERHIPFVFLDRTVPGITSDIAGD
SLEGAIELIRYLVQLGHRRIALVNGSSEVSTARLREEGYVAGLREAGADIDPELVLR
GYRDFSDEEGLDRLLSQPDQPTAIFAANNMLAIGVIRLLRKRLRPEDISVVCFDDL
DLASAFDPFLTVAVQPAYDFGFQGVQMLIDRIEGKSPSEAQTVILPSELIRIRASATTP
REQK"

CDS 1955432..1957222

/gene="fucI"

/locus_tag="EFAGFIKM_01726"

/EC_number="5.3.1.25"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q97N97"

/codon_start=1

/transl_table=11

/product="L-fucose isomerase"

/db_xref="COG:COG2407"

/translation="MTHQDYRYKQAFPKIGIRPTIDGRRKGVRESLEEQTMRMATSV
ELLAELRYPDGSAVECVVAETCIGGVAEAAAASELFSRSNVGVITITPCWCYGTET
MDMSPSIPTAIWGFNGTERPGAVYLAAVLSAHAQKGIPAFGIYGEDVQDGGDITIPDD
VREKLLRFSRAGLAAATLKGQAYLSIGSVSMGIAGSIVNDSFFQEYLGMRNEYVDMSE
LTRRIEEIYDPEEYKLALAWVKENCSEGPDNNAHLQTDKRKEYEWETVVKMTQIV
RDLMAGNPRLAELGFTEESMGHHAIVSGFQGQRQWTDHSPNGDFLESILNSSFDWNGK
RAPYLVATENDSLNGVSMLFGSLLTHTAQIFADVRTYWSPDSVQRTGHQLEGNAKD
GILHLINSGSAALDGTGQQSREGKPVLPKFWEITDEEVQDCLKATSWRPASVEYFRGGG
YSADFLTKGGMPVTMTRLNLVKGLGPVLQIAQGYTVDLPEDVHDTLDQRTDPTWPSTW
FAPVLTGLGAFTSVYEVMNQWGANHGSISYGHIGADLITLASMLRIPVNMHNPETEI
FRPRAWGLFGTSEPESADYRACSVFGPLYR"

CDS 1957348..1958838

/gene="rhaB_1"

/locus_tag="EFAGFIKM_01727"

/EC_number="2.7.1.5"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P32171"

/codon_start=1

/transl_table=11

/product="L-Rhamnulokinase"

/db_xref="COG:COG1070"

/translation="MGNQATHVLAADYGAGSGRVVRGSFDGSRLSLQEVHRFNNEPVQ

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YREARNAQWMEEVLHVMKEEELYAMSGVLPQQINTVFQLLGSVREQAEVLRPDVRMLF
MPDLFHYYLSGQQACEYTIASSTGLLHAGEARWNEHLIGRLGIPESLFPKLVQPGTVL
GDLTNELFAELRTGPMQVSVSGSHDTASALAVIPAMDSDFAFISCGTWSLMGVERDTP
VLDDRSRALGFTNEGAVSGKVRTLKNRSGLWLLQESKRQWERENQPFTHEELIQLASL
AAPHQSYVSPGDGVYLAPGNMAERIRQQCSASGQTPETTGAIVRCILESLALEFRQT
LDELQLITGIRPRVIHVMVGGGVHNRLLCQFTANAAGVPVWAGPAEATSAGNCMLQFLA
HGEVSSLAEVREVMAASFSPETYEPEDTELWQEAYENYQSLNQIKR"

CDS 1958909..1959571

/gene="drdA"

/locus_tag="EFAGFIKM_01728"

/EC_number="4.1.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0DTQ0"

/codon_start=1

/transl_table=11

/product="5-deoxy-D-ribulose 1-phosphate aldolase"

/translation="MSEQQVREELTKYARRAVAQGLVVGPGGNLSARSGGTMLLSPSG

YALEDLPEDEWIAIDIETGATSAGATRPSSSEVLMLHSYRVNPNIQAIVHTHPAYTIA

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TGKNLREAYYRTQVVEESAKVYMIAKAAGEPKVLTAEYKEIQSLESEAYRVQLLQQL

KS"

CDS 1959813..1960541

/gene="lutR"

/locus_tag="EFAGFIKM_01729"

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/inference="similar to AA sequence:UniProtKB:O07007"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator LutR"

/db_xref="COG:COG2186"

/translation="MGPELNEMELEYELLKQLRDANAPIGASTLVHTLGKTYGLSQAT

IGRRLMEMDVEGFTVLKGRKGRTLTEQGLDRMKTLERDLQQSVNSQLIQMLNHSGEK
ALLDVLVARRALEREIASLAAQRASKEYIVLLQASIANQHELLSKNIIPYEEDREFHR
LLAYAAQNQILLHAVELVWETSRDFLETAYIRRRVGSELVVDHQQILDAIVAGSPEQA
EAAMVNHINQMIDDVKRYFAMQNNQ"

CDS 1960583..1962631

/gene="apc3"

/locus_tag="EFAGFIKM_01730"

/EC_number="6.4.1.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5P5G4"

/codon_start=1

/transl_table=11

/product="Acetophenone carboxylase gamma subunit"

/db_xref="COG:COG0145"

/translation="MDTIYRLGIDIGGTFTDALVMDHQGRVIAALKTPSIAVAPEQAI

FNALDQLKETGVNIHEIDLFVHGTTLGVNTLIERNGAVTGLLVTKGFRDILEIRRLRL

EDTTNLYGDKTDALVPRHRVKEIDERVIASGGILQPLNEEQLLQAVDELVEDGVTALA

ISFLHAYVNPAHEQLAEDLIRERYPQLFICRSSAIWPQQREFERTLATAMNAYVGERM

GSYFLRLQEGIQAYGLKANLLSTMSNGGIMTAARAANEPVRTLLSGPASGVIAATHIA

ERAGIHQVITFDMGGTSVDVALIDKEPSYSENKVGDFPVIIPAVDVTAGAGGGGSA

WLDSVGVLKVGPRSAGANPGPACYQRGGEPTTTDAYLQLGILHADRFLGGQMRLYPE

LAERALGNLGQKLELNAEQTAQAILDVATANMYAQFSPLMARKGVDPDFTLLAYGGA

GPMHAFLMAREVGIGRVLIPSPGTLGCTVANLRNDFVHTLHKSTQTLEPGELSS

LFAELENQGRSWVDEEARGGVKLDNIYCLYSADMRYEGQAFDIEVTLLEEIEDPKKA

GIKFHESYQNVFGISQPEAEVMFVSLRATIVGVLPHTNTVDPADLPFDESAAEERLIT

FDHVQQTAKVLKRGQIPSVDAPIPGPIIVEEYDTTIFIPPGYKVYRDGHGNAVIGEVEA

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CDS 1962628..1964601

/locus_tag="EFAGFIKM_01731"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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LNEQILRMFLDNSRIPEQNLGDLKALMAALNRGEQRLEELIARYGVEKIQQGIEQLLE
YAEKARVIVQDIPDGSYDFWDYLEKGPGGYPIRLRCKMTIAGSDIHLD FSGTDPQVR
ASFNIPTHNQQGHYMLVPALIRYFRTLDP TIPWNSGMIRMVRNYAPPASVLNPEPMAA
VGARAATFIRLMDVITGALGKAQGSMPAAGAGQACIVMMAMTDASDGKKKVGVIQPI
CGGSGARPMKDGIDGMDFAVGH LNRNIPAE TVESEMPVLIEHYGLRADSAGAGTFRGGS
GIDLCVRILTPDTVMTARNMERMEFQPWGRLGGGVGSHGEAILNAGRA SEDHLGRIDE
LLLQPGETVTFLSQGGGGYGDPYERDSRLVLEDVRSGLVSPEKALELYGVVIDDLKLN
ESDTEQMR AKRPRQQEEFAYGKAREQFEDIWSD EMQVT LNQALLNAPLALRDYLKRQT
MGVVEEKYKDSL SVDPREISDIMEGLRQQIGLH"

CDS 1964670..1965806

/locus_tag="EFAGFIKM_01732"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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SGDKVKLT MFIWAGSNQDVVPKEVVAEYVKEHPNVEVT FEESSNSVMYPKMVASKQAD
ANNPVWNFGYFNADATAGLND DMWEPLDTSIVTNIKDIPESFHKPDNKG VVWGVSSF
ALVYNKDLVKTPPTSWNDLWDNEEFKGKTALWDYMFYSYISPLIAAKGQEIGATYENP
EPAFQFWADRSDQIGTLVSSNDQLKALLES GDALIA PFSAQVAQTWIDGGSPLAVAYP
SEGAISFPYTLQVVKGSTPEQTRVANEIINELLSAEALSQYAEATGTPVTSTTA AVPD
KYKDDPSFSVETQSNGINPDWDVLAQNSSSWKELWDR LVKTKLQ"

CDS 1965879..1967009

/gene="potA_1"
/locus_tag="EFAGFIKM_01733"
/EC_number="7.6.2.11"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P69874"

/codon_start=1
/transl_table=11
/product="Spermidine/putrescine import ATP-binding protein
PotA"
/db_xref="COG:COG3842"
/translation="MSSGQETISIETREVTKYGKRAAVNQVTLQVKKGEFVSLGGS
GCGKTTLLRMLGGLEQPDQGTIMLGDRDVTGIPAYGRNSNMIFQQLALFPHMDVFNNI
AYGLKVKKLPKADIQRQVGEMLDLVQLGDYGRRAVSELGGQAQRVAIARALINRPEV
LLLDEPLSALDMQLRLDMQRELKRIQREFGGTFIFVTHDQSEAMNMSDRIGVMRAGKL
LQYATPDEIYERPADSFAKFIGDTNLFETEVLGHDVSGIRVECFGKPLWVKVSDGNA
VPKAGARHSLIRNEYIRLGEDASHCLNKLDGHVIEAVYGGANIRYSVQIAEGFLVQA
SVLHQRGASRYSPGEPIQIGFDPEDALLSEPIDDRVQGARI"

CDS 1967006..1967923

/locus_tag="EFAGFIKM_01734"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNRIAERIVNLYSFGNRTWVTRLLLLLPALALMGIVYLGGLLIF
GRYSFDMYENGKLIRGWDLGAYRAFLSDPYWKLIGTTFRIAFKVTLSLLAYPLAY
CIAGLKPKGMKQLLLLLTFLPLLVS AVVRSYGWQLLSKQGFMNWL FIRLGLTEEGFS
MIYNETGVVIALVHIFLPMVFPIILNVLSQSDASLKAAAQDLGAGSLRTFLTITLPLS
ARGIASGVQIVFTLCLTAFTTPQLIGGGRVMTLPVFIYQRTLDTNWPMAAVASLFLLV
SSIVVSLLVNKAETLMFRRSRKGGQAYG"

CDS 1967916..1968761

/gene="ydcV_1"
/locus_tag="EFAGFIKM_01735"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AFR9"
/codon_start=1
/transl_table=11
/product="Inner membrane ABC transporter permease protein"

YdcV"

/translation="MVKSNSGTKLLLYIFVGAVAIYLLLPLLMIMLTSVSGSGSASKFP
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RAFFVSPMVMMPKITLGIAYLILFSKMHIAGGLFALILGEAVIVLPFVLTIVGSALANL
HPAHREAAADLGAGPLRIFFTITLPQLRLSLLSGSIAFVFTFDQVEALLLRQDSY
TLPIQLFLYMEKWQDPTIAVVSVVLIAFALALFMTIKLVLRVPGLESFGRRKTKGG
LDQNE"

CDS 1968754..1969971

/locus_tag="EFAGFIKM_01736"

/EC_number="3.4.11.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01974"

/codon_start=1

/transl_table=11

/product="Methionine aminopeptidase 1, mitochondrial"

/translation="MNNSQHLSHSSGLNRDRAEEVMKAQGLSALIATTPENIHVIGS
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GKPSTDDIDLFIYLLQTTVIHPGPVEALKAALKQLEIEDQPIGIDEMRIAPDILARIR
EEAPDRPVIPAYKLFRKIRLVKTPFEIEQLRQAAQLNERIEQELIDLIAAGVHEKQLA
DHYRLAVMRAGGTPAMTAVGAGPRSALPLIENYFHTIETGDQIRFDLCLQLEGYWGDT
GRTVVAGEPTAWMIKHFDKSGWETALETVRPGVKASEVFHAAVSRVQREGIPHYRR
QHVGHAIAGLELYDDMTLSPGDHRVLEPGMVLCEVPYYELGAGGFQIEDTIVVTPDGY
EFLTHMERKLFTK"

CDS 1970054..1971241

/gene="ynfM"

/locus_tag="EFAGFIKM_01737"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P43531"

/codon_start=1

/transl_table=11

/product="Inner membrane transport protein YnfM"

/translation="MIQQGKTKFRNLSLALFAGGFVTFALLYSLQPLMPEISDAFSIT

PAHASLALSVTTIAMALTMLFIGSLSDSVGRRFIMTAALVISSVIALLSVFSPGYTEL
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WFSWRAAVGFIGILGLCAAVIFWVIPP SRHFVKAAPGFKNPIPLLWSQCRNPRLLCL
YGLGFLLMGGFVTLFNYIGFELTGEPYHLSQSIVGSLFVVYLMGTVSSTWMGRLADRY
GRSHVLGIALGIILAGAVCTVHPALWVKIIGLALFAFGFFGGHSIASSWVGLVANQHK
SQANALYLFFYYLGSSVSGTGGGLLYSHLGWTGIVGMIGVYVLIGFVLCNLLVHRLKG
QAT"

CDS 1971327..1971677

/locus_tag="EFAGFIKM_01738"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

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RKLETMSRASAGHQ"

CDS complement(1971791..1972417)

/gene="azoR2"

/locus_tag="EFAGFIKM_01739"

/EC_number="1.7.1.17"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32224"

/codon_start=1

/transl_table=11

/product="FMN-dependent NADH-azoreductase 2"

/db_xref="COG:COG1182"

/translation="MSTLLYITAHPHDHETSFSMATGKAFIDAYRESHPSDEVVHLDL

YRSDIPHIDADVFSGWGKLQSGSDLTSEEQTKVSRLNELSDQFASADKYVFVTPMWNF

SFPPILKAYADSICVAGKTFRYTEQGPVGLLTDKKALHIQARGGIYSEGPAQMESGH

RYLSIIMSFLGVPKLDGIFVEGHNQYKDRADEIKQQAIEQATTLAKQF"

CDS 1972648..1973592

/gene="deoR"

/locus_tag="EFAGFIKM_01740"
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/inference="similar to AA sequence:UniProtKB:P39140"
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/transl_table=11
/product="Deoxyribonucleoside regulator"
/db_xref="COG:COG2390"
/translation="MGMDLEKQRLSIEAAKLYYQSDYSQQDIAARLGVSRTVSRLLQ
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YLQETVQDADIIGVTWGTMMHAVARQLRPKQVKGVVQLKGGVSHSHVNTYAAEIVH
LFAEAFHTVPRYLPLVIFDNIEVKNMVEADRHIGRIVELGRQANIALFTVGTVKEDA
LLFRLGYFNEEEEQQLMNSGAGDICSRRFFDAEGQLISEEINSRTVGIDLAELRNKEKS
ILVAGGQRKIEAIHAALKGHYANILVTDQYTAQALLRF"

CDS 1973782..1974456

/gene="deoC"
/locus_tag="EFAGFIKM_01741"
/EC_number="4.1.2.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39121"
/codon_start=1
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/product="Deoxyribose-phosphate aldolase"
/db_xref="COG:COG0274"
/translation="MTPQLAKMIDHTLLRADATQSEMAKLTEEAKQYQFASVCVNPG
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GKDDFVEQDIRAVVEAAAGKALVKVIIETCLLTDEEKVRACQAAVRAGADFVKTSTGF
STGGATPEDIALMRRTVGPDVGVKASGGVRSLEDMQKMIEAGATRIGASSGVKIMQGE
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CDS 1974687..1975874

/gene="nupC"
/locus_tag="EFAGFIKM_01742"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39141"
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/transl_table=11
/product="Nucleoside permease NupC"
/db_xref="COG:COG1972"
/translation="MKFLIAIIGLLVVFGLAYIASNGKKQIRYRPLAIMILLQVILAY
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VISALIGILQYIRILPFVIKYIGLVLSKINGMGRLESYNAVASAVLGQSEVFISVKKQ
IGLLPKHRLYTLCASAMSTVSMISVGAYMTMIEPKYVVTALVLNLFGGFIIASIVNPY
EVTEEDILEVQEEKQSFFEMLGEYILDGFKVAIIVAAMLIGFVALIALVNGIFSAV
LGISFQELLGYVFAPFAFIMGVPWKEAIQAGSIMATKMVSNEFVAMLNLKETAMSART
TGIVSVFLVSFANFSSIGIAGAVKGLHEKQGNVVARFGLKLLYGASLVSVLSAITG
LFL"

CDS 1975904..1977082

/gene="deoB"
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/EC_number="5.4.2.7"
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/translation="MSTFKRVHLIVMDSVGIGEAPDAAEFDDFDVDTFGHIARERGGL
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VFENGFPDELIQRIEKTGRKVIGNKPASGTEILDELGAEHVETGALIVYTSADSVLQ
IAAHEDVVPLKELYEICEFCREITLEDPYMLGRIIARPFVGEAGNWKRTANRHDYALK
PFGRTVMNELQDGGFDVIALGKIADIYDGEGVTKAVRTVSNMDGMDKLSETMDEEFTG
LSFLNLVDFDALYGHRRDPQGYAQALEDYDARLPEIFAKMTNDDLLLITADHGNDPTY
RGTDHTREYVPLLAYSPRFSEGKKLDRSTFADLGATVAENFGVKMPEYGTSLKDLK
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CDS 1977179..1977886

/gene="deoD_1"
/locus_tag="EFAGFIKM_01744"
/EC_number="2.4.2.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q5EEL8"
/codon_start=1
/transl_table=11
/product="Purine nucleoside phosphorylase DeoD-type"
/db_xref="COG:COG0813"
/translation="MSTHIGAKPGDIAETILLPGDPLRAKYIADTYLEDVVCYNEVRG
MLGYTGTYQGHRISVQSGMGIPSAIYANELISEYGVKNLIRVGTCCGGMQEHVRVRD
VILAQAACDSSMNKHVFGGYDFSPIATFSLLKEAYDRATAKGMKIHVGNVFSSDSFY
RDDRSVTEKLMKHGVLGVEMETTALYTIAAKFGVNALTILTVSDHLLTGEETSAEERQ
KTFNDMMVVALDTAILT"

CDS 1978121..1979422

/gene="pdp"
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/EC_number="2.4.2.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39142"
/codon_start=1
/transl_table=11
/product="Pyrimidine-nucleoside phosphorylase"
/db_xref="COG:COG0213"
/translation="MRMVDIIAKKRDGKELTTAEIDFVVQGYTQGEIPDYQVSAWAMA
VFFKDMTDKERADLTMSMVNSGETIDLSAIEGIKVDKHSTGGVGDTTTLVLAPLVAAL
DVPVAKMSGRGLGHTGGTTDKLESVAGFHVELEKEEFIRLVNEHKVAVIGQSGNLTPA
DKKLYALRDVTATVNSIPLIASSIMSKKIAAGADAIVLDVKTGAGAFMKTTEDAKELA
HAMVSIIGNNVGRKTMAVISDMSQPLGLAIGNALEVKEAILTLQGKGPKDLEELCLALG
RQMVFLAGKADSLEHAEELKEVIQNGKALEKFKDFLANQGGDASVVDHPDRLPQAQY
LVEVPADKDG YVAGIVADEIGTAAMLLGAGRATKESEIDLAVGLMLNKKVGDPVKAGE
SLVTIHANREDVTDVIAKIKENITIADHADAPVLVHDIVTE"

CDS complement(1979525..1980508)
/locus_tag="EFAGFIKM_01746"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNHTIYTMKPPVSRSHLIQWHNLIRAAWIGGLAVYIIHLNSSD
SLHYYLAPTMQKLLCCPVPLLFIAVIMAWHGLLGRNEVHCDCEHPPPSGFLRSSMVY
GLIAIPLLLGFLLPDRTLGGSSMASQKGMSTLYAPPEIRRKEPLDPATQLNVQDLTQQ
PTAVQSVSATKVQFIPPDEYSREFAELAEKLYAEQIIRVYPEIFSETLGTIDMFQRQF
AGKDISLTGFVYRDKSMDQESHFALGRFLVMCCPADAAPFGVMIHIPEADSFPDTSWV
QIDGSIGSAQVNGKDTIEIRATKVTPVSEPTTPYIYTNADSVMAYEKIKSQ"

CDS complement(1980591..1981625)
/locus_tag="EFAGFIKM_01747"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q8DUY3"
/codon_start=1
/transl_table=11
/product="Putative two-component membrane permease complex
subunit SMU_747c"
/db_xref="COG:COG0701"
/translation="MKMAANLKLLSFLIPCAFLVPVLITMAPDLKEAWKSEALQNMKT
VFIGIFLEAAPFLLMGVLLSSLMQWVSEEMVRRLLTPKNPIGGVLVAGLLGIIFPICE
CGMIPVVRRLMHKGMPAYIAVTFILSGPVVNPIVFTATLLAFPSHPEITIARMGLAFA
VAASIGMLVYVFVRRNPLRMPKVAATEVKTHPGFKMAQPHSHANAHDHNVKNWRSFF
IHAGDEFVDMSKYLVIGALITACIQTFISRSDLISLGNGPVASYVFMMGFAYVLSLCS
TSDAFVASAFSHTFALGPLVSFLVLGPMMLDFKSTLMLLSTFRTRFVIGLSLAITLVF
AGSWLINLLV"

CDS 1981859..1982008
/gene="rpmG2"
/locus_tag="EFAGFIKM_01748"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P66231"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L33 2"

/translation="MRVIVTLACTECGDRNYTTTKNKRNHPERLEMKKYSPRLKKMTI
HRETR"

CDS 1982058..1982765

/gene="znuC_2"

/locus_tag="EFAGFIKM_01749"

/EC_number="7.2.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34946"

/codon_start=1

/transl_table=11

/product="High-affinity zinc uptake system ATP-binding
protein ZnuC"

/db_xref="COG:COG1121"

/translation="MILSSMHDVVFGYGKEPVIDQLSLDIHVGEFIGITGPNGSAKTT
LLKLLGLLKPWSGTIHMSPQLKRGKNSNIGYVPQQVASFNSGFPSTVNELVRSGCYT
RLGLFRRITATQDAIVERSLREVGMMWDYRNTRVGELSGGQKQRICIAMAGQPQVLV
LDEPTTGMDRHSREGFYNLMRHYADVHGLTIIMVTHGLEEMGDRLDRTITLERQESEE
WQCLSTNSCNVPSGQVD"

CDS 1982717..1983610

/gene="znuB_2"

/locus_tag="EFAGFIKM_01750"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34610"

/codon_start=1

/transl_table=11

/product="High-affinity zinc uptake system membrane
protein ZnuB"

/db_xref="COG:COG1108"

/translation="MFEYEFMQRAFWAGGLIGVIAPILGVYLMRRQVLMADTLSHVS
LAGVALGSVMNLPVICGFAVAIIIGALLVEQLRRSYRTYSEVPVAIIMTSGLALAVVL
MSLKTNLSTKTFSSYLFGSIVAVSDMQLWMMAGVCVIGLLFFILLRRALYSFTFDEETA
SIGGVQVRGLSFAFAILTGMTVASAMPIVGVLVSALIVLPAALALRVSRSTAAIIV
AVITGLIGIFSGLTTSYHLNTPPGGTIALILLVILLTGISAQKLIARYNRKRHRKERN
QQEQRETLVIHSRRNTSHEIQ"

CDS 1983597..1984703

/gene="znuA_2"

/locus_tag="EFAGFIKM_01751"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34966"

/codon_start=1

/transl_table=11

/product="High-affinity zinc uptake system binding-protein

ZnuA"

/db_xref="COG:COG0803"

/translation="MKFSKKTALGLLFSLTIVAGCGQKSASDTSAAPTGAPVPAETE
TAKLNVQVSFYPMYEFTKNVAGDLADVHTLVAGMEPHDWEPTPQDIASIEKADVLVY
NGAGMESWIDQVTGSLSNASLIQVEASKGINLLEGGEHDHGHEDSDGTDTHDHADESA
GEAHDHDADEGTAEEDHHDHDAEAEAGHDHDHGGLDPHVWLSPALAVTEVRNIEAGL
AQAAPEHAAQFKQNADAYIAQLES LDQDFKAAVTD SKRKDFITQHAAFGLAKEYGLQ
QVPIAGLSPDQEPSAAQMASVIDFAKEHQVKTIFFETLVSSKVSETIASEVGAKTAVL
NPIEGLTEEEIAAGMDYISVMRQNLEALKLALNE"

CDS 1984869..1985351

/locus_tag="EFAGFIKM_01752"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNLNEEHELLSEQPAHLWRRRKLELMHWTERDKHTVSAKKTEI
WNGVEVDAELVNALSILQNAGVKTEFSCAGVSPLDEPVDHSLYAYVTLVQSEVADQFV
NYALRRMRNRLLVTLAEKGRYDLSSFFIGHNRSFCWWMEHCALQFGSRNESSEKSVV

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CDS 1985394..1986095

/locus_tag="EFAGFIKM_01753"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKWVKTILFLLGSVFLTRFIPFSSLFRNLDTMIHEFGHALMTL

VLSGKVLRIELYADHSGVTYSSMLTPGRSILVSLAGYISASLFALLLFYLYRKGLHMW

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SVVSAVYVGLMSWTQPSRAGDAANLAQQTFLPALFWGTLFALFALWCAKGALSFFRK

EGTSRSSRSRGLRRA"

CDS complement(1986211..1986582)

/locus_tag="EFAGFIKM_01754"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKTRFWLLYVLPFILILVFVAIMASGSFLKKPFGTDDRLLLESIQ

TLEKQVESKKWTEAKSQVDYAMKAWDKVVNRIQFSVERETIYDILGTLARIKGGVAAQ

DDKAIMEEIYFYVLWDNLGD"

CDS complement(1986609..1987337)

/locus_tag="EFAGFIKM_01755"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31533"

/note="UPF0702 transmembrane protein YetF"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMEETWVVAVRSIIAFLTLIIYTRVLGKQQMGNLTYFDYINGIT

IGSIAGTFATDLSSKAWIHFVALTIFTIITIIIFQYITLKNRTISKLMDSPTLIIQNG

KILEQNLSKMRVKFDELTMMLRQKDVFDTITLDYAILEPDGSLSVVLKPENQPVTAKD

MHMHPPKSKLMTEIIIDGLLIKQNLEERNKDINWLSEQLKKQKITIQDIAFAAILPND

KLYVDLFEDKITEKIDMGDYEGPF"

CDS complement(1987544..1988407)

/gene="uxuB"

/locus_tag="EFAGFIKM_01756"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34896"

/codon_start=1

/transl_table=11

/product="putative oxidoreductase UxuB"

/db_xref="COG:COG1028"

/translation="MSERQYERSSRLEGRTAVITGGAGVLCRSMAEELARHGASVAIL

NRTVSKGQEVVSAIEAAGGKAIAIACDVTQADSVQAAADAVLEQLGPCDILINGAGGN

NASANTTNEIFRLEDLEKSDVTTFFDVSVEGFRQVMDLNFVGS LIPTQIFAKHMIERD

VPATVINISSMSAPSPMTKVPAYSAAKAAINNFTQWLAVHLAESGIRVNAIAPGFFLT

EQNRNLLLQPDGSPTERSSKIIAHTPMRRFGKPEDLLGTLMWLADERQSGFVTGTVIP

VDGGFMAYSGV"

CDS complement(1988404..1989471)

/gene="uxuA"

/locus_tag="EFAGFIKM_01757"

/EC_number="4.2.1.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34346"

/codon_start=1

/transl_table=11

/product="Mannonate dehydratase"

/db_xref="COG:COG1312"

/translation="MRMVFRWFGEGNDTVTLDIRQIPGVEGIWWALHDVPAGEEWPM

DKILAVKTAADKAGLHLDVVESVNIHEDIKGLPSRDKYIANYIKTMEKLAQVGKVI

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ERLQYLTGLFEAYKDVTE DHMWEHARYFLQEIMPTAERLGIRMAIHPDDPPWPIFGLP

KIITSQENVRKYLNLVDSYNSVTLCSSGLGANADNDIIGMIHEFKDRIPFAHIRNVK
IYENGDFIETSHRSQDGSVDIAGWEAYHDIGYEGYARPDHGRHLWGECRPGYGLYD
RALGIMYLVGVWDSLQRRAKA"

CDS complement(1989512..1990246)

/locus_tag="EFAGFIKM_01758"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEYTLKLSSKAGLLPVASNMSMNNKQSYSTRDVVYFTLKQLIL

SLKMPPGTAISEKEISLEFQVSRTPVRESFVRLAQEGLLEVYPQRGTYVSLIQVDLVE

EARFMREQLERAVIRLACENFPNEQMVLTLEQNLAWQQECRVKPDDERMFQLDEEFHST

LFAGCNKSNTWTVIQQMNVHLNRSRMLRLSSDHQWDHLIEQHRSMVKAIQQHDADTAE

RLMQEHLHLTVTDLAVLQDTYPSYFQ"

CDS 1990461..1990763

/locus_tag="EFAGFIKM_01759"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGQKAISVFQTCIPLFQVLSDNHRQSILLTLTEKGRMTVNEITE

QSSLSRPAISHHLKLLLEKGLISVEQKGTQRYYSASLNASVELLKELVAALEEECL"

CDS 1990854..1992257

/gene="aldH1_2"

/locus_tag="EFAGFIKM_01760"

/EC_number="1.2.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2FWX9"

/codon_start=1

/transl_table=11

/product="4,4'-diaponeurosporen-aldehyde dehydrogenase"

/db_xref="COG:COG1012"

/translation="MTMTIQEVTSQEVEQILEQQRQFFRSGATRSAEARIARLTQLKQ
AIQKYESRLTVALYQDLGKSEFESYTTEIGFMMDSITHTIRKVNKWWKPVKVKTMAL
LGSKSYIPEPYGAVLIIGPFNYPFQLLIEPLVGAIAAGNTAVLKASENTPAVSAVVR
EMIASVFEPAYVQVLDGAKDTTALINAPFDYIFFTGSPVVGKIVMEAAAKNLVPVTL
ELGGKSPVIVDEQADIKVAAERIIWGKLLNTGQTCIAPDYLLVHEHVKEPLITEMKAA
IVSFFGSDIQHNKDYGRIVNKGHFKRLTTLIERDQAKVIYGGASDEEDRFIEPTLIDA
ESWDAATMEDEIFGPILPIISYRNLEAIVEIVKRPKPLALYLFTSDTRVQDKVLREV
SFGGGCINDTITHVANPRLPFGGVGHSGVGSYHGQYSFETFSLKSVLKKKTKLNLPI
LYPPYDNKLKLIKRLK"

CDS complement(1992337..1993248)

/gene="rclR"

/locus_tag="EFAGFIKM_01761"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77379"

/codon_start=1

/transl_table=11

/product="RCS-specific HTH-type transcriptional activator

RclR"

/db_xref="COG:COG2207"

/translation="MSSTYLPPTLGESVHEVFYPDVQTTVNLFATHLRSVGMDWDYPA
HEHPQYELNYVTEGEQRMMVNGTLYIQKAGELLIPPGSIHSSQSHNGKGFYFCMHF
DIDDQLFLSLLARIKQVRFSADSPVTQQIEPVLRLKMSSADDETNTMVQRMQLQSAV
FELFGHLWEAVSKEAAHWFTDGHEKIELAHQIRNRLQGLMSQQFKQGHESNHGYIDD
IAAELGISSSHCNRVFKEVFGQSPRAVLSQLVLHEAKLLLGNPKLSVQNIAVMLGYKD
IAHFSRQFKRWSGMSPSRYRQEQPALE"

CDS 1993468..1995657

/gene="xylA_1"

/locus_tag="EFAGFIKM_01762"

/EC_number="3.2.1.37"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P45702"

/codon_start=1

/transl_table=11
/product="Beta-xylosidase"
/translation="MNTSKSIFYNAHHAPIGAFASFTLG YKGAKGGLGLELGKPADQN
VYIGLQSHDGDNYQALPFYEASEDESSRYDVEKLENGDTASTTATKVPQPLITAFRDE
DITREFTSGTDTWTAGDLTFRIYSPVRPVPDPTNGDREELMDALVPAVLVEMTIDNTE
GQQSRKAYFGYQGNDPYSAMRLIGGPEGGSITGVGQGRLTAIMSADDGLWPARGFTLE
KLLQEKHRENLAFLGLSTAALLMEVPAGEKRTYQFAVCFYRGGIVTTGMDTTYWYTRY
FSDIQAAGEYALQRFSELTASCGEVEQRLGSAALTEDQSFMLAHSIHSYYASTQLLDA
DGEPLWVVNEGEYRMMNTLDLTADQLYFELALNPWTVRNELEWFVKRYSYTDQVRFPG
EEKLYPGGITFTHDIGVANVFSRPGHSAYELVGIDDCFSQMSHEELVNWLC CATVYIE
QTQDQAFVKNTLPVIQDCFESMLNRDHPDAEQRNGLMGLDSSRTQGGAEITTYDSL DV
SLGQSRNNIYLAGKCWAVYVALEKLFATEKLADLSHQAGLQADRCAASIAAQLTDGGY
IPAVIAENNDSRIIPAIEGLVFPYFTGCEAALDVNGRFGPYLKALQTHLKT VLPGTC
LFEDGGWKLSSTSNNSWLSKIYLSQFIARELLDVEWNETGKAADAAHVNWLLHPEESY
WCWSDQILSGVAVGSKYYPRGVTSILWLLEGKGNHLGQIYASKEAVQ"

CDS 1995654..1997801

/gene="aguA"
/locus_tag="EFAGFIKM_01763"
/EC_number="3.2.1.131"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q09LY5"
/codon_start=1
/transl_table=11
/product="Xylan alpha-(1->2)-glucuronosidase"
/translation="MSQSVVQAALSGPQYDAWLGYHSELPGANGLAQKTAPAWSKLIL
VEENHGVITTALIELSRGLERLYGVKPSVSHLSDTQESERDNHASTPAIRIGTWTGSD
SVAGSFSETERSTVQGEGYIIRENETEGVLVIGSETPQGVLYGAFHLLRELTMDQGIA
HEADDAVNKWSFITEQPTNALRMINQWDNVDGSIERGYAGDSIFYDNGEFTLDLGRIR
DYARLLASTGINAISINNVNVHRRESLFLTERYLSDVAKVAAEFRAYGVRLFLSANYA
SPIEIGGLRTADPLDAQVREWWNIQTAKVYAAIPDFGGYLIKADSENRP GPFTYNRDH
ADGANMLAEALRPFGLVIWRCFVYNCKQDWRDRSTD RARAAYDHFTPLDGRFAENVI
LQIKNGPMDFFQVREAVSPLFGAMENTNQVIEFQITQEYTGQQRHLCYLPQWKEVLDF

DTYAKGEGTEIKRIADGSLYKRPYSGFAAVSNIGADACWTGHPLAQANLYGYGRLAWN
PELSAEEIADWVRLTFGHEDEVVRQVMGMLLTSLDIYENYTAPLGVGWMVNPETHHYG
PNVDGYEYSKWGTYHFADCHGIGVDRTVNSGTGYTSQYHPENADRYESVDTCPDELIL
FFHHVPYTHVLHSGKTVIQHIYDTHFEGVVQAEALAETWRWLEGKIDPVIFSKVASLQ
DNQAEHAKWDRDMINTYFYRKSGIADEQGRTIY"

CDS 1997912..1998979

/gene="gutB_1"
/locus_tag="EFAGFIKM_01764"
/EC_number="1.1.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q06004"
/codon_start=1
/transl_table=11
/product="Sorbitol dehydrogenase"
/db_xref="COG:COG1063"
/translation="MGQHELPETMKAAIMTEPGHIIIEQPVPQPAADEVLIQVMAVG
VCGSDVHYFEHGRIGRFVVEKPIILGHECAGIIAAVGSNVSRLKTGDRVAIEPGVTCG
RCSACKEGRYNLCPDVQFLATPPVDGAFVQYMVIREDMVFPIPDHLSYEEAAMNEPFS
VGIIHAARRSKLAPGTTLAIMGMGPVGLMAVAAAASFGVEKIIVTDLEEVRLAARRMG
ATHTINVRNEDALAVIRELTGGVGVDTAWETAGNPKALQSALYSLRRGGKLAIVGLPA
QDEIALNVPFIADNEVDIYGIFRYANTYPAGIEFLSSGQHDVMSLITDRYSLEETQQA
MERALHNKSGSLKVMVYPNGM"

CDS 1999146..1999412

/locus_tag="EFAGFIKM_01765"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRVHEFMIHADFHRRDDLMSVSSQASRFSSDIILSYMESEHEHRV
DVKSLLGMALLPIRYGSVRLQTRGRDELEALEYMLNVLEKGTA"

CDS 1999557..1999808

/gene="rpmE2"

/locus_tag="EFAGFIKM_01766"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34967"
/codon_start=1
/transl_table=11
/product="50S ribosomal protein L31 type B"
/db_xref="COG:COG0254"
/translation="MPKVDIHPKTQLVIFYDASADFKFLSSSTKFSNETMEWEDGNSY
PVIRVDTSSASHPFFTGKQRNVDIGGRVDFNRKYNINK"

CDS 1999958..2000263

/locus_tag="EFAGFIKM_01767"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSSITHMVTFTLYAGKDTPEAEAFLEKSSDALAVIPGVEQFQVL
KQVSEKNEFDYSFSMVFADQVAYDAYNNHPVHRQYVEERWEKEVSRFQEIDLIQNHN"

CDS 2000415..2001176

/gene="fabG_3"
/locus_tag="EFAGFIKM_01768"
/EC_number="1.1.1.100"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O54438"
/codon_start=1
/transl_table=11
/product="3-oxoacyl-[acyl-carrier-protein] reductase FabG"
/translation="MQLDLSGKTALVTGATGQLGRVIARTLAACGANLALHYINNDTK
ARELQGEIEALGRQAVIVQGDITKQDTAFRIRDEIQPVLGGVDIVVANAVIQYEWTTV
LEQSPEDYLSQFESCVMQSVYLAKAFIPHMQNVKAGRFIGINTECAMQNFAHQ SAYTA
GKRGMDGVYRVLAKEVGEYQITVNQVAPGWTISERDRSSEPGHDEAYTRTVPLKRRGE
DQEIANVVAFLASDLSSFITGAYIPVSGGNVMPAI"

CDS 2001421..2003148

/gene="poxB"
/locus_tag="EFAGFIKM_01769"
/EC_number="1.2.5.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P07003"
/codon_start=1
/transl_table=11
/product="Pyruvate dehydrogenase [ubiquinone]"
/db_xref="COG:COG0028"
/translation="MKKTVADVLLVESLLNAGIKRIYGIVGDSLNAVLDLSIRRSKIEW
IHVRHEEVAFAAGADAQVSGSIAVCAGSSGPGNMHLINGLYDCHRNRPVLAIAAHI
PSDEIGSEYFQATHPEYLFQECSHYCEVITAKQMPRSLTMAIQTAVARSGVSVVLP
GDVAGLEAADIPVEHVYHVTNPVHPSEPELVKLAEYLNQGKKITLLCGAGCAGARE
PLMQLCDRLKSPMVIALRGKEYLEYDNPYSVGLTGLIGYSSGYHAMMDCDVLLMLGTD
FPYRQFYPEDAKVLQVDIQSSHLGRRTKLDYGVCGDVKATIELLPYLTEEHSDKHLR
KSVDRYVKVRKDLDELAVGKPGKKPIHPQYLTKVISDAAAENAIFTCDVGTPTVWAAR
YIEMSRNRRLGSGFSHGTMANALPQAIGAQVADPGRQVISLSGDGGITMLMGDLLTLK
QHNLPIKVVVFNNAGLGFVELEMKAAGFLESGETLVNPNFAMVAQAMGMEGIRVEDPD
ELEGAVQRALQHDGPVLIDVVNRQELSLPPKIDIKQAEGFTLWMMKAVLNGRGDEII
ELAKTNLLR"

CDS 2003472..2004227

/gene="lvr_1"
/locus_tag="EFAGFIKM_01770"
/EC_number="1.1.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9LBG2"
/codon_start=1
/transl_table=11
/product="Levodione reductase"
/translation="MSHAGKVAITGAGSGLGQAAALKLAEKGASIVVVDLVEETGLE
TVKQIEKLGSKAIFVQADVSKAPEVENYVKKTVEEFGRIDMFFNNAGIAGPGIKLIEH
TIEQFDQIIDINLRVFGYGLKYVITEMLKTGGGSILNTASTAGIVGPAVAPYAATKH

GVVGLTRTAAIEYGKDNIRVNIAIPGTIETPMVVQFGKDNPEVFKATVDSIPSGRLGR
PEEIANLVSFLLGDEAPYINGAVYPIDGAVTAQ"

CDS complement(2004336..2005520)

/gene="pbuE_1"

/locus_tag="EFAGFIKM_01771"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q797E3"

/codon_start=1

/transl_table=11

/product="Purine efflux pump PbuE"

/db_xref="COG:COG2814"

/translation="MSSTLKIYVLALVSFLVGTSEYVIAGILDRIADTMNISLIAAGQ

LITIFSLVYALGTPVIIALTSRWDRRKLFLGLFVVANVLAYLLPGYGLFVAARVL

MALGAGVVVVTALTVASQIAAEGKQASAIATVITGFTASLIVGVPIGRLVAASWDWKL

VFAGIAVLGILAMLVIAAAIPPSKAEAPVPLKKQLSLLKQPRIVLALLVTFFWLGGYS

IAYTYISPYLVSVSGMSEALLSSALLAFGIASLIGSKVGGFSADRWGVKRTLITGMTL

HIVSLVLLNITASSHLAVFLVLILWSFAAWSSGPTQQYNLVTMAPESSGIMLSLNSSV

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CDS complement(2005749..2006033)

/gene="sdpR"

/locus_tag="EFAGFIKM_01772"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32242"

/codon_start=1

/transl_table=11

/product="Transcriptional repressor SdpR"

/db_xref="COG:COG0640"

/translation="MQSNSNEIEQVVKIHKALGEQTRYKIIQLSGESNLCPADLESR

LVTVALSTLSHHLKQLSDCGLLTSQKKGTIYYSLNTETAQKFVPYLLNK"

CDS complement(2006205..2006546)

/locus_tag="EFAGFIKM_01773"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEMNTLVWIVLSLLILVLLVRVTSLQHQLNELKRDIERLENGST
GSVRSDFNITLSPKEAPPSHTSQPAQTDLQELLTIQQGKKIMAIKRLREARGLSLK
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CDS complement(2006587..2007786)

/gene="pksS_1"
/locus_tag="EFAGFIKM_01774"
/EC_number="1.14.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31785"
/codon_start=1
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/db_xref="COG:COG2124"
/translation="MNPNEPNESSKPAFFTKEFTHNPYPVYEKLKKEEPVFRVMFPQG
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QFRIWSNTVIDASTAESAELEQHSKEFTDYLTAWFAKVRQDPGTDLISQLVIAEESG
QQLTEQELLGVVSLIIAGHETTVNLIGNGILALLEHPEQRELLIKQPELIHNAIEEM
LRYNGPVEFSTSRWALEDIEFRGQHIAQGELVIVALDSANRDEQQFKDADIFDITREK
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EIPVQLK"

CDS 2007941..2008954

/gene="ydhF_1"
/locus_tag="EFAGFIKM_01775"
/EC_number="1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P76187"
/codon_start=1

/transl_table=11
/product="Oxidoreductase YdhF"
/db_xref="COG:COG4989"
/translation="MLGKNENEVNADMSYAQLPLHHHQIPASRMVLGCMRFGGEWDGL
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ALAELHHSGKVRHFGVSNMGSEQIRLLQLHSKVPLIVNQLEMSLDKIGFVEAGVTVNR
PQARDNVFPYGTMEYCQAEHIQLQAWGPLAQGRFTGRVVDGQRAEIEHTAQLVDRMAK
ERGVTPESIVLAWLMKHPAGIQPVIGSIRPERILACRDATNIELTRCEWYELYSASCG
RRL"

CDS 2009375..2010475

/gene="yehL"
/locus_tag="EFAGFIKM_01776"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P33348"
/codon_start=1
/transl_table=11
/product="putative protein YehL"
/db_xref="COG:COG0714"
/translation="MEMLKPPAETLYEVELRALREEDQGKRPPNWLLSPAYVRDFIIG
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RRFNFETIKPIHNVKMEAKIIESQARSLLLHSGIDIEINPDVVELLATTFMELRTGMT
REGYKLDTPQASMSTAEAVSVYVQSAMTSYYYEDKAIALDRLVQNMLGTIAKENDKDL
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CDS 2010463..2012931

/locus_tag="EFAGFIKM_01777"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"

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NRLCQKTNCRSFDELWEKVFEIGGLEKSTRAVQDVFTYCTLSRMCYSTERLQSSGDL
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QGKPGTSQQSAVNPDTVHQQMYPMVYTFADRLNGYASGMPYVNYDQIWNQLLRKK
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TTGQHKKVLDLYAKPEHRQISQLIQCITYLVPEFAKRQSGPDWIAERDMNLVRETWVY
MYSSRIEARLIENSLYGGTLAGAATRKMEEQMQEVPDHHSGELARLMLQALLMGIQDT
AMKLYEQVRSALRTDGNFLSLCNSLHVLNRIHQHRRLLGLSDEQQLPELVSEAYRNAV
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GVCVAISSGLGDRPRDEIVDRARGYIHGTPDQTRQTALFLQGVFTVARDAFLYEDQLL
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CDS 2012916..2014139

/locus_tag="EFAGFIKM_01778"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEANMNEANRTTDETGEINESSNPDGSNRGDQHSATLNRWRLI
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GEVLKSAKDIVRTVVEELRSKLESQTRASIMGKRSRYTSSSVRSLRNLNFKRTITKNL
KNYDKNKRRFVIDRLYFDGNIQPHNKWNIIIGVDESGSMLDSVIYSSVMASIFYRLNA
LRTKLFIFDTQVVDLSDRLEDVPLMNVQLGGGTHITKALRYGETLIDNPGKTIFIL
VSDLEEGYPIAQMYKACKDIIDAGCKLLVLTALDFNGDSVYNKHAAQTLTNMGAHVAA
ITPNELADWIGEIT"

CDS 2014159..2017716

/locus_tag="EFAGFIKM_01779"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLTADRAVELVEKFAVTCSEYSLKTDRSSEIIDYVLGTTDKF
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LHTLIEPVVVSNIQGKHNGSSQELKDEFLKEKRSQLIAELYPNTSFSSKEQCSNTVFH
QTMVLVSGALLYLINISGGKQRFLDTNSEIGHVLLHTIHLHEIYPLEVRRYLLSMDP
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PPFLKLCIQKFMEDQGLTLPNAEGSLEQTVFHALRHPLDGGRQGLAIARYLSGENTLE
EYWEDPNSRGLFNQLNRDKKRVHNLISISFLPLDSEAMRRFAILTTHPDWTLDIISDM
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ALFVQNVIMQKFAVGLIWGTYEDGALISTFRYMEDGTFNSVDEDEVDLPSGAQVGLIH
PLELDQATLEGWTTQLEDYEIKQPFEQLNREIHQPEDEDKTKNEYDHLPESDFSPTAF
PKALEKYGWIKGPAQDGGWYHEFYKEYGDLVAELQFSGTSITYYEGLDDITLES LHFF
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CDS 2017778..2019553

/locus_tag="EFAGFIKM_01780"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIRYANKGLYKRSLKELDNGVSVTYTWNASSVSCQLSDGTHCTL
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VPKNVSVTESASNLVSNVDDPSEIPHTVSREIESRFRWMTESDLTMLIKSYSSSMIEE
VVFRLRYPEEIKIFEDSLTLVHLTTQNI EVSFTEEPNLAKALCKVQQTAGKMAKLEAL
LRYRNLKGLDDTDALSGRVYEAKFSLQTVQECRVMLAGLLKTGLARLPQSYMAQLETL
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VIQQSQLIGSFRSKYFTVPSLHLYGLGADAWETRSGFRGITYYFYCFDDEEIYTSDV
RAVYYDDQQFSYTEHYGAFTPWLPNLTFRQFVGEEVQFHSVKVNEERRISSGEGAKLA
ILPRTGVETLNLGKTMQDVTTLQEESRFDLFAAPKERLAVIKVARIVDHNFKQTQ
ELVLTVENTEGERLALTPYSSDWQAMIQRLESGYGSQSLEHFYAFVRVEPKRISPIS
FLKGKTVLSLKLDIGNGRMGRLGRI"

CDS 2019540..2019818

/locus_tag="EFAGFIKM_01781"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEEYNQFMQKINGWSEELLLRGLSQFTIRDIEVLEQLTAESLRL

QMSFLHELLNHLIKEGRSVALGQGNEELLLFYCRLTQYVQLSVQEEA"

CDS 2020042..2020584

/locus_tag="EFAGFIKM_01782"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEEEQIRKAVANRDPEAMEWVMNHYAGLLWKIAHSILHHASVEE

IEECVADTFFAFWQNPDAFQSGRSSLKNYLATITKHKAIDRYRKLNRRTELTYEEIHH

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CDS 2020598..2021992

/locus_tag="EFAGFIKM_01783"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MRKSEKEFTEQNLFNKKLFYDKLAMNEPPTVTRSDSSFYPPI
YPSAPSAQTKKSMNKRKRYRKAIYIPVTVALSLCLVTGAAASVGII DLSTVLHFLGAD
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GNANNAQIIHYDDANQTAIVRFLIQGKVSKNRITVQINTLMSGASQQDGYNVQVDWKQ
LLQEKQNNSYEILERDRISGLGGKTDPIPVLHQDVTNIPVEGIDWVHISNIGFVEGKL
HIQINPDNEIGEYNHGYFYFTDEQGQKLDIPEYSISYGHYLGKRVRYGGDYEEFVYDL
SAVDDLDKRLQGSFTSISEVMQGNWKTTFNLSQNGLSKEGNIQFDANGVLQANVALS
AVGVTLTGEALSKIRVEDLSIEVHLKDGTKLSGASGFLQLDQDLIKWISPKTIPVNDV
SYLLNGEKVNFER"

CDS 2022170..2024677

/locus_tag="EFAGFIKM_01784"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSMSEPLLTQIVKQHIPAGATVVTIDKPVQHPAIYAADLTGDGM
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AYRVEIIRWQNGKWVPAPDVYATYYPKVQYQEQLTQQYPDYIFYWYYLADAQYHAGQ
YPAALASVQKALSFPEAYPSREVLQELEKKIKQAMVPVSHARVATWLYPISVRTTSGT
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SEERAITIDSQGFKMINEQGTVLTKRAYPYISNMNDGRALFYDSNPGQADGTVSRYGY
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LAFQKETSGKYGYIDERGNIRIQPKFSSAFPFSGGQAIVNTAEDYKSIYGVINTQGSF
IIQPAYNDIRELGEHRYALGQAIHPEQPYIGSVYAIADTNGRRLTEFLYREVGNYNKNG
LASASNGRQTYLLDLSGRPAAGYPHVEGSGTLEV VAPDLIKAYVDQRLSYVNRAGQII
WRQNTIVPLHPPYRVREEKYKPNRDYLVYYPQVEGLTNQAEQLALNAKLKQLSQVKPI
PADQQLDYTYTGDFDITFYQQQLQLQLTGYNYPAGAAHGMPTMIYAIINLTNGLLYE
LKDLFKPNSDYVKVLSQIVGDQIKNDPQYSYVFPDITYTGISADQPFFVTADALHLYFN
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CDS 2025104..2026057

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/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNNTSEVSGLMQVTKERKGLLIASIFSTLSSLLQIVPYVGVIK
IVEELLTHAGQPSAMDKDLLIYWGIVAFVALIAGLIALLYIGGMCSHIAAFNILYQLRV
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FWLDYRMALTLLIPIGIGFWLQSRLFRSEKGRQAYRDFQLAIEEMNATGVEYVRGMPA
VKVFGITADSFLTQAVTRYRDISLKITDLCKTSYGLFFVIMISLFTFIVPVGILLS
SGNAGNQSFATFILITPSLSAPLLKLMYLGSGIREIV"

CDS 2026112..2026903

/gene="msbA_1"
/locus_tag="EFAGFIKM_01786"
/EC_number="7.5.2.6"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P60752"
/codon_start=1
/transl_table=11
/product="Lipid A export ATP-binding/permease protein
MsbA"
/db_xref="COG:COG1132"
/translation="MPKVPDYEVAFRQVSFAYERKESEAYKPVLDQVDFVANAGEMT
ALVGPSGGGKSTIANLLLRFDVQEGEITIGGIPIQEMGTEKLMDTVSVFVQDVHLFY
DTIEENIRMGNTSASRQDVIAAAQTACCHECIKKLDAGYDTKIGEGGYLSGGEAQRI
AIARALLKHAPILVLDEATYADAEDEHKIQGLAQLVQGKTVLIIAHLTTIRAAEQ
ILVIRKGTIAERGTHDQLRALGGVYEHMWQAHISAASWKLGGTGR"

CDS 2026900..2028021

/gene="btuD_6"
/locus_tag="EFAGFIKM_01787"
/EC_number="7.6.2.8"
/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01005"
/codon_start=1
/transl_table=11
/product="Vitamin B12 import ATP-binding protein BtuD"
/translation="MKNLYLNISGGNPRSLPSVIAAILDGIKIVPAALLVDIFNTI
YKSFADPGKGLDINRMWIVCCILFAWLLVEYAAAYASLYDKTYRAAYSLSAASGRLKLA
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WRMAVAMFVAVPLGVALLWLTDSIQARMSENHVRKNEAASRLQEYLSGIREIKAHNM
GGKRFERLRRSFDELRSASIRLEGIMGPMIMGAMLLARSGMTWMILVGSYLLAGGELS
LKNASIVLLDEATASLDPENEAQVQAINELVADKTVILIAHRLKTIQNADQILVLDQ
GQLVEQGTHAHLDDHSGIYARLWQLQQDAEGWQVKVNGS"

CDS 2028104..2029066

/gene="fhuD_1"
/locus_tag="EFAGFIKM_01788"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37580"
/codon_start=1
/transl_table=11
/product="Iron(3+)-hydroxamate-binding protein FhuD"
/db_xref="COG:COG0614"
/translation="MFKRIPVWIALCCMLTLAACGTTQTTSEVASSEGTAAATTKLI
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AAEMLYGEWGLKRTDGIPDEGWGGKEIALEALVTVPDRLLLMENSENKMVDSKVWN
NMNAVKNKDIYKISNVDNYSYNTAMGRMELMDRLGTMILGGQK"

CDS 2029187..2029495

/locus_tag="EFAGFIKM_01789"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MSLILGFGQYLVAFYVVILSPISWLLRKYVRFP MVGTFIYMIGF
GWGGLWVFDLMYNPYFVNGYHLNRMTSIWIFAIGLVYAIVENKIWRRGQMNEQKAT
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CDS 2029801..2030199

/locus_tag="EFAGFIKM_01790"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYKAGFWIRLGANVLDSLIIISIPLVIIAGILTGNFDTDEPIAKL

LSALYSILLPVYWYGRTIGKRICGIRIRKYDTHEPPKIGTMLMRVVAGLVVYVLTGLI

GVIVSACMVGMRREDRRAIHDFVAGTEVVWD"

CDS complement(2030405..2030575)

/locus_tag="EFAGFIKM_01791"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIGCFIQLTDRI LSRLDAVNHTKSIDEFIVLATIKQDNTVSGSN

LVGGKLEWGGWI"

CDS complement(2030641..2031408)

/gene="gpmB_1"

/locus_tag="EFAGFIKM_01792"

/EC_number="5.4.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01040"

/codon_start=1

/transl_table=11

/product="phosphoglycerate mutase GpmB"

/translation="MGIKKRNIRLKLAVEDKNMFLFPIRRITNHHLAIQFIKLTGSIV

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ERITRWGANWREQNLGMEDFKMVAKRGLTFLEKLINEYVDKRILVISHGALIGLSLQH

LLPQHFKQTYIDNTSITILHTNKNWACQLYNCTKHL"

CDS complement(2031539..2031652)

/locus_tag="EFAGFIKM_01793"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MFTLAAKHLTDFLFYRYKFLAQAKDKNLYRLPELTRN"

CDS complement(2031704..2032324)

/gene="xerS_2"

/locus_tag="EFAGFIKM_01794"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A2RKP9"

/codon_start=1

/transl_table=11

/product="Tyrosine recombinase XerS"

/db_xref="COG:COG0582"

/translation="MGRIDDKLSELPWYVTEFIDSKKRKLSASTLLNYCHDYIIFDW

LITENFTTVQKRTEIELSTLETLTIRETESFLSFLEYQLGNNKLTINRKLSSLKSLFD

YLQNKAETIDLKPYIQRNVMAMKMDLNAVKESQETIANRMEGKILRENDFEAFRVFVAY

DYGELNKTNKRIMNFHQFNRRERDTAIIISLILGSGRLRLSEVSGILRI"

CDS 2033278..2033412

/locus_tag="EFAGFIKM_01795"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLAAIHMVDLMRYLFGEAVEVVGTAAPDGEHHPISISLKFAMV

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CDS 2033761..2034144

/gene="mhqP_2"

/locus_tag="EFAGFIKM_01796"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P96694"

/codon_start=1

/transl_table=11

/product="Putative oxidoreductase MhqP"

/db_xref="COG:COG2259"

/translation="MLIIRIVIGFIMIGHACKKLFGIFGGEGISGTAAFFNAV GIRPA

WFMALCAGIIELVGGLLFTLGLWTVVGAILLMLTMFVAIVKVHVKGKGLWNLNGGFEYN

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CDS complement(2034977..2036632)

/locus_tag="EFAGFIKM_01797"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRNVRLWMLMLVFVFLTSACSPAGNNSDSPQNEGNITVEDNM

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DPNGNGKADEIPLAGAVGGWNTIEGFLMNSFIYNPMGSTQTGMMLDQGKVVAFTQD

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RYKEYVALPPLAGPDGTRIAWTNPYEGITSGRIVITNNSKYPEVAFRWADGLLDGGEV

SLRSDTGTMGEYWDWAEETGINGKPAVWEKLKEKTADSNVGWQTRAPRYYPADLRLG

EKRNDEFPLEVILFEAAKQYEPYKVDSSLVIPPLFYDEEQAAELVNLEKTIIDYKKEM

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CDS complement(2036700..2037596)

/gene="araQ_8"

/locus_tag="EFAGFIKM_01798"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1
/transl_table=11
/product="L-arabinose transport system permease protein
AraQ"
/db_xref="COG:COG0395"
/translation="MSNISIRKSKGDLIFDIINHSLIILLAVLYPLVYIVSASFSA
SESVVSGKVWLWPVKPTLDGYKAVFANGMIWTGFMNSWVYAVAGTFINVMFTILAAYP
LSRHDLKGRGIFTFLVFMTMFSGGLIPTYLVRDLGLLDTRLALIFPAALSVWNMLI
TRTYFQTTISRELLEAGQMDGCNDYKFLWKIVLPLSGPIVAVISLFYAVGHWNQYFSA
MIYLRDPQLFPLQLVLRDILIQNQIDFSTMSSTEELVKREGIRELLKYSLIVSTLPL
MVVYPFVQRYFVKGMMIGSLKG"

CDS complement(2037616..2038578)

/gene="yteP_8"
/locus_tag="EFAGFIKM_01799"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:C0SPB3"
/codon_start=1
/transl_table=11
/product="putative multiple-sugar transport system
permease YteP"
/db_xref="COG:COG4209"
/translation="MQKPQVQVTRPPKEMTESGHRGRPWIQSWQLYLLILPLAYLI
IFKYVPMYGTLIAFKNYVPTKGIWGSDDWVGLLHFERFLNSYQFVRILKNTLSLALYEL
AVGFPLPILLALGLNYVRNTFFKKSVMITYAPHFISVVVLVGITMQFLQPGTGALNV
ILGFFGVDSVHFMAKPEYFKTIYVLSGLWQNIQFSCIIYLAALSAIDPTLHEAALMDG
ASKVRRMWHVDLPGIIPVITVLFILQMGNFMDLGFQVLLMQNPLNMRTSEIIDTYVY
NIGLKGAVPQYSAAAAIGLFKNVIALILLVIANRMARRTGNSLW"

CDS complement(2038846..2041110)

/gene="rhaR_8"
/locus_tag="EFAGFIKM_01800"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01533"

/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaR"
/translation="MNLAVVRKWINNRPLFFRLVIPYIAVVILLASCLGFTYSKSLKI
VKKDILYANDMALEQTRRTLEIRISEMEQTMWDIVSLPSVRRALIIREPFEQANPYRF
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DRFFQLNGNFQPAMQLTLAGKTVSGIPFIRPMGNGREVGALLVLMNDRKIHELLGSM
QLSEGSLSYIADQKGQIISYVSGTGVEGLVPSVVKDVNLKDMITASTTSHQLGWTFVT
AHPQAIVAERSLEITQSILNLLIFVLGLVISIGLAHRHSLSLHRLTRHFTEQSEPK
LFFGNAYSWIEQKVGGLSERQHIMEKLHKEQLPILQTTFYEQLLKGYFSSEDHLQSLM
KHAGLEFDSTGYLVLTIHFTGYGDGVDADILREVEGKKITVKEALRFSDAAKSIHVHD
WDTYHLSIIYCCGDKEIQDLHLVEQILLHILGNHSLYLEEELDVVVTASSMVTNLWEL
PHAYQEAMTAFRQYVWDPRHRFVWYDGQPENQSFAYYPPELEAMLVQCTLTGDIERMQ
DVLHGLYQANMVMNRRLSLSMMQLFLNELLGTLAKVLIELKNLQTSPEEYVQIRCVKDA
VDYYGQIHDRFLSIGSLIHLNKRSHNIELRDRLTAFIQKNAYDSDSL SASKVAREFNIS
SAYFSQFFKEQVGSNFSSYLEQLRIARAKELLNGTDSNVQEIAVSIGYNSSNSFIRAF
KRSEGRTPSEYRQA"

CDS complement(2041517..2041888)

/locus_tag="EFAGFIKM_01801"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNTEQDLRVLKTLEHIKSGFSLCVSQKTFKSITIKDISTAAKVN
RSTFYTTYTDKYHLRDELVKATLQDLDHADLTFTFDDQSPWQTRSVIVQHLEHLWS
QKEWYLHLWNKNLELYVFEDM"

CDS 2042193..2042723

/gene="linC_1"
/locus_tag="EFAGFIKM_01802"
/EC_number="1.1.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:D4YYG1"

/codon_start=1
/transl_table=11
/product="2,5-dichloro-2,5-cyclohexadiene-1,4-diol
dehydrogenase"
/db_xref="COG:COG1028"
/translation="MYNLMKAGFVTGAGSGIGRASAIAFAQAGAKVMVADINEEAG
LETVQLIKGFGGVASFVRTNVAVEEDIIRLVQATVSELGQLDFAHNNAGITLPPAPMA
DSSSEAFDRVVKINLYGTYIAIKHEIQAMLKTGGGAIVNTSSGFGLIGGQNQAIYSAT
KICNKRNYKKCSYGIC"

CDS 2042710..2042955

/locus_tag="EFAGFIKM_01803"
/EC_number="1.1.1.119"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q5FPE5"
/codon_start=1
/transl_table=11
/product="Glucose 1-dehydrogenase"
/db_xref="COG:COG1028"
/translation="MEYAEKGIRVNAICPGMTATPILSWLDNAPEQAAAFRSTIPSGK
LQTAEDQANA AVFLCSNLAGQITGVTL PVDGGYTAGR"

CDS complement(2043131..2043952)

/gene="rhaS_10"
/locus_tag="EFAGFIKM_01804"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaS"
/translation="MYNPLDLVVRIVWSSRKQTPMDWSDIRNNTSVHTFYWIHEGKGM
FQTEDQTYEVLQGMLFYMEPGAQMKMESSKESPLTISMILFDCCAVSYQTPEWQLPQP
IHRMDIPFFSRYHSERALRLDHAFNEITESWLLGNHYREMESCALLKLLAILHRPDH
FSEPGNTTSIIFKIKEELETRFEEQLYIREIASKYAISESHLRKMFMSHIGQSPKEYL

TEVRLRQSERYLTYNTYFKRIARQCGYHDEYHFSKAFRNWKGVSPSTFRKNEKS"

CDS 2044126..2045814

/gene="uidA_1"

/locus_tag="EFAGFIKM_01805"

/EC_number="3.2.1.31"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P05804"

/codon_start=1

/transl_table=11

/product="Beta-glucuronidase"

/db_xref="COG:COG3250"

/translation="MIRLFDTHHTRISTELEGMWEFSPVDNIGERPKEFPFKLPVPGC
WESHPHFGTYRGKAVYRRVISVSSQTHIRLEFKGVSHTAHVYFNGEFVKTHYNAYTSF
EVIIPNAISGEHEILVYVDNSFSEASALHFPNDYYTYGGLIRPVVLEEISDLYIENIM
FTPLRQANQWNGRWKVMIRNISQFPQQVQVIGELAGIKSILGSCEVGPGGQAELIQT
SYPNVLEWSLDHPSLYQLQTKLITNGRLVDDLVDRIQFREITISNGQLLNHGHKLK
GVNRHEDHPMVGCSFPLSLMVRDLDLIEEMGCNAVRTSHYPYDERFLDLCDERGIW
EENHARGLSLEQMRNPFAWQSEQVTREMVEQHFNHPSIIWAILNECASNTEEGKVH
YAKQLTIIRELDPSRPRSFASHHRDQELCFDLAEIVSFNLYPGWYTDEKPEELALEAI
QWANKLGGADKPIIMSEFGADGFYGFRRSNNREKGSEERQADILRNCLNAYQASTDICG
MFIWQFSDCRVTEGEGWLLTRSCTRNSKGLVDEYRRPKLAYDVVSFIYKSEDKK"

CDS complement(2046057..2049968)

/locus_tag="EFAGFIKM_01806"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVKTQETGSVLTAKDWVERAVVGTEPGQYAESDWKTIVTLVEA
EEQTQRDKSTIRHLLDGMDQFLSRVHCSNRVINKENNLLEYSTYRRELTRLVFKARAI
LFIDAEQYTEGAKVALTDQITRAEAALNGTYTAPFVRNRAFIEPRPDEDIQAVTEHCT
MAPSYNMGTYGLRPAIEWYTYQHIMADCYETEKVYASSIGCVNESTADLSQGDLPAVE
LESCSIAYLTFDLPSLGQRRRLRHARLRLVNHHTDGKSVDLYALEHSNHHFQTLEQLTY

RQIERHPKMQPSADQYLRSFQLGFAEGFSYADLSEYVIRSMEEKGGKLLALT LGEGEL
PCGFYTCNHPEQQKRPLIELFWDEVQEDVWQQKVREICQRAKQILANEKPGSELGQVD
PEAYQQVQQELSNAECLALSQKTEKVSESGSALVRLLNAMRHLRHSRVLRSDDLKGW
NLFFTTQGLTKLREKTVRNDELEREFQKVREWSERRSLADLQSYASVMQDEPDWTLN
KQFGLWTRSRLTFTPPENTASASLAFVLPSEDNEEHDKLGHVWIDRVSILPAHDANL
EIENSGFNEGNQLPNHWTPVAIKGKPVLHWEDRGEYVQDGSHSIYLENPTSGDEGAWI
YDKDIPLQGGVNHTLTYFAKVEGKFKEGVQAVLTFKDAVGREVGSGFHGIHNKKS LPGN
PELRLTVSFQADALIYAMTGERSYAEKVKLQMLWLLNDYCQGVESWL VHNVRPDGLDA
YGAVQIGRVTTLIATSYSLIRDANVFSQEEYDRMMAQLDYLRDLMDLRDRTEL GAYR
AQQGTSNWHTDMAAGAAMLALAFPEMPHARQWLDNARLILKGQLDYHINEDGSWPESI
RYLFAVIQRYGTFAKTLRHMTGENWFGQTRFSSTFKYALSVQTPPYVFFDNKISTPNF
GDHTLDNGGGFAVLGLYVDEIISDPELGAQVYETWIRAGKPLCGFGVESNMLENFFM
PSSIDTLASDSKTLNLISQSFENIGLYLFRQNFNCPDEGYLSVISSRTPVGHGHHDQA
SFIWYVNGIPLVDPGVESYFDSTFAWYKGSSSHSVVQFRHNGYYVDMPRVSEVQHLL
TSDLLDEITIRIQSPTGAGNHTRHITYMKNGLDALILWDVIRNAEEGTRMNLPLAAKS
TSIEGQRALSIGHYGMDETISLLPQCADIIEWGRSYPIAPLVEGKSQ LNYLRIKAG
RNEPLLTVLFAHPTGGEGQLIKPIRCSEKHALAYQIRKLDRVEAILVNTSDECVTTE
LRYKHTLMDTRNKEIIPDIKGQIRLSLDGGQLRVLIPNSNT"

CDS complement(2050003..2051571)

/gene="xynB_2"

/locus_tag="EFAGFIKM_01807"

/EC_number="3.2.1.37"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9ZFM2"

/codon_start=1

/transl_table=11

/product="Beta-xylosidase"

/translation="MNINFQGKSKPLNHIWSACVGAGRANEGLRADWQSHLSKAVKHG

GFRYLRFHGLLHDDMHVYKIVDGQEVFNFYVDALFDAMLDQGIRPFVEFGFMPNDLA

STERTQFWWKGNISPPNDYAKWANLISKLVEHWIQRYGLEEVKNWYFEVWNEPNLSAF

WDGTKEQYFKLYQVSAAIKAIDDLRVGGPATSNFVPDARFDGELEDISTHLLTVTE

ELDSLEWKGVWIEEFLAFCERKKLPIDFISTHPYPTDFALDGHGEFQGRSRHASSTKD

DIEWLKRVIASSAYPDIEIHLTEWSSSPSSRDYSHDYLPAAAYVVKTNLEVSDLIDSL
SYWVFTDVFEFVGAGPAAFHGGFGMLNLQGIPKPTFHAYSFLNQLGEHELARSEGTVI
TRTDNGELRGLFYNYPEDYKGTVPMSVYPDQTVTAQTAQSFGISRTFNLVVEQVTPGGQ
YVLRTVDRDHGVAVQLWNEMGSPNSPSREQTEQLIAYADQLNERKFTADSNGRLLTDF
NIGPWAIALLSEEV"

CDS complement(2051632..2053977)

/locus_tag="EFAGFIKM_01808"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMVRGNAKSNHSAIWFEDEPAKEWNECLPIGNGLGGMVYGGITK

EVIQLNEDSLWYGGPTDRNNPDAAAHLGNIRDLLMEGHLQEAERLALLALSGVPESQR

HYLPLGDLTLTFRNALPGKINAPQSYRRELNLEEGHVAVTYIQNGISHRREIFTSYPD

NAMMIHLTAEQPGSIHVDVQLSGGVRKRHMDGMIRLRDNSMAMHGSTGGGGVNAAAAI

QVQTVGGSVQILGETLLVKDADEVFISLTAATSFYDQPLEECDTRLLQLTKYSIDTL

KERHRKDYQALYHRMSLQLGPVDKELEHLPANARLERVQAGESDHGLVGLYFQFGRYL

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EDHEEAEPGHRHMSHLFALYPGNRITPTNTPELSRAARVTLERRLENGGGHTGWSRAW

LINFWARLLDGEQVYQNLISLLKHSTLPNLLDNHPPFQIDGNFGATAGIAEALLQSHT

GTLSILPALPPAWSEGKVKGMKARGGYIVDIEWFADGRLVACITATQTGMGSILAQQI

NEIRQQGAGTNLSDDINTNGEPITLELEAGYTYELFGRYRI"

CDS complement(2054014..2057058)

/gene="lacZ_1"

/locus_tag="EFAGFIKM_01809"

/EC_number="3.2.1.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P81650"

/codon_start=1

/transl_table=11
/product="Beta-galactosidase"
/translation="MLDITKHWEDPTTLHVNRETARAYYIPYHDAVSAKTRKRGKSPY
FQTLNGQWKQFQHASVAQVHEAFYQKKFDVKEWDNLTVPSCWQVNGYDQLQYINYNY
ISCDPPFVPNDNPAGLYVRDFEISSEWDTKERFVVFEGVNSCFYLWVNGQYVGYSQGS
RIPAEFNLTEYLQPGLNRMALMVLKWCDGTIYEDQDMWRYSGIYRDVYLLARDKAHIR
DVFHKQQFAAAGNQVTLVSEIETTGRLYVKAELKDASGRLVAAADGVIEDKGALKLEV
EKPGMWSAENPVLYDLYLTAGDEVILSSVGFRTVDVHEGVFRINGKAVKLKGVNRHDS
HPELGQTIPMEAMIEDIKLMKQYNINTIRTAHYPNDPRFLELCNEFGMYVIDEADLEC
HGIGQAGNFKDGCYQQFSADPTWKEAFIERAVRMVERDKNQASVIMWSLGNESGYHDN
HIAMAEWIRSRDESRLVHYEGTAAQFGGHPNTQSLDVESKMYFTYDEVRYKIEDETNI
KPLFLCEYSHAMGNSCGDLGDYWDLIYAYPQLMGGCIWEWTDHGIASKTAEGQSYAY
GGDFGDSPHDSNFCIDGLVSPDRKPHSGLIELKQIHAPIHVEAIDLSQGSFSVINRHD
FVDLSHIGLHWKITSDGVTVQQGQIWQLEAQAGSEQRISLPYDFTALNGQAAELTSLF
WNNKETTWASMGYEVAFAQFIIHETQSLARMQDEITTKPIAYRHVHADEHQGTLVMTG
HGYRYEFNLDQGAFASITREGLEMLAKPLRFHIWRAPIDNDTYILGKWREEGYDRAKT
KIYGTWEQTENGVSLSVKYSIGASDRYPILHGEAIWNVQHNGVQLQTRVNVRENFP
YLPRFGLEWIMPSGNEEVEYYGYGPHESYLDKHSARRGRYLTRVHDLFEDDYVMPQE
NGSRFGTEWAMVTNLLGMGMKFASSQPFSFNASHYTPEDLAAASHTYDLKPRQETVVQ
LDYKMSGVGSSSVGPQLLDAYQLVDKAFTFELWLKPIFKEDE"

CDS complement(2057369..2058973)

/gene="rhaR_9"
/locus_tag="EFAGFIKM_01810"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01533"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaR"
/translation="MKHTFSLVIVDDIPAVVDGIAHDLPWDDYAIEVVGTAYDGLDGL
KLIQEKQPDIIVTDIRMPKLSGIEMIEQAKQSGAKLIFISGYSDFSYAQQVLNLGGFD
YILKPFTPNELLETCRAKVQLEKEKESRHHLMMDVERKLRESMPLLRQEYLNLLVRY
SHPETVKEKWDFLNVNMNDHYFTVFTVEMDNYYTNKAGVSDVELQRFSLQNILETIR

TFTGAVVFRDDINRFVCIVNDRADADNEEMLKIAEACRENNVERYTRYSSISIGVGTKVE
HIHELPITYQQAMYALSYNFYTGGSNVFAYPIYAENHATYVKFSSEKERELVYLLRSG
ATSKINEVLGDIFSEWKDSQAMPTPDVKVMFWIELMVNVRNAINEDLEFVEPHFFDRK
IHKLTYDTSLTELSQIVAEICHMYCENIGKKQKETAHVVINESIAYIREHLHLNASV
ADYAKQVHLSTSYYSNLFKKVTNQSVLQFVVQERIEKAKILILQGITLQEVA MEVGYE
ERSYFSDVFKKKVGMTPSEFKKQYQN"

CDS complement(2058975..2060735)

/locus_tag="EFAGFIKM_01811"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKWLYSTTFRERIQLSLILFTMIAVVVCGGTSYLIASRVLENK

SYSLNQGIIDKSAQSLEEKLRKIRLAVLTFMSSDQFNQLLKETAKGGELSYDHFKN

QSLQTPIFQMKLIEPGITSILVNTPVGEYFSNPDNRTGGIPFSESNVYPFLEKGHLPG

WVESHPPDDLFRGTQNVLSLMFVPIVQNAPADTHIVVDVSESALKEYLLKNSGDAIPV

FTENGKLAFEADSLSSQLASDSDFRSRLKDNKGHFEYTVNHIRYLVNYSTVAFPDNWL

IVHLTERNVLLKDVRILQLVTISVIVIFGLLALLVSRKLTSLLRPLNQLQSVMKKVE

HNDWSVRFQGEYKDEFTHVGFRFNSMLDQIELLTRERMDAQHAERIAEMKALQAQMNP

HFLYNTLNTILWKSHSNKQEEVREMIMSLSALFRVGLNNGEELTTVGKELEHVTQYLK

IQKLCYASLFEYTIECDEEIKQLSTLKLLQPLVENSILHGFKDYRNEGQIHIRVKVV

NKFLQMKVIDNGQGFDVQEHEADNPHLVSDCEGFALRNIGKRLSLYYGSRAEFNVTS

TPYIQTSIEILIPLEIEGAS"

CDS complement(2060847..2062403)

/gene="lipO_5"

/locus_tag="EFAGFIKM_01812"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37966"

/codon_start=1

/transl_table=11

/product="Lipoprotein LipO"

/db_xref="COG:COG1653"

/translation="MKKKAALLMASLLLSASVLGACSSDKTGSNTQTPSQSSSSQESA
NLSIFYFDDAGVVKMDSPVLKKAELTGVTLNNVASAGGEEKQAYNLMLASGTLPDIV
SYTADLNSIGAEGALEPLNDYIDKLAPNFKKFLDEHEEVKRTITAADGNIYAIPFVA
DGSASTGWFIRQDWLDKLETPKTVDEYYEVLKAFRDQDPNGNGKKDEVPMQRDNV
VGAYSLPLWDAYHSFYIKDGKIVGYPYEDQFKTGIENTIAKWYKEGLIDKEIYTRSKA
REVLGNNNTAGSTHDWFASTANFNQSLSKDVPNLDFIPFAPPASISGNVYEVGKRAQL
SGFGWGVTAQSKHIEDAVKYFDFWWSEEGRRLFNFGIEGKSYTMVDGKPKFTEEVLSQ
PAVNGYLVEAFGAQLPKMGAWQDFSYYEQWTNEIALKGIKEYQDKNIISDNYVLPTLN
FTKEEQKRLDALKGQIDTYFAEKAQTWVMGGENVEAGFEAYKTQLKNLGVEEYIQIYN
DAYARYLSIQ"

CDS complement(2062477..2063340)

/gene="ycjP_2"

/locus_tag="EFAGFIKM_01813"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77716"

/codon_start=1

/transl_table=11

/product="Inner membrane ABC transporter permease protein

YcjP"

/db_xref="COG:COG0395"

/translation="MMESRGEKVYFVFNYYILGLFACLTLYPFLYVLSASISSPQAVV

SGEVLLFPKGITWEAYTSVLGEKGIWTGYGNTIFYTVVGTLTSMILTICGAYPLAKKR

LKGRTTINLIISFTLIFNAGMIPMYLNFQSLGLLDNRFGLIIGFAISTFNFVILRTFF

QSLPEEIEEAARIDGAGDIGVMRIVIPLSKAPLATIGLFYAVSRWNGYFWSMIMLRD

ESKFPLQVLLNRLVVQMKPSENMMNDVSFTTGETVIYATIVVAIPIIAVYPFIQKYF

VKGVMIGSLKG"

CDS complement(2063351..2064307)

/gene="yteP_9"

/locus_tag="EFAGFIKM_01814"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11
/product="putative multiple-sugar transport system
permease YteP"
/db_xref="COG:COG4209"
/translation="MTTNTKIQTYNKIVKRTSTLWALIKRDWFLYLLLVPFLLWYVM
FAFKPMYGIQIAFKDYSIFRGIQGSEWVGLQHFQEFLKSEYFYRVLKNTLIISLYALL
FVFPAPIIFALLLNEVKSSKFKKVQTFTYMPHFISVVIVAGIVTNFLAPGNGIVNLI
IEKFGGDKIYFLADASFFRTILNSMNIWQGTGFAAIYIAALSGVNSELYEAAVIDGA
SKWKRTLHVTIPGILPTIMIMLILQIGSLLEVGYEAILLYQPVYATADVISTYVYR
EGIVNGRYDMAAAVGLFNSVVGFIILIAANKLSKKYTESGLW"

CDS complement(2064532..2065689)

/gene="ugl_2"
/locus_tag="EFAGFIKM_01815"
/EC_number="3.2.1.179"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9RC92"
/codon_start=1
/transl_table=11
/product="Unsaturated glucuronyl hydrolase"
/translation="MLNIEKQSIWLQDIEQRILQKLDWVSDKSKNKIPYTTVNGVHDD
RSVENPSSTHADGINWWTNGFWGGMMWQMYHNTGQEKYKAIANISEDKLDAGLQYYG
LHHDVGFMWLPTSVANYKLTKNPESRKRALHAANLLAGRYNPMGEFIRAWNDISGEDT
RGWAIIDCMFNIPLLYWATEETGDPRFMQIALKHADTVMDTFVRPDGSVNHIVEFDPF
TGDVIKSYGGQGYAEGSSWTRGQTWGLYGFMMSYIHTGKKEYLDTAKRIAHYFIANIP
DNGIIPIDFRQPKEPAYEDSTAAIAACGLIEISKAVELHEKDLYLKPALKLLKTLDE
DRADWTTECDCILKNGSAAYHAKEHHQSIIYGDYYFIEAIYKLKGTDLFW"

CDS 2065869..2066759

/gene="araC_2"
/locus_tag="EFAGFIKM_01816"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A9E0"
/codon_start=1

/transl_table=11

/product="Arabinose operon regulatory protein"

/translation="MEVGFESEVPFHGQPLIWTDHRHRTSKTNSSFYHWHQCCEFLIVFE
GKGTVMNNKTYPIKPGMLYVFQPFIEHKVFAKVTHESHYERAVIHLDHVVIDQYLKD
YPRRREWFDRLCYSSEIERAFDLSDMDLFSYCMEDYGQIAHMEQGESREEITVFLVQ
FLSAMARIFPKDQSEPSLTRRKKEHSELMQWLDEHYMESNILNKLADQLHFTRSYVS
RLFKNETGSNLSEYLTAKRIKVAAHMLETMTMSVEYISHHVGFQNVSHFISCFKKTYQ
VTPLKYKLNQKKSGLESHEV"

CDS complement(2066880..2068853)

/locus_tag="EFAGFIKM_01817"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPQQSTKAKLMSIMLVIIIMLLIPAYSVLSSETAEAAFTTHPGIM
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GNSALENDARAAYYNALLWNVTGTQAYANKAIEILNAWSSTLTSIAGTDAQLAAGDNG
IFLANAGELLRYNSNGWAAANITQLENMLTNVFYPHIQSPGDANWGGSAMKSMISIAI
FTNNQTMFDSAISNFRTNACASVTRNVMSTGQISESGRDQVHALGGLGNLTVVAEIAW
KQGVDLFGDGDNRLLAGSEYWSNYNLGNEPTSWDSTYGRCTMGPWSGINGTGRSDTIG
WAQNEIIYAHYVTRKGLTAPFTTSYMNGMPATNTDAALLTFAYRLGTTTDSTKPSAPT
GLTVKPLSDKVINLSWTPSTDNVAVSGYKIYRNGTIVGYSPTS DYTDAGLTASTAYNY
QVSAYDAKSNTSTTSSTVSATTLSSANAQIPFSSQDIGSVGVAGSYSYSAGTYTIKGA
GSDIWDKSDQFRFAYVPLKGDRTITARVASLTNTHSSAKAGVMIRESLFEDASNVYAA
MKPGLAVFQNRAPGAINSTTSATVSAPYWARATRSNTVTYISANGVTWTQTGTS
SISAASTAYVGLAVTSHANTTLTATFDNVSVQ"

CDS complement(2069011..2070048)

/locus_tag="EFAGFIKM_01818"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRSKTNVKKMEMRKVWTSFLVLLMICTTSVNAATIEQLARPSFE
LKLKSVNNKLVEVSVIGHDLEDLYAYEMNLEFDADRLIFSKASAGSVGYTVVPKAE
GN
YLKIAHTKVGSVKGDSDGQLLTTLQFNVQRAGNSKITLQTIKLVDSKLNMSNMTPALQ
ETIQAESATSFSDITGHWAEASILKAVEAGFIDGYTDGTFRPNHEVTRAEFAVMFSRA
LKLDVNESDATFADANQIPAWASSHVQAAVKKQLITGYVDHTFRPNAKMSRAEMASVA
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CDS complement(2070117..2075468)

/locus_tag="EFAGFIKM_01819"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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NFYHNNGRWMNQHGIIQAYMMAAIFSDNQQWYQEAVEWATANKTATFKGQSGDIFHQ
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TFGEVTDASDGVGIFFLDNRILAGANELAKYNLGYDILYTPVNISNAVVGDPGTGNYA
DTVSDNGRGLGYASEVTYGYMHHLTQPLDPGDERIKYLAQAIEKQGGLKAIPSYVLL
QGTSDLATGEVVGPPKPLSNPPYIEVTAAYDRLQAFDYMGRSETTSTSTFQMDGMRS
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DLAKGEVLTTLQVPNTGWWTNYATVSSKLSKPLSGKHIAFKYYGSANALSYQIAFDW
FAFSDGYAGDEHPALSGVLSGEATKASDGVNLSEGGAITFGKMNFDSGNNSIELQAKT
TDATGKLLLYSGETLVASYKLPNTSNAMVKFTSEVASADLAKIKGIHDITLRYKGNP
ITLKTYRNIERNRLANVETGSGANFIADQAIPISGTFEIGSEGTRSYILTKNESIVY
LSKAALQVDRTKDSIVSFTVRTNGVAKLQLQRDSSTPPFATIRVPDTKGDWLRVSTNI
SNKYVKSDDYPTYLKSFLVSIETDKEDTEVKLSYTLDPADTSPVLKLTSEQGFELTS
VAAYENGADMNLKVSVEDLDSVNVSLSTDNQDYIDSSGLNGKAGGT LIVKPAGLAPGE
YVFHIYAEDDTSNYVDKEVKLSIYPEEENKAPEGLTAALTGPTSVLLNWQEVNGATYY
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STIQVTQSMVKASSKQWDASDSTGIGTPESNGWRAFDGNIETAPDALTNPSWILIDLG
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KGYRYLRYYTPKGNANVAELEYQKAVDVPAPNQAPVFADLAPVTVTAGQEVKQTLVA
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TVKEIAEPQPGTENSATLRGPLTAAPGQPVDLNIGVQGVTDGFTTAQLTVTYDYLRLQ
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ALHGQVKVDATTGKAQVSLSDFEVSADGNSNMLDTSTASIAIQIQVDKTQLTAAIQSA
QSLHDMAVEGSDTGQYPVGSKAVLLTAIEHARAVAANETPTQAEVDAKVVELNQAVES
FTELVIGVSKAELQQTILQAQWLSAAAVVGSSQGQYPFDAKNAFDAAIQNAVTVRDNS
GTTQAEVDKAVIALQPAITTFRNSIYTATPQPTDHTGLAVQIQSVQKQLDKAVAGTKI
GQYPQQAISILKAALNTANEVKNNTAATQSSVDEALANLQSAASTFAAQMITLVPQGT
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CDS 2075939..2076730

/locus_tag="EFAGFIKM_01820"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIHLTIEVQREDGTILAEHTDTNHTHLVYDQPYQLGDSIVLRSS

RDGVYLYIQLDDALNPDFVYLSGQEYRLSIPFNEKKTSYSPKSFTGQLHLLTVRVASN

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ESWGINQRLDAEFTLHFGRLEIDKIVLYLRADFPHDNYWKQVTLFSFDGSSITSSLE

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CDS complement(2077435..2077611)

/locus_tag="EFAGFIKM_01821"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGKLNQLDDFVENDETSSIILWDGNGDFGYRRNRQDRSESWIHI

QRVDHRFFRSQPVS"

CDS complement(2078357..2080120)

/gene="cotA"
/locus_tag="EFAGFIKM_01822"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P07788"
/codon_start=1
/transl_table=11
/product="Spore coat protein A"
/db_xref="COG:COG2132"
/translation="MVQLLDPKRIPKYMNQIGNTPVYMPTVLRQPMTGKLIGHAYKIY
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DGYPDAWWTADGKTGMAFTTNNYIFPNVQQSTTLWYHDHTMGITRLNNYAGLTGIYVI
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VNGKVWPNLNVKPQQYRFRVLNGSNARFYHLHLSNQHKFIQIGSDGGYLPQPAELSSL
MIAPAERADILIDFSSLAPGTTVILMNTANAPFPNGATADPETVGQIMQFTVINGSVI
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PPIDPYLLGQPISPPPNEKGWKDTIQMNPGEVTTIRVRFTSQDGSFPFPDPSLGPYV
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CDS complement(2080700..2080981)

/locus_tag="EFAGFIKM_01823"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSNYHELVKGKVYIGGADAALSAIKEQGVTDVFDLRDDGKPQEG
FPDSTNRHHYPIVENRNDQEESIKFAIQAVTEAVQAGKNILSLCWWPEQ"

CDS complement(2081009..2081185)

/locus_tag="EFAGFIKM_01824"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MISILKTEGLKNDVVQEINKIRVAVDPEIVTTVESITLDVERYD
DGLGLVVSGGSSCF"

CDS 2081727..2082059

/locus_tag="EFAGFIKM_01825"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSLTTGLQYNYLESEGKLIYCKNISNKEITIFLKLTEKSFGQT
NSIPIFQRYFILDPMCCKEFNFTFKKINFFEVQVAFSELSKTICSVSLLDKTGIQYEE
YKLYKSSK"

CDS 2082737..2083183

/locus_tag="EFAGFIKM_01826"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVRTL DARTSLASTGISPLNILLPSNTPTLLGIVGLNIFNPGPL
IRTQFNGTYRFSVASLSSLPSTIRLEIFRGATNTGQPIYVVSQPIFSSTNTILASFEG
SDYNVPPPVNGQLIYSCYATFVPASGMEQATRIGPECFNAV TYSDD"

CDS 2083225..2083677

/locus_tag="EFAGFIKM_01827"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVKTL DARTSQGSNGHNILTPSFTNGVPQLFAQVGLQVSNPGMF
IRTF FSGIIEVTANQLPVNGNFVIEVYRGLSSSQQLVYRAGTIVQANAFFSPCVLSFT
GSEYNVPPPGSGQLVYSVYAIFTYDPSFSINNLR LGPESFNATVYSND"

CDS complement(2084257..2084448)

/locus_tag="EFAGFIKM_01828"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNNVVEGQEYIPIEVANLAAFLFYRYKFLSQAKDKNLYRLPKWT

RTCYYLRLGEYLSGSRGLC"

CDS complement(2084496..2085503)

/locus_tag="EFAGFIKM_01829"

/EC_number="1.8.3.7"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9F3C7"

/codon_start=1

/transl_table=11

/product="Formylglycine-generating enzyme"

/db_xref="COG:COG1262"

/translation="MEDIEQDKKSSCCTPGHERASIDIKMSTRFNTKPVIYQDHGKEH

TKSEPTASSMIRLEGGDFCMGTDGNEGFAEDGEGPARKVWISPFYLDYAVTNAQFQD

FIRDTRYKTEAEKFGNSFVFYLLASDQRRNRATMVAQTPWWHVIEGANWMHPEGKGS

DLEERMNHPVVHVSWNDALAYCEWAGKRLPTEAEWEYAARGGLFQARYPWGDELTPDG

KHMCNIWQGEFPTNNDALDGYVGTAPVDEYEPNGYGIYNMAGNVWEWCVDVFNPHYHQ

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CDS complement(2085729..2086778)

/gene="ssuA_1"

/locus_tag="EFAGFIKM_01830"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40400"

/codon_start=1

/transl_table=11

/product="Putative aliphatic sulfonates-binding protein"

/db_xref="COG:COG0715"

/translation="MMRITTNRGRLLFVFMVMAIVIAGCSNAGNSTSERTPSNASEGK

TDSNAQPAGGEETVKVRIAVNGNLNPLIIAQEKGWLKEGFEKLHAEVEWSKFASGPPI
LEALVSGRVDLTFLGDGATITGLSNNLPLQVVGLIGEGKNLSILVPVDSSIAKVQDL
KGKKVGLGRGSSSHVYLIKVLEANGLKQEDLTIIINLTPEDAQAAFESGQLDAWVTVDP
NVTNLNVANHKAKALDANIELFAPLSMVAHSEFTKTHPELVVEYLKQFKRSLEWQSEN
DEAAQIYSEQTKLPPEIHKVVLERSNNLLTAYSEEALAAQEATTAILLQNDFLKREID
FTQGVNDSFVLQALE"

CDS complement(2087013..2087600)

/gene="kstR2"

/locus_tag="EFAGFIKM_01831"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0R4Z6"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional repressor KstR2"

/translation="MPRNVLRDTQMREQRRKEILDAAASVFARRGLLTKIDDIASEAG

RSHGYVYSYFKSKEELLLAVIKRGQDLYGEQLNKAIELEGKASDKFMYIATKVLSQES

NADSYMVLLQAIFTDLLDDQEKKKIRERGKKNRQLLVQLIHEGQADGSVRQGDIHLA

TLFATLIQNLMLLKAREYEPANETTIQLLMQMIGP"

CDS 2087839..2088603

/gene="ssuB_2"

/locus_tag="EFAGFIKM_01832"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P97027"

/codon_start=1

/transl_table=11

/product="Aliphatic sulfonates import ATP-binding protein

SsuB"

/db_xref="COG:COG1116"

/translation="MQPLLHIHEVSKTFHTDQQITPVLDGISFDVHEGDFTAVIGPSG

CGKSTLLKIVAGLDGEYDGNVLLKGEPILSPSQEKGFIFQEHRLF PWLTVEKNIAADL

SLREASVRRVDDLIKLVKLNGFEKAYPRQLSGGMSQRVAIARALLRKPAVLLLLDEPF

GALDAFTRSHMQEALLDIWRSNRTAMVLVTHDIDEAIFLSTRVIVMDARPGRIKAIVP

IDLPHYRSRTTRSFTLRLILNELGHKEELEGYHI"

CDS 2088631..2089461

/gene="ssuC_2"

/locus_tag="EFAGFIKM_01833"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40401"

/codon_start=1

/transl_table=11

/product="Putative aliphatic sulfonates transport permease
protein SsuC"

/db_xref="COG:COG0600"

/translation="MEVPIRSNAHSEKKHKTMPRSSGGSWHLFVRGAILPVLILSIWQ
ILSSTGTISTQLFSSPALILRQYWELTSGELMHHLRISLVRALLGFLGGSCGLLLG
LFVGMFRKIEETVNPTVQMLRTVPLLAITPLFILWFGFGELSKVLLISLGAFFPLYVN
TFLGVRNVDAKLFDVARVLEFSRFSQMMRLVLPALPNILLGIRLSLTIAWLCLVTAE
LLGADTGVGFMIQDARAFMQTDIVFVGITIFAIVGKLSDSIVRFFEIKLLRWQDSYKG
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CDS 2089528..2090979

/gene="betC"

/locus_tag="EFAGFIKM_01834"

/EC_number="3.1.6.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O69787"

/codon_start=1

/transl_table=11

/product="Choline-sulfatase"

/db_xref="COG:COG3119"

/translation="MTSKPQNVLFIMSDQHNRDILGHNGHPLIQTPHLDQLARDGVNF
TNAYSNCPICVPSRASIATGRYPHDNGSWDNAAPYSGNKPSWGHRLGNQGIHVTTIGK
LHYRDAADDTGFDPQRLPLHVLNGVGDLFTLIRETGLPSGNLGRKQVLAAGPGESSYT
QYDRAIAKEAVNFLRDEAAGIDRPWVLFVSFVTPHYPLTAPQEYFDLYPLESIALPKN

YGLDQRGSHPVIDEYRRLGIVDELEEGDVRNALAAYYGLCSFMDAQVGEVLSALRET
GLDRSTRIIYTSDHGDSMGEHGLWFKSTMYEGSVAVPFIMSGPDLPKGEQIQNNISLV
DCFPTILEMVGAHPEPEDHDLPGKSLLPLAKGEIEPNRVVFSEYHAAGSITGFFMVRE
EQYKFIYYVNYPPQLFNLA KDPGESNDLASDPYADVSRMNQKLREIVDPEKTDAEA
RQDQQRRLDLHGGREQIVAKGFKVPYTPAPKVE"

CDS 2091007..2092146

/gene="nylB"

/locus_tag="EFAGFIKM_01835"

/EC_number="3.5.1.46"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P07061"

/codon_start=1

/transl_table=11

/product="6-aminohexanoate-dimer hydrolase"

/translation="MDLQQIDIIRQNMHFAHRFLPTATVHRSGGDVSP IASEPLHLDE

LAFVDATGRATTLSQALERTHTDAFLVMHRGKIVYEKYYSGMEPTLRHGLASVTKSFI

GTLISIELFVGNLGANDRVDRYIPELADSAFGDATIQQLDMQISCKYPIFFPEANYI

DNQRNLLLT AIGTIPAKEGYTGPKTIHEYLASITKSQEHGSAFLYSNGPTEVLGWILG

RVNDTSLAELLSQRIWSKLGTEEDAYFVVD SVGTEQACGGLHATLRDVARFAEMMRND

GLFNGYRIVPKAVIGDIQQGRRDLLAASNRAKARPGYSYRNQWWITHNRFKAYEANG

LYGQRIHIAPLAEMVIVQFSSYPGHSDETARLFSHGFEAIANHLN"

CDS 2092862..2093002

/locus_tag="EFAGFIKM_01836"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAFVSASPAARLTDVGKDDADGFFPTVAVTLRMEPHLFDAYEKP

LP"

CDS complement(2094344..2095180)

/gene="bpoA2"

/locus_tag="EFAGFIKM_01837"

/EC_number="1.11.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29715"

/codon_start=1

/transl_table=11

/product="Non-heme bromoperoxidase BPO-A2"

/translation="MAKVVNNGEENAPIELYEDHGEGKPIILHGWPLSGRSWEKQV
PILIEAGYRVITYDRRGFGQSSQPWDGYDYDTFASDLHLHLDLRDATLVGFSGMG
GEVARYIGTYGTERVSKAVFAGAVPPYLYKSEDNPQGGLDDATIAEFQNGVKGDR
LAF
LDGFTNNFFAAGDRTDLVSEPFRLYNRDIAALASPKGTLDCAAFALTD
FRQDLEKFN
IPTLVIHGDSDAIVPLEVSGQRTHE
SILGSRLVVVEGGPHGFNATHPEAFNAALIEFL
KS"

CDS complement(2095676..2096671)

/gene="xsa"

/locus_tag="EFAGFIKM_01838"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P49943"

/codon_start=1

/transl_table=11

/product="Xylosidase/arabinosidase"

/translation="MNQQQLPKPHQPLVTHIFTADPSAHVYEGKIYIPSHDL
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SMNNFDSPVVDHGEALHL
RDIPWASKQLWAPDAAYKDNTYYL
FFPARDHDSIFRLGVATSESPAGPFRPQPNYMEGSFSIDPAVLVDDDNQSYIYFGGLW
GGQLEKWQTGSFVPDAEGPAPDQPALGPQVALLSDDMLS
FQSKPAEISIVDEDGNPIL
AGDEDRRYFEGPWMHKYNGYYYLSYSTGTT
HKL
VYAIGKNPIGPFTFKGEILSPVIGW
TTHHSIVQVEDKWYLFYHDSSLSEGVN
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CDS complement(2096668..2096886)

/locus_tag="EFAGFIKM_01839"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNYRNRWILERYSEPSTGMPTCWTMKRLPCSRASASCFTGVYLG
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CDS complement(2097412..2097984)

/locus_tag="EFAGFIKM_01840"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRFQNKSGVRRAAIQSRLPAGVTAQLRTDRDSYVLLNFSGAV
ARVELDQNGYVDVESGEVVTGQVELPVNGAYILRRNANTVQKDSLARYVKGNVVPV
SATRIFPDSRVTFQNDQAKSEKLNIQGNEVYFIQSDTRDKETNYVTYHRIGWRDDHN
HLLYEISNNTDSDLGKEDLVKLAEMITSR"

CDS 2098452..2099660

/gene="setB"

/locus_tag="EFAGFIKM_01841"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P33026"

/codon_start=1

/transl_table=11

/product="Sugar efflux transporter B"

/translation="MINRFISLFSIPSYALLFMCMALQGMGISLSTPFLSIYFTEQLG
VSIGMFGLYLAVTLIAGIWISTLIGRRSDLGLNRKSVYLFSTLSNVLAFSGYLFIQDF
PILFIYMTVFTALGATGMPQLFAISREAVIKSNFTERAFA NSTLRSFSLGFITGPLI
GTL LLAIGFGKIFLGTIGAFLLVTLVFLFLKSNT EMKSSNAE ANIKSFRLAQNRDI
LIPFLIMILMYTAHWMSSINTALFITNNLGGTTNHVGLVSSICAALEIPFMIVLGLLS
AKYSNRILVFCGAIFGGAYYFVILISNAMWQMLAAQILLAVFVAVISAIGISYIQDLL
PSMPGYASTLYSNSSTIGRLIGSLVGGGVASIVGYRYSFIFCFILIIVAVIMLVVSGR
QPVDEPQIST"

CDS complement(2099818..2100738)

/locus_tag="EFAGFIKM_01842"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTKQDRILIFGAGVIGSMYAIKLIEAGFDVTLFARSNKYKSLR
ENGLRYEGKGTVRSIQVNVIDTLENDDIYDFIFVTVRYDRSESALLALKDNQSKNVVT
MTSNSMGFSSWLDIVGDRLLPAFPGFGGQIKDGV LHARFLPKIIAATAFGEINGVSTE
RIENLAKIFKTAKLPYVIKKDMQSYLITHSVSDIAMLSVLQSENKIIDKKTARTRRTA
RKITVTLKAYLRAIQKAGVLIDPPMLKMVLNIPNLILDFFMTWLRNMMVRDMMLPDY
ANNANNEIVLLSNDLMKFLNQNDIKSEIY"

CDS 2100787..2101275

/locus_tag="EFAGFIKM_01843"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYDVIINFHYSLINHQQFFMICRMIFFEKISVQEIANNSGFNRST
FYQYFPDIYELLDSEVENELLNDIKKELANKELSMHTVQDTLYCLDSREHLLVLNALIV
NNVFLNIGKASCSKHS�KKKPTLFLHKTGSRSVSLIIAARKSYTEPEQLLLWLSFQQG
SR"

CDS complement(2101199..2108515)

/locus_tag="EFAGFIKM_01844"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTMISKKWKPLMIALLLAIPSLPIQVSALPAAATDAVKTGISNA
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TNGQFPDNRDGFVEVD TNKTLAAGGSTQYSTINPDNPYMNK TASADGKKVEVNYIGQN
LNSTDQRMKGFDVKS VFNMETDDGSMLWEITVK NKS NQYIEFGDIGLPMPWNNKYQT
LSDTYDDRVTVHN FAGADSGYSYAIRTS GEGNFMLFTPVPESGARIEYVDYWMHEAGE
RRAADTFKNWTGDSGGWYPGLNVLYIHSKEIQKTGRGYFTDASSLV LGPDESKTYKFK
FSAVRGGDNTPQESAQSPNNSSTSMEDREANLRSILYKSGMIDAVAVPGFQTAINMPV
KLDLHYDDNIVDVQSIDIQNVAENDPFDEAHIPDIKPGKSRKEMVDNSRAGRGLPEGN

PGYNESVEFVETKIVNGEQHHIYSLQFDSIGNNSVRIDYKLKDGNEWVDKFTQFEFNV
LAELDAISDAHSEFMVQQTQDKNPESPTYGNYFDWYLSSGMDLNTNHWGDDWSHDNIN
FMTMKNYLAPNPDEIRSIETYLIDFMWERYMKNTQDSYIVANWLKDSGAYTDKDKPYT
RTFSEIMEATGFFNMYRIQKAYPNLIEYRESPQFYLEKAYNIYYKRVSTGAIGFYGEQ
QIPDMIEALKEEGMQTESANLQKKFALDKGRNMTRATYPYGSEFEYDNTGEEGAYAAA
KALRTYYPADALTGAAEKSMEMADWKTRAMRGIQPTWFHYSVPVFRGGEGWWNFQYTA
SLAGYIMDDWLRYENDGRSVEQKAIAQQRNYAAKISNFNAVNMGQISANSVGSTSWRY
SMYKGGTGTKDVYDGGSRVMSNGWNDFSGESEEGLYGSLLSISSDIVTDPIFGLFGYG
ALVTDEGDSYNITPKDGFGRINLIDEKIYLELESDKVESAQIQKDGGKFTLQLLNPS
GKGHTSRILFDGVGIENGYYSMKLNGAAAGQFYVQNNNEGVAMFQMGSVQRAELIEKS
AGGENEAPQITVELATQHPQALIPFMLNGIVTDDGAPEGTLSYQWEVWSAPEGGKLT
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VANNSIVVLSGEAIPDPVHSEAEPPQLKYTWAVKQKPQGSADISFVDGDKTAAYARVS
MAGTYVFTFSAADGDKKASKDITIEIKEDTVDVYRALSVVTKKDIEPELPRQIYILSE
EGYLEQEITWDAIDPSGYASVGQFEARGTVNGSALEVWATVHVNTLQNAALTAKAS
ASFSGGDGYPEAMNNGIEPKSSTDFSPNRGAPNSAWHNWGREGDPAWVMYEWDPFLA
SSMDVYVFQDGGGNFRPKDMQLMLRDEDGKWYTPRAIKGLGNELNQYNTTTFEPAYIT
GVRMDMKPLVNGSGILEWKVNGYTGAVDKSELIKVYNYVNTLNVTLAEPGLAPIEAA
KAEASAVIKNMNATDEEIALTLEKLLTELRLLSRPDGNMAFLANASSSYTSPWESLAA
VNDGNKNGNINSHWGTWGHEGAEWVEYEWPPQASIRSSNLLLWSDGGGKIPPTQIVY
SYIPADSATDEWVTAGTVTEGIKVVEHTPAESSNPYTFDSVLNVKAVRVTLTQSQAG
DNGVGLWEWEVPQAGSTQDREAPVTPAGVAPSVLHGDDGKLIGVTTEMEYKKEGEEEE
TAIAGIEVTGLTAGKYYVRYMKTGSLASLDKEVVIPQGQTQEQAAPDASGWGISHAN
SNTNIKGII EGLNDTMEYRKLG EEDYTPVTDSSINDLEPGSYQIRYAATDILKASPPV
TVDIRNEARADREAPTA EGLVITPPTAAGGNDGRIENVTADMEYRKVDQGGYMPVSGT
SIEGLEAGSYELRYAGTDMSPNPAILIVVPDGTKQEQSPPSSAEVKAVNVSAAGAKD
GKITGVSPVMEYRLVGVDASSWNAITGTEVTGLGNGIYEVRYKETATHYASQSLTVVI
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RQEDLNEALEHVKANSSNIKTIMVDIPKAEGAHSYAVELPAAALTAAHANIKIEINTE
FGTIAVPSNLLKYVSDAKNVELSLSRLD TVKLHSDVKSVIASRPVIAFAVQLDGEEMA
TLNAPVEIRLPYTPDVEELANSKYLTVSYMAANSTFVQLLNGKYDSALQAMVFPAANT
GQYAVVYTKKFFNDVIKDSWYAPAVETMASKGFIDGTSATSFSPEQKVTRGEYLAWLV

RTLDLKAEFNTTFSDMKRTDLYEEIGIAKALGIALGTNGSFYPETEIARQDLAVLTM
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CDS complement(2108835..2109689)

/gene="araQ_9"

/locus_tag="EFAGFIKM_01845"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

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/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MGTRKNKINAASVLLLVLVVLAVLMLFPLYALILASLKPAEL

FRYGLNVRWDWALMSLDNYKTIFAGSGAASHYFTWYKNSLVITALFTVLSLLFSSMVG

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PIFFFFRQFAQGLPKDFMHAGRIDGCTEFGIFFRIMVPLMAPAFGAIAILQAMNSWNNF

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LTVGGVKG"

CDS complement(2109694..2110626)

/gene="araP_1"

/locus_tag="EFAGFIKM_01846"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94529"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraP"

/db_xref="COG:COG1175"

/translation="MQLHKETTASVHANRRRSIRLNSRTWAPYWFVLPFILSFLIFFA

YPLFRAGMMSFQQVLPGDVQFVGLEHYSKLWNADFRDAMWNSTRYTLWTLVVLPVPM

VLAVLLNSSRMMARNLLRSALFIPALTSVVVAGVVFRLIFGELDGALMNSILSVFGIP

SQQWLYSSSLAMVALVVLAGWRWMGINMLYFLSALQSIPKDLYEADIDGAGVMRKFT
NITVPMLKPITIYVITITLYGGYAMFTESYMLWAGKPSPQNIGLTMVGYYQQGFQYF
NLGFGAAIGITLLVITLLISMLQLTVLGMFRKED"

CDS complement(2110693..2112003)

/gene="araN_1"

/locus_tag="EFAGFIKM_01847"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94528"

/codon_start=1

/transl_table=11

/product="putative arabinose-binding protein"

/db_xref="COG:COG1653"

/translation="MKKMQVWLGVCLLVVVMALSGCSTTKEASGGTSGEAGNGGVTKL

VFWTFVDAHQKFYESMAEQWNQNHDPDQQIELEATTIPYDDMHTKLLLALQSGVGAPDL

VDIEQSKFPNFMKGVPQLVDLTDMIQPELNNIVQSRVEIYSKEGKYGIDYHVGATVM

YYNRDSLNLQAGVNADDIKTWSDFEQAGKQVLEKTGKPMITFEGNGNWSWWPAISQQKS

DQVDADGNVTVNAPINIETMKFFQKMVQEGVAAPGAGHDTEEYFGYMDKGSAAAVF

MPFWFMNRFTDHIPDLKGLMIIRPMPAWEEGGNRSAGMGGTATSITNQSASIELAEQF

LAYAKLSKEGNIQIWKQLGFDPIRTDVWTDAAWKESNKYTDYFGDDIFDTLLEVKDEI

APVHIREKSPEVFDVAVRNKAMPEIFINMKDPEQVLNDVQAELTR"

CDS 2112163..2113083

/gene="rhaS_11"

/locus_tag="EFAGFIKM_01848"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MDSPILHFITPPIPYFIDCGRAYYEAGEYHISRSEIGVFDLIVV

TRGSLAISENGTEWFLKQGEALILKPDGHHYGSAAACKAETEMIWIHFQTYGSWRESAN

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RNWKRQATFQQFMQHLDLGLSSLSDVAAIRIAEKIELYIRHNYPQPISNPMLQKELNY

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FSKKEGISPSNFRSKFTNTENKLTHSEPMT"

CDS complement(2113322..2115307)

/gene="hypBA1"

/locus_tag="EFAGFIKM_01849"

/EC_number="3.2.1.185"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:E8MGH8"

/codon_start=1

/transl_table=11

/product="Non-reducing end beta-L-arabinofuranosidase"

/translation="MTKPVVPHHPQTPGYSHKINDPFWSHYIELVRNVVVPYQWEALN

DRIEGAEPSRAIRNFRIAAGEEEGVHYGMVFQDSDVAKWIEAAAYLLSAKPDPELEVL

VDSVVDTIAQAQQADGYLNTYFTLREPGARWTNLAECHELYCAGHMIEAGVAYYHATG

KRMLLDVVIRLADHIGTVFGTEPGQLPGYDGHQEIELALFKLYETTKVEKYLELSRYF

LDQRGASPHFFVEEWEQGRGRTVHFGELEMVHRHTYSQSHLPIREQTTAEGHAVRLVYM

CAAMADVAAKTGETSLKEACERLWCNTVSKRMYITGSIGSSAKEEAFTGDYDLPGDTA

YAETCASIGLIFWAKRMLQMKPDSKYADVMERALYNTVISGMSLDGQRFFYVNPLeVD

PEIQRVNPNYAHVRTRRQGWFGCACCPPNIARLLASLDQYVYTPVVEQATLYVQLYIG

GEGEFTLKDRKVALTMASDYTSTGEVKLIVRPDSSEGMEFTIALRKPDWCEIPELWIN

GQKTEQSGFISECGYMKVTRTWragDEIRLHFPMELLRMKGHDHIRATFGKVAIQRGP

FMYCLEEVDNGRGLHRIQLPRDAQFHIGSGDRMPLGVPAFTTIGQRIVSHEDWGTHLY

RSDVHWDAPADLRFIPYFTWANRDEGEMSVWIRECE"

CDS complement(2115611..2121970)

/locus_tag="EFAGFIKM_01850"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAKKKRKWATKMWVAALATVVTlNTGIIPASANYTTDFVHEGVG

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VVEDKGARKNYP SHADQTYNSGGLDISQRKFITSSNSAVTLLKLTNNGNAPITLTMTV
KSPFVTETEGDELIGKRVAAPIMVGRAGEKYVEAMSHVDVHLSGDGMMPVGNLDLVKEI
TVPAGTSVDEKVVMGWLAEGIPASKTQYAEFKTSTNEKAFSEQVKEYNEWWAQNIPYI
DIPDENVKKVLYYRWWSNR FN LLEANIPGNDWQFPMNMEGV LGYNNGITVSVPWVLQD
LKWLRDPSYAYGTWLSQGEYSENANYKNNPGRPNIWTWDMMQNTSQVGWEAYKIYGGG
EKVLKKFADFSASDVTGTLNHFRGTNPDLVYYNHGPITGNDGDTVSMHWKGNGNYARL
DGSSTAYANAVATQQMYEQLGDNTNAKRMEEVAQRIRNAILNNM WYDETFDGDGEAD
TNGEGSFLHKKVINQQDVFN PWRDNNMFVFNFGVVPKEGEAGYESKYLTQLADYGDPN
YYPIFPFFTADQHSIMKRVEAFQNGETSAFGTDQFAWCNFGNYINTIRASLRHYPMEN
INSDTYKTLFDWGAWLHTVEPGNTDHLDSNEFFWLEDYFFGTPWTPQNPPNPSGKMVR
AWIHHDTLGMMNYSVMEDMAGLQPRADDKIELWPLDIKYDHFVADNVRYHDANLSIVW
QDPAKYSDSDPYYKDIPVGYSLFINGERVMTTDEM SHIIFDTATGKVEKPDGDVPGAV
GDNTNTNVIYEIGSAVNLASADDT SLESDDKKA VDMFNKAGVDVEHKGVNLATASGTTV
ESSYIHSNSNVNRLADGSTIASINHTSNTALFGGSPNPSESVTFHFDFGFSVDNVKVY
FYNDRRPSGYAAPQTFGVEYLDADGTTWKPV EGQFRYPNYVAANYNNVEFNAVNTAAI
RVHFTHASGYSTGIKEIQIYNNDLNVTPSEN LAPKVLLDLPVNVEQGTPLKLAPVITD
DGLPSGRLTYAWN LVSGDAGAVQAETLDQSTLNVTFGGVGEYVYELSVSDGIAITKVE
VPITVYVATAELSNVIAKFADRISPQGKLV RNADDFTSESWQALQAALTEAKELLAQD
DYSLDEVQSM TNRVRLAEESLR YRNAALLATT SASYTSAWESLNSVNDGYIPLVSGSI
GNPEIETQYGNW GSPNQNH WVEYTWKNPVTL SGSSMYFYDDGGGVQVPVDYDFEYFDQ
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PEGEEPPQTEHGAITAIEPASVNTTINVMP ELPSQVTVTYADNTKGLANVWDEIPEN
KLSIATDFVVLGSVEGTDLRASLRVYVKYD KSRLKAAIDAASDPSVNEENYIGTPEQW
QTLQTVLQLASDMYDNDASTEGDIDSAYKALLEAFEALEPVEEHNVTIIGINIPGGSV
DQLAKEIVIPESTTLEELKTGLNVPASVTFAYESDGFTSAIDLKTGYKVMVTGADQI
TTKTYTVLMVTKNPPVNTAALEAKLNESKALKQERYTAASWQNLA EKMASAEQLLTSG
SASQADIDA AVLALDSAIAGLKLLSTPTPTPTSPSPSAPTVPVPEPAPAPT PSDSK
ELTPVTVNQ GRIEVKAVASGKD GKAKAQLTDS DINA ALEDMKD GKLTIVIKKDLETQQ
VEAVLPWKT LN TTKSLTSIKIEMGSAGLTIPHQLTTFKDINTLGVVFEAVEPSQLPK
QAGKLREAGAVSNFTVNADGKNISSELHGKGLRLGMPYQLKAGLKGHQVVAFTL NDA
GVAQAVVGKYN ESTKMFEFNMEQNGMFGVLGVNA AFKDLNVNVN WAVEGIQALAARGA
IEGTGAGEFNPTSQVTRAEFLKMLMNTFDLLDETATPAFSDIKEGTWYSTPIASAYTL

GIVK GKADGSFGPN EPITREEMAVMVYRLAGNLNVT LSTEGEDDSAKFVDLENLSSES

TAAVEAVRMGGLITGMPDGRFNPNGQTTRAQVVTVIYRLLTNLEK"

CDS complement(2121989..2122870)

/gene="araQ_10"

/locus_tag="EFAGFIKM_01851"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="METAPAPVKYTSIKQAKNRRKAIHFGLILLSLLALIFAFPLYW

LLRGAMVSHSEILARPPVFFPKELGFENFRLGLERIQFWRQLWNSVSIVVPYVIGTVI

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FFCAGGNAYFVLLRQFFMTIPAELSEAAKIDGAGYFRIYYRIMLPLIRPAMIVVALF

SFINCWNEFFYTM IYLKTEADYTLPMGLYMVNGMRIPNYEQVMALALIVTLPCLVFFL

IGNKYFVEGITLTGIKG"

CDS complement(2122870..2123847)

/gene="araP_2"

/locus_tag="EFAGFIKM_01852"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94529"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraP"

/db_xref="COG:COG1175"

/translation="MNPERKISSETVPARRFAKGATKEA IAGYLFAAPAIIGFLVLT M

YPMLASLYYSFHKITIMSGSQVMEWIGLDNFRYIFS NPSSEFKKSITVTLVYAFVNVA

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LLQMGI PPWDFLNDPLQIFYTLFIMSLWTCGGTIVVFIATLQDVP GELLEAVEMDGGN

AWHKFLKVITYPTIKPVLFFQLIMCMMTSIQIYTQSVVLSRNGAPDRMTYFINVMIYDH

SFVQVGMRGLASAEAWIVFLITLVITGVLFYFQGALKRDDAMGKRKWVR"

CDS complement(2123890..2125263)

/locus_tag="EFAGFIKM_01853"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRFGKRKLVLSLALTAFSTLAGCSGNAKNAAGNGDPSAGGIT

LELLYWGDDVQKQLVESAAEKYTADTGVKINAQVLPADGTFTFIQTRLQSGELPDIS

YMGEADIQKYNEMGILEDISDLLADGSIPEKLPITHTPEQKVIGVGLSNQMELLFY

SKSKFDEAGVPYPPTKVEEAWDWDTFVANAKKLTKDSSGKTAADAGFDAALTENYGLG

FTAGREFHHFWAANANGGGIVSPDGKEFQWDSPQTTEGIQKLADLVNKDKVSSAFSYT

WSSGIGSAVDALSGGYAMTVSGSWDLANIKGNEDIGVGVLPKMEKAVTMNAGAPLVVY

NTSKHIEEAKKFYAYMVNPENSLDLLKSGAWLPNQADWYTDQALIDKWTAEPAFAKE

TILSYATTKDAIVQWPAYYVPAYLKMNTHEYEKSIDQALSGQKSVKEIYDAIMPAIKSL

WESGKVS"

CDS complement(2125433..2127895)

/locus_tag="EFAGFIKM_01854"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTILSNEKFRIEFGERTVQSLVMKDDPHEMNWVVDPHYLQEVG

FQEDKDLFGESMQLNDRFVQSSMFEPNITKHSTNHVTVEFKDVQVKILFSYLLEGD

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ISNPVVEQEFIVTLPADVPERKLELILKDGRDMLVWNVLEPVHTLLEKRAEWLALN

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WFIEGDLSPKPLYGNFYRIYDFDYIAHVFYLLSQMDEELLHLHSPSEYLKWAAEVMC

LRLDPDCHSGQREKDESRLNGVFILYIRELLQALKDKEYAELHNQLRQLWDRFGQEME
IGVRHYGGAVTEHFYDNAGFGPTCNALCFLGHTDEASQYQGLILANIGFSNDYRLQNP
DRWWEALSPMIHSLWGGLVASSALVAYEHLGNTEYLEAAYRSTMAIFHCYDWNVRSTP
RKMEPGEAASTYSVSAPNLNMPSLSRNRFGQSVFVEADDPLFAALFSDVSGDDWDMGE
ELVAYLLGFGTTTYLYRDEEGRLSCVNGFVTEEHDGWTVKSYAAYPSRYVFREEHLEF
RAPLGLTLQKSIRLENGKFRVCL"

CDS complement(2128029..2129066)

/gene="ccpA_2"

/locus_tag="EFAGFIKM_01855"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P25144"

/codon_start=1

/transl_table=11

/product="Catabolite control protein A"

/db_xref="COG:COG1609"

/translation="MRKTSIKDIALRANVSIATVSYVLNGTRNVRPETRRRVQEAIEA
LNYKPNEIAKSLQRNRTNTIGVITEDVTVFNAPDIIDGINDFGDRHDLHILLVNLRLD
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YTQDDISIQYNDEQASYEAMSYLVQMGHSRIAIISGLMDSIPSRRRLNGYYKAVTDFE
LPFDPSLIKMGDWERDSGYRYANELLDMDNPPTAILSMNDVMGVGVLQAAKEKGLSVP
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CDS 2130207..2130851

/gene="gntR_1"

/locus_tag="EFAGFIKM_01856"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8GAL4"

/codon_start=1

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/product="putative D-xylose utilization operon

transcriptional repressor"

/translation="MKTPKIVTIKEQVYEIIKNRILTQEYQFGEKINIGSLSKELGIS"

NSPIREALSQLGQEGLVSTPNSGLRVVNMSKRDLFEQAQMVFYFWMTGSYRYCAENDK
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FLASGSYLQGSEKEWHLSIQEHEKILLAIKEKKHDEVQEAIKVHYFKPSWTLDI"

CDS 2130885..2131817

/gene="rarD_2"

/locus_tag="EFAGFIKM_01857"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P27844"

/codon_start=1

/transl_table=11

/product="Protein RarD"

/db_xref="COG:COG2962"

/translation="MKFKQSNEQSVGVISGASAYIIWGILPVYWNLIGSLSAKEILAH
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NNHLVEASLGGYITPLVSILLGLIFLKEKLSFWSTVAFILASIGVLNMTLNIGTFPWV
ALSLAITFGMYGLLKKITQLEPMTGLTIETLIMAPFSLFLGNLQMKNESVFTQGSPQ
TIWLLMGAGVITAVPLLLFAITAKRVSLAMIGFLQYIAPTIMLILGILLYHEPFNYEQ
ISSFIFIWISLILYTLSSKSKWFIKMEKKILYLKG"

CDS 2132237..2133508

/locus_tag="EFAGFIKM_01858"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISHaha5"

/codon_start=1

/transl_table=11

/product="IS110 family transposase ISHaha5"

/translation="MNPVIGLDISKEESHGQAFLDRGKPYRGIFYFQHTRDGLEILLQ
VIQDIERESGHRPTIILEATGHYQSPVVQFLEEHHYVFIVINPLISNRFRKTNLRKVK
TDAADAYLLGELYREEFEPFKKRGVQLLNIRYLTRQHESFSKMCVQTKLQFQAVLDQ
VFPAYKGVFGAMYSNVSLRFLHEFPTSSYVLKVSEETLKTINALLSSKRGRSERWIN
ERVQRLMVAAKQNPFQQTMYESHNLNKLISLILQYQEHLAMLEKTIDALATEIEEY
DLIQSIPGIGPKIAATILSGIGEVD RFDHPKKLVAFAGIDPSIFASGKFTATRNRIK
RGSRQLRYVLVMAVQCGLIRSRDTRIKEFYERKRAEGKPHKVALVACANKLVHWLYAI

LKSKKSFRSVLQNNGVTFQLSSDWKVIWYAY"

CDS complement(2134640..2134798)

/locus_tag="EFAGFIKM_01859"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQIDTFIHISRLTRNLAGSGDKRNISTVTWFTSQHLKGNGRSGA
KIREVENT"

CDS 2135034..2135234

/locus_tag="EFAGFIKM_01860"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKILAISILGMGLTGAVLIISIALLFNPPIGSVLKMVTAASTL
SFIIFAVSALIFRRRLDDENRE"

CDS complement(2135650..2136417)

/locus_tag="EFAGFIKM_01861"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNYINIQHPYLRQIQLKRQQVPTYNRYPFDLAVIRNLNTLDFHP
KVTYIVGENGMGKSTLMESIAVAWGFNPEGGTINFSFSTQATHSSLYEYIQLIRGPRR
PRDGFFFRAESYYNLATTIDELDSQPSFGRPIRPIKDSYGGKSLHEQSHGESFFSTFI
HRFGENGLYILDEPEAALSPLRQMAMLTRIHELVLQNSQFIIATHSPILMAYPDSIY
NLKPDGIEVQVLEETDHFMMMKEFVNNKDRMLRELFE"

CDS complement(2136836..2137906)

/locus_tag="EFAGFIKM_01862"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MIRLTRYEFVKIMTRKSIYLALTGLLMLLVLYAYLGHPGPMNGT
SFYKPYEGAITAEKVQAAQEQLQNKGYSDANQNRYGVFYEISIFSPESIKNYTKTDD
SGNVMERTVNVTEIHYNKPWGYLLEYIDQFGLFMMIMILLGLAPVFAEEYALGTAAL
VRSSKRGKSQIVSAKLMA SIVYIILCVILFTSINLLIYWLRFGNLAGADTPIQSVGMY
FQSFDEYFSPYRLSALQYYVVQLVTHLVGSLVFGCVLWVSSLSTAFVAIIINVAIV
GVPYLA FDMNFNPGWAKWIEEFSFSTMMRVTRLFQTPVNYSIFRVEVSYLQLYLLIM
TVVTAVVIGTYRAFRNREVFS"

CDS complement(2137903..2138778)

/gene="yxIF_1"
/locus_tag="EFAGFIKM_01863"
/EC_number="3.6.3.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94374"
/codon_start=1
/transl_table=11
/product="putative ABC transporter ATP-binding protein
YxIF"

/db_xref="COG:COG1131"
/translation="MKLTMDNVSKKYRNKWAVKSFTLGLSSGGVYGLLGPNAGKTTL
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TAGLDPKERIRFRNIIGELGRDRIVLLSTHIISDLEFSCKEMILMNEGQLITQNTPEA
IMNSMQGSVWTATLTEQQLVELTSHFKVSGLSYQSDGIVARILAKERPVPQAMPEAPR
LEDVYMHYFDEEATS"

CDS complement(2138759..2139604)

/locus_tag="EFAGFIKM_01864"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MKRTENEDRRKRRAELEMEEYAEIAPFLDDYVVEYPSEMEIDRT
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NMVFVLLLMLLVSGGRGSFISWSGVALWYTQLLIAAGASLWLMRVRGGTAVSIFLVA
WFGLFWLMLSNPRFVTLVQSIQTPVLIAIALCGVLLISQIRQMTRKYTSQTERGYSF
EIDHG"

CDS complement(2139579..2140151)

/gene="sigE_2"

/locus_tag="EFAGFIKM_01865"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0R2D4"

/codon_start=1

/transl_table=11

/product="ECF RNA polymerase sigma factor SigE"

/db_xref="COG:COG1595"

/translation="MDDEELIHEIREGSRAAMEVLVKRHYKSIFSIVYRKTGDYHISF
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CDS complement(2140536..2140976)

/locus_tag="EFAGFIKM_01866"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MDKYKIKVKTRKNVLSLVAAATLLIYVGLIFYRGGLPDLPSFIK
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CDS complement(2140977..2141183)

/locus_tag="EFAGFIKM_01867"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
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AYKIANFFGLAIEDVFDSEVEEM"

CDS complement(2141505..2141942)
/locus_tag="EFAGFIKM_01868"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKNTRRKRIKLGDYAIPLPNGKFAFGRRLLKDASIAIYNVISDT
IEELPQEEYQFIVGVYDDVLKSGDWPVVENRPFDPDEEEAWPPPACIIDRISGGYEIY
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CDS complement(2141975..2142349)
/locus_tag="EFAGFIKM_01869"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDQKEFDSVINLPANIRYEYCIKKVVDSEEVWGLYENGWSVTED
DKGNKLLPFWPKKEFAEYCATEGWEIYSSKSMDLYEFIDDFLPNLKKEGFKPSIFLNN
ADSAVLEVDIIIEDLKTELEKY"

CDS complement(2142552..2144600)
/gene="glcA"
/locus_tag="EFAGFIKM_01870"
/EC_number="3.2.1.39"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P23903"
/codon_start=1
/transl_table=11
/product="Glucan endo-1,3-beta-glucosidase A1"
/translation="MKPSHFTAKRFMKKVLGMFLVVMLASIGILPASKVQAAGTTVT"

LMEYFSPADGPVISKSGVGKASYGFVMPKFNGGSATWNDVHSDVGVNVKV/GNNWVDID
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AMNATQGPQITASFTGGAGFTYPTFNNNPAVTYEAVADDLKVYVKPVNSSTWIDIDNN
AASGWIYDQNFQFTDGGGGYWFNVTESINVKLESKTSSANLVYTITFNEPTRNSYVI
TPYEGTTFTADANGSIGVPLPKIDGGAPIAKELGNFVYQINMNGQWVDLSNSSQSKFA
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FIGNPANAPRPDVSDQEDISIGTPTDPAIAGMNLIWQDEFNGTTLDTSKWNYETGYLNL
NDPGTWGWGNAELQHYTNSTQNVYVQDGKLNKAMNDSKSFQDPNRYAQYSSGKINT
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SGTIHFGGQWPGNQYSGGDYHFPEGQTFANDYHVYSVWWEEDNIKWYVDGKFYKVTN
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CDS complement(2144754..2146295)

/gene="rssB_4"

/locus_tag="EFAGFIKM_01871"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00958"

/codon_start=1

/transl_table=11

/product="Regulator of RpoS"

/translation="MINILIVDDQKHIRDGLQAMLHQFPLELNNIYCAASGIEALCLL

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WILQIEEQNDALWRNYRLALLREEVCMNQPGASSAHSMEAIAYRVFGRQGCICLQHRP

YLILAVDASIDPSVLPAALKEGKINVITAMTNPIQGLKELPDSYTVLELYRHSYLP

DQYSIFPAHIEHMEQQWQLPYEDLYELFQSVGTDNSGTITQGISAIFHKKVLQRYPIR

YTQQLCAATVQMMEYQRVHPYMGEEMLDLESRLNLFNYQGMREYIQAQQQLRLN

QLYYDYKCSYRHSQDLNEAIRFIHESYHKPLDLAMVSNHVSLNYAYFSNLFKKNIGKG

FAEYLRDVRLDKARRLLAETDCHKIVEAAMVGYESYKSFTRAFRLVMQIQPTEYRQMM

RQKAN"

CDS complement(2146299..2148137)

/locus_tag="EFAGFIKM_01872"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKYLLTRLRKLYRNARISQKLFLAFSLMIAIPVILISFVYIRMQ
ETQLYKDAMATGNSHVSWLNEQLRRRMDMIENASNTALTQKSFVDFIHSNMLVDGLRL
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GGAAAYRLFSFRDGEHTLSYYRLVRLQGGEQKRPSIMEVRVPHSMFFSDLLQESKGDF
SVLMNASDPPQYVYNPQHEFSEKYGGMEELGSIHRHLDILPQERALQVKVGDSFY
ALYRYIAPLNTYVVEIASHQALMKGPRSWYAFVVTITLCVLLLIMLLVSQTTRRIFRR
LDSVLVSMRQVRKGELDAMIDTGLDENERGDEIDEVAVNKNMLHEVKRLMTQVVDKQ
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DTVAFREELANIQSYIEFINFMEGSSIVMTADLPQEILHYAIPKMCMQPIVENAVHHG
APSGGRVTIEITFSVENDSLLFINIRDDGKGLEPEMLHRLQAVLRSESDTPMVTSRSG
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CDS complement(2148211..2149869)

/locus_tag="EFAGFIKM_01873"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MFMLRSPFIALLMMCLISGLTACSESEQWEDKGASTKADFTEQ
IQLNLNLLEPSWKLDTPMNLTWVFVGAEWYGHTWGESLTSKYVTQKTGVNIEFEVST
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GALQWYRQEDGHTYVIPNDAYSPEQMRSTGLTGANQTLVRKDLYESMGKPDLTTPKG
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DYIEWLKTFRAYEQGLINVD FMVDSSAQVQEKTNHAQYFMMIREWTDISDLNSKLEV
LTNQSSYYIAVDGPRSSRGESAKLFPGSMDGWMVTMISKSTENPERAIRFLTYLASEE
GQRDLFLGKEGETWAMKNGKPQLTAAMVQLHDTDRERLEKEYGIMDTYWMLRNPAFVN
KWRPENAPSIKQMEEFANQQADLD SGYKGLYPIGDS DIALAWSRISQNWEEVLP
PELL
TAKDEAAFNKIFENFLIRRVNYGFNQVMEYRQAELELRKAKIAR"

CDS 2150076..2150333

/locus_tag="EFAGFIKM_01874"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MYLIWILIVGGLIGWLSGNLIGRDVPGGV LGNIIAGFVGSWLG Y
ELLGPRGPVVGGFHIIPAIVGSIIALLIFYALARAGAFRRR"

CDS complement(2150498..2151289)

/gene="fabG_4"
/locus_tag="EFAGFIKM_01875"
/EC_number="1.1.1.100"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O67610"
/codon_start=1
/transl_table=11
/product="3-oxoacyl-[acyl-carrier-protein] reductase FabG"
/translation="MTKLYGKTAIVTGTSRPGGIGTAVCRTLAQEGANVFYTHLYDYD
KTENPGDADKNWPD LFAEELRSYGVKAAHMEVDLTDPNSPAQLLDACRSALGLPTILV
NNATYSVAADFRQLNASLIDAHCAMNIRGTFMLSAEFARMLEVELAVHQDL CGGRIIN
LTSGQGKGPM PGNLAYAATKGAVSTFTECLSAELAPFHITVNAVDPGPTDTGWMSEEV
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CDS complement(2152704..2153222)

/locus_tag="EFAGFIKM_01876"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGILSGNPKNEPMHYGEIFSVWQCSTVAKGALSFYQAFLNHAGD
KDLKKILDALIDQAKLEIKECDTLLTDNGIAPTPALPERPPVKLEDIPVGARFTDPEI
AASIASDTSMGLVACSQVMGQSIREDIGALFAKYHVTKTALGVRILQMSKEKGWLIPP
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CDS complement(2153675..2154040)

/locus_tag="EFAGFIKM_01877"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSNNKAFRETLAFLIVRDNAHQNAFAMALETLGVNWGVFPVPN
YDINKYPECQKYVDLSFHNAQFNFRLDNTRIAEVFSGQTPSRNGGELQVTEPPQGFPL
PYMPDLPNEHSPGLHDLNT"

CDS complement(2154042..2154413)

/gene="ydbD_2"
/locus_tag="EFAGFIKM_01878"
/EC_number="1.11.1.6"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P80878"
/codon_start=1
/transl_table=11
/product="putative manganese catalase"
/db_xref="COG:COG3546"
/translation="MHYFFQSSNFRGKGKQYRDLIRGVFMEELSHVELVQQTINQLLT
GAGAEGVGNAGIDGAPLDEAIKHANPHHYIMGAQSSLPVDVAGNPWLGNVYVDHGNLV
SNLLDNVVLESTGVLQKNTDL"

CDS 2154675..2155388

/gene="yflN_2"
/locus_tag="EFAGFIKM_01879"
/EC_number="3.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34409"
/codon_start=1
/transl_table=11
/product="putative metallo-hydrolase YflN"
/db_xref="COG:COG0491"
/translation="MNQEQLDYGTDYKFVPVTSVGSVGVGIEILPDFCYTIQIVNICL"

VGNPESDEFVLVDAGMPKSANEIISVIEERFGANSRPAVILTHGHFDHVGGVIELVK
HWEVPVYAHPLELPFLTGVKNYPEPDPTVEGGLVAKMSPSFPNESINLGSHVQTLPPD
GTVPHMPGFRWIHTPGHSPGHISLFRENDGALIAGDAFTTVKQEYMYKVFNQELEISG
PPRYLTDDWVAAKKICCSP"

CDS complement(2156413..2156775)
/locus_tag="EFAGFIKM_01880"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNDSRKQRTEVADPTLEQIQSFRVSVQADLDDLKNRLERTRWP
DELPGVGWDYGVPLNYVKELVNYWSKNYDWRKHEARFNEFPQFITTIVGENIHFLHVR
SPEPNALPLLMIHGWPVR"

CDS complement(2157039..2157461)
/locus_tag="EFAGFIKM_01881"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MYLIRGLGLDALTAGLVLLPGGILQAIMSPVMGKLFDRFGPRWI
VPLGLIVISTALFFLKGISESTSLILIMIMHTGLMVGICAVWMPSQTNGLNQLPPELC
PHGKRDIYEYDSADCRSNRYGSRHQPDISRQSCFYGNNGN"

CDS 2157495..2157788
/locus_tag="EFAGFIKM_01882"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQTNNMSVPIENMGYLSARGIGIGMGLLSMFNFIAAAGSTAVIG
KVLDDGGTSTVQLNPFVHDKVAFVYSNILLALAVVVVMTVLYYYQFGRKFNNK"

CDS complement(2158334..2158762)
/gene="slyA_1"

/locus_tag="EFAGFIKM_01883"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01819"
/codon_start=1
/transl_table=11
/product="Transcriptional regulator SlyA"
/translation="MHSREDTPYMDLFQIIIGLKLKRADESIKELGLSSQQGKVIAYI
YENQDNHIIQKDLADRFHLRGASVTSMLQGLEQKGFIERKIPANNERQKNIYVLPKAV
DLIEDFNNSFQKVEDEIVQALNDEEKQILKKLLIRINERI"

CDS 2158932..2160242

/gene="ade_1"
/locus_tag="EFAGFIKM_01884"
/EC_number="3.5.4.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01518"
/codon_start=1
/transl_table=11
/product="Adenine deaminase"
/translation="MEKLNQNAGLEEITAITNVRIFDGYQIIAPRHIVIKGVSIISVG
GDIPSDATIIDGENSTLIPGLIDSHVHTSIGGLRDALRFGVTTELEMNGDFTKRGREI
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AHDHDEIPQVTTVEEAIKHVHTQVENGSDYIKIMIEEGTVMGAPGLPVLSDEILKTAV
TEAHKFDKLVIAHVLTALSSKAAIDFGVDGLGHLFIDRPECTSELVKSIA NSGAFVTP
CLVLNSSIIGNPASELANDPRVH SKLSPDWIDLNSSFNTPQGNMENSFKNVMDLHR
AGVDILVGTDVAPVPV PNLGGLAHGASVHHEMQLLVKAGFTPIEALQSATSKPARCFG
LHDRGRITEGARADLILINGDPITNISDTLSIKSVWFNGSRKLG"

CDS complement(2160376..2160768)

/locus_tag="EFAGFIKM_01885"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MHRFTNFINTASKELAEELIAPDAVFYVPMQKEPMNGPSGYLSI
IHMMRSGFSDIQWTVKELVAEKDLIAAHFVMKGTQDGEFLGLPPTSKKIEVNAMNFYR
ISNGQIIIEYGQPDMLGLLQQIGAIPKA"

CDS complement(2160743..2161480)

/locus_tag="EFAGFIKM_01886"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPIEIKDIVSKKILSEVKGYLDIGFTHSLNPYTGCAFACEYCYV
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RIFSPYAPGIDLRVKALKKINDAGIHTQVSISVLPFSPNFANMLQGITDRIWIDTLL
IGDGQMGMRSERLGMPQLFDASFHELH"

CDS complement(2161719..2162846)

/locus_tag="EFAGFIKM_01887"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRWVEKFIISGVSCILLAALAGCASDKNLEDATVPLALGLDVK
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QLLQYKDWFNILDVTFRDPRNTITDRIVAFDGPDIADIFNFQAKDQPPLPLFIKALVDS
GSRSSATVKTTAQELHRQLYDRAMTPSISEIKIENNKIMLKGTLLSQKGQYRTSLTY
QETSLHILKNEAKPGVSLTFPVDDLQQTMPFNIDKVSFSLGDISVTKSTHENGRFQ
FNIKVKSIVSITEKFLEFELLGNSEEMANKLSKEMKKSMEALIKKCQNYNIDPFGYGF
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CDS complement(2162843..2163937)

/locus_tag="EFAGFIKM_01888"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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STLSRAHWLYLLPIFKEGWFPVLSSVTYMIYPLLIGLVLFLYPHLVNKEKALPAMII
SNTLTCIVYLGITLICVYFSPDEIGEYNDPVISIMKSIEFQFIERVEVVFIAFYLFV
FSCIWIPSMYLVSRCSASLVGKGQERYHLAVWCIVIEISFFLYRPSFIESAQVNYALN
YIGFMMEFVLPAGVFLYVAIRKRMGGGQRT"

CDS complement(2163941..2165434)

/gene="gerBA_2"
/locus_tag="EFAGFIKM_01889"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39569"
/codon_start=1
/transl_table=11
/product="Spore germination protein B1"
/translation="MDEQSATNTNEENITKSLNESLGRIEEIFTNTPDLIRKLSIKQ
TGELAAIIYMEELTDKASLNQNVLAPLQLETGNPSGDFITTVGYVKPHSKWEELRLSI
ILGYSVLFIGRSTAYALDTKGFPQRAIEDPQQEPSLKGAHQGFJETGSQNIAMIRRY
IADKELKVKRYIVGQRGQTPVSLLYLEDVTQPDIIKALEERIQSIDVDIINTGELAE
FIEDQPLALLPQMITTERPDTAASQILQGRCVVVVDGSPSVLVAPATFMSFFQTVDDY
SSRWSISSFLRILRIFAFFIAIFLPGIFIAVISFHFEIIPMKLLTLGESRGQVPFPP
FVEAIIMEITLEMLREAGVRLPAPVGQTVGIVGGIVIGQAVVEAGLISNVMVIVVAFT
AISSFIIPNQDMMAAVRIMRFMMILATWFGFVGLVVGMMMSFIGRLITLNSLGISYST
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CDS complement(2165736..2167022)

/locus_tag="EFAGFIKM_01890"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MKEFLSEQSIEAFRSIINYNPDATFIVSNEGATIVEVNEGVTECL"

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SPSHKMVLGFDPKKEYIGKWVYQPNGDVDDKFRTVFMSMLLLRKPFTCEIERQHEQGY
PVWLEMKGTPMFDGDFKNMMLVGREITERKKYQVQLEQLSYHDALTGAPNRRYLNK
MLSDALSAATTSGQLAVMFADLDNFKQINDTLGHDAGDELLRQFVKRAGACLQEHDV
LARMGGDEFVFLPHVKSSSELSLLAENILETLQLPWILDGKELYTTSSIGIAFYEED
DSVKELLQKADAALYLAKAEGKNTYRIYSFRDLSMR"

CDS complement(2167577..2168104)

/gene="nusG_1"
/locus_tag="EFAGFIKM_01891"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00948"
/codon_start=1
/transl_table=11
/product="Transcription termination/antitermination
protein NusG"
/translation="MNWYSFFVQSGKEEEIKLFMDRFYALQHLSCLVPKRMIPERKQG
KTRHCTKVLFPGYIFIQTGGQIHDLYYNIKKTPYILYMVNGGIHKHDQAANFFTPIPKE
QMDWLIQLCGDNGTMGYSDIILGGNQIKVTSGPLLKEAMIRKIDKRKSRKIEVQLL
NEVKLIDVGINVLLA"

CDS complement(2168250..2169449)

/gene="yjiB_1"
/locus_tag="EFAGFIKM_01892"
/EC_number="1.14.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34374"
/codon_start=1
/transl_table=11
/product="Putative cytochrome P450 YjiB"
/db_xref="COG:COG2124"
/translation="MNIKERSSFPDLNLVTGFKTNAEKYEPFAWYKKMRQEDPVHYNE
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KAMSSWASRVDMIVQELMESIEGRIEIDMVQDFASPLPMIVISELLGVPTSDREQFRD
WANTLT LAPQENTPEEYMRIYQLQAQASTQLVAYFQDIIE LKRRNPADDIISDLTQAE
EDGEKLSPDSL IASCVM LLIAGNETTSLITNSIYTFNDYKLIKELAQHPQMIPSAVE
EMLRYRSPLQRAIRKVLKRTEIGGKVL EPGDYVVNWIGSANRDENIFEEGDKFILGRK
NNPHLALGKGIHFCMGSHLARMEAKAALTAMLTYPGLQVHPEYEVDVNPSNVYGLKN
LSIQLQD"

CDS complement(2169503..2170018)

/locus_tag="EFAGFIKM_01893"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MWIGFLLIVISLIRIPSVVIAMRNEKKIVAGGGTEYGNLNSKVL

FVLQNLIYLSCIVYAFIYDVQFNVLTVIGLVVYVFALCCLIVIRKLSPFWTYKLYIA

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EKVMKQTFTQY"

CDS complement(2170122..2177573)

/gene="acpP"

/locus_tag="EFAGFIKM_01894"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01217"

/codon_start=1

/transl_table=11

/product="Acyl carrier protein"

/translation="MTLPATESFLQRLRHSDYFVRDHRVHGVCTLPGVVLLDMVYRLS

GSHLRRTTSIELRDIVFTQPIVTSTDFDVIDRLTLSMKLDEGQVTIHSRKVPKNGEQPS

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FSFMKNNGDVYRQDQMEWMDIRLSSLAEQYLDKFHAHVALLDGATFAGSSFR LGIVDG

LDAEVPPYIPFMIERFVIYDRFPAEIRTFTEQTPSDLSGGDIISRSIAVTDTEGRLLA

EFVHLKAKRVRHAASITGLTNPMTTGRNNKPTSETTTESSEWAKTTVMSAGSQDQIR

TTISSYVKA EIARMLHILPEAVDERTGFYEQGLDSMHLL ELVKRL ENRVNMELYPTLL

FEHSSVQALTDY LHTHCSDAWNEAAVVSERVNLNTLPSQSSHSTDEQPATHSEIPATA

REIEGNGEPCYEPKWIETRDIHEAESARHTIADGKELQSDHTSYRIVVLYGNYPDLA
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VCIWYKGDLSLQRHVRKLVEIPVPGAALKTYKTDGVYLITGGMGGLGYALAVHLSRQC
RCKLVLIGRSLLSENIQRKLNLSHINGAEAMYIQADTTVLAEMKQAVLQIRDQYGEIT
GVFHCAGTAKDQLMLQKPLSDLEQVLKPKMDGLWNLEQALNDLRPEFTVAFSSLSAIV
GNKGQADYAVANSCMDRLLLNHQENSGTEGAIPRQVTVNWPLWADGGMQVNDHIRSSM
YTSSGSMPLPLAEGMALIDRIIAQDVSQVVLVYGNKSRIQSAMGDDMAIHLPPSPDPE
DIAVIGMAGRYPANNMDELAQILKEGRDCITPMPDERWLGLHLPYFASEYYPAGGFL
DMIDDFDPAFFQISPLQAERMDPQARLFLQAAWTACEDAGFAIERDKHHDASAAKRN
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PSRLFLLSAKSEASLQEHVADWQQWFDRHSNAEDTLRAISLSLLKGREHFKYRFGGWA

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CDS complement(2217719..2218960)

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/EC_number="1.14.13.232"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q3S8R0"

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LPGQRLRSYLALRKDIWQRIREDGIESLRGM LLSLCPHLQQEITQIVDFKQVQSIPAY

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/inference="ab initio prediction:Prodigal:002006"

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TGYAPAAGMFELGGKVQVLKKG VYFPARANKLHELRYRQYDSIDEIDEKTKTRLQEYF
KRSFDSIYAEMESALTTQERALAERSPKARMAVIFKWYLEHS AKLALQGDENHQHRVD
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CDS complement(2222909..2223796)

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TAVGNNKYNQCSVNNWSDILAVSAGYLHTVGLRSDGTVVAVGRNNEGECDVSGWRDIV
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CDS complement(2223989..2225920)

/gene="fbp"

/locus_tag="EFAGFIKM_01902"

/EC_number="3.1.3.11"

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/inference="similar to AA sequence:UniProtKB:Q45597"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG3855"

/translation="MDEQFLDLLAEKYDTEEKIITEIINLEAISNLPKGTEHFVSDLH
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FAHPEETEDLATDMVWYIWTGECSSLFGKREMTTFERYFIQDKEAHKERKNPYHLRE
NEEICRKILQEFDLNPDHGHVINGHTPVKEISGESPVKANGKMIVIDGGFSKAYQSTT
GIAGYTLLYNSFGMQLVAHKKFNSKEDVLCNGTDVLSLKRVLVDKELERKLVRETNVGE
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CDS complement(2226245..2226961)

/gene="COQ3_2"

/locus_tag="EFAGFIKM_01903"

/EC_number="2.1.1.222"

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/inference="protein motif:HAMAP:MF_00472"

/codon_start=1

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mitochondrial"

/translation="MIPLVYDQINHWGKDDEFFLALLKRLQVESIADLGCGTGRWTTTH
LVQYGYKITAIDPNEEAEMARSKDTSGNVDWIIGDSADLQNTYDAVIMTANVAQVF
LTDDSWKRVISDVFRSLKTGGHFIFDTRNPLVKVWEEWEKDKAPDLAKDRLSGEPLEI
YTEYEGFEGDIYTFYEIVKNTKTDKVLVHEKMQLRFQNGEELDESLKQIGFSKIKTYG
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CDS complement(2227028..2227936)

/gene="gltR_1"

/locus_tag="EFAGFIKM_01904"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94501"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator GltR"

/db_xref="COG:COG0583"

/translation="MELRQLNTFCTVVTTLNFTRAAEALSYPNVMTMQIKALEDELG
VRLFDRLGKQLALTAGKRFLTHAQGVLEKMEEARSAVHDNEKLSGTLTISANEVICS
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LEEHFRLLAAPDHPLAKRTLQLEDHFHDEVFLTNEKGCPYRTMFDRSFEKEGIDSITY
LEFQSAEAIKQCAISGIGIAFLPEIVAEESEVERGELVLPWQIPDLQVYTQMLWHKDK
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CDS 2228080..2229099

/gene="metXA_1"

/locus_tag="EFAGFIKM_01905"

/EC_number="2.3.1.31"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:K4ICC9"

/codon_start=1

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/product="Homoserine O-acetyltransferase"

/db_xref="COG:COG2021"

/translation="MDYEIFNLGDVLLQSGVTLPNAFLAYKTYGKLNEQKDNVIVYPT
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DNVRFQHQLLTEKFGIQKIALVVGWSMGGIQAQWGASYPEMVERIAPFGGIAKPWPH
TFVVLEGVKASLLSAVGFDSSKLNQLSSTDMAVGRVYAGWGLSHAFYREELYRDMGF
DTLEDFVAGVWEDSFMNMDPHNVLAMLWTGQHADISANPSYNGDFDKALQSIKAYACI
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LSTNE"

CDS complement(2229104..2229217)
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/inference="ab initio prediction:Prodigal:002006"
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CDS complement(2229319..2230359)
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/EC_number="1.-.-."
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P32382"
/codon_start=1
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/product="NADH oxidase"
/translation="MNYSQSVEALFQPIELGHLKLSNRIVMAPMTRQFSPDGIPGSNV
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YEKTSRTDRYGGDMMARTRFAVEVIEACRKVVGSEFPVLRLSQWKTDYQAKLAET
PELLEQLLAPLVQAGVDIFHCSTRRFWEPEFEGSDLNFAGWTKKLTGKPTITVGSIGL
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VPFTREAMTVLT"

CDS complement(2230564..2231139)
/gene="comR_2"
/locus_tag="EFAGFIKM_01908"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P75952"

/codon_start=1
/transl_table=11
/product="HTH-type transcriptional repressor ComR"
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YCIFKDKRSLFLKALALYREQVIAKLKEIEALDSSPGDKLDALRYSLLDDETGCQGCL
IVNASLEFGTDDEQVTREAEMLMVEEVQLVLEKIISSGQKQQLISNRYTSIELASYLNN
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CDS complement(2231380..2231943)

/locus_tag="EFAGFIKM_01909"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MLELEFTTIEEWDEALWARMERIYHEAFQSGAKTKAILRSMMLDR
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ALREHRIKGMIIAEFGTTEAHQERIQFWQRNGFILTYSYVHQYRMVPEPYQAMMLPLD
TNMHVPDDGEALFRYINAFHKVAYRKS"

CDS complement(2232370..2232615)

/locus_tag="EFAGFIKM_01910"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNKYVLHIVASVICILLPAVGLLYVLWDSHQPKIGPVGDKPKNY
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CDS complement(2232704..2233678)

/locus_tag="EFAGFIKM_01911"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MLSEEDYAKVAKEALQQYPIYWEKLVYLGKSDNVTFQVQTNDNDN"

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LYSSLNQLKQLVNLELISRELFVHVEESAHKIANVIQNHKRLPSNWGIIHSDLHESNY
VFYKDTPRPIDFSNCGYGFYLFDMAETFLHLSSDNRKVFISYSKVNQLEENYVELLE
AFFIWTIIRTFAFHSLNPNEQQSLAANFPSVIENYFRKYLKGEIFLLN"

CDS 2233984..2235069

/locus_tag="EFAGFIKM_01912"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTIIPVIVMIFVFVPTVILMVSMPLYLTRETISFGVTVSAVQFHS

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CDS complement(2235613..2235960)

/locus_tag="EFAGFIKM_01913"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAVSAGYLHTVGLRSDGTVVAVGRNNEGECDVSGWRDIVAVAAG

SYHTIGLKSDGTTAVGSNKHHQCDVSVWHDIRAVSAGCAHTIGLKTDVTLVTVGDND

YGQCDVSGWSNIH"

CDS complement(2236509..2236877)

/locus_tag="EFAGFIKM_01914"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"
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CDS complement(2236861..2237226)

/locus_tag="EFAGFIKM_01915"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MSKKLEANGLWESSRMMLPQHKERIIQHRTQIHQTKPLIHQDE
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DQLVTVKLEEGGVYSETDF"

CDS complement(2237223..2238464)

/gene="dinB_2"
/locus_tag="EFAGFIKM_01916"
/EC_number="2.7.7.7"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q47155"
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/product="DNA polymerase IV"
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MIAKKAEGGIFHLKKEELHLHIGDKPIRDMWGIGSRMEKHLWKMGI RTIRDLANTPLS
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ICTEVCRRARKKGLMGSVSVSVSGADFDQPTGFHRQVKLSIPTNITVDVCKLAKRIF
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CDS complement(2238727..2239629)

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/locus_tag="EFAGFIKM_01917"
/EC_number="1.1.1.25"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q8Y9N5"
/codon_start=1
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/product="Shikimate dehydrogenase (NADP(+))"
/db_xref="COG:COG0169"
/translation="MNNDKNLAKIDAKTTLVGLLATPIGHSVSPQMHNVGYSGLNY
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FARNDKFFSKAEENAAAYINNEMKHFGVKANVPLEDKEAFRKEIAESAILANATSLGM
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CDS complement(2239657..2240844)

/gene="ydiN_1"
/locus_tag="EFAGFIKM_01918"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P76198"
/codon_start=1
/transl_table=11
/product="Inner membrane transport protein YdiN"
/translation="MKNPYIKTSLGMYLNYFMLGMINIIIASNMSSLSDNYNQPV EKI
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GWSFYALGILFLISGIYLIFMPFPSFKSHSKDEADSETYKNRFKEEPKFWGEG LAIIL
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VFQ"

CDS complement(2240890..2242077)

/gene="ydiN_2"
/locus_tag="EFAGFIKM_01919"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P76198"
/codon_start=1
/transl_table=11
/product="Inner membrane transport protein YdiN"
/translation="MKYPHLKMGLGIYLSYLLLGMSIMLASNMNFLSERLHVVPDI
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IGFFSVSLSTVIQTWLPTYGNQVLQLNEKKAVELLSFYSMGGILICILVLAFLKKFIK
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FSK"

CDS complement(2242519..2243541)

/gene="cytR"
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/inference="similar to AA sequence:UniProtKB:P0ACN7"
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/db_xref="COG:COG1609"
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ISADYAGIDYEEGAYLATTHLAKKGHQRIAFLGGVKESSTWVKRMDGYRKAFKDHNLE
LEESIIIASDPTSEGGEAAARLLLKSPNPPSAIFCFSDLIAFGVMKVLTKEGIVVGRD
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CDS complement(2243875..2244576)

/locus_tag="EFAGFIKM_01921"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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KDAKVESIQIYSLLD"

CDS complement(2244681..2246075)

/gene="sasA_4"
/locus_tag="EFAGFIKM_01922"
/EC_number="2.7.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01837"
/codon_start=1
/transl_table=11
/product="Adaptive-response sensory-kinase SasA"
/translation="MLSFGIIIFAVNKAIDYYSFITIEKQMMEKADLSELFREVLSQ
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GAGGFIVLITLSSLWIARN TT KPIKQLLGAAQSFSRQEFRRVHLNRKDELGMLADGLD
SMGRQLHDYIQYQKQFVSNVSHELKTPLAAIRGFSQYLVEGETENKELQNIYAHLLQE
SDRLTRLINELLLL SRFDKAGSNELELEKTEMNELIQQVAMNMGAKAKDKEIEIRVSQ
AEEEPDDEGKTRVYANVNPMLMSHAIANLVDNAIKYSGSPSLIELNLEYTPSEVIRI
RDQGIGISGEELERVQERFYRAKNASTANGSGLGLSICKEIVERFNGYIDIESQIGEG
TTVTIVLPRAETQS"

CDS complement(2246117..2246824)

/gene="walR_2"
/locus_tag="EFAGFIKM_01923"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37478"

/codon_start=1

/transl_table=11

/product="Transcriptional regulatory protein WalR"

/db_xref="COG:COG0745"

/translation="MKKILVIDDEIAIRDLIELVLRRENYVVQTAENGKIALQLLDTF

QPDLVVLDLMLPDCSGYDLCKEITGKRAVPVIMLSAKNEVIDKVLGLELGAEDYMTKP

FDNRELLARIKVILRRNESKEESSEGTEVKSTRIIHEELTFDLESRRVLKNDVAVSLT

AKEFKILETLLKRPDKIFTRDELLQIGWGYDFMGDSRSVDMTIMRLRKKLEDNADEPK

YVRTIYGFGYQLGGGEA"

CDS 2246979..2247236

/locus_tag="EFAGFIKM_01924"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDLLWVLIVGGLIGWLSGNLIGRDVPGGVLGNIAGFIGSWLGT

ELLGPRGPVIGGFHIIPAIVGSIALLIFFALARGGAFRRR"

CDS complement(2247574..2249265)

/gene="ilvD_2"

/locus_tag="EFAGFIKM_01925"

/EC_number="4.2.1.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WKJ5"

/codon_start=1

/transl_table=11

/product="Dihydroxy-acid dehydratase"

/db_xref="COG:COG0129"

/translation="MENKKDLRIRSKVISEGANRVPNRAMLRAVGFQDEDFKKPMIGI

ASTWSEVTPCNMHINDLAVQAKQGARNNGGAPLIFNTITVSDGISMGHGGMLFSLPSR

EAIADSIEIVTGAERFDGVVAIGGCDKNTPACLMAIGRMNIPSVVYVGGTIQPGNLDG

KKVDIVSAFEAVGQYQDGKMTDEQLHKVECSVCPGPGACGGMYTANTMAAAAEAMGMC

LPGSSSTSAISADKALECEAAGKQVISLLEQEIYPRDIMTKKAFENAITVVMALGGST
NAFLHLLAIAHSVEVDLTLDDEFERIRLRVPHLADLKPSGQYVMQDLNDIGGVSGVMKL
LLAEGLLHGDCLTVTGKTLAENLAEAAPLQNDQEIRPLNNPLKPDGPLVVLRGNLAP
EGAVAKMSGMKIQFSGPTKVYDSEDEATEAIMNDEIQEGDVLVIRYCGPKGGPGMPPE
MLSVTALIVGKGLGGKVALITDGRFSGGSHGFVVGHVSPEAQVGGPISLLQNGDIITI
DSDIQEIKVEVPEEELAARAQAWVQPPLKVKSGVLAKYAKLVSSASRGAVTDWME"

CDS complement(2249281..2249946)

/locus_tag="EFAGFIKM_01926"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPIPKDFSLPVRMSAKERAFSQIRWIIDGTLQPGEKLIDAEMA

ESLGVSRTPIREAFQLLEVQGLVSMHPGKETKVTNIEKNDIFKMYSTMAALQALAAEI

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KIL"

CDS complement(2250543..2250758)

/locus_tag="EFAGFIKM_01927"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAILSTGPIENNPVSGVRPTQQLTINIDNRNLVTNAIVLIQGY

LNGTRTEYILELISVNPQNQAIIKKDYFA"

CDS 2251055..2252611

/gene="opuD"

/locus_tag="EFAGFIKM_01928"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54417"

/codon_start=1

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/product="Glycine betaine transporter OpuD"
/db_xref="COG:COG1292"
/translation="MVFTITIIIVALFAIWGAVAPDQLADVANVAYNFSIQNFGWFYL
LATLFFLIFAFYLAFSRFGSIRLGDDDDPEYSTISWLSMLFSAGMGIGLVFWGVAEP
LSHYLSAPEGAVPETTQAAILSMRYSFFHWGLHPWAIYTVIGLALAYFQFRKGYKGLI
SSTFIPLIGERLAAGWLKGKVIDILAVISTIFGVATSLGLGALQIGGGLNHLFGIPNST
LTQVVIITVTVLFLISATSGLDKGIKILSNVNLVIAVLLMLFVLVTGPTSFIFDTFT
TTLGSYMQNIINMSLRITPFSRETWIGAWTLFYWAWWISWAPFVGTFIARVSRGRTIK
EFVIYVMVIPSLFGFIWFSVFGGTGLHMELFNAAHLAEAVKEDTTTALFLMLEQLPLG
TIVASIATLLIMIFFITSADSATFVLGMLTSDGKLDPSTRVKLTWGIMQSAIAVVLLI
SGGLTGLQTASIVTALPFAIVLIGMCFSLKALKAEKERRQKEKRQRQKLKRLLEEQ
EISLNEISGR"

CDS complement(2253188..2254420)

/gene="yycB_2"
/locus_tag="EFAGFIKM_01929"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37482"
/codon_start=1
/transl_table=11
/product="putative transporter YycB"
/db_xref="COG:COG2807"
/translation="MPNKQNKKFVPSSVALIILGIIVIAANLRTPLTSVGPLVSFIRD
DVHISNTLAGLITTVPLLA FALLSPLVPKLGRRYGVERIILIALIFLTVGIVIRSLSG
AVNLFIGTAVLGFAIAICNVLLPSIIKRDFPNKIGSMTGVYSISMNLCGAIASGISVP
LAMNAGLKWQGALGIWGLSFVSILCWLPQLRNQTKQTATTSQQMANNDVNVVRSPLA
WQVTLMGIIQSMVFYVLIAWLPEILKQQGIDSNQSGWYLSIMQLAMLPTFIVPVIAG
RMSNQRLLVITTILLTGTGLLGYSSNVILLWIVILGIGGGFAFSLAMMFFGLRTE
NAHQAAELSGMAQSIGYLLAAIGPALIGYLHDATNSWNLPLFILLGASVLLFVVGIGA
ASNHVVGSRDGYELPRKG"

CDS complement(2254637..2255197)

/gene="sutR_1"
/locus_tag="EFAGFIKM_01930"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77626"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator SutR"

/db_xref="COG:COG1396"

/translation="MDEIDESKQIVLQIGGALKKYRKEKNMTLDDLSELTGVSKLTLG
NIERGETNPTLAIWKISKGISLPLLALFTSEKPVSLYRAGEGLRFSNDEKNWIIEPV
FKSNDIEMCRAYLQPNSSYYPEGHHVNTTEIATVMTGSIELQVNGENYTLNQYDTISF
RADHPPHAYTNHTNSETVLHISLKYGF"

CDS 2255379..2256323

/gene="ghrB_1"

/locus_tag="EFAGFIKM_01931"

/EC_number="1.1.1.81"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01667"

/codon_start=1

/transl_table=11

/product="Glyoxylate/hydroxypyruvate reductase B"

/translation="MKILIVGYFCETSKSNIERSFPQDWNVIVPPGKEMLHHIEDCQ
VIIPEHIKVDHSLLSNAKKLKVQTGAGFDNVDVPACTQLGIWVANAAGVNAQAVAEH
VMALILSYKNIPFLDTFMKNKMDENQLDYTGSELKGKTIGIIGLGAIGKKVAAFCRV
FDMNVLAYARNATAQSDDLVKMTDFDTLVSTDIVSVHVPLNEQTKQLINKAAFKKMK
NTTLFINTARGGIVNERDLIDALKNGDISGACLDVFESEPLPIDSELRNLGNVILTPH
TAGMPDGRKFHKTRYDFFINNIKGVENGEEPESKLNQL"

CDS complement(2256355..2256840)

/locus_tag="EFAGFIKM_01932"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLSDLEGDMGGPSEFLEQSVSQDLILELLNHAVWAPNDGLREP"

WRFIFADNQYGDIMQGLQEPAPAYLLVLVKEEADQYKREEDFAAVCCLIQNFRLAHE
QSLGVRCTLHDWMYDPSRTEMFGVLSNERIAAVLELGYGANQWKGNTLPETQLHFEL
L"

CDS complement(2256858..2257433)
/locus_tag="EFAGFIKM_01933"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSLAELIRERRSIRKCNSTPVDQELVVELLRKAMRLQPSVESGS
WRVYAGTPEARKRLVDCMLEQMSQSKLGKLIPGKLLDVFKKRFTDIPAHVIVMSTVG
PNRLTNDRNYYAACGVMQSFQLLGWEQGLGMLWDTESMIQHEGFFNGIGLREDERFVG
ILHIGYYDKAPRSRKRTPAEQKWTVLQGQST"

CDS complement(2257454..2257936)
/gene="pchR"
/locus_tag="EFAGFIKM_01934"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P40762"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator PchR"
/translation="MISKDRTKQLLYDQFIRFLHUYENHKDTEIEHFLSIAQRESIEK
IPQHLTAVHMDICIGKHEPINNTGIAEAMNLSKASITKIGNKLLEEGFVKRTKMNDNK
KESYFRLSPQGRKIFELHERLHIHEAERFYRTLDKYSETELKIIHQFLQDSSINIESR
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CDS 2258322..2258738
/locus_tag="EFAGFIKM_01935"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDDKTVIIDQGPFFHGTAKELQIGDLLEPQFLSNYQEKNSNHIY

FTATLNAAKWGAELARSTNAKERIYIVEPLGDFESDPNVTDKKFPGNPTRSYRSKSPLK

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CDS complement(2258823..2259785)

/locus_tag="EFAGFIKM_01936"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFNPVIDVHHHHISKEMQRKQRELGMEIPSFMPKWTPEIGMQKM

DVCDISFSFLSAPSDLTFIDQSSANALARKMNEELASYAQLYPERYGAFATLPLDPA

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IAGLSPALLEGTFTTTRAVTTMAVHRIFDQYPSITFILPHTGGMVPYIKWRIALAAIG

QDSIQVETTPEQFQAEIAKLDHLYYDSTLNLGTIQKLIAPDRILFGADIPWPADSVLR

IQRESVFHEAQVSEENAKAIAYGNAFRLFPRIKSLFDIEKKLI"

CDS complement(2259802..2261295)

/locus_tag="EFAGFIKM_01937"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFKKRLPAGFIKVMSLICAAPLLLTACGIPDSKEGAEPGKASAT

DMYEVMVTYPAFGDVTDVKEIQEAISDITSEKVGATVKLLPVNGSNYANQMNLMLAGS

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PSIKAWALSPSFVMDKELADKHDIDLSAIKTWNDISAVLQLIKENEPGVTPIVSYTSQ

ETPGQAMLNFDPLGTAPGVLDFFGGEDFTMQNLFATSRFSTMADLMRDWYQKGYFSKDV

ATSQETGSNLIKAGKAFSYIRNINECYSESAAAGTELVCVPLEDSYMTRNSVASNMMS

LARNSEQPDKAIQVLELFYSDEAVINLFTNGIEGKHVYKRDNDLIGKPEGVTAIGYDS

NQYAVGNNFLSYIWEGNDPDMWEHLRGENEGALKSRAMGFSFDINPVKTQITSVANVQ

NQYDAGFQTGTDFPSELGAYLDKLNAGVEKILTEKQNQLNQWLENK"

CDS complement(2261352..2262233)

/gene="araQ_11"

/locus_tag="EFAGFIKM_01938"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MYSNRIYQMAVHLVLIMMGIAAVFPFILLISASLTEEQAIIRDG

YRLLPAQFSFDAYVYLFNQYSLILRSYGITTFITVVGTVGLLITTLVAYPLSRNVLP

FRSFLSFFVFFTLFNNGGLVPMYLVYTDLFHLKDTIWSLIIPNLLTNGFYILLMRSFF

STSIPGEVVESAYVDGANEWVIYCKIVLPLALPSLATIGLMLMISYWNDWFNGLIFIN

DGSLYSIQNLLNRMLSDVQYLQQNSLSGQTAVVSSVPLGSVRMAIAVIGVLPLIAAYP

FFQKFFVKGLTIGAVKG"

CDS complement(2262251..2263183)

/gene="yteP_10"

/locus_tag="EFAGFIKM_01939"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system

permease YteP"

/db_xref="COG:COG4209"

/translation="MRRGFHANRIQSIRKHGLLLVMILPGIVYLFINNYLPMFGIVIA

FKDINFAKGIWGSWDVGFDFNFAYLFQTQDAWVITRNTLLYNGAFIVLGTVLSIAVAVL

LNEVKKRFASRLYQSIILLPYLISMVIVAYLVALLNEENG FVNHYVLP LLGIDPVSW

YADSGKWPFILSVVYLWKNVGYTCIVYLASIVGISQEYYESATLDGASKWRQVWSITL

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CDS complement(2263517..2264737)

/locus_tag="EFAGFIKM_01940"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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/product="hypothetical protein"
/translation="MEKGLTLVKNVKWSENLFDLTIDQATGLIVSIETAGTDADLTSV
NIAGRPTTVIDADGLHYVPPMTDMHTHLDKHFIEGPWKS LQPFVTLPGQLEFEKSM LG
ELPTGAGERAKRMLDLMLAQGTTAIRTHVDVDPQIGLSHLEEVLEVREMYQGRIDMEI
VAFPQQGLLRSDSVSVMREALRARANYVGGVDPAGLDRRV DASLEAMFELATEFSAGI
DLHLHDPSHLGIYTISRFAELTEQAGMSGRTAVSHAYCLGQVGETEVRSLAERLCATG
VAIMTSVPIDRPMPPIKLLMETGVS VHIGSDNILD SWSPFGNGDMLSRGSRLAEASGW
VEDFWLLETYKLISNAPLTPKVGERGT FSLVNAINAMHALAA APPREAVFSGGVLVGG
RMFPNSRQMAAIHS"

CDS complement(2264761..2266020)

/gene="codA_1"
/locus_tag="EFAGFIKM_01941"
/EC_number="3.5.4.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P25524"
/codon_start=1
/transl_table=11
/product="Cytosine deaminase"
/db_xref="COG:COG0402"
/translation="MIDLLITDTVISGDERRMDVGISSGKIAFFTPCGERKTEASRVV
QKG GLLLPGLVEPHIHLEKAYLLDSMDREAESLQDAIQITSKLKSSFTREDMYHRSL
VVIREAVRNGVTHMRCHAEVDPVLGLRAVESALRLKQSLKHQLDLQVVAFPQEGVFKS
PGTAGLMEEAIRMGADVIGGITYQDADLGEHLDFAFSLAGKYGKPLDFHADFSVDSND
RAVVEIAKRAIAAGMQGHVAAGHVTSLGSLPEHEASAIGELLCLAGISVITLPMTDLF
LNGREGSEGYHRGLTPVKLLQDCGVNVAIGVNNVRNPFTPF GKADPIEA AWWLLAITSY
MGSKRDALILT NMLTHNAAQALGIDNYGVKVGAPADMVLFRRERSEREVLLNKPEARTV
WKSG LQVACTDSK LLELTWLS DGMETI"

CDS 2266223..2267884

/gene="pucR_3"
/locus_tag="EFAGFIKM_01942"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32138"

/codon_start=1

/transl_table=11

/product="Purine catabolism regulatory protein"

/db_xref="COG:COG2508"

/translation="MLLTDLLKNGIYDDARVITGHKGLIREVQTVNIMDCPDIIIRFLR
PNELLLTNGFFMKQQPEMFIHLIRDMQRLHCSGLAIKTKRFELPIPDEILWEADQNEF
PIIEISDVRLSLGEILQRSTSVILNNKSDELQYALSIHKKFSEMIMRGKGISSIISL
SKLFSSPVILLNYKWQTISASDQNTSVAELTAAVNTLQDLSDISSPTSLCFINPSVR
ERCCMLVYPVKTYRHEGYLLSFHSPDQWTGLFGLTLEQASNVIGMELTKSQAVKERSR
RHKNEFFSDLIEGYITSEQEALNRGKRCGLIKGRASVVLTMRNDEVHMHQRFKNEG
SAPPKRDNITEQEEQYEHKRVFGGLDHSFVMFTKHDTYCLLSIPESGWDEAKITEQ
LSGMLKELHHEIGLSLSIGIGKPATNVLGVRHSYTEAVNALQFGYWLKRKQFVQSYQA
KDIGYLFHMLPHNELKQFYDATLNGLLQIADEHEKKELLRTLNAFYDTQCQLVETSKQ
LFVHRNTVVYRLEKCEKILGVKLKDPTESLRIRIAIAIEPLLQD"

CDS complement(2267991..2271794)

/locus_tag="EFAGFIKM_01943"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKDKSKFVICLLMATGLALTSNGIFTSKSIAASAVLADQETNKQ
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VEIGQIYHLKVKAVGSSLKVYWGNQYKPMIDVQDISYQSGKLGLHWWDGSAFNSNIVV
SDLKGNLGTVLSSKGKWQPDINGKRGRVEQENRAQQIYNKEAADMVYEGNITLRPDSI
SALAFRSSTDGAEGYEATLTKEGDQVRVSLTNTKGTVIASSQRTYPSQMGAKHHVEIK
AKGDRIQVFLDGYTTAAIDVKDSTYRSGSTGIVVKKGTAYFQDTYVTELSQYYNEIYR
PQYHYTPIRGSASDPNGLVYFEGEYHLFHQDGGTWAHAVSKDMLNWKRLPIALPWNDH
GHVWSGSAVADMTNASGLFGDSGGKGLIAYYTSFNPDSPNGNQRIGLAYSKDQGRTWE
YSKERPIVIENPGKSGNEVGNWDFRDPKVIKRDENNRRWVMVSGGDHIRFYTSTNLLD

WTLTDNWGYGDYVRGGVWECPDLFQLPVDGTSQKKWVMISTGANPKTGGSDAEYFIG
HLTADGK FVNDNPAGKVLRTDFGKEFYASMSFANMPDHRTVMMAWMTNWDYPFAFPTS
NWKGELTIPREVSLVTTKDGIGMTQSPIKELESLRKPLYASNKSVSPSSGNLLKGII
SGAYEIEAEIEIPEASTVTEFGFNIREGANQKTVVGKASDSHMFVDRTASGETDFSN
LLSKKHEAPAQMENNRIKMRLVDESSVEAFGNNGKVVFSDVIFPDASRAMSFYVKG
GNVNVVSLKVHQLQSVWNEDIPSKAQIKMDTSVRELGVGESDTLQAMVEYGPGLGVQP
LKWNSSNNDVIALDLVDNSHAVIKAKKEGESTVTVSTPNGKTSSSVLIKVSNGGEFRTN
LSGWTKDLSAASWLSEHGIRGKYFSDANYIAKEKAGNFTYEADMMLGETGGAGSVLF
RASEDGRSGYYLNLDPNMKAIRLFYKINGAFEERQVLAKVPTFIRPGQTYKVKIEANG
PHIVVHVDSQKVIDIMDGTFAEGHFGLNVFGGSASYQNVNVSNGEPANLTKSSLVNAA
TQKSIYTVNLVNGEPVTLQDASAASVQKWVFPVTGDEAGSYSIRTTAGQTLDLDIGQN
KLQLYHYLGYNNQRWVLHENKDGSVHITSAHHQKALEVSEDGTEFLSELNPSLDRQK
WILTK"

CDS complement(2271922..2273514)

/gene="sacC_2"

/locus_tag="EFAGFIKM_01944"

/EC_number="3.2.1.80"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P05656"

/codon_start=1

/transl_table=11

/product="Levanase"

/db_xref="COG:COG1621"

/translation="MNKIKILLSGENNISKGPENFIYKNEYRPQIHYS PNGNWINDP

NGMVYYEGEYHLFYQYTPHDTQPDFGRMHWGHAVSNNLVHWDELPPAISPGE DGAIFS

GSAVVDKNNTSGFFNEAGSGLVAIYTNNDNSAQPGKPQVQSIAYSKDKGRTWTKYEGN

PVLFPMETLDFRDPKVFVWHEESSKWVMVLAVSDRVEFYTSSNLKDWSFASGFGSDIPG

IHRGIFECPDVFKIQVDEDPNTTKWILTLSVGDRNGVNPNDSEPPAGGSGMMYFIGHF

DGKAFTLDETLESFDTIQWIDYGSDFYAAVTWDGIPNEDGRKIWVGWMNNWRYASTLP

SKEWRGHMSIPREIQLRQTYSEGLRLIQAPITELNQLRRSILSLQDITIKPDMNVLSAV

SAAKMEIIAEFEIGNAIEFGFKVRKSSSSNQETVIGYNVLNEELFVDRTKSNTVDFHP

DFAAKHKAPMKPEHKRIQLSIYVDWSSVEIFGNNGTTIISDTIFPDLGSRGLELYAIG

GELKVMSLQINDLVSIWENQSV"

CDS complement(2273909..2274055)

/locus_tag="EFAGFIKM_01945"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVKKKISTAISAALIVSMLATGVIVAIEGKTTLEVAKSAGDKKV
EVIK"

CDS complement(2274255..2275283)

/locus_tag="EFAGFIKM_01946"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVIERVKRDFLDDIAIIGLTGSFSTGDFHEKSDLDLIINNTEK
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DFQQKALDALAKPIGEACLN RANKWIDLAKQAYSDTMLSEDIGSVRYASAEVLYNLVN
ALVSMNNTCIKRGIKRYLEEIRSFYVPDNLESLYMSIIEAHTIEDIRITSFNMLNSV
TRLHNTMCDNFIVKPAPTFDNLRGTYEELWCNYRNKILNSVTANDASYVFLSAFGAHE
YLDEMA MEKGTKKYDLMQYFDASNLPVMKEKLLEVMD DYREEYNKVGRKVERFTTFEQ
LYAHYMNQ"

CDS complement(2275493..2275759)

/locus_tag="EFAGFIKM_01947"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKYSKAESIFPEELLRIIQEYVQGELVYIPKPKEAHLKWGEKTE
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CDS complement(2276054..2277139)

/locus_tag="EFAGFIKM_01948"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLPMEEYFGKLELVHSFYGAMPTGVSSETARIFICFPKWGDDV

KFTVAEIVEGHMQYPNVETNLINPLNIVMSFISVQSVVADGRGTLWVLDTAAPNFSE

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GPGAIIVVNLENGNAYRRLHGTSTSPDPYFVPKVEGKILKNRNADGSTSPFRLASDG

IAISPDGKMLFYCPLTSRQLYSISTESLRDRTIPDFKLSDLVQYWGEKGASDGMITDA

KGNVYAGDYENDSIRKILPNGIMETIAHDPRIWPDFTSIGPDQYLYVIVNQLHRQAR

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CDS complement(2277392..2277673)

/locus_tag="EFAGFIKM_01949"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPNKNKIDLATENARKPAEGALNSSGSITLEQHASNAVYEVQTA

LNQAISSLNESDATNSQALEIARQQLTRADEFDQALTSANALRLPDQQ"

CDS 2277862..2278104

/locus_tag="EFAGFIKM_01950"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTNPRTLAPHESMELHEALNFKTLCLAKSKLMQGLVFDQELKALM

QKDVIQSIQQIAELQAIYARAPFQAPVPNNPTPITH"

CDS 2278116..2278502

/locus_tag="EFAGFIKM_01951"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MNTDYLDPINSLNMPPEMADMTFAMDFLIRAKEGVRNLSIALTET
ASPDVRALLHHTLKQGIAMHQEISELMIRKKWFHPYELNEQYQLDQLSAKNTVMIGQM
NLFPGDTSRKGMFDRTPEHIGGHKA"

CDS 2278499..2279635

/locus_tag="EFAGFIKM_01952"
/EC_number="1.1.1.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07737"
/codon_start=1
/transl_table=11
/product="putative zinc-binding alcohol dehydrogenase"
/db_xref="COG:COG1063"
/translation="MKAVTYQGVKNVVVKEVPDAKIVKPDDMIVKITSTAICGSDLHL
IHGMIPNLQENYVIGHEPMGIVEEVGPGVTKVKKGDRVIIPFNIACGECFFCQNQLES
QCDNSNEHGDMGAYFGYSGTTGGYPGGQAEYLRVPFANFTHFKIPENCEQPDEKLSLI
ADAMTTAFWSVDNAGVKNGDTVIVLGCGPVGLLAQKFCWLKGAKRVIADVVDYRLKH
AKRTNHVEIVNFEQDKNIGNTLKEMTKGGADVVIDAVGMDGKMSDLEFLASGMKLQGG
TVSAFIASQAVRKGGTIQVTGVYGGRYNGFPLGDIMQRNVNIRSGQAPVIHYMPYMY
ELVTSGKVDPGDIVTHVIPLSEAKRGYEVFDTKTDDCIKVILKP"

CDS 2279667..2279867

/locus_tag="EFAGFIKM_01953"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDSTYALHEMLEVHEIAAFKTVCMTKSKTMQALVTDPELKQILQ
QDATLSQQQLQELGGVLSKATV"

CDS 2279879..2280175

/locus_tag="EFAGFIKM_01954"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MNPILEHMTGLNTLTDDVIAMDFLMNAKSGVRNYAMAVTECATP
EIKQILMKQLDEAIDSHEKISNYMVQHGLYHPYHIAEQIQLDLKNIQTAMNIPS"

CDS complement(2280464..2281126)

/gene="tenA"
/locus_tag="EFAGFIKM_01955"
/EC_number="3.5.99.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9K9G8"
/codon_start=1
/transl_table=11
/product="Aminopyrimidine aminohydrolase"
/db_xref="COG:COG0819"
/translation="MLTISERLYQAAQPVWKECLEHPFVKGIGDGSALTVEQFRYYLLQ
DYLYLFDYARVFALGIVKSHDPKLMQFFSKNVDNILNGEMKIHRSYMDRLGITEDHVF
QVKPALKNAAYTNYMLSVSHAGGIAEVLVSILACSWSYAEIGQVLAQKPDAADHPFYG
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EP"

CDS complement(2281773..2284214)

/gene="xynA"
/locus_tag="EFAGFIKM_01956"
/EC_number="3.2.1.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P36917"
/codon_start=1
/transl_table=11
/product="Endo-1,4-beta-xylanase A"
/translation="MKRLGQWNITALVLVLVLA MLPFSNVSHA AKAVTEVEGGHLSTN
FEDGTLQGWT PRTGNERLVTQ QEAHEGQSSMLVANRERSYHG PMLSMKDMLKRNQEY
EIAAYVRLTQEPTTDQTLQLTTYKKTAE SWNPIGSVKIAKAEWNTWHKITGKFQYSD
DPTELNLF IETPYISED SVDTL SFYVDDVSFTLAEQLEIEEGILSLEDLYQDDFPIGA

AVYRWQLEGAYGQLLTKHFNSLTATYEMKPKYMSPSEGVYEFEAADQYVQFAEEHGMG
VRAHALLWHIDAAEWMFKDPQGNPASRELLLARIQDYVETVMTRYKGEIYAWDVNEV
IADSNGDANGLRKSPFYELIGPDYIEKTYEFARAADPNAKLYYNEYFTEIPEKREHMY
QLVKRLKEKGLIDGVGLQSHYNLESPPIKEIEKTINMFAELGLDIQITELDVDSGIPF
GEEMSDEVAVKQAYRYKELLDLYKKHKDHISSVTLWGLQDEKSYNNQAMLFDSALKAK
KAYWGLVDESSLPVLTRAVSLSGKPDIKKQSQDPLWNKAVSTPLKGDSSGSASFRTL
WDRSNLYILVDVQDAKADVNDNRVDIFVDLNNGKTTSYEADDRHVIIKRSKVEGAEQR
SYRVRETKAGYQVELSIPWGGIQVVSEYETGLDIRVTDGGASGTEPHNPLYWNDRTQS
QEQDTSKYGVIQLAPMPKSAQAVQGIVQIDGKKDALWNKAVPFEVKRLNQSEGAEAVA
RAMWSGEYLYLLIDVTDPNITDNINPWDQDSVEIFLDENHQRTPYFYDDAQFRISA
DNVGTFAAGGAHPDAL"

CDS 2284703..2285113

/locus_tag="EFAGFIKM_01957"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTFLPPFGPGGGFGGPGGGPGGGPGGGPGGGPGGFPGPPSFP

GGGGGGPQGVQAPTGPPPSFIPQQPASLYAVDPRAISGCLFRYTYIWPDRGPGFWMYP

VFVGRNSVAGFRWNGFFWLYTGLDLQRISFSCF"

CDS complement(2285184..2286923)

/gene="ettA"

/locus_tag="EFAGFIKM_01958"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A9W3"

/codon_start=1

/transl_table=11

/product="Energy-dependent translational throttle protein

EttA"

/db_xref="COG:COG0488"

/translation="MIKVENLSFSFPQKELYKNISFTFEEAQHCFIGTSGSGKSTLI

DILMDPERYLFEGKLEIDPDCRIGYVSQFLQVDKTKEMTVFEYIAEEFIKIQDEITAI

YAEMATTSDMDSLMEKLQLALDAFEAMDGDNFEKNINKQLNLANLMKLDLSISAVSG
GEFKLIQVMKEMLNRPDFMIMDEPDVFLDFENLNALRKLINTHKGMLLVVTHNRYLLN
HCFNKIIHLENTELQEFDGRYIDYNFSLQTKIELQEIAVAEAEIEERYDHIIDNLRE
IATYNSEASRGRALKARVKFQERLEARRIKEPFVDIKQPNIRFGIDKEMEDTVVVNLN
NYSVSFDELLLENVNFEIKSTDKVALIGPNGTGKTTLLREIFKNNQDSIEINADVKA
YLSQVQGEMLKDSNTILNEFIDSGFQTYDEIRSYLPNYGFEGEILDQKIESLSGGEKN
MLQLAKVSASQANILLDEPTSHLDIYTQIALEKAIEDYKGAIIMISHDFYSVVNGMD
YVLIIEDKTISKMSIEEFRQMIYASHFDENYLENEQKKKSVMKIELALKDTNFELAK
SLVDELEELIKLL"

CDS 2287231..2287635

/locus_tag="EFAGFIKM_01959"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNFASVRIITDDVNRLVEFYEKITGVSAERPAPVFAELVMP SCT

LAIGHSQTVQLFGAGSAVAANNRTVIIEFHVHDVDAEYERLKPFDVDEWVKEPTTMPWG

NRAVLFRDPDGNLVNLFTPVTEEASQRFSGRL"

CDS complement(2287654..2288514)

/gene="gltR_2"

/locus_tag="EFAGFIKM_01960"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94501"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator GltR"

/db_xref="COG:COG0583"

/translation="MEIRHLVTFITIVEHEGFTKAAEHLGYAQSTITLHIKALEEEIN

YPLFDRIGKR VILTETGKKLLPHAQKMLDLYHMIKEVTAAQGELTGNIVISIGETLLI

YRFPPIIEEFKKLHPHVNIEWHQLDSVHYKENLMQGKSDISFMLGTEVHDPNLYSEKL

AEEPMMLLYPNSFELQRDIVRSNLLFTERGCGYRTLFEQCIEEYQIGITSNIEFWSIE

AVKQSILSGMGISLLPRITVEKELKEEKLSGQQYKQNLATQLLYPKNKWISPQVEAFI

EIVRKHAFLW"

CDS 2288669..2289508

/gene="oleB"

/locus_tag="EFAGFIKM_01961"

/EC_number="4.1.1.114"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8EG65"

/codon_start=1

/transl_table=11

/product="Cis-3-alkyl-4-alkyloxetan-2-one decarboxylase"

/db_xref="COG:COG0596"

/translation="MQTAATSSILINGYRIAYEQYGEGSPIWLLHGTPSYSYEWKVI

PALVQKGKVVYVHDLGYSERPLEADTSVAAQYTLFSQLLDELGMDRLHVAHDLG

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KQLPMAVYNKELMTGDTLEAYLEPHAGSLGKSSFFSHQVAHYNKYTESYGTDLPKLK

VPVQILWGEEDWQPLAYAKRLVQDIPHACLHVIPRAGHFVMEDEPGQCSDYIDRFCN

KHP"

CDS 2289792..2291555

/locus_tag="EFAGFIKM_01962"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRQTRKKMDLRFKLYLIILVPLLAMGGLIHWATIDSSNASLM

TMQHNNQQLAVNTASQLGQESLIKLSSTASEESNEYKSLRDELVKVRLQSGALVY

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LLSSFTPIKDSQGTIVIGYLGIDISAGAVNQVSATSVNNAYQTIIPIFVVVLISLVMM

LFVVRGILRQVRDIKSSLEQVADGNLKVSTHMSNDQLGDISDLINIMVAQLTNILMG

IQQGSNTLQSSKDISETAQTNQRQSEELSRAIEEIAIGSMKQAEETEHSVQHSENLG

KIMDEVGSYVKQFTYTSQQLSSVQVQVTREHEVLLEKGRENAKRVEHQDISRSLTQ

SELASSISGQIHNLKQTQILSLNASIEAARAGEAGKGFAVVAGEMGQLAQQSERSIQ

EIDEILGSFVQEIHMRMGSHFDANMVAVEEQEKQIADCLQAFRQVSRLSTEVHELAQSL

DSRTMDMHSIRQEQNLSYIASATEETSAMAE EVTASAVEQQRSASELSNISGELAG

LAGNLKSYSDQFQIEVRKSGP"

CDS complement(2291651..2292019)

/gene="pucR_4"

/locus_tag="EFAGFIKM_01963"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32138"

/codon_start=1

/transl_table=11

/product="Purine catabolism regulatory protein"

/db_xref="COG:COG2508"

/translation="MTAKAGKLSVVQEDLLKLQGI PRDQMQQYVD RYLG SLLAEEGY

DPELLQTLETYASCNGHINEMSSRLYIHRNTAAYRLEKLERLIGIPLKEPETLMLLNL

VFLFRRLL EQRRPRCPTIVS"

CDS complement(2292066..2293466)

/gene="allB_2"

/locus_tag="EFAGFIKM_01964"

/EC_number="3.5.2.5"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9KAH8"

/codon_start=1

/transl_table=11

/product="Allantoinase"

/db_xref="COG:COG0044"

/translation="MKSAIPYDLVIAGGMIVTEAAVERKDIGIIHGSIAEISDNIDPM

GASVINARGLTVM PGVIDTHVHFNEPGL EAWEGFQTGSAALAAGGGTFFLDMPLNAIP

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DKDGFMSDDDTLREGMRIIAETGKVLALHAEHEPTVTRLTREARSLGQFGPESYTAS

RPIKAEVEAVETALRYAAESGCRLHFVHISSEAAAGRIREARKAGVDVTLETCPHYLC

LTDKDFAVIGAVAKCAPPLRDAEEQDKLWVKLKEGWFDLSSDHSPCPASMTGNDMF

ESWGGIAGVQSTLELMLDEGYLKRGVPLPLLARLLSAAPAERFGLAPVKGRIAVNCDA

DLVLVDLNTYYTLQASDLYQKHRHSPYIGRSFGCKVKMTLLRGRLMYSEGSPLLNQGT

GKEFRSACPGAMNISS"

CDS complement(2293519..2294574)

/locus_tag="EFAGFIKM_01965"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLTFDHNQEQPQKRTPDERSKWNESFYRRSMELPDELLIGAIDSH

VHAGPVLNSNPGHLDPIQVAQEAAAAGMKSIYYDVFGWASGMAWVVRHVPGIHTYG

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PRFAEKELSVATSIPLEGPVPEELDEILKMVAEHPEVYLNTGHVSVPEAFRLDLAEQ

YGIKVLIAHPVRGQMTIEEQKSAASRGAFLEACLDWLYPDVPRTHYYVEREYMDMG

AELGRYSNATKWMKTIREVGIDQFVLGTDYGIRAAPTPVQGMRTMIASMLDYQFSPDD

IYRMVATNPARLIGIQS"

CDS complement(2294614..2295483)

/gene="ngcG_2"

/locus_tag="EFAGFIKM_01966"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O50501"

/codon_start=1

/transl_table=11

/product="Diacetylchitobiose uptake system permease

protein NgcG"

/db_xref="COG:COG0395"

/translation="MELQLELQRQRSTRFLPSPAKLAVNALMLLFTASCILPLLWIG

YSSLKTQAEFANNILSLPSAPQFGNYLEAIKLTNMLQLSWNSARVTLLSVIGITAISY

VTGYITARIDFKGKKVMIFYLFGMLVPIHALLVPLYLLFKNFGLADQWYTLIIPYIA

FNLSLPIMLISSYVAGIPKEIEEAAIDGLSFSGTMYRIMLPPIAIPVLTTVAILQFFS

CWNEFSFALVLLNDESLRTVPLGMSYFKSQHSTNYPQLMAGMILSMLPVTIYFVFSS

RIIAGVMAGAVKG"

CDS complement(2295483..2296379)

/gene="melD_4"

/locus_tag="EFAGFIKM_01967"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34706"
/codon_start=1
/transl_table=11
/product="Melibiose/raffinose/stachyose import permease
protein MelD"
/db_xref="COG:COG1175"

/translation="MGKALRPGKWVLLAYLLPGLIISFVVLVPIFSAFRDSFYSWG
GPKKTYIGIENYKEILQDNVFWHSFLNNVLMTAYGLIGQVGFGVFALLLMSKMVKLK
GLHRTMSYFPSTLAPVIIAFLWMLIYNYNYGLLNAGLTKLGLDVLVQSWLDLTGPVL
LASIPLSWQNIGFFTLLMLAGLSSINKEVLEVAELDGATGVRKAWYIIPLAKPTLVV
ASLLCIANNMRGFEHIYALTRGGPGNSSVMALYAYETSFLRFYGYGSALAIIVL
TMLLILLSTLALQRRNSKGGAY"

CDS complement(2296403..2297740)

/locus_tag="EFAGFIKM_01968"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MNKRSFMLGLLVTSSVLSACGSGDNEEATAESGKNVTISLLHR
YQESNIGKSPEDTAVLDGLKRFMEDYPNVEIIIEQLQNEEDYSIKAQALAAADDMPDVF
IVPGSWMTNFVDNEIVLPLNEELDKRPEWRDGYRAGTL DAGTREGQVYGIPIAAGPTH
LIYYNADMFGSIGYDQFPSTWPDLM DAGEKLADKGINLFSYGDKSKGYAMSSWISALT
DRINGPQWTESILNGSGAQFTDDGFVHGISMRELAKAGYLNKDLNSVDADTMVNYFF
EGRSAAFVSGIWSAMNIVNNAPEGIAAGTRVAVFPGVEGGLGNPLSSSGGAGVYYSVN
SGVEAGEKLDAIMTMLEYMTGSASAKLMAEVGGFPAYDPGDFDTGKLHPVALAA YEAS
AAADATKIFDLWFDASIVEVLNTGIQGVMAGSRTPEQLAEETQQAYETFLNNP"

CDS complement(2297815..2298477)

/gene="rspR_2"
/locus_tag="EFAGFIKM_01969"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ACM2"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional repressor RspR"

/db_xref="COG:COG1802"

/translation="MTKGKEREIYQDIKLAIQHKLLPNSQLVEDALAEAFEVSRTPI

RNVLRRLAMEKLVTVIPYRGAFVSCPSVDEAREVFEMRRVIETSMVRKLCCTTVKPEQL

SPLEVLIREEHQASHDGDVVGALDVTVDIHLKLAELSDNYYYHFLEELISLTSVIA

LYGTNQSFCHDHVDLLAAILQQDGELAARIMTEHLWQIERSLNFTETAPNVLNFKEIF

QK"

CDS 2298954..2299205

/locus_tag="EFAGFIKM_01970"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKEKLYYGKDIEVMFNSDVCIHSGICVKGLPAVFDLSKRPWVD

PDGDTSEAIARHIDTCPSGALTYKLLDGEYSTKKEDEHA"

CDS 2299198..2299479

/gene="yjdJ"

/locus_tag="EFAGFIKM_01971"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39274"

/codon_start=1

/transl_table=11

/product="putative protein YjdJ"

/db_xref="COG:COG2388"

/translation="MHNVEHEPANKRFLIQDNGDIAAVMTYVISSPELYIIDHTLVEN

AYRGQGLGDELIKAMVEYARENGIKILPLCPFAKGRFERISEYVDVLHQ"

CDS complement(2299579..2301249)

/gene="mall_1"

/locus_tag="EFAGFIKM_01972"

/EC_number="3.2.1.10"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P29094"
/codon_start=1
/transl_table=11
/product="Oligo-1,6-glucosidase"
/db_xref="COG:COG0366"
/translation="MKRVWWKEAVAYQIYPRSFMDSDNGDGVGDIQGIISKLDYIQDLG
IDLIWICPMYKSPNDDNGYDISDYCSIMDEFGTMADFDQLLNEVHLRGMKIMDLVIN
HTSDEHPWFIESRASLDNPKRDWYIWRDGKNGDEPNWESIFGGSWEYDEVSGQYYL
HLFSKKQPDNLWANKEVRKSIYEMMNWWLDKGIDGFRVDAISHIHKEEGLDMPHIEG
VKYVSSFEEKHMNVKGIQSYLQEMKENTLSRYDVVTVEANGVKVEDQEDLRDWICEVR
GKFNMVFQFEHLDLWKNSTDRQLDVPKLNVLTKWQKSLEGVGWNALFIENHDQPRKV
SSWGNDTEYWYESATALGAMYFFMQGTPFIYQGQEIGMTNVAYPSIADYNDIADRNL
QIKREEGMSHEEIMNIIWASSRDNSTPMQWSSAKQAGFTTSTSWLKVNDNYVNINVE
KQLQEPRSLQFYKQMIQLRKEHDTLTGYIELLLPHHPSVYAYTRTLADQQVLVIN
LSEHMLEEDELGLNFSEIWLNTNYENGLVPLVLRPFETIVGLSNKVK"

CDS complement(2301302..2302930)

/gene="malL_2"
/locus_tag="EFAGFIKM_01973"
/EC_number="3.2.1.10"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P29094"
/codon_start=1
/transl_table=11
/product="Oligo-1,6-glucosidase"
/db_xref="COG:COG0366"
/translation="MENKKWWKETVVYQIYPRSFQDRNGDGIGDLEGIVSRDYLQQL
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LHLFSVKQPDNLWENPKVRQEIYNMINWWIDKGVGGFRLDVIDLIGKEPDLKITGNP
NLHQYIRELSKETFQKAEDLLTVGETWGATPEIAKLYSNPDGSEFSMVVFQFEHISLDE

QEGKGKWDLKPLDVMALKKVLSKWQTELKGDWNSLFWNNHDLPRIVSRWGNDGEFRV
ESAKMLATLLHGMQGTPIYQGEELGMTNVQYAIEDYRDIELNIFYKERMKGKGYPEQS
VMESYAKGRDNARTPMQWDTSDNAGFTQGEPWIKVNPYKHHAEESLNNPESIFHY
YRKLIQLRKDHEVIVYGDYELIFPENPDVFAYTRTLNGTTILVVCNFFQGYTTELSLQE
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CDS complement(2302953..2303846)

/locus_tag="EFAGFIKM_01974"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSYSANFKDRIGRFAIYAIVLMALVCLLPLWNIVAISSFSSSEA

VSANAVGLVPVNFTTAAYTKIIEDAQFWRSFGISVLRVALALVLNMILIIMAYPLSK

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MNFFSAVPKALEEAAAFIDGANPLQVLFKVVYPVSIPALATVALFSIVGTWNDFFGGLI

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LIYPLLQKYFVTGIVVGSVKE"

CDS complement(2303860..2304774)

/gene="yteP_11"

/locus_tag="EFAGFIKM_01975"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system

permease YteP"

/db_xref="COG:COG4209"

/translation="MKQGNSKIKGRLGPGAMYHMMMLPGILFLLVFSYVPMVGIITAF

QDYIPAKGMFGSEFVGLKHFMYMFKLPDIAQVVSNTLVIAIGKILLGTMMAIIFSVLL

NEIRIKYVKKSVQTIVYLPFLSWVVLASVWNMFSLDGIVNQMLAFFGLENINFLGS

NTWFQPLIIGTDVWKEFGYSSIVYLAITSIDPGLYEAAGMDGASWWRKVWHITLPGM

LPIILLMGVMSLTNLSAGFDQVYNLYNPVVYETGDILDTYVYRIGLVGRQYSFGTAV

GLFKSVIGIVLLMSANQLAKKYTDRKIF"

CDS complement(2304837..2306573)

/locus_tag="EFAGFIKM_01976"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRTKWSMKSNRLTKRLAVLSMSALMVATLAACGDSSTPPTAEEA
GKYEVTGDPFSAKYKDEITVTMGRVTTANPKLPAGDTYENNAYTRLVKDTFNAQITDQ
FEANGEDYSRQVSLAIASGELPDMMRVDSKDELKELVDNDLIEDLTAIYDQYATDNIK
QMYDSYDGRALDNATIDGRLMGLPATSLDSAPTMVWVRQDWLDLLGIQLDADGDGALS
LEEVEQTALEFLKRDPGQSGNPVGIPFVNTMNTTDYNGSAYTMLGVASTEGAFPQYWM
NGEDGKIVYGSTTEETKKMLGTMADWFKNGIIDPQFGTRTFDDITALYANGQSGIAFG
PWHIPDWGLISAKQMDKNAKFSAYTLEDANGKVNVAHANPSNQFIVVRKGYEHP ELAV
KIVNLFYDKLANDKNAATTMPEAAKYQETGVDGSTRPFNIEVNSATSLDDYSDVVRG
IKGEINLDEVRTTESKNNIGSIKTYLSMDTDDVTAWSKYHSRINGVGLIDKLTQENK
FVWMTPAFSGTTPSMKQTSWANLTKLEQESFIKIVTGSESLDYFDTFVSNWKKQGGDQV
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CDS complement(2306824..2308230)

/gene="cheB_4"

/locus_tag="EFAGFIKM_01977"

/EC_number="3.5.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00099"

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KTQPVDLMLTDLAMPVMSGIELMRAARQLYPELHIVVLT LHQDFDYIQEALRLGAIDY
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TWSQIKNWIMNYTETSLFYAYNPNNQVIAVSMNEENTFSKEPQDEDLNRIKQSWFQTP
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EVEEWIKQTAVSIRKSDEQTSYSQEIIDAVKKAVMIVQHDLEQAYTASGLSQQLNISR
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CDS complement(2308227..2309939)

/locus_tag="EFAGFIKM_01978"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTLKKRIFLLFFLSAFIPFISIFAISYYTIDSIFANKIDDGIRS

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FDDQLVLSAMRKVQLSERNDVFIYVESGFRLTQDILGYNQYNGALSHLILDGEGNIVY

SEIPEAMKVGENFSSLTVDPAKDGISRGYHWFKEDASQKWSVSVISQAQYQQEKNQW

LLQILLVALFFLGFTVFLAWLLWKMVYKPLGLFHSEINGMSKNPQTTGRRARTQIPEF

DFLGGEFSNMQHQIGDLFREYQQKEKIRADLEVEKLLYQINPHFLMNTLDTVHWLAVM

NGQGEIDKLQVSLNKLYYNLGKLGQVSTMEEEIDALRQYLILQQIRYDFEFDVRITA

DEQVLQIPVPRFILQPLVENSLEYHGLSDEGFIQIEVTCTSTLNIMIQDNGAGMTEETI

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DISA"

CDS complement(2310225..2316608)

/locus_tag="EFAGFIKM_01979"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIRRTVSIQKSMFVSFLALLMVISLAVPPAPIRAESSSSQPGRQ

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LVAYDYVGGELVKRWTFDTNQAGSQYQSQGNHNLSVLDVDKDGKDEIMFGALAIDDDG
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KYPNGINDNTHFSSYGAQKIAGLVAGAVKDMELSISSLVIDPDISEPEPEPEAQLYEE
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CDS 2316817..2317689

/gene="rhaR_10"

/locus_tag="EFAGFIKM_01980"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MVHTVSYAFRNDTSIMTLDSIGWQIVSSEEYRCPSDDRPDPGH

VVFQYTLNGQGYLDIDNQTLPKGHALLVKIAGEHCYYYKQENNEPWEFIWINIRGD

EANRIWDMMHDDNEGHVIRRNADSPLIQELWQIIHLIHQEKVTDKYRLSMQVYRWLLIL

VQTSRDAEKDIGALSITTIEKCKKFIRENYASPLTDLASHCDINKHYLCRLFQKSE

KTSPLAYLKDRRIEVAIRLLRTTELPISQIGQQCGFESPSYFGKVFRQYMSMSPKEYR

LNKLEFPYEAIIYE"

CDS complement(2317820..2318557)

/gene="bacC"

/locus_tag="EFAGFIKM_01981"

/EC_number="1.1.1.385"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8KWT4"

/codon_start=1

/transl_table=11

/product="Dihydroanticapsin 7-dehydrogenase"

/translation="MGKLQDKVAVITGGASGIGAATARLFVSEGAkvVLVDLNEEKgk

AFEQELKALKAEALFIKANITSEEEVSEIFKQTVEAFGQVDIVFNNAGIGRVHPTHEL

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GVVNLTRSLALEYAEQNIRVNSLCPGFIDTPIIPEESKQALSAATPMKRLGQAEEMAK

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CDS 2318734..2319348

/locus_tag="EFAGFIKM_01982"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNNELIVTSQHRNRTKEHLKTALIQLIKKKGFHGVSVKDIVDQA
GYNRSTFYLYHQDKYILAEELLILTLEGLRGAVGKPYWHGQKVSTNKLDAESFQIVDY
IYHRDFFELIQYDDTLPGLHTGFPQTILKIYQEQFVFETINNSPVNMDYFKYYTAYG
FFGLNNWILSGYRESREAFIKNVIELTKTHHSFHYVGNTFES"

CDS complement(2319372..2321441)

/locus_tag="EFAGFIKM_01983"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNGILHKIMQERLGNC DYEVWISSNWADWWLIEAIGRRESTPPC
FAEQLPLQHPKVEWESEENMLVFLPYNNNICVAIRVFKNWEFSAEDLVTLSLLYPYY
TEAVASKNERALNEIMNSIRDVTQLLDLNELLGRILVSALSVIPYECIGVLWRYDPAI
DALTVKARAGEMGEGMLRMKLKPGEGIIGNTEFKRGTPKLYNGLSTVEDDFGNMTSENK
YHLNSAYNFQDIGSIISVPIKVEGQSDCVLIVYQKGRVPLFTESDVRLQLQSFADQVSI
AITNAKLYENLSKQNETLMKRDEIHSSLMRLSLQNKGAVSIVNELARVIGVSMFTFVDF
IDNEWIPKRSKIMNGWNAESLRSLYESLHHPDYLTCEGVADRSYQYLYPIASANQCL
GYLIIQMNTKLEPLQLIALEQGSSILALELMRKQSLAEFYFKKTQQFFNDLRLSQDSE
DYWQKSGEIGIVPSTSIVVGLLEFAEWWNPSTLSALSVQLVAYLREKMPAGALPIAFG
NERRITVLLMLNESHKPGKLEQQFSALLPEWEHRNHVKLLGGLSSVRSGVDAINTGYQ
EADKALAYQKTRGEQGTIRYTDIGVNRLFIRQPAEDLNAFMAEIFEPLRPAKGQTGGL
EETLMTYMACGSSAVQAAAALHIHINTLYQRIHKIEEILGMSLSNQEHLHLQLACYL
RQTYRSS"

CDS 2321588..2322832

/gene="sauU"
/locus_tag="EFAGFIKM_01984"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q0K843"
/codon_start=1

/transl_table=11
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/translation="MSKIMHSHKHFYIVLTLLFLGWCLGNLDRFVINYAIVGITQDLG
LGASAQGIILSSFFLGYAIMQIPGGALADRFGRKVLVSLFSWSVFTILTGSAWSLF
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LVTIGWRNLFYIIGAVGILITALMFFLLKEPAKPALATSGSAQQPKTSLKTVLKTPMI
WNLFISYFSIYAVNWGLQSWMPTYMVNVRGLDMTQMGLLAAIPALVSIFTMILSGYVL
DRIPAGKDRMIASVFGVLVALFLYLMGSAGSITTFITYMTIVTAMAGFISTLIISKSL
KTMPEVVATANGFINTGAQLAGFLTPMLIGFLVEASGGSYATAFIMLIAFALICSIT
LMFSRRSNSGQDNTTEMQAKAV"

CDS 2322927..2324369

/gene="abgB_3"
/locus_tag="EFAGFIKM_01985"
/EC_number="3.5.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P76052"
/codon_start=1
/transl_table=11
/product="p-aminobenzoyl-glutamate hydrolase subunit B"
/db_xref="COG:COG1473"
/translation="MTTVDLTQFISEAIEGKRDMFTNASDQIWGFAETRFDEFQSAE
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VQPRGNHGHGCGHNLLGIGALAAVAVKDYLQEHPEPTGTVRFYGCPAEESGYGKTYLA
REGYFKDVDAALSWHPHSLNAV MHGSSNAVIHGTFTFKGISAHAAAAPHLGRSALDAV
ELMNIGSNYMREHMIDQARIHYAITNSGGLAPNVVQAEAEVTYLVRAPKSAQVRSLE
RLVKVAEGAALMTETTMNFKYEGACTNLIPNSTLEKIMHQHLVAFGAPQYEEDEYNYA
KAIYDTLPLQNQQEAGTLVGPELAPLLAERPLPNFIAPYSDERETFMGGSTDVADVSW
NVPTAQCIITTTMAFGTPLHAWQTVAQGKSSFAHKGMLLAAKAMAATAIESILHPEIVK
EAQQELLDRLGGEAYDCLVPADVQPPKRGE"

CDS 2324374..2325042

/gene="sdhB_1"
/locus_tag="EFAGFIKM_01986"

/EC_number="4.3.1.17"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P33074"
/codon_start=1
/transl_table=11
/product="L-serine dehydratase, beta chain"
/translation="MRFKDVFSIIGPAMVGPSSSHTAGAARIGRTARHLFGECPSHAE
ILMFGSFAATYKGHGTDTAIVGGLLDMDTDDPRLPDFAHADTAGMETIIRPGTGLYP
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VIAVTRLLVDNHINIGHMSVDRKNRRGEAMMVLECDGKMDPVVVRQIEVLPEVHDVT
LLCL"

CDS 2325089..2325964

/gene="sdhA_1"
/locus_tag="EFAGFIKM_01987"
/EC_number="4.3.1.17"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P33073"
/codon_start=1
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/product="L-serine dehydratase, alpha chain"
/translation="MNFRTLKQLAELAETRNLTLGQLMLEEQCHESGEDKNVVFSSQMH
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EVNASMGRIIATPTAGSCGIIPGVFISSQERFGWTDEQMVYGLFASGAIGYVIANNNSF
ISGAEGGCQAEVGSAGMAAGALVDIRGGSPSQSIHAVGLALKNTLGLICDPVAGLVE
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QTPTGRKITRDLQHK"

CDS complement(2326102..2326569)

/locus_tag="EFAGFIKM_01988"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MKKRVSVKIGDVFSIKLNQDLDCYGQVSEGRISDCMIVFDLIS
MEHPTVSEITSKPIIFLIQTVNSRIEDGIWKVIGNAPIPRMTFPMYKEETEDGYTLVD
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CDS complement(2326636..2327367)

/locus_tag="EFAGFIKM_01989"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYLKELNLDLPYIVDDENIESIMKKQKCEYNEATKLDYALNWKW
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LNDFSGKNELEKKKATLRLMEGIEKLALRNNWDIDPFREIALQIEELDYNVNEWTWKK
DVKSPNKKYNARVICHNNVDSMDIFLSILQRDGTQVLVEKVISEQPDEFAYAEHLGEL
TWVSDFEVALINKAGTEKYSATLNN"

CDS complement(2327409..2327708)

/locus_tag="EFAGFIKM_01990"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDILKWIQSWYYENCDDGDWEHLYGVRIDTVDNPGWSVEIDLTD
YLEDVPFDSIEEERNEEDWFYCIVRDGVFHSAGGAKNLEEMLNCFKNWASSLERS"

CDS 2327885..2328244

/locus_tag="EFAGFIKM_01991"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKIILFIFISMIILSGCSNKDEKENYPVFEGTVVFKTDENDKY
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EPSPIRTVVSIEKIND"

CDS complement(2328465..2329736)

/locus_tag="EFAGFIKM_01992"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MKKRLTILATVLSLTMLSACSSTSISGTSKQEEIPKPKENKVASD
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LRDELLVRLGGTAGGEQLFDSNFKTWSYDDLALSEKEKQYPVLFFVHGAGAYPQQGTL
FAQDLASAGYIVVSIGHAESGVYKLKDGRTVGMSEKFMDEVTKYGMEAATLTPPEIVT
EKLEEEEAIEIARKLTSAPKAVKFANYAVLQSEDIRYVADNLYKMNTGDMESMFKGRL
QLDLGMGVFGHSFGGTAAIVSRDDDRFVGAVNLDGNMLGALDSDFKKPFMQLSTVLA
YNTNAFLLESNSKDTYFAIIDNVVHGDFSLSLFTTTDKASRGTRDAMEQRNIITSYTK
AFFDEYMLKKDADIDSLTFDGVEMIKKPQKP"

CDS complement(2329852..2330499)

/gene="degU_1"
/locus_tag="EFAGFIKM_01993"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P13800"
/codon_start=1
/transl_table=11
/product="Transcriptional regulatory protein DegU"
/db_xref="COG:COG2197"
/translation="MTIKILIVDDHFVREGLKLILETNQRYEVVAEASNGMEAIRRV
DTYKPDIIILLDLNMPGGLDGMTALRAKGMDIPIIIITTYNEDEMMIRGLALGAKGY
LLKDTGREMIFRSIDAAMRGETLLLPEISEKVFHAKTSEKAKESSSARISLTDKELIV
LQAIARGARSKEIGFDMGISERTVKTHLTSIYNKLGVDSRPQAVAVAVERGILHL"

CDS complement(2330496..2331719)

/locus_tag="EFAGFIKM_01994"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MSDYSINKPYTSSRSDIQNVLRDSRLPALIWGILIYFSALYSQL
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KEVKEEAHFHSHITGICVVTRLSPHLLVVPKLIFEHSLHIIRECLANTAKYANATNVE
VVVAARENEIELSITDDGIGFDTNLIEKQSGSYGLIGLYERTRIMGGEIEIESGKKGT
KVSVRIPLQQEDTNA"

CDS complement(2331993..2333609)

/gene="xynB_3"

/locus_tag="EFAGFIKM_01995"

/EC_number="3.2.1.37"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94489"

/codon_start=1

/transl_table=11

/product="Beta-xylosidase"

/db_xref="COG:COG3507"

/translation="MNKIKKMITNPILPGFHPDPSICRAGEDYYIATSTFEWFPGVRI
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FKDTHNYLVTATDIEGPWSDPVYLNSSGFDPSLFHDEDGRKWLVNMIWDHRKGKNRFA
GIVLQEYSVQEHKLIGPAMNIFKGTELGLTEAPHLYKQKDYYYLITAEGGTGYEHAVT
SARSRTLQGPYEVDPANPILTSYGRPDALQKAGHGSLVETHTGEWYMAHLVGRPVQH
KYCILGRETAQCTWSEDGWLRLASGDTYPEVQVPAPMIQSHPFEPIDHDFHFE
LRHDWNTLRIPPDSTWLSLTERPGYLRHLGMESMSSTHRQSMIARRLQALECEAETCL
EFAPDHPQQMAGLILYYDTQDYLYLRVTYHEEKGLCLGIIQSKYGVYDELLEDIPLES
VSTLRLKVVVDQDRARFYAINSDSSWNTAGGWVDITHLSDESPEYIRFTGTYIGLCV
QDLGGTRKHADFDYFMYKETKHTAGVSENM"

CDS complement(2333670..2335646)

/gene="yagF"

/locus_tag="EFAGFIKM_01996"

/EC_number="4.2.1.82"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P77596"
/codon_start=1
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/db_xref="COG:COG0129"
/translation="MYEQITSIMGETASNCFDIIAHAPGAAGRPLTDDLNRNSPSGD
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VATCDKGLPAMMLALAGMPQLPGVIVPGGVTLPTNGEDAGKIQTIGARYVNGELSLE
MASDLGCRACATPGGGCQFLGTAATAQVVAEAMGMTVPHAALAPSGQPIWFEMARQSS
RALIHMESQGMTMADIVTDASIRNAMTVHAAFGGSTNLLLHIPAIAHAAGLTVPTVQD
WIQVNKNVPRLVSALPNGPIFYPTIRVFQAGGVPEVMLHLRQLGLLDESVPVTGTSL
GQVLDWWESSERRHLMRKQLKEQDGIDPDSVIMSVEHAQRLGISSTVTFPTGNIAPEG
SVIKSTSIDPAVLDEHGVYRHRGRAKVFTTEREAIHAIKTGCILAGDVVLLGRGPSG
TGMEETYQLTSALKHLPFGKYVSLITDARFSGVSTGACIGHVGPEALAGGPIGKLQNG
DLIDIAVDRNTLEGSINFGEGDLEFSPEEGALILAQRPFHPDMPDEALPDDTKLWA
ALQSVSGGTWRGNVYDVERIVTALEAGKKALGWY"

CDS complement(2335663..2337129)

/gene="aldHT"
/locus_tag="EFAGFIKM_01997"
/EC_number="1.2.1.5"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42329"
/codon_start=1
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PEAKGETLRGVAILRYYAGEGMRKTGDVIPSTDSEALMFTTRVPLGVVGVIAPWNFPV
AIIWKTAPALIYGNTVVLKPAQETAVTAAKVMECFEEAGIPAGVLNLVCGRGSVIGS
ALAEHPDVGGITFTGSNEVGKRVGGAALARGAKYQLEMGGKNPIIAADADLDLAVEA

TISGGLKSTGQKCTATSKVIIERKVYDTFKEKLLSQIQEVRLGDGMSSGSWMGPCASE
GQLNTVLSYIQKGQDEGAVLLTGKRGDGPGLLEEGFYVQPTVFEGVESHM SIAREEIF
GPVLALIAVDSLEEAEAAANDSDYGLSASIYTQNVGAMLSFIRDMDAGLVRINAETAG
VELQAPFGGMKMSSSHSREQGQAAIEFFTAIKTVFVKS"

CDS complement(2337151..2338026)

/locus_tag="EFAGFIKM_01998"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRIIRFLDGQQKWLAAVTDDEQAYRLPQADFMTLIHQARKQGIS
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KTFYDKVYDAERPEIFFKSTAARTVGPNEAVTLRSDSNWQIPEPELGLVLAADGSIVG
YIVGNDMSCRDIEGENPLYLPQAKMWRNSCSIGPAIRLAETVQNPYAFSIVCEIYREG
EVVVKSEASTSELNRKLDLVSLARDNDLFDGTVLLTGTSIVPPNDFTLAPGDRIEI
SISDIGTLINPVISN"

CDS 2338243..2339154

/gene="virF"

/locus_tag="EFAGFIKM_01999"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0C2V5"

/codon_start=1

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/product="Virulence regulon transcriptional activator

VirF"

/translation="MTKLSDAVYLGRLPDVRMSFQLLGLHARKVDSSWTYPSHEHSMY
EVHWMMDGQMNMVVNGQSYRQSVGDLLFIRPGMTHSCTGAGPEGFTYFSVHFSIHDS
FCRELNRCIDIYPANSNLALGLSPSLSTLYGLATEHLSSSLSSSKQMKVHAADFELL
GSLVGQLSQQASVTLRKHETIAHQIAEHIEDSVRYIHLHGEIQESDRTWIQDIAKSLS
ISPSQVNRIFRQVYGIAPRKFLSETLLNEAQRLKQTDLNIDHIAMMLGYKTNAHF SR
QFKRWTGIAPSEYRSRSQHAGEAQSDV"

CDS complement(2339671..2340624)

/gene="nlhH"
/locus_tag="EFAGFIKM_02000"
/EC_number="3.1.1.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P9WK87"
/codon_start=1
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/product="Carboxylesterase NlhH"
/db_xref="COG:COG0657"
/translation="MSIETRILPELKEVYSQFPGFELERNLEWSRNLVSAASVRKSEH
VNTTSRKIPSDGGEMLVKIYEPADRTNDLLPAMLWIHGGGYVLGHPDMDDKLCERFVQ
TAECIVVSVDYRLAPEHPYPAAIEDCYAGLVWMTEESAMLGIDVNRVAIAGASGGGGL
TAALALMARDKGGPSIIFQMPLYPMLDNRNITPSSHEITEEGSIWNRTDNVAAWNMYL
GEENDVIESSFYAVPSRAESLAGLPAYTCVGQLDLFRDETMHEYVARLAQAGVDVEFH
LYPGCFHLFEILAPETEVSQRTVKGYMDAMARALHPNRTLN"

CDS complement(2340682..2341734)

/gene="fgd_1"
/locus_tag="EFAGFIKM_02001"
/EC_number="1.1.98.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_02123"
/codon_start=1
/transl_table=11
/product="F420-dependent glucose-6-phosphate
dehydrogenase"
/translation="MEIGVTSFVETKPDTKTGVM SHAQRLQEVVEIVLADQVGLDV
FGIGEHHRDDYAASSPAMVL SAAAPLTKRIRLTSVTVLSSADPVRVFQDFATLDGLS
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NLGVYPRPVQNSIPVWIGSGGTQESAIRAGILGLPLVLAIIIGNPTKFAPLVELYKKA
ATHAGHDVSQLRVGSHSIGFVAEDTEKAAELFFPSTQYGMNKLKGERGWAYYDRSSYD
AARRSDGALYVGDPETVAQKIIHLRKHVGITRFMMYVPLSTMTHELVMRAIELLGKEV
APRVREEISKWEAEKR"

CDS complement(2341764..2342633)
/gene="mmsB"
/locus_tag="EFAGFIKM_02002"
/EC_number="1.1.1.31"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P28811"
/codon_start=1
/transl_table=11
/product="3-hydroxyisobutyrate dehydrogenase"
/db_xref="COG:COG2084"
/translation="MKVSFIGLGNMGLPMAQNLLKAGYEVVIFNRTPEKAEPLIKQGA
RYVQTPLEAAKESNLVITMLSDDAALREIVEGPNGLNGLSENGIHVSASTISVDLAR
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GDHGEEGNIVKIGVNFLIASMLESLSAQLMVEKHGIKPSRYMDVVNALFQSPVYQNY
GAIMTEQRFEPAGFKMKLGLKDVALAIEAAKSVQAPLPLGQLIHQHLSEGITHGYGEL
DWAALIRCLEHSS"

CDS complement(2342793..2343320)
/gene="comR_3"
/locus_tag="EFAGFIKM_02003"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P75952"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional repressor ComR"
/translation="MLLFWKKGYEAASIPDLLEVMGISRSSLYDTFSDKQTLYRDALE
HYKKGSSNKQTILEQASSVRDGILQFFEYHIASAYDTSLPGGCFVTNTATTLESPDEQ
INVLIQTSFSDLEQAFCELLEKGQQSEEIDKTTDIKLSYLLNLHQSINIMAKTGQN
PERAKEMISFIIAGI"

CDS 2343531..2344016
/locus_tag="EFAGFIKM_02004"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MKKFFLSCIAMLLFLIPFSPATSAASGDRLIYDIMYNVAGGGLV
SNNNRFSFQFDNYGDAQIWDVKSRKMIWHSNTKDTRIHKLQINYFSGKLVISDPQNT
YWTSDNLAWAKAWYGADNVPANLRGNVLIMQTDGNLVLYNNENPALGWYPVWASNTGG
Q"

CDS complement(2344220..2345392)

/gene="pbuE_2"
/locus_tag="EFAGFIKM_02005"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q797E3"
/codon_start=1
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/product="Purine efflux pump PbuE"
/db_xref="COG:COG2814"
/translation="MKNKWIIYILALAVFLIGTLEYIITGVIEMIASDLSVSTSEVGL
LVTVFALAAAIIPILIAFTINIDRKKLLVSTLSVFIASNGLMLVDLSYETLLWVR
QGASGGVATVAMAVSTRLVEKEKRGNAIGIILMGLSSSLVLGVPLGTFFSEMFGWRV
LFVFIGLLSVLPLLIYKKVPAIKEEEKITLRMQLSILKNPLILTALLITLLYIGGYS
TLFTYITPFLQATSSLSMTEISGVFLAGICSFVGSKVGGQLADAKGSKFTICLGLLL
QGVTLFFFALAGVNLIMLILVLMIFMLATWSISPAQQLYVTLAPRNPDIASVNTSF
IQFGFALGSGLGGLVISRTSVMYLNWLGFAGVIALLLAILLFKKSRSRTGTPDPV"

CDS complement(2345417..2346235)

/locus_tag="EFAGFIKM_02006"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLFKISAFSRLSRVSLKTLRYDQIGILKPRKVDHDTGYRYSA
DQLEELNRIFIYKELGFTLPQITQLLQEHITLENIQGMFKLKRSEIQIIDTEQAKLV
RIEERMQLIEEEGHVETGQEIRIKEEGARQFLFQTGCGREEEIPSLFRQFDQSVTKEM
RQLIDGPQVVLWKEIAGQEEFEFEIGYFCCDLRSPDPFQLRTLPAEPMMATFAYRS

NATFACKACVHLATWIENNNYQIKENGAGRELYLPLSQEQDVQFIEIQIPILNR"

CDS complement(2346481..2346900)

/gene="arsC"

/locus_tag="EFAGFIKM_02007"

/EC_number="1.20.4.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P45947"

/codon_start=1

/transl_table=11

/product="Arsenate reductase"

/db_xref="COG:COG0394"

/translation="MSKKTLYFLCTGNSCR SQMAEGWAKKYLS EDWNIYSAGIEAHGL

NPKAVEAMNEVALDISTQTS DIIDSELLNNAD FVVTLCGDAADKCPMTPPHVKREHWG

FDDPAKAQGSDEEKWAVFQRVRDQIGERIKTFAETGK"

CDS complement(2346926..2348221)

/gene="arsB_1"

/locus_tag="EFAGFIKM_02008"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AB93"

/codon_start=1

/transl_table=11

/product="Arsenical pump membrane protein"

/db_xref="COG:COG1055"

/translation="MFSTLLACIIFLITLV LVIWQPKNLSIGWSACGGAILALLVG VV

NFEDVWDVTQIVWNATLAFVAILISLILDRIGFFEW AALHMAKAAHGNGVRMFVYVS

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NLVNIVSADFFGITFMEYAGRMFVPNLFSLAASIGVLYLFFRK SIPKRFDASELKPPL

SAIKDMKMFRLSWVVLGVLLIGYFTSEFIGIPVSFVAGIVAIFFLIMASRSSAVPTTL

VLKEAPWAIFFSIGMYVVVYGLRNVGLTDLLAVVIQAVADQRLFAATMGMGFIAAI

SSLMNNMPTVLLDALAIDATTATGTVREALIYANIIGSDLGPKITPIGSLATLLWLHV

LSTKGVKISWGTYFKTGIMITVPTLLITLVGLYLWLSIL"

CDS complement(2348295..2348621)

/locus_tag="EFAGFIKM_02009"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDSMQEAADKLKLLGDKTRLTILLLKEREWCVCEFVEILDMSQ
PGISQHLRKLKDQGLVKENKRGQWVYYSLNVENTPYITSVLELMPDTATILKSLNKEN
FTSVCN"

CDS complement(2348764..2351232)

/gene="cdr"
/locus_tag="EFAGFIKM_02010"
/EC_number="1.8.1.14"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01608"
/codon_start=1
/transl_table=11
/product="Coenzyme A disulfide reductase"
/translation="MSKKVLIVGGVAGGASAAARLRRRLDEHAEIIIFEKGPYISFANC
GLPYYIGGSIDDRERLLVQTPKGMADRFRIDVRLRSEVVAIDSQKRVVKIQSQERGAY
EESYDELILSPGAKPIIPDLPGKDNPLIYTVRSIPDIDRIKDQISSSNNQYAIVIGGG
FIGVEMAENLKEAGLDVTLIEGNAQVLTPYDTELAALAAQEMENHGVNLLFSKRVQGF
HSLEQGIGVELADGHVLTADMVILAIGVTPDTYFLKDSGVSLGARGHIIIVNEALESSV
PHIYAVGDAIEVTETIHGTKATIPLAGPANKQGRIVADRIAGLPSTYKGTQGTSIIKV
FGMTAATTGSNEKTLQRLGVDYQTVIVHPASHASYYPGSSAITLKLFTPQGKILGAQ
AVGYDGVDKRIDDIIVAIHFGGHVRDLTELELSYAPPYSSAKDPVNMAGYAAENMITG
RVQFTFTYNQLADRQPGQSILLDVRSEIEHQNGHIPDSLSIPVDELQRRLDELDPSKEI
WLYCQVGLRGYTASQILRQHGFVKNLSSGGYKTYRQAQFKPAPFTEKQDHHDPADV
KEKKSIPDSTQPQRIDHELNVCGLSCPGPLIQVKQKMDQLSNGETLRVKASDPGFYE
DVKAWATMSGSTILQLERMKGGTIESVIVKNTAQPVSDSPISDPASTMVVFSGDLKA
IASLIANGAAASGRKVTLFFTFWGLSIIRKPQPQKLSKTMIGRMFDMMLPRGSQKLG
MSKMNMLGAGPKMIRGLMKKHHVPSLEELIESAIAQGVEIVACQMSMDLMGIQREELI
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CDS complement(2351229..2351543)

/gene="pagR"

/locus_tag="EFAGFIKM_02011"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31178"

/codon_start=1

/transl_table=11

/product="Transcriptional repressor PagR"

/translation="MNTPAFDSNNIKQFDEPANLLKALSHPIRLCIVRGLMMKKKCNV
SYMQECLDLPQSTVSQHLQKLRSAGIVATERNGLEVNYVLADQRVEQIIKTLFEKDDC
ES"

CDS complement(2351776..2353590)

/locus_tag="EFAGFIKM_02012"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTKTPNYDGYL FVHFIDGEQPDGEQVYFSYSEDGLHWKDLNGGS
PVLFSDLGEKGV RDPFLVRSVKDKNFYLIATDLRIASGKGWTHAVNAGSRDVIVWESS
DLLNWSSPWNVT LGVEGAGCVWAPEAVYDEMADEFLVFWASATQEPQE QERKQKIYSA
RTKDFRTFSASEKYIERDNHII DTTILPADGSYYRYSKDETTKNIRVEKGDSL DKGAF
VTLQAPVLEAMAGVEGPQIFKFNDREEWCLIVDRFAEGKGYLPLLTTDLGSGDFRIVP
DGEFDMGSTQKRHGSVLPITAECSLLLA AFGDGHQVLPGQYADPDIAQFGDRYYMYP
TTDGFEGWSGTQFKVFSSSDLKHWQDEGVILD LGTEDVTWATGNAWAPAIA SRNGKFY
FYFCGKMLNGESAIGVAVADTPIGPFLAESQPLITMEQLKRLGITMGQAIDPSIYVEE
DGRTYLLFGNGHAAIVELGEDMISVVEDTMSNLAGLHDFREAVAVLKQGGLYHFTWSC
DDTGSSEDYHVNYGTAEQLYGPITYRYPILSKNVEKGMLGTGHHCIFNENETGQLRIAY
HRFVTPLSRFSSGKGYHREICMEPILFGKDGLIQPVIL"

CDS 2353947..2355305

/gene="phoB"

/locus_tag="EFAGFIKM_02013"

/EC_number="3.1.3.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P19405"

/codon_start=1

/transl_table=11

/product="Alkaline phosphatase 3"

/db_xref="COG:COG1785"

/translation="MKLSKRVLPAVALTLAVSASTLLSAGQASAVQAVSVEKKQIKNI

IFLIGDGMGTSYTSAYRYMKDDPSTKGMDKTVFDPYLVGAQMTYPDDDKQNVTDSSASA

ATAMSAGVKTYNAAIAVDPEQKEVKTVLEQAKENGKSTGLVATSEITHATPAAFGAHD

ISRKNMDAIADDYYDELINGKHKVDVLLGGGKSNFVREGRDLTKEFQKAGFSYVTDSS

SLLADKNQQVLGLFADGGDLKLIDRTAATPSLAEMTNTAIDRLSSNDKGFFLMVEGSQ

IDWAGHDNDIVGAMSEMEDFAAAFQAAIDFAKKDGETLVVATADHSTGGLTLGKDGEY

NFFVDPIKAALRTPDFMASKIAKGASVEETLKSYLELKPEDIQSVNEAAKSADVTK

IDNAIEAIIIDNRSFTGWTTGGHTGEDVPVYAYGPASHRFAGLIDNTDNAKIIFDILSK

HQ"

CDS 2355777..2356217

/locus_tag="EFAGFIKM_02014"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLGNILLGMVIPILGVWILRRNFTILILYYPLGVAISASINNI

GFNYFWNILPNTHNQSLAALPMDLGVYPIAGCLMMYAIIVKGAGPWLAILVASLSLTV

IEWFAKMMGHVIYFNGWNIIGTFLSYLLPFFLAYGYSKLLRYTK"

CDS 2356324..2356794

/locus_tag="EFAGFIKM_02015"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYVAYPYGYRYTFTPWWATSSVEALELIKTAQGERNDEMFDYS

LIQLSPDANQATIITSIRNDERGHNQMFRQMYKDLTGQEISGVNSEPVETVTSYLGGL

QKAFQGELAAVEKYRKIWFGLPYGIYKDTVWGIILDEQKHADKYNNLITYNLPR"

CDS complement(2356922..2357809)

/gene="mneS_1"

/locus_tag="EFAGFIKM_02016"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P46348"

/codon_start=1

/transl_table=11

/product="Manganese efflux system protein MneS"

/db_xref="COG:COG0053"

/translation="MDQLKYDNLKLGERGAIIISIIAYICLTVLKLIVGNMAGSEALKA

DGLNNATDIVASIAVLIGLKLAQRPADTDHTYGHWRAETVASLVASFIMMAVGLQVLF

QAIGSVFQGKHESPDIIAGYTGIFCAVIMYLVYRYNKRRLATRIKSQAVMAAARDNISD

AWVSTGTVIGIAGSQFGLPWLDPVTAIVVGFLICKTAWDIFKEATHHLTDGFDVELIQ

EYKKTIAGIDSVETVKDVRARNYGNNVVVDVWITVDAELDLQQAHDICTDVENELIEE

HDVYTVHVVHVEPDTLEECI"

CDS complement(2358148..2363217)

/locus_tag="EFAGFIKM_02017"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNCMVKRKLFFFIVFMLTVVVPSSLIGTRTAYAETLPYQTIID

DGSIKINDVVTLDAGNENNGYVAPNWTSTGVKGYDLSSTKYTSTAGRTITWNPRLA

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GEEFVQLTRSTGTTNTILTRADAVKFEGNITQKEPHKTIIDDGSLTIDHVTVDSGN

VSNGFSAPYWTTSSAGVKGYNNSSSKFTDAVGRSITWNPRLAAGTARISFYKLDWADKA

DSNVKIEIVHNGITDVKFMDLRPSSGPSVGWVDLGEYEFSGDDSEFVRLTRTQPSTGT

IITRADAVKFEGNIRQQAPPLSPLRSRTLANSYTEKGSIENTDNYKATFYEAAWDGGK

SIVRDMFYKNTETGNWVPINNESERLEEQWVLLDGNAGSRTNYYDTMNKRWITFDGVH

FPDSQTAVLTDSTHGSYDFEVNWSMAGDKPDVSFAFTPRRDGNYVIGYQSFTTEAVS

GINEVLNGFRSHAKMVGTVESTSLRELSAPMSLVEKNDGSGNPLTYGVFVPSAELPVE

FEPTGGVTKQRLGMSLVNNEGSVQPILYAPQLGTYSQMTAESTYQFHMGLIAQKSNLY
ESYADILRNEYDYSAYRENVSESLTDAMFNMIDLLKIEPQGDDSVNYVPSPSGWWSRA
KGFIDIENEDSVRTSSNAVLLGAYYLTGDDQLYDTRALPSVQYGVSRNGIGWSPTQKK
VYGVPSLWKMATLPFDVSSVTAVHQMMGTTAGIGALAEYLVDPDQKDRGPVIQPL
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HNAVIGRYSSYPGYYYKGAFAVSQLEPDFPLEGPSGATSIYYHHIPGQLGQTM DYLISE
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ITGESRDKFYIGLSNASSEEVQTPIELNEHIIGFNPAQDYTVTIVRDNGTPEQAVMSG
GIIQATVSGKGITAIIVEGLNINVPLHQVRTADTSDASYFFDIHSPIDAVKGMLMVKP
DETVYDAYVQAKTKPATIHYSLDGGATYTTIPDTIYPMIEWSIRVNDLSQTFTYYVES
EGKQTRKRTL YLPDQVSETPLQPDGQDSSTIIVDNTEAETEGVWIRDTTANDYYYDNY
VYAKSTTGATSKMRWRPELPESVTYSVYYKIPQITTASENWATNASFTVYYSGGSDT
VTV DATTANGTWVHLGDYPFAAGDSGYVELTNKANKSRVVADAIMWVDPNRVPQLESA
VILSDRNELQMTQTAQLTVTG YLDNGLVGDLTQADVQYFVDRTDLAEVNSSGLLTLN
LDGNTDHI EVWATVTIDGVTLTTPPLNISIRDLTVIVDSTNTTGLYTTEGSWSQSNLA
GYKIGVKSRYSTVQGSSATWKGQFPEGKYTVSIYKLVHTTANDNNVKVEVKHKTGTEI
TYIDATVGSSGWVNLGTFDFTGDGSEYVRLTRVPTTVPPTLPADMIYTRVDAVMFE
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CDS complement(2363480..2364688)

/locus_tag="EFAGFIKM_02018"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKEFFPRRGLPNVIQKLENGETVTIVYFGGSNTRSKGYRVMTAD

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GVAVSQLVSDGKLIFTSRADVSIPGAVIFTHDSIHPTIPKGHQIYTDITRSFEKIRE

LRDHVGKVEHHLPQDPLVPSNPWEYATMLPLDRLTHFSAGWSYMTDPDDFPLVREYDWL

FPGLWRAVDAGETITVEFEGTHIGLFDIGGPDSGRLKVSVDGGEPFLVDRFTPYNDHN

RNQYVFLPELPNGKHTVRFEIGHEKTDKAVVFEASGNERGMEHVRQHPAWYDQTVIQL
GKLLLVQPPL"

CDS complement(2364705..2366921)

/locus_tag="EFAGFIKM_02019"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MELMKADVTVIGGGIAGICAAIAAARQGLLVSLINDRPVLGGNA
SSEVRVHINGSAYLGNSPSYAREGGLVEELKLKIFHCNPLYNKKLMLSLSDTVLLDM
VYDEPNISLFLNTCVHETGMENGRIQWVEGLQLASERKFRFESPTYIDCSGDGIVGYQ
AGAHFRWGREAKHEYQEELAPEVADHYTMGDTILFQARDVDYSVPYKRPGFAYDITKL
EFFDSIRKGLNHRSFPRKINGLGGLWWLEYGGHMDIIKNNEDIALELRKLVYGIWDYI
KNSGEFDDVDNLILDYVCPPIPGKRESRRFIGEHMLSQNDLTTKTHFEDAVSVGGWYMD
LHANKGIYDEGPATAWNFVPGLYNIPFRSLFSRNIPNLMFAGRNISATHVAFGSTRVM
ATCGCMGQAVGTAAALCAKYETDPAAIVKAHMGELQAQLLRDGGQTIVGLQEPLDPYFA
DGLTIRASSQRSYEHLPTEEASLDKALCLVLP IQTSVVESVQIKIKNSSEHSETLQV
KLYGGDRKENYIPTSELKGYNLVISAGHDDWITLDLSCKKPEDDKIYIVLEGTADLTV
HSNEEKMTGAVSFLYRPEEPARLKKLNKSICFKDLIPFQDMYNPANVVNGFSRPYGLP
NSWISERTEGQEWLEFGFASPKNLDEIHLVFNSQLNLEHFDDPIEPLIQDYDVTLTLE
DGTESVTKVRGNYLSLNKHQVHAQAVTQIRFDFCATYGSPYYEVFAVKLFAPNNAK"

CDS complement(2367033..2368643)

/gene="cheB_5"

/locus_tag="EFAGFIKM_02020"

/EC_number="3.5.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00099"

/codon_start=1

/transl_table=11

/product="Protein-glutamate

methylesterase/protein-glutamine glutaminase"

/translation="MGRDYTCFIVDDEDLIIQRLELFFNELSHRDRRFVLVGKANNGL

NGIEEIIKLKPDIVISDIVMPRMDGISMIEQLKAELPHTQYILLTAYSSFEYAQRAIQ
ANVLEYIVKVPLREADLNRAIDKAAGILNEFEKKEAEFHSLNVSVLENKYRVRKQFFN
ELIRGEIPSHRASDFANRMQFHFFQANYCCFIVEMNTYESFRNEYAATDQNILKYAIT
NIIETVMNGSSGVAADLSDNRFIGFLSWENNRSDMETEYACLSLGGQIISHLHQYLN
KRVSVAFGSPHRGWESIKQAYTEAKNVSEDFYYHTEKVVKTPMHRFQYHNDKKADFQQ
KLADFLIRLKRKISKEELDNLADLSQFVTDHKKHKSIMVPMIRDLYRDITLKFKSGN
KMATEVPDFPMEFMAFQEQLAYIGDFTFEYVHAGQLLHREEIMSAMHYIETNLKQRLT
LEAIAEEVNLAPSYFSSLFKKTMNEGVISYINRKKIHLALELLNGRDYSLLELCEEVG
IVNEGYFCKLFKEYTGDTPKQYRIKMTR"

CDS complement(2368643..2370382)

/locus_tag="EFAGFIKM_02021"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRRRISLPLKLFVFAFVLGCIIISQLSYRYVQKEIRTNDIF

YTNQILDKVDQYFTVNFSSFQTLFSVETSVKANINNTEVIKKQLRELYELNSIYVSN

IYLIKSDLSILGGSTPTRIFDEPLSERAPLFDAADKNRRTTFVSEPYKSKYSGWTVTM

VRYLNGAPFPMAIAVDLDLNAIEETLFKINKQEQMNLALITASGKIIAGFSENKGPLS

IQDHTFSIGETSAAEILDTSSETTLQVHTKDGPVSLKKPTEKFNWTIVSVNDESRLK

AALSRLETYIELLAAGLLLSLFISFLVAKYIRKPLYTLKTKMKQVEQGILTTVTIN

RNDEFGDLSRAFDRLQQIVELIRRAELHNELERKLEIQVLQSQINPHFLYNTLGSIS

NVIRLGQIEKVDVIGSLISLLEYGIDDASEKVSLRQELRNVADYIEIQNIRYNRNFH

LIEDIEAGLMDFPVFRMLLQPLVENSIFHGYNGGGIEGPITIHAYREDGIVIEVVDQ

GEGIPADKIKHILISEPSEEEVKRKRIGLNNIHGRIRLHYGDQFGLDIISIPKEITRI

RAVFPAELPKGDA"

CDS complement(2370475..2372061)

/locus_tag="EFAGFIKM_02022"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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IAGGDIPDLIFLKSRADLAQYYDQGV LADLTPYMDQFPELQKRFGNDSWEAMSYQGKT
IGVPGYDNVNGISRSFFIRNDWLKKLNMEVPTTPDELFEVMKAFTEKDPDGNGKNDTY
GFIGGMNKEGNLQTYGFDSLMWMFGVNPSSAVEIKDNEPVFLFIDPKMKEALAYINKM
MAAKVVDPDWVTMNSPDLLDQKMFKGRVGMIRDARRLEPDYQQKMKEISGEVPEWIV
IPPMKGPYGDQIVERKSFQGNSSWAISAKVDEDKIIRILSMLNYLFTDEEAYPNFAYGI
KGIHWDVVDGKIKNKTSELSKEMKEKYLWVDHYRMPRRGDDAEYFSFQNPKTAEAFKD
NQQYVGPTLPGNLLTPDPSDTLDADRTRFINESLVKFMTGKEPLSNWDNFLQTLDTKF
DMQKYKETAIQQFKEAGLIK"

CDS complement(2372127..2372996)

/gene="dasC_2"

/locus_tag="EFAGFIKM_02023"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9K489"

/codon_start=1

/transl_table=11

/product="Diacetylchitobiose uptake system permease
protein DasC"

/db_xref="COG:COG0395"

/translation="MIHMTIGEKVWQTVVYVILILLSLLCVLPFLYVAVSVTPSEV
LRRGIVIIPESFTFLAYKEVFISHGIWQAYKITLFRITVGTALNVFFTIVIAAYPLSKK
YLPGRSPFLLFIVFTMMFSGGLIPTYLLIRSLGLLNSPWVLIIPNLISAFNLVVIKGF
FEQLPGEIEESARVDGASELQTLWRIILPLSLPVLSTISLFYAVGHWNSYFDAIVYIN
DSNYMPLQVILRNILLNVATQSADSLANSGAVSTFAVQMATVVVTTVPILIVYPFLQK
HFTKGVLLGSVKG"

CDS complement(2373010..2373957)

/gene="yteP_12"

/locus_tag="EFAGFIKM_02024"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11
/product="putative multiple-sugar transport system
permease YteP"
/db_xref="COG:COG4209"
/translation="MQAKLAADAIPISKKRKTWIRTIRRHKVMYALLLPALIYFAVFK
YIPMAGIMIAFKNYNLALGLWDSPWVGFKNFTDFMNGVYFWDIMKNTIVISLYKLLFG
FSAPIVLALLLNEVYSQWFKKIVQTITYLPHFLSWVIVYGIMVALLAPGDGLFNMILK
DFGVEPISFLTEPAWGRMLIILSEVWKDIGWGAILYLAALAGIDPSLYEAARMGASK
WRQLWHITLPGIRGVILMLILKLSHILDAGFDQIFMFANTFNQEKIDIIDTWVYREG
LERLKIGLATAVGLFKAVIGFALVLAANKLAKKFDGQIW"

CDS complement(2374157..2374912)

/gene="COQ5_2"
/locus_tag="EFAGFIKM_02025"
/EC_number="2.1.1.163"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01813"
/codon_start=1
/transl_table=11
/product="2-methoxy-6-polyprenyl-1,4-benzoquinol
methylase, mitochondrial"
/translation="MNNRERFSSRVDSYLKYRPSYPKEVIDYLDVVGLRVNSNIADI
GSGTGIISKLLLERGSYVIAVEPNQAMREAAEQMLESNPKFQSTSGSAESTGLPDQSV
DFIVCAQAFHWFDRSAAQIEFRRILQPGGKVILIWNSRLTNGTPFREEYNQLLHTYGT
DYEKVNHNKISQAILLSFFKEGSMHEMRFKMSQEFD FEGLKGRLLSSSYSPVPGHANY
DPMTELRNLFDKNNQNGLVEFDYETEIFWGEV"

CDS complement(2374933..2377218)

/gene="secA_1"
/locus_tag="EFAGFIKM_02026"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P28366"
/codon_start=1
/transl_table=11

/product="Protein translocase subunit SecA"

/db_xref="COG:COG0653"

/translation="MNVVVKLIREFKERDTRRLKKNYRDRVELIRKRNLETWDDQRLQ
AESLRLQEEARSGTPLDELLVDAYALVCEAAKRTLGLKPYDVQIMAAIALHERFLIEQ
HTGEGKTL SAVMPVYLNALTGKG VHVLT FNDY LANRDAAWMGPIYRFLGLTVSSVQAG
MSLF EKREAYAKDITYVTAKEAGFDYLRDTIAFNEADTVHRPFHYVIVDEADSLLLDE
ARVPLVISGDSSASKSDGVLFAEVARQLQPGEHYDFDEFQRNVYLNEAGAAKAELLG
CGNLYDSHNSHWLTS LNCALHVESLLKKD VDYIVRDGVIELIEEHTGRVAENRYLPDG
LQAALVSKEGLQWKAGGRILGTITIQHFISLYSGICGMTATAHASAMEFEDIYALQVV
QIPPNKPNIRIDHKHRIYTHKEAKYKALVQEISSVHRVGRPI LIGTSSVEESDMLAEA
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AKLSGLYVIGTYVNESMRIDDQLRGRCGRQGDPGSSVFYISLEDELMLRFGIHKLFRA
PNQDEVLD DPALHSKIEHIQRVIIGQNF DIQRELNCYS DMVEDQRRILYEERFGILKA
ERLMSPSERRVRLFYIDEFWADHLAYVSYIRESIHLESITSRNPIDEFHTQITQSFEK
IPAKIDHESANMLRKLGGSDNPEIWEQFGLKSPISTRTYMINDQYSQDKRSSWTGTTV
FAFWGSKILKLLLPVYRMSK"

CDS complement(2377336..2379636)

/locus_tag="EFAGFIKM_02027"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNMKKKLSIFTALAVFQAFVGSVSAQSAPQGDTASVNTANVES
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TTNETGTPV VQEETPEKVETPATPAQIEQPSVDGTSPAVAGGNLTLYMNSNKMEQDG
KTYLAGQPM AIKNGVSYVAIRALVDRVG YGVKYDNKTKETIIISGEDELRFKTN SKDY
TVNGETRTMKGPAYQQKSTFMVPLTSITQALNITYKVNQSAKTVVLNLNTPVASFTI
SQKEIFAGDQVDYVTSSSSPNGMDIVDERWTGRQDSFDQAGTYTISYQVQDSNGQWSD
PYSTTIEVLAPNLPPVAMFATDKEQYKMGEKITYTDQSTDENNIVKAVWENNSLAFF
EPGPKTVTLTVTDNHGATNTYSKVITITNETLYSFTDFNLLFTPVGQKFTFNGGEVTT
MEKVPTYMDEPSLLIRSNSPETVNT EGIVYKESSSGQTRFMIHHVNNTGKRVKMYVI
ATNNNP NPAVFEQQNMGFAGPTPYATVAGKLSIDKWFKSIQTGADQKKEYLQPGESKL

ILTELNKTPMKEGQVISLYSDAYS DYSLDYNVILVEENKDPFEALPLLVLDRDGVHN
RGTYPNATRIIKYDEHVGTKPARLPIGDNSSDPNLVGTDPMAYTDASNAGNFGVLYKI
TLTNVAPRTLISFNPRGGKYSGVALVNNQLVAIAEGNVAVSNSSEQSVLYRTGLTGES
VTILFSAAPGSNLPVNLLFTPLPSEK"

CDS complement(2380212..2381651)

/gene="clsA_1"

/locus_tag="EFAGFIKM_02028"

/EC_number="2.7.8.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P71040"

/codon_start=1

/transl_table=11

/product="Major cardiolipin synthase CIsA"

/db_xref="COG:COG1502"

/translation="MVTILLSLVMIIINILLSAVFLFFERRDIGYTWAWLMIFYFIPIL

GFIVYLFLGRNLKKKNFYGLSAEERNSLKLIVENQLVTLKEQRKENNPLLMKYADLIQ

LNLTSNAILTNDNEIFIFDDGQEKFDSLFIADKEAKKEINIQYYIIQPDSLGGKKLRD

ELTIKAKEGVKVRVLYDEIGSKKLSLKFFRELISAGGEVEVFFPSLIRPLNFRMNNRN

HRKLCIIDGEIAYIGGFNLGNEYLGMDDKFGYWRDTHFKMHGDAVNHIQGRFILDWKH

ASKSDQVSYEQFSFNTARLDGSSPVQIVSSGPNSQVEHLKNMYIKLIVNAKKSVMYIQT

PYFIPDGTGFMACKIALLSGVDLRIMIPNKPDPHPVYWAYAGELLDYGAKILLYD

NGFLHAKTIVVDEEVASVGTMNIDSRFRLNFEVNAIVYDERVAKQLQELFHQDSQLS

TELTSDRYRNRSIIKFKEGISRLSPIL"

CDS complement(2381863..2382207)

/locus_tag="EFAGFIKM_02029"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAQIGNCNNTVSPA VND AVCTTISLSDTGGTPTIIYENSSTFL

VNGTILIIENNGVGASPTAALLIDGVQIPGFVAPGSSRSYTAPTINSISVIGAGAGTT

SIKIAFSLNYRF"

CDS complement(2382292..2382639)

/locus_tag="EFAGFIKM_02030"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNTRLAETTICGEFHINSATITEVLTLSASSTLNVHGTVSIYN
HKQSNSSVFLNIIHNEGTCSLPVLPGNTCAFSCAGMHIEVEIEKSLNNIASGTFGID
IYYQVLNEEEDDEE"

CDS complement(2382781..2383476)

/locus_tag="EFAGFIKM_02031"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISBth8"

/codon_start=1

/transl_table=11

/product="IS3 family transposase ISBth8"

/translation="MMAIHFENREFGYPRMTTALWEAGLNVNHKKVWRIMRELSIQSV
IRKKRKKSSYTPSVIYPNRLKRQFHATAPQQKMVTDITYISDGNSFVYLSVIQDLFNN
EIVAWQLSKRNDVQLVLDTVEQWTQKRDVSEAVLHSDQGFQYTSQAYNTRLEAFGVKG
SHSRKATCLDNACIESFFSHLKTEKLYLNQCNSEAEIRQAVEDYMYNRYRRFQAKLK
QRAPIEYRCALAA"

CDS complement(2383641..2383961)

/locus_tag="EFAGFIKM_02032"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAKKGQTFQTYTEEFKLNAVRSYVEGSSSYKVAEREGIRNCSQ
LKVWVKWKKGAEFDERKNSVPNPLKGRPRTAFGSVEEERDYLQAQVDYLLKKRYPNLV
KEKR"

CDS complement(2384123..2384602)

/locus_tag="EFAGFIKM_02033"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSNYHFEEKESFIVLGIGTDLKSDYTDYVGISKEKADFWSTVKE

DGSLDKLKSLATNDYIFAVNEAVNNQMMHYAGVMTEESLPEATRVIQFPKG EYLVVKG

EAETADALSNMLTGIAFGQVLPVEKDYAYVGGPNTTVEMGERNGVVYGEMWIPVVRN"

CDS 2384708..2385682

/locus_tag="EFAGFIKM_02034"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKVERINIITRYINNRAHFTISEIMREFNISRSTAIRDIREIE

AMGMPLVAEVGRDGGYFVMNNSLLPTVRFTDNEIKALFIAFMATRNNQLPYLKSRQSL

AEKLLGLISENQQDDLVLHLNQILLFEGTNPHNPDLLDLSLPHPTLEKLIQILLIERY

LLVTVQEENKTKSYPIVLLHLHHQKGHWIIEGFDLEEEKRRIVSVDNLIHVEAYPAKK

RLSTKKIVEQLKRNTQAEVINLVLELGPKAIAQFKKYHPLKFSIAYTNPYQTTALLKA

FMNVHNSEELTEITNWLLFLGEDIKVKEIPKEALNAVQERLSLYQMKQ"

CDS complement(2385854..2387083)

/gene="bcr_1"

/locus_tag="EFAGFIKM_02035"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P28246"

/codon_start=1

/transl_table=11

/product="Bicyclomycin resistance protein"

/translation="MAKSTNWNVFGLAILLGLFSTLGPFTIDMYLPAPFPEIAQNMNTT

ASLVQFSLTACLLGLGVGQLVMGPLSDAYGRRRPLLICMAAYIICSLACAFAPNIGLL

ILFRFTQGFAASAGIVISRAIARDLYSGHELTKEFFSLLLLVGNLGPLAAPIAGSGVLS

FTTWIGVFICLSFLGIFLLIMTKWSLKETHPVEKRMVPDFKQQLGNYRMLLRDRKFVG

YMLAQGIMTAGVFAYVAGTPFIYQNIYGVTPTVFAILFASNGISLIIGSQIVGRLAKR

IPEQTLLLSGLWLAIIASVAALVVTLVHGPLFALVIPLFFFVCSIGITSTAAFPLAME
SQAKMAGSAAALLGVVPFLLGALVAPLVGIAGEDTAVPLGLTLLMTSIIAIVTYFLFV
KNVPQHPTPNHAQSNADF"

CDS complement(2387253..2387885)

/gene="yodC_1"

/locus_tag="EFAGFIKM_02036"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P81102"

/codon_start=1

/transl_table=11

/product="Putative NAD(P)H nitroreductase YodC"

/db_xref="COG:COG0778"

/translation="MNALTKDFSEVLHGRRTIKKYDPNYKISREEIEMLEDAALAPS

AFNLQPWRFVIESDQGKEDLLEIAPFNFSQINTSSAVIAVFGDLNFDVSAEEIYKET

ADLGYITQEIKDKMLAMVVPMYNQFSMDKKRESVLLDGGVSMQFMLTAHAHGYATNP

MSGFNKEKIAAVLGLDPDRYVPILLISIGKAASDARPPVRLPISQITEWK"

CDS complement(2387928..2388521)

/gene="betI_1"

/locus_tag="EFAGFIKM_02037"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00768"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator BetI"

/translation="MTRVSKNPQERKNEILTVAMELFNSNGYENTSVSEIVRKVGVSQ

GTFYNYFQSKEDVLNAACERTLASRLEAINHLVENCELNAREKLIRIFMDATPDEQDE

DVFEYLHKESNSTLHQKWIVIEINALIPHIKKIVRQGAEEGEFLAQPELKAEFLLVG

AAFWLDRGVFTWNEQEYLERKNALNGIIDQLLAVNKQ"

CDS 2388648..2389829

/gene="mdtL"

/locus_tag="EFAGFIKM_02038"

/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01530"
/codon_start=1
/transl_table=11
/product="Multidrug resistance protein MdtL"
/translation="MNKRLLFILGISAAIVSLAQSLYIPLLPDLQQLNTSLHLVNL
TVTLFTVAMATMQIILGPIVDRNGRKKILVPGIIIVYIATIGCMFSGSIEMLLIFRVI
QGIGASSVPLVAATMIGDVFEGKERGESMATYQMILGISPAIGPLIGGIIGSKFGYTG
TFGFAAISALLILIAAIFMLPETKPVNIKPVGTLGLKLSFGKILGNKTGVVLLSGFI
MYDVFYTFIVFLPTILQTKYALGAASIGFFSLALMIFNLVGSKMSGSLQAQIGSVRTL
FWAGIMTILSLVIFIFAADYSLIVLLLSLMLTGFMGLATPVMPTLLSSEFVEERATA
MGVYNFVRYLGMATAPLIGSFLFPLGNIQLLIGITALLVVMVVFVINRLLPVKKA EVS
N"

CDS complement(2389976..2391199)

/gene="tylCV_1"
/locus_tag="EFAGFIKM_02039"
/EC_number="2.4.1.318"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9XC67"
/codon_start=1
/transl_table=11
/product="Demethylactenocin mycarosyltransferase"
/translation="MARVLVVITPAEGHVNPSLGLVTQLIDNGEEVIYVCTEEYRSRI
EQTGAQIITYFPFPQDAFSHDPVLKPQEYKHSYQFIYMMVSGIIRRIIPNVLQVVEDQK
FDYMIFDSLMGWGGTILAEKLGIPAVCSIASFAFVEPLGSSSVLNETETKELYEATMK
ITTELAEEAFQVSIPAMEEIPAHAGQLKLVYTSRYFQPQAEKLDDRFIFTGPSIITRQD
APTFSFEVLRERYPQTVYIAMGTILNKNLDFYQLCFEALGDLPVNVVLSSGKYTDMTP
LANQVPPNFIVKPYIAQLDMLQHTDVFITHAGMNSTSEALYYNVPMVMIPLTSDQPLV
ANRVQELGAGITLNKHNL SATDLREALTEVLHNSQYRRQAYLIGESLRQAGGYKRAAE
MIMGHMGSERELTKF"

CDS complement(2391270..2392634)

/gene="bmr3_1"

/locus_tag="EFAGFIKM_02040"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P96712"
/codon_start=1
/transl_table=11
/product="Multidrug resistance protein 3"
/translation="MLVLATVAFEGLAITTIAAKMAQSLEGIHLYGWIFS AFLLSQLI
GTLVMGQQVDKRGVFTSMLVSFSV FVLGTVVSAISFDMHMLIAGRALQGFGAGALITC
VYTCVTLHYPDTLRTQILAAFSLAFVLPTLIGPYAAGLIASYISWRYVFWIVLPLIGI
ALSLTFRSFRNLQLQQDLSGPARATDSKIMYAILLAVGTG LLLTGLGMITDWRGILLT
LAGLVIMITPMRKLLPVGTF SVKKGLPATLVSRGLYVACYFTTESFVILALTEVKGLS
ADLAGLIVAAGSLSWSA AAWLQAKLDARDQGRARKGRVMTGIGIMIVGTALVILALIL
TDGGIILILLSQMITGFGVGLANPTTAAIALQHALPRKEGEMSANLQFVDSFYMGVSI
GVGGALIALSETLQWGISTGVLIVLTQLLWVLLSFLASLRITKLVHQEHHPINQVKD
NISM"

CDS complement(2392831..2393118)

/locus_tag="EFAGFIKM_02041"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MISFVISDQAIDLFKNEWEEEDQYVRIYAKYVGGGSDAFTIGI
NASATPVPDPALVQSIGGFHFFVEKTD AWILEDELLQIDCNENGIFSSKISY"

CDS complement(2393140..2393499)

/locus_tag="EFAGFIKM_02042"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O67709"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/db_xref="COG:COG0316"
/translation="MII EVSDTASDKIVEILSGADIQNAFLRVGVDEGGCSGLSYTLI

VDEQQAEDTVLNKKQFKILVHANSIPYIDGLEIDYEESGMLGGFTMNNPNNAKVSCGC

GASFRMANYRGEVKKCD"

CDS complement(2393849..2395207)

/gene="ycaD_2"

/locus_tag="EFAGFIKM_02043"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01149"

/codon_start=1

/transl_table=11

/product="putative MFS-type transporter YcaD"

/translation="MSSNHQSIFSPRYFALSIGIILSVMAVGFEGLSVTTIAPSIAGD

LNGLSLFGWIFSTYLLAQIIGTLVVGRIIDKRGPAAPFTFALLLFIVGLIAAATAGDM

YTMIGSRALQGLGAGAMMTCVYTAISLSYPDELRAKILGAFGTAYVLPSMLGPYVAGV

IADQWSWRFVFWGILPVLVVSALLSLPAFRKLKVQKTGGDSGSSSTWMALLLTLGTGI

FLVGLSRLPSIMGFVLVIIGFVLMIFPLRKLLPKGTLTLRRGMPAILATRGLFFAAYT

STQNFLVLALIDVKGITPSQAGLIVASAALSWCIIAYLQGRWDAADQSGRHMRIILG

VLLLAIGIAIVFWVPVTVTIAVIGQIIAGVGIGLAHPISGVVAFSQTGEEGVGQTSA

NLQFADSFTPGVVIGIGGSILVVCQAGGMSLQSGLIVAMGFHLLIVTSIIASTRISP

RG"

CDS 2395373..2396032

/locus_tag="EFAGFIKM_02044"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSGNQTKKDASTSTRRAIINLLKERGGMDVMALSTQFSLSGMAI

RQHNLNALKGEGLVTTVEEARPMGRPTKLWILTPAANRFFPSGYSDLSVSLINSMKEAF

GTEGLDKLLDVRNKNMQEQYLQHLGDASDVREKLEKLAEIRTNEGYPMAEVQEQQDDGSL

LLIEKHCPICEAAVCTGLCKNELHLFKTVLGDNVHIERGEYILAGGRNCVYTVRQNK

S"

CDS 2396233..2396634

/locus_tag="EFAGFIKM_02045"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSQKIWMNLPVKDVVKSTTFFNEIGFHGENVGNERAQLVIGSTT
ILLFPDATFEKFTGAKTADTSHSAEVIFSIGADSREEVDAFIEKVELAGGTIFGKPGE
IDGWMYGAGFADLDGHRWNLLYMDESKMPKR"

CDS complement(2396664..2397875)

/gene="sotB_1"

/locus_tag="EFAGFIKM_02046"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00517"

/codon_start=1

/transl_table=11

/product="sugar efflux transporter"

/translation="MLTGISLNPWHMTTKRNLHLLVFILTFGVFSILNTEMGVIGILPL
IAEHYEVSISTAGLIVSLFALAVAVSGPILPLLFSGMNRKHVMLFVLGIFIVGSLVSA
ITSNFTVLVIARVVPAFFHPVYCSLAFTVAAASVPKEEAPKAVAKVFVGVSAGMVLGV
PLSSLIATSTSLFYAMLFFAAVTIVAFVATLLFVPSMPVTKRISMGTHLYVLRRSVMW
LSIVGVIFMNGAVFGVYSYLAFLKTVTRYDWNTASVLLFLYGLANMVGNMIAGKLLA
NFPLRTIKMYPIALITVYILLFTFGQFSVPTAFLIFIWGILGGIGGNITQYWWVSAAP
EAPELSNGIFLTSSNLGTTLGASVCGLIVTGISTQYIVVGGIVFLIFSIVTNYFRISM
TGRFEGFKVGG"

CDS complement(2397832..2398689)

/gene="hcaB_1"

/locus_tag="EFAGFIKM_02047"

/EC_number="1.3.1.87"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01647"

/codon_start=1

/transl_table=11

/product="3-phenylpropionate-dihydrodiol/cinnamic

acid-dihydrodiol dehydrogenase"

/translation="MKGMIDMDKKKWWFITGTGRGMGTTIAKAALTAGHKVVATGRNP
DAVVRAIGESENVMVVSLDVCEPADAHSVKAALIERFGAIDVLVNNAAHFCGGYFEEL
TPDQIEHQLQVALVGSMLHVTRAILPVMRNQRSGHVISISSGAGISGFENSAKAF
ALEGWMEALAPEVAPFGIHTTIVNPGFFRTEFLTDASSTFAKPSIEDYDDRRAGHMEF
FNNQNGQQPGDPKKLAKALLKIANEAQPPQRFIAGADAIDIAEQKIANLQTEINAYRD
LSKSMAYDN"

CDS 2398827..2399717

/gene="oxyR_2"

/locus_tag="EFAGFIKM_02048"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ACQ4"

/codon_start=1

/transl_table=11

/product="Hydrogen peroxide-inducible genes activator"

/translation="MEIRVLRVFLTVAREGSITRAADFLHVTQPTLSRQLKDLEQELG
KKLFIRSSYSIILTDEGMLLRNRAEEIVGMVDKLEAEFESMEETISGDIYIGGGETEA
MKQIARVAKDVQNKYPNIRYHLYSGNEDDVTERLDKGLLDFGILIQPADVSKYNYINF
SDKDVWGVVMRKESPLASKHTIRSTDLLHVPLICSRQSMKQTFSKNEFADWFGEDFDK
LNWVTYTNLAYNAAIMVEEGIGYALTLDKIVNTSSESDLCFRPLEPRLESGLNIVWKK
HQVFSTAADLFLKEIQAKIV"

CDS complement(2399721..2400608)

/gene="rhaS_12"

/locus_tag="EFAGFIKM_02049"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MVKQLYEDILYSDFSFPYIMYHTRHTSIPPGRGFNDLHWHEDL
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HVDSAMEKNYVLPYTNSSLVSLVIKKDSEWETQILDMLWGMRETFAEKKWGWYEIS

IKTVQLWFLNISIPSGETPRSEKRQQRQLQLMLSFIHQNYAHPVTLREIADVAHL
SISECTRCFKKTAHMTPEYLYNIRIKKSKDLLSTNDTITEIAEKVGFNVNHFHFIQS
FKKHEERTPKFRCSPHPV"

CDS 2400764..2401696

/locus_tag="EFAGFIKM_02050"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKENKLSLLFHPYVLLFIAILSVSVSSIMIKSSDTPTAIAGMYR

LYISAIIMLPFIPWKTIRFLKMNSKDWSTVFLAGLLGLYFLFWMESLVYTSVASSMV

ILALQPLFVMIGSYFMFKERASIPTILCLITALFGSVIIAWGDIGVSREALIGDGLSL

IGTILVSAYMLVGQKVSRIKIDANIYSVAVFIIGGSVLLVYSLNNFSLTHYDSSDWMY

FLLLAIIPTIFGQYIFNLLLKSIGATTVSVGIIGEPVLAIMLAYLMLGETISAFQFVG

GLITLLGMLMYFGLKSYHVQLSKFLRFNRFRKLG"

CDS complement(2401733..2402416)

/gene="tetR"

/locus_tag="EFAGFIKM_02051"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P04483"

/codon_start=1

/transl_table=11

/product="Tetracycline repressor protein class B from
transposon Tn10"

/translation="MKKQQPQISEDKILEISWELLGEEGIEKFSMRRADKLGIQAPS

LYWYFKSKQTLYQRLANQISKIILDEFHTEGDWKEQMEGLAVTVRSVLSRYPCSTQLM

MMTLPHEPDMIRFTNRMLLCMESTPLEQEQLQAVLTLVNYVFYVLDDYQHQRNISA

VLKDQESFQGEEMIQLLDSMSEKEAGLFSRMYKNGLFVMTDGAFAFGLKLILLGIE

QVIKKPTEK"

CDS 2402553..2403905

/gene="mepA_1"

/locus_tag="EFAGFIKM_02052"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7A7N0"
/codon_start=1
/transl_table=11
/product="Multidrug export protein MepA"
/translation="MDAENLHYFEKAPIAKAVAHFAVPMMLGTSM SVIYSILNAYFLG
TLGNTAMLTALALTPLFAVIMALGNLIGSGT FISRLLGEEKVDDLKHVSSFAFYS
SLVLGIIVMAVGLPLIEPIVHGLGATPESFGFTKEYVTIMLMGSPFVILFFTLENIVR
SEGSAMTSMTGMILSVVINIILDALFIFVFHWGVIGVASATVISNLVASAFYAYHMSY
KSQFLT VSLKWFKVTKDILSNVFKIGVPVFM SVFLGAMSLILNLFVEYGDQAVAGY
GISSRLLQFPEFILMGLCEGVPLIAFSFTANKLRMKQTIGFTIKAILGLAVLFGVIV
YLISDHLIGLFTTDPQLIEMGSYILHVTFLSLFITGMTSLFMGIFQATAQGTAAFVMS
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CDS complement(2404003..2405019)

/locus_tag="EFAGFIKM_02053"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MFNWKKRYISVIVAILLMVGAGLYIVDQSDFDMEEQTIEIQSPQ
GKLTGTLTLP RNHSGKLGLVLFHGDGSIDSTQGEGYKPLWERLASIGYASLSLDKRG
IGGSEGNWLDQSMDDR VVEAQQAIAWAKEQSIIDDSKIGVWGASQAGWVIPKLAGEH
LAFSILVSPAINWLEQGEYNTRSRMAKDGHSTEEIQNQVDYENQIKEILKKHGT YEEY
TKIAREDDLISKERWNFIKKNFASDATADLHHFKTPVLLLLGEDDVNVDIVDTEQAYR
KGIQPSSLLHV KIFSNTEHSMLPTS IAGSEWKQSLRFLFAPRSITVDGYMDEIEHMLT
AFSL"

CDS complement(2405012..2405656)

/gene="mshD_1"
/locus_tag="EFAGFIKM_02054"
/EC_number="2.3.1.189"
/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01698"

/codon_start=1

/transl_table=11

/product="Mycothiol acetyltransferase"

/translation="MTTSIQIEPVCPPQFHQAVAELMAYGFGHKFKITSLSITDLAYV

FEQLLNYPPEQSTLRRIARENEEIVGTMCLKWKEADNRAAITSVRANPHWWSHCNRV

GMWKLLQLITGLHLLKHTPKLGECYVEDLVVHPQHQQKGIGTQLLQWAQKYMLQSKSM

SSLSLHVASQNHQAIQLYERYQFRKQYSTNSFLTGLLLGENQWHYMIYKGDSYV"

CDS complement(2405669..2406436)

/locus_tag="EFAGFIKM_02055"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSDEITISELAKLMKVSQHQRIFEEKGVLPAYIAENQYRMYG

VDEIYRLSHILLRLKMGSLVQMIKECLSNLTTVQITSLFRQALADTEAAITQLQQTKH

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FEADIHAYDETDTVGIYTQKEGANDLVLPBGKYLSRHVVYQIEAELKEHINEFYAYA

EDQGYPHYHGPLIMVEKSYLSLFTPEKLHYELLQMID"

CDS complement(2406579..2407556)

/locus_tag="EFAGFIKM_02056"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAEAVDVTTTGTGKRKKRYLWLKIIGGIVGALVLFMGITFVVHT

ISNGAEKKKIESYGQYVNVGKNNMNSIQGSGETIVLLPGQGTPSPVLDKLLIDEL

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TYVNTYPDEVSAFVGIDSSVPNQPGMDVKLPLNLMKFFQKSGLMRVLNKVSGDSYASL

DYDEHTKEQMKLISNQVSTNPTLVNELKHLGSNFKNGEKLTPSDLPVLLFVQSNNEK

NPQWIPLHEAQAKQSAQGMIPMEGSHYLHHTKYKEIAEEFKSYMKQIQ"

CDS complement(2407721..2409019)

/locus_tag="EFAGFIKM_02057"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A0A2A5K5H4"
/codon_start=1
/transl_table=11
/product="Nucleobase transporter PlAzg1"
/translation="MDKWFKLKERGTTIPTETIAGVTTFFTMVYIVIVNPGILSSTGM
DFNGVFIATVLAIVGTLMGIWSNYPVIAIPGMGLNAFFAYSVVAGYGVSWQVALGA
VFIAGILFIILSLTSFRYMLLDAIPASLKHAIAGIGLFIITVGLQNAGIADSESNL
ITIGNLAEPMAYLTIIGLIITVVLMAYNVKGYLEFIGMVVTAILAWIMGLFQMPESIVS
MPQGLASTALQLDLAGVFSNGLYTIIFTLLITLFDTTGTMLGVAEQAGLLKDGKFPR
SRGALLADAVGTTSGALLGTSPTSAYIESSTGVAAGGRTGLTAVTVSVLLALTFFTP
IVSVISSIPAITSPALIIVGYFMINVISIKIWDDLEEAFPAFLIIILTPLTHSIATGI
GVGFIFYPVLKLLRGKGKDVHPIFYIFAVLFFIQLVFLDH"

CDS 2409590..2410441

/gene="yvgN_1"
/locus_tag="EFAGFIKM_02058"
/EC_number="1.1.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32210"
/codon_start=1
/transl_table=11
/product="Glyoxal reductase"
/db_xref="COG:COG0656"
/translation="MQKVILNNGVEMPILGFGVFQIADANECEQSVMDAISAGYRLID
TAASYLNEEAVGRAIKRSGVARDELFTTKLVVQDTGYERTKQAFEKSLERLQLDYLD
LYLIHQPFQDVHGSWRAMEELYREGKVRAIGVSNFQPDRLIDLILQNEVTPAVNQVET
HPFNQQILTQFMKENNVQIESWAPFAEGKNDLFQNEVLLSIGEKYNKSVAQVVLRLW
TQREVVVIPKSVRKERIIENFNIFDFELSQADIESITALDTKQSLFFSHNDPEMVKWI
STRKLDI"

CDS complement(2410569..2415017)

/locus_tag="EFAGFIKM_02059"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRKGLACMVAWSLMASLVYPATAGAESVQGQAEVGNVQAKSLHF
SVPYTDLTGHWSQSAVTRLQDLNLLKGYTDGTFKPSQVISRAEFVMILDRAFGFTGNA
ATGSYVDMTSDDWYYDVMVRANGSGIIEGTDREHLSPQQPITRQDAAVMVDRAFQLSA
TSNEDSEGLKFEDADELSSYAKKALTYLVNENIIKGFQGKLNPKAPITRAETAELLSA
MIADVKSTPGTYESRVDGNLIIKSTDVTLKNMIVNGNLLLAEGIGEGSVVLQGVTVTG
SVIIKGGGSHSININNSKLKRVVVDKRGEVPRVAITEESNIQEMHVKQKSILEISSNS
LIDSMNIIHAEASQTQMDTKGTIQKLSVDAIDVVINGEKVIQGLRTSMVGEAQQPVSAQ
PGGSTNVTSTPTPSSPDGQSPSTPSNPAGEKPVPAITPHDQWELVWNDEFNGPSIDS
SKWTVQDTGLVYNNEMQYYSPDNTRITKDQNRSVLQIEAKKGPKNGKDYSSGKLISMG
KGDWTYGKVVVRAKLPIEKGMPAIWMMPTDEAHYGGWPASGEIDIMELIGGKESNNK
VYSTLHYDSVKPDGSHGHDQGSLLPKGETFADDYHDFQVEWLPGMIRFYVDGKLHHE
VTNWQTKAAGQPEYYTFPAPFDRPFYLILNLAVGGDWPGAPESNFTSEKMNVDFVRVY
TYKNLDIWPDVTTNPIEPAQQRDPQTNGNQIYNDRFAEGSADNGVPLQWKFITNADGA
GSVKVVTDEQKGKAAEVTIDASGTENYSVQLTQMMPYIKKNKKYKIQFDAKASANRTI
MSKLNQFEKSWTNYSGDNTFALTDDWQSYDYTFNMRDGTDNARFEFNLGLDDTTWWF
ANARLIEVGEADPLPVERNALPDGNFIYNGTFDQGKERLGFWSSSIQDSAAANISVNN
FSKFPIMERQLVVDVTQTNNDPQQVSVNQPDLEANTTYGFSLEDAKADTPRSIDIDV
VSSNGHTVQVHQGNLSLNQEMKFTGEIIIIGDGASIAQSELRLFGSSKGKVYVDNV
RLTKRGKPLSVNGYAHVPATEAWMMQGLQLEDSEGGKHVSMDQGDLLQYKIDVAHD
GVYVLSARMASGKSDSKVQFSIQDEQGTVAQSDLSLGDGGWQAYKTVYFPRVNLTA
GKPYVNFEGADYNTRWVDISQNKIQNSELTADLNHWEIIPNDLTASHDEGEGLTINL
PGTSEQWWDALLQQDQIKLDANKTYRLTFEASSSSPKSMQAVLSQNAGDFVKYFEEEV
ELTADQKSYSYITMGDTSDSAAMLAFGLGYPLSTGEHSIHINNVLQYEVNPNADQGG
QPAHVNLIPNGDFSKGKEGWFTHADGNAADLEMQVNNQQQLQAKIGHAGQHPWDRQVIN
EGFGIQQGFKYKLTFFAKAEKSRKLGLGIGWVDAAANYEWHGFFGARVDLTPEEQEFT
FTFDATEDSYANTRISFDLGNIDGEQDGNTTVSLSEVSLINLGPAN"

CDS complement(2415061..2415939)

/gene="ycjP_3"

/locus_tag="EFAGFIKM_02060"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77716"

/codon_start=1

/transl_table=11

/product="Inner membrane ABC transporter permease protein

YcjP"

/db_xref="COG:COG0395"

/translation="MYKTKGYRIFSIANYTFLGILSILCILPIIHILAVSFSSMAPA

SSNLVTFWPIGFTTDAYVKTFGNSNFINSILVSLKRTVIATIIGMVIMLITAFPLSKE

DISFKGRSLYTWFFVFTILFSGGLIPSYILIQKLGLMNTIWALILPGALSVWNVILMM

NFFRGLPKELAAAYLDGAGHIKTLILVYVPLSLPAIATLSLFTMVYQWNSWFDGMIY

MSDIKNYPLASLLQTIIVQQDLSKINVDPSMLENISQRTVRAAQIFIGALPILMVYPF

LQRFFVKGIVIGAVKE"

CDS complement(2415955..2416905)

/gene="yteP_13"

/locus_tag="EFAGFIKM_02061"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system

permease YteP"

/db_xref="COG:COG4209"

/translation="MKEHTLETPHKRRSTRVKQRWNMQRNWTLHMMLIPAVLLALVFQ

YIPMGGIVIAFQDFKPYLGFSESKWVGWDNFRYLFLYPDVGQVIWNTLVIAFFKIIAG

LFAPFLFAILLNEVRLTAFKRVSQTLVYLPHFLSWVILGGILLDILSPQGGMVNQLVV

AFGGEPFFLGDGTWFRITLILSDVWKEFGFGTIVFLASLSGINPALYAAEVDGANR

FKQTLHITIPALMPITIVLMTLSIGNILNAGFDQVFNLNPLVYDKGDIIDTFVYRLG

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CDS 2417052..2418761

/locus_tag="EFAGFIKM_02062"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MFTRLNVFTKITLLFVMLLILVLFLYTYSNRESVRVIEHEIQNN
TMNHLSTFADSVESNIYQLSLYGMSIGQDSSIQEYQRPDYKDIPYERVKVGSAILKEM
NLYNAASKWHSTITLYFPRMQKVISTDYAYIPYRDDEFKEPLSQSWTYADNQFIWYT
TDPTTAMARPGKARLITKISFPVHHLTALLNQNKLNKGDPMFHPDYGLISNSSGKE
TLNAILPSLKEAKLQASGGFSTTLNKTEYYVSYIQSKSLGWYYVDYVPMQQILKPITS
SRNLFYASIAVLIVMSVVVLYTLYRSVQLPLLQLVKGTNRLSTGDFSVRLHHSARNEF
SLLFARFNIMAQRIQELIENVYEEKLRSREATLKQLQSQINPHFLYNCLFYIKNMARM
KNEKAVVAMALNLGEYYRYITRSEKDQATLREELTMVKNYLEIQSLRLERMHFTIDVP
HDILDKTVPRLTLQPIIENAIHGLEPKSVDGEIKIYADCEDDVYTIIVEDSGLGMSE
KQLDHLRDNLLKPLDENMGCCTWNVHQRLSFLYGEGLSYDHSSMGGIKVNITWHDN
TDK"

CDS 2418773..2420413

/gene="rhaS_13"
/locus_tag="EFAGFIKM_02063"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaS"
/translation="MLQILLVDDERSVETLAETIPWESCGIGTVHEALSGAVALEIM
DNHDIDIVITDIRMPMSGIALITAIHEKWPHVQTILLSGHADFEYAKQAISQESFDY
LLKPVSDLEDLIESVQRLVHRIEKEWETAASHQRALHAFQDHLPLLQSTMLHELLTGKV
YDQKTLADKLDLLELPYSVGEDLGMLIIRMEKHLSDMAHGDLALMEYAICNIISEVMH
NHFHIWHTRDVHDYIVVLVSMKHSTTMSYSRSETPQTLLEQYAAQIQTNVQLYLKGAI
SISVSSWGKFPHEIGELYERTVMSMRKRMGQVQGLFVTASDETDANPLHTIRSLYQPP
TLISLLEAGRFEDVEQKIEHIFEELLHSNEHHDAESTFEVYFAIAGAFAYIIHKNGK
QISSLIPAESYRYFQAPSYSTAQQLQDWSVRTLHYIRDDAEQELRDNHSTIVRSVKSF
VDLHLAGDVSLPAIADHVHLHPVYLSKVYKAETGEALTAYVYRLRMEKAAYHLRTSTA

KVFEIAELVGYNNNTAYFIRVFKKFYDLTPQEYRENLPV"

CDS complement(2420570..2422216)

/locus_tag="EFAGFIKM_02064"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIGVLALSAALSGCSNGSDKKTESSTPATTLELKNGKYDPPVSI

TYLRPWGPDVKFKSGEDQDNNVHTKWAKEKLGIELKNQWISPSTNNAFETKLRLSLAS

NADMPDIISYRGEFNLVRELIESGKFVDAGELFDKYASDTWKA AVNEDPSVWYPYMQD

GKKIGIPILDYSYNGDPVMWIREDWMKKFNLEAPKTIDDLEVIMETFTNQDPDGNKQ

DTYGLTIGFKNWLNTWMSEAGWVFGAYGTMPNQWNLTADGKLEYSVTPGAKQALAKL

QSWMSKGYIP EEAGVYDETKAAEEFTAGKAGIVGPHWMP SWPLEDVKKNNPEAEYKA

YIPSGPNGQAGRHGTSNGNGVILINKDMKNPEAFFTYQNYLFDHYANPKEGDEF EHG

FAEGYDWVMVDGK PSTDASLTGGYAPEKYLTFTDGARIPNLSMTTLAKLASGEEATTP

FEKKIKSGVPV PMLDAAKIVLDQKDIVFNQMFTGAPSMTMQMNN DILTKMEKDTFSQI

VYGKTSVDAFDSFVEKWKSSGGDQITKEVNEWYDSVKSGK"

CDS complement(2422444..2423157)

/locus_tag="EFAGFIKM_02065"

/EC_number="3.2.1.73"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P23904"

/codon_start=1

/transl_table=11

/product="Beta-glucanase"

/translation="MKRKSWYTLAVTGVISLFFSVSAFAGYVFW EPLTYFNASTWQKA

DGYSNGNMFNCTWRANNVNFTSDGKLKLG LTSSAQNKFD CGEYRTTNTYGYGLYEVSM

KPAKNTGVVSSFFTYTGPAHGTQWDEIDIEFLGKDTTKVQFNYYTNGVGNHEKIINLG

FDASQGFHTYAFDWQPGHIKWYVDGVLKHTATSNIPKTPGKIMMNLWNGTGVDSWLGP

YNGANPLYAEYDWVKYTSN"

CDS complement(2423470..2424174)

/locus_tag="EFAGFIKM_02066"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKSLIIVVLISMLIVQGCVPEMRNDSNVEKKAMTSADEQLFK
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MKNTPFYAGAEGYLDILKLTIEAGADPAITNRYGGTALIPASEHGVDVVQELLTQT
SVDVDHVNQLGWTALLEAILNDGNARQQETIQLLIDHGADVNISSDRDGVSPLSHAKN
NGFKEIEDILVRAGAK"

CDS complement(2424185..2425693)

/locus_tag="EFAGFIKM_02067"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNSTTRKIATFLTITALGTAVFPLTANQVHAATYVTNIAATTTQ
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TDVNPNAWYAPYASKLVELGIMQANDGQFNPQTQVSDAELEQVVSAMQRDVKSVDHWW
MSEFYSENGTATRGETAVLLQTAHQAIPEQAQIKSVRSLNAILVTFDKPLTAANE
AFAKAQTDFAFSGGLTLTNMPRLKTGSIATYIVPTSVQDASEVYNLTYPKQDAGSFEG
SGTKINMTTVSQVTNDTFEIALQVNSVVDYGYIISAYSGGRGANAFVLNDQEQAGGK
TYQIISSMQARQVVITPEGDEPIVARYVPFTQSTDGKQEPKFRLEPQTLKSGVTYTV
SSDWANIENASFTAKSFDALVVASAQAVSETSIEVTLDDPGDELFSGRSVTLTSPSG
DVLATYKYSSRKATGVFDLTNDGKLTGTTYTINPVGDWSIASSVTLTLE"

CDS complement(2425813..2426505)

/gene="srrA_4"

/locus_tag="EFAGFIKM_02068"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9L524"

/codon_start=1

/transl_table=11

/product="Transcriptional regulatory protein SrrA"

/db_xref="COG:COG0745"

/translation="MANILIEDETTIAELERDYFELNGFSVDLCHTGDEGLKQALEG

DYNLIIVDLMLPGLDGFECRRIREVKEVPILVVS AKKEEIDKIRTFNLGVDDFITKP

FSPSELVARAKAHLTRYERLLGKNKPAEQDEIHIRGLHIDKGSRRVFNNGEEVAITTK

EFELLVFLASHPNRVFSKSDLFERIWGMDSTGDIATVTVHIRKLRGKLETPKNPEYI

ETVWGAGYRFTA"

CDS complement(2426512..2427981)

/gene="sasA_5"

/locus_tag="EFAGFIKM_02069"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"

/codon_start=1

/transl_table=11

/product="Adaptive-response sensory-kinase SasA"

/translation="MSIRIKMLLSFTGMLVISLLFILLTASLYTIAATGDLQSFRDIY

KVHYQINPLTEQGESIFQEMKFLAKNDPDDLQNKVLLREYDMKLRAEKSGLYIRRENS

QIFESLTFNQPELKQALPAYDLNNYQIRSTFNIGERFYAYAKFDFQYSDGERGSIFVI

RERSPFAELTRKLLPVMSFLLIGVLIANLLLFRWITRSFIKPLNQLRSSAEHIKDG

LSFKLQLNSNDEVGQLSEAFESMRNQLQRSYALRQQDEVNRKELISNISHDLRTPITN

IKGYIEGIRDGVANTPEKMESYVNIHSAVSMDKLVDELFLYSKLDLNQEPFLFKTV

DLADFLEDSIEELRYDLEDKGVALDWINQVSGPAMAAVDPEKLRKRTVVNVVDNALKYM

ENEHHRFEITLQADENWITMAFKDNGRGIPEEALPYIFERFYRAEQSRNSSTGGSGLG

LAIARQIIDGHGGFIWAESQPNDGTSIYIKLRLNEERN"

CDS 2428147..2428755

/gene="rhaR_11"

/locus_tag="EFAGFIKM_02070"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MKLDQTVFHRTDWEYILVLYRICSSDLEETSFSHQHFELSTGQS
PRLIELITRLWHVYNQRRGGISKFQTEMLFRDVLNETLICVDHRQNSCESDVLFEVST
YIQEYYDQSLTVASLAEQNNVNRNRLSYVFRRHAGMGPAEYVLKYRINMAQQMLLASD
AYVQQAIESVGIADPFYFSRVFKKQCGISPTEYRLKFINNPS"

CDS 2428835..2429173

/locus_tag="EFAGFIKM_02071"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHYQAIKLNEEF SKLNDLWSPKLIGEMNDYQFKIVKIAGDFEWH
VHEETDKLFFVLEGEMIIDFRDGQVKISKGEMCIVPKGVEIKPSAEKECHIMLMEPGS
EVNNGGTAE"

CDS complement(2429304..2430440)

/locus_tag="EFAGFIKM_02072"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKTYDVFPEPIGAYTVGRTQMDFEYTASDYSKRELTA FVYPSD
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VCGGGGSPEWGTVLCTDLASMGYVVVSIGHQNSTMYKRKDGRLFNVSKNFSDVITAFG
EDSEMLALAGKMEMRPDDETA IEMCRNVLALPILSKITEFSELQAEDVRYVADYLYKV
DSGELNSIFKGRLLLDIGMGIIGHSYGGPTTAMVCRDDRFTCGIGLDSGAFGLLDSD
LKKPFLFLFCEPNYNMNAVIGANNSMKTYFVSVDRAHLDYCDIVFTSVNEELRGERD
AMEMRNIVTNYAKNFFDHYILQKAASVESLAYDGVELIRKTSNK"

CDS complement(2430437..2431096)

/locus_tag="EFAGFIKM_02073"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPKNTFFRLDEARREEISNSAMHLFVDNLYEDITMKMVLDSLSM
HPGTFYRYFEDKDDLYCHLIRNVTQKRAAYFSNSNEDSLYSYFLTGLFGNVNGMVTEP
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SFMFESMQLNLILFFREFDIKDSELQHKISKYFAEFMGHGLLEDHKYSEMVSCLKGER
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CDS complement(2431309..2432391)

/locus_tag="EFAGFIKM_02074"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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AAELMIRLGLIDKLVGVAALFGSPEDIADEFKQIPVLAEGYVGKEVTIGATPDLVVG
RGGLFEDADWGVGTVSSLNDMGIKTYVQSTSVPDASLDSLYQDITELGEIFNVQANAA
AYIETLKARENALSARASAETINYASFSDNGDGTIGIYNGNGDTFIESAMSLINMHNH
LINETGTLSEKLEINPDAMIISRYAGGIDPEQTIEKLLANKQVQNINAVKNKKIYI
IDFNNFWGYGDSIFTGVEGLADDLGL"

CDS complement(2432650..2434923)

/gene="bglB_1"

/locus_tag="EFAGFIKM_02075"

/EC_number="3.2.1.21"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P14002"

/codon_start=1

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/db_xref="COG:COG1472"

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LLLPGVNMKRTPLGGRNFEYSEDPLYTGELGAAFINGIQSEGVGASVKHFAGNNQE
FEKMVTSSSEIDERTLREIYLSAFERIIKSDPWTVMCSYNLLNGTYTSENEHLLHDIL

REEWGYEGVVLSDWTAVNDRIRGLKAGLDLEMPGPANYNAKAIEAVQNGSLSEEQLD
RSVGRILKLVERVTGKKDMDSSPDSYHTLARKAAAESIVLLKNENAILPLRQESISS
IAVIGRFAKKPRIQGAGSAKVTPTTRVDIPWDEIKKLAGDAMTMNYAEGYPEDDSINDE
LIKESVSLAMNSDVAVLVFGQPEYAESEMHDQLQGIDLPEHQVKLILAVAAVQPKCIVV
TSSGSALAMRPWVQHVPQVIHSWLSGQGMGKVIADVLFQTNPSGKLSETFPVKLSDN
PSHMRIRGENGKLYYREGLFVGYYDRKELAPQFPFGHGLSYTSFSYTDLEVAQHTT
GVTVSFQLKNTGKRKGKEVVQLYVHDEECTWTRPEKELKAFKVELEPGEERKITFEL
EERDFSYYNTKYNRWVAETGFFQISLGSSSKDLRITERLHCDFGKEEITFQKFSLLSE
WMSDPAAKKELEHCLNEMNEHVTDKVYLNEEFVGFWADFPMIKVFQMFGQQWMNERSP
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CDS complement(2434943..2436175)

/gene="licC"

/locus_tag="EFAGFIKM_02076"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P46317"

/codon_start=1

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/db_xref="COG:COG1455"

/translation="MKRFMKWMTDSFAPRLEAFTNNIWVSSIQEAIMVAIPMIFIGSI

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PEFIMDWFDLVPIALVLATGWVLVYQLHFDIFGLIVNVFEPINAVGQSLTGFLLFNF

IGVVLYSFGVSPWVMTPIWYAIWIPAIEENAALVAAGQDPVNINTFETFFSGWLIGIGG

MGATLPLVWVFLMARSKKLKS VGKATIIPSLFNINEPVVYGAPIAFNP LL MVP MWINS

LITPMIVYLALDWGWVRIPSQIFQLWYTPIGLSTYIMSGLNGLILLAVVLVIVFIVWF

PFFKLYDAQELKKEQEQN"

CDS complement(2436377..2438836)

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/locus_tag="EFAGFIKM_02077"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1
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/translation="MKLFVNSVKHIDFHWHEVEVYVLHGSIIIMYLDQQQYTLHEDD
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TYIDLHYNEKITLQDMAHSEHLSLHYFSHFFTDKIGIPFQKYLTIRLEKAQAQLAAN
DKNISEIALDCGFANVKLFNKYFKEYGCTPGSYREDSRTPELHQLNVNRKPKTYEES
SSGDYYEMETLNAIGLLYRYLDVKVDADQDTLPVPSVHLSDQTYIEIRADQTSSVYEK
HWNMTMTAGRAIEGLREDWRKQLSALKGKIPFQYIRFHGIFNDELMVYSENEQGTPLY
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PAFYKESIELMRQKMNASSYGHVELHVTEWNFSLYDRNLLHDTMFMAPFVIYHTMNTL
GDVKAMAFWSFTDVFEESIVPASPFYGGFGLINRDGLKKPSYYAFELMQKLGDELMVK
GDGYVGTRKGDGSMQFLFYHYVHVDQLFASGDWSELSSSTRYDVFEKGSKAYELTSL
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WHREILLPPHGVMLLILDRQY"

CDS complement(2439042..2439923)

/gene="pdxS"
/locus_tag="EFAGFIKM_02078"
/EC_number="4.3.3.6"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37527"
/codon_start=1
/transl_table=11
/product="Pyridoxal 5'-phosphate synthase subunit PdxS"
/db_xref="COG:COG0214"
/translation="MQTGTDRVKRGMAEMQKGGVIMDMNAEQAKIAEAAGATAVMAL
ERVPSDIRAAGGVARMADPTIVEEVMKVVSIPVMAKARIGHYIEAKVLESLGVDYLDE
SEVLTPADEVFHIDKHEFTVPFVCGAKDLGEALRRIGEGASMIRTKGEPGTGNIVEAV
RHMRLINSQLRKVQNMSKDELYAEAKNLGVAYELLREVENHENGKLPVVNFAAGGVATPA

DAALMMHLGADGVFVGSGIFKSDSPEKFARAIVEATTHYTDYKLIAEVSKNLGAPMKG

IEISKLAPEERMSNRGW"

CDS 2440074..2441564

/gene="gabR_2"

/locus_tag="EFAGFIKM_02079"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94426"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulatory protein

GabR"

/db_xref="COG:COG1167"

/translation="MQFHVAYSSYLNRKYTKMKALYHAIRDAIHEGNLIHGEKLPSTR

ELAATYHISRGTVNQVYDTLTAQGYIHSEHGRGTFVAYQLDLNNNASTEKACTHHLSA

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IRQREHHLKTTSAMVSSTGDPKLREAIAAYLRRMRGIQVDPDHIAVTAGSMQAIALLT

QLLADPGDYVVTESPCYVGISKAILAAGAKLIEANLDGQGQVVPQDWEARMFLVTPSRQ

FPTGEMLSLERRQTLTDWAQRNDAMIVEDDYDSEFRYRGMHVEPLKTLDKAGRVIYLG

SFTKTLPLEVRLGYVVLPTLADTFRKAQALYEPRPVNLIEQRALAAFMTSGQYERHL

RRMNRLYSRKFHLLKLLNKQLSTWFDWVENEAGLHVFGWWRGNVTTYEAFRESARSQ

GVVYSEVSSSTSVGMKYGIYLSFAHLSDEQLQEGVSRLKNAVTTAL"

CDS 2441624..2443645

/gene="yoaA_2"

/locus_tag="EFAGFIKM_02080"

/EC_number="3.6.4.12"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P76257"

/codon_start=1

/transl_table=11

/product="putative ATP-dependent DNA helicase YoaA"

/db_xref="COG:COG1199"

/translation="MNWLNELYKMNKQEPDKEIERSLVNAIFRIYDRFPRIGLRERIG

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EIDERADIKAGVSDAEWSHVSVNDCKFERCHHKNACLFYDMRAKLNKAHEIDFIIVN
QDLLIRDLMKKKEGTKSIIESEQPALIVIDEAHNLEAKVRDARTLEFTYRGICRILDNA
VQLLTQSGDKSLFSQSKFIKNCAERIFKQVNADLLHHAKQDNDRIKVSEIKGIPLNQ
VLNDLKDSLRLSILTSRHEREIDDAFEAINGLITLINVLSEIEDNYLLWASSPLRVT
TISICPKDISQFLKYALFNGKVPVILTSATLCQGGDTLEEQYSYMTSLGYKGDFLER
QPSPFDYTNHATMYISNKIPYYQHDQREIYLEAAYKELVQLCNLTQGRTIVLFSAKED
MKYIHKKLISRANEYTWAVHVQKEGSSQDSVIAEFRKSKGVLLGTGVFWEGVNIEGSD
LSQVIIFRLPFPVPSDPVYEEKSSVTENPFMEVFVPDMLLRQRGTGRLIRSETDLGI
LSILDSRLSEAAKKSIRGQVLDTLPPFKKVTEDFAVLEKQVQTKGIRRTD"

CDS 2443792..2444319

/locus_tag="EFAGFIKM_02081"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVERPTTEEYAAYYEGYIQLVPEGNIIERLELQANIPTLLSSL

TEEQANYRYAEGKWSVKEVIGHLLDNERIMSSRLLRIARGDQANHPGYDQDVLMTQTHP

FNAYTLADLSEYAVTRRSTILMLRRLTPEAWLCRGIVSDNTASARSIAFVMAGHELH

HCSVLRDRYSLDLKL"

CDS complement(2444398..2445339)

/locus_tag="EFAGFIKM_02082"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNNQLTNGGIWNDSSGQPIHAHGGHMLFHDDYYYWYGEDRRDDI

YVSCYRSKDLFNWEFRNHILTTSTPAAPIRVRTNLALVNDKGGKVNLERPKVLFNTVT

KKFVLWVHYENGNNYNDAACSIATSDSPDSHFVYHGSFNPYGYMSRDCTLFQDDDGTA

YFISAARDNADLHIYRLQKDYLNVESLVGKLWQGEYREAPAVFKRKGKYYMVTSFCTG

WAPNQGKYAMANTMDGPWGMLSDFGDETTYQTQPAFVLKRSAAEYLYFADRWNGSDYF

QSSYVVLPIEFNGDIPILNDYSTLSLREDAHLIHFER"

CDS complement(2445370..2447085)

/locus_tag="EFAGFIKM_02083"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIKGKSWMAIVIALMLLIVHLTSSAQTVHAAGEETHIAATLFLV

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SSGGFGEMIQQTSTDDITYGNDKVLSYTDHPDLANSKFEGINILYHAPTNKFVFWAH

YENSTDYTLARVSVASATPGEDFTFHKSFRPEGNQSRDISIFKDDDDSDAYLISTANN

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SATSIDGDWSELRTIGNTSTFSAQSGSVMRVKPDGMNNVVMVAYRWMFGWAGTQNGTT

EERLLPVWFSDGYAFYDYFDQVLYNTSDDVVPVQNGKLLSQGKPATAQTATGTNPAS

YANDGNYQTEWVGTSWPHWWKVDLGSVQQLNNVQISWWMQKGSEGYKYKIETSTD

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GSDTN"

CDS complement(2447157..2448842)

/gene="lipO_6"

/locus_tag="EFAGFIKM_02084"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37966"

/codon_start=1

/transl_table=11

/product="Lipoprotein LipO"

/db_xref="COG:COG1653"

/translation="MKKRTDLWKMVSMVMSAALVAGCNKGESASETAPASVLKDGKY

DPPFTITIAKQQDENAGKYINGETLNDNVLTRWGEQNLGIKIQTLLGGDASQYNTKL

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PVVREGKVYGMIAPNLTEGEVMLIRQDWLDRLKLKAPTTIDEFEQVIAAFTNEDPDG

NGKKDITYGFTFSGKDSYNTGWVSDPVMIFSFTGKHLPRQWHNDNGKLTYGTVAPGNK

EALAKLRDWYAKGYLNKELATQGAWDALSDFTGKAGIIIGRPWLYDSVKDVEKNVDG
AKISAYPTIQGVNGDKTYQSAQLNDGVFMFNKDFQNMEAFFLYDKMYDAAFSTGEFK
YGYAQGYDYDIVNDKVTDFPTKFNTPLEAVQGVGKMAFTKNTPSVDGPGQSYDLANG
VKADTGVLISASKDQTTQDGYRISYENRDVLLPNEFNGPPTPTMQNVWEQLTTMEQE
TFTKIIYGNEPLEAFDTFVKQWHEKGGDTVIEEVNEWYNQASETDVMTLMNLK"

CDS complement(2449004..2449873)

/gene="ycjP_4"

/locus_tag="EFAGFIKM_02085"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77716"

/codon_start=1

/transl_table=11

/product="Inner membrane ABC transporter permease protein

YcjP"

/db_xref="COG:COG0395"

/translation="MYHKTTGYKVFSYFNAYFAMILAGLACFLPLLHLLAQSLSSKAAI

SGNMVSFWPVGVFNVDAYIKTFNNSNFNGAMLTISITRTLGLTTISMFILTCAGYALSKE

FRGRNVLMWFFIFTMLFSGGLIPSYILITALGLKDTIWALVLPGAFGAYNLILLVNNFF

KTIPKALEEAAFIDGASFFVILSKIYLPPLSLPGIATVSLFIMVGHWNWSWFDGILYMSD

ASKYPLASFLQTVVVQSNMQNMAMSQSEVAAMSEQSIKAAQIFVSTLPIILVYPFLQR

YFVKGIVLGAVKE"

CDS complement(2449892..2450686)

/gene="yteP_14"

/locus_tag="EFAGFIKM_02086"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system

permease YteP"

/db_xref="COG:COG4209"

/translation="MAFQDYKPWLGITGSRWIGLDNFERIFQYKEATQAIVNTLIIAV

SKIIVGIIVPIVMAILLSEIRNMGIKKSVQTLVYLPHFLSWVTVAGLMIDILGLDGGI
NHILTQIFGNDPIYFLGDPDLFRFTVVISDVWKSFGFGMIVYLATIAGINPSYEEAAE
IDGATRRQQIRYVTLPSMLPMIIVISTLSLGNILDAGFDQVFNLNPLVYSTGDIIDT
YVYRSSLNGQYGFGTAVGLFKSGISLILIVVSYRLAYKYANYKIF"

CDS 2451094..2452803

/locus_tag="EFAGFIKM_02087"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIRKMYMKRFIYFFVFFLLTSLFFVMNRLSSKTLEENLIGAS

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IQKSGQNEPTQYVVGKLN TDYLNLLKAVNNDSSNAFFWFNSHQLWSEKEVDNDLL

KAVTEMISPQPEITLKYDYHTKSDDYVLSRYIESIDAYLITYTQTNDFLQPIDRNRK

VFFASILAVFTLGLVVIFTFYRNYYRNIRLLERKFSQVEQGNHNTRITENTDREFYSL

FRSFNHMVTEIQDLFVSLKTETELRRSAELQQLQAQINPHFLYNSLFFIMSVAQFSPD

SVMRMSKHLAEYYRYLTKLDRHEVTLESELQFAEHFLIIMALSKKMEYSIDLPSSELSS

LPLMPLIIQPVVENAIQHGIEGQQGAHRVTIEVKQTEAAITIKVSDDGKGLSLDDIRS

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GDN"

CDS 2452803..2454152

/gene="rhaR_12"

/locus_tag="EFAGFIKM_02088"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MRLLIVDDGHYVVEYMKHLLDWNTFGIDQIETMTNSIEARELLT

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EFLGRRRMCCFKLDGFTQEHEDVIKHAVGDKLDRLVWAAGTGLFGLVPEEAAGELTIK
LEQSVASPPFSLTDRNVTRQMFYRFFLNEDVHSEDFNGIFNHSPSCGDWESAGNIIKK
YEHIHLHKQKIIFLMETILYVYLTDKDRDPSETVDWIFNQLRYPDELSSTLMDRVSRI
RNNKQMSIQTIVDKVQTYIEDHLSHGLSLDELGKVAHLHPVYFSKLFKQETGENVSNY
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CDS complement(2454272..2455618)

/gene="ntaA_1"

/locus_tag="EFAGFIKM_02089"

/EC_number="1.14.14.10"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54989"

/codon_start=1

/transl_table=11

/product="Nitrilotriacetate monooxygenase component A"

/translation="MTKKRQGQLHLGAFIYFTGHHHAGWRHPDSGVEKMFDIEWYKRI

AQTAKEGKFDMIFFADLLHLIYPSRAAAGMLDPVSLLSALSMVTDKIGLTATLSTTYN

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AALWDSWPQDSLVMNRRASGTFVDESKLRVADYKGKWYSTQGLLNVPRPPQGYPVLIQA

GSSDPGQDFAAKVGEVIFTAQTSLAAAQDFYRTVNEKLLAMGRERGSLLIMPGLSPIL

GSTVEEARRKERELLDLIDPQEAVMMLSGMLQTDLSGYPVDGPLPDISDPVEASNGMK

SRVQLIMDLARDEQLSIAELGRRLLGARGHMQFVGTPQLTDLMEEFNGYGCDFNI

MPPVLPGLDLDFFVEHVPELQRRGLFRGEYEGTTLREHLGLSEPTVVVSHKQQVHG"

CDS complement(2455654..2456409)

/gene="ssuC_3"

/locus_tag="EFAGFIKM_02090"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40401"

/codon_start=1

/transl_table=11

/product="Putative aliphatic sulfonates transport permease
protein SsuC"

/db_xref="COG:COG0600"

/translation="MPNWLYGWVLPVILALWEAGSALGLLSDSALPAPSRIARTFWQ
LCVNGDMTQHLLTASTIRAIGGFLLGAVTGLLLGVTGLGKWVEQTLDPITQMLRTVPL
LAVIPLFILWFGVGELSKVLLIALGSFFPLYFHHLGVRSADRKLVEVTRILQYSKFR
LLTRLIIPSAIPNILLGIRLSVGASWLLLAEMMGASAGVGYMIQDARVYAQTDVVF
VGIIMFALVGKLSDSAVRLVERRLLRWNNNTYKG"

CDS complement(2456494..2457288)

/gene="ssuC_4"

/locus_tag="EFAGFIKM_02091"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40401"

/codon_start=1

/transl_table=11

/product="Putative aliphatic sulfonates transport permease
protein SsuC"

/db_xref="COG:COG0600"

/translation="MQISGNKLVFRTIHLIGMSVPAAILIHWQIVSSNGWVNPVLVP
PPKDIAEFGRMISSGELLTNLRISTGRAALGFLGGGLGLAAGLWVGFSKKAERLLD
PSLQLLRTLPHLAVAPLFIWFGFGETSKIVLIAKGAFPLYVNAFLGVRSVDRQLFD
VASVLQFTKLQTITKLIIPASLPSLFLGVRLSIASWLGLVVAEMMGSSSGIGYIIND
ARSFSLTSVIFVGIIVFAIVGKVTDSLVLKLAEEKLLRWQDSIEGDG"

CDS complement(2457304..2458335)

/gene="ssuA_2"

/locus_tag="EFAGFIKM_02092"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40400"

/codon_start=1

/transl_table=11

/product="Putative aliphatic sulfonates-binding protein"

/db_xref="COG:COG0715"

/translation="MVKKYNLIAVILVLVAGCGNANNNAGNGEDAKPVEGSSNP
ASYDDVTVKIGVQKGGLFGKAQEQKWFEDAFGELGVKVEWLEFQSGPPMIEAMASNH
LDFAGMGNMPPISAQAAGIDFKIISQLLDGKNNVAIVPNDSPIKSIADLKGGKVAVT"

KGSNAYNFLYQVLQKDGLDNSDIQEIQLPDETQPSFESGKVDAAVWDPYITLNTLS
GKGKVLADGESEGLSPSFQLVRSDFANDYPELVTLYLKTFEQARQWEANNQEKAQFQR
YADERNIPIDLVKGIQSRAAMINIPVSDETIANQQNTANFQFELGTIRKEINVADVFD
NQYIEEALK"

CDS complement(2458382..2459149)

/gene="ssuB_3"

/locus_tag="EFAGFIKM_02093"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P97027"

/codon_start=1

/transl_table=11

/product="Aliphatic sulfonates import ATP-binding protein

SsuB"

/db_xref="COG:COG1116"

/translation="MLIIERLNKTFASPTGPIVALSNIRLQVEPGQFITFIGPSGCGK

STLLKIVAGLDTTYEGTLELNGKAITGPSVDKGFIFQEPRLFPWMTVEKNIAANLSLG

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DAFTRTHMQEALLDIWQNSRTTMLFVTHDLDEAVFLGEKVVIMNPRPGHIRNVIPVDL

PYPRKRSGGSFQELRSRVLGEFEKVEHSPLIDKGAGI"

CDS complement(2459338..2459958)

/gene="fadR_1"

/locus_tag="EFAGFIKM_02094"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94548"

/codon_start=1

/transl_table=11

/product="Fatty acid metabolism regulator protein"

/translation="MSPRNIEKDLQREKRINHILDTALEIIALKGIGSVSINHIAVA

AGMSIGNMYHYFKSKDEIIEILRRGQTSYGEHVSQLAEQSGDALNKLKLLSSEWLAL

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LAYFVSLIQGLTLQMPGAEVPIRAQARSIVSLFAVSLHNSKRND"

CDS complement(2460169..2460462)

/locus_tag="EFAGFIKM_02095"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYYNQTAGFGLLAPEGYPEGGESLTLERLSSMNPDIHQHRID
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CDS complement(2460627..2461130)

/gene="ntaA_2"

/locus_tag="EFAGFIKM_02096"

/EC_number="1.14.14.10"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54989"

/codon_start=1

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/product="Nitrilotriacetate monooxygenase component A"

/translation="MPGLYFFLGDTHEEALHLKAAHSHLNIERRHASLQSVMLDLT
GYPLDQQRVTAEMLANPSQAVRSRTHAELLRSFITKYQPTVKEILDRPEVVGSAHWVSV
GTVETVLNDIERVEAGIDGFIALPGGSEKSMEIFFEQLIPKLVERGMFRSEYEGAT
LRDHLGI"

CDS complement(2461163..2461735)

/gene="moxC_3"

/locus_tag="EFAGFIKM_02097"

/EC_number="1.14.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34974"

/codon_start=1

/transl_table=11

/product="Putative monooxygenase MoxC"

/db_xref="COG:COG2141"

/translation="MTSNQELYIGLFLNATWNKGDGWRHPDSGVEQIGTIDYYIHWAK"

IAEKFKLDFLFRADYLYISPQMLSDSSNFGSPDPTLFFAAIARETNRIGLVTISTTF
NPPYVVARQLQLSLHWLSNGRAGWNIVTSIEGADNFGNSPMPSPEERYAKAMELTDIVC
KLWESFPNEAIVDRKSGLFSDKDKVTAMQ"

CDS complement(2462039..2463547)

/locus_tag="EFAGFIKM_02098"

/EC_number="3.1.6.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q0TUK6"

/codon_start=1

/transl_table=11

/product="Arylsulfatase"

/db_xref="COG:COG3119"

/translation="MNKPNILLITSDQQHWNTIGAFNSEIETPNLDRLAQEGTSFKRA

YCPSPVCTPSRSSIITGMYP SQHGAWTLG TKLLENRHTVGEDFHENGYRTALVGKAHF

QPLRGTEEYPSLESYPILQDLDFWGSFHGPFYGFDRVELARNHTNEAHVGQHYASWLE

ERGCTNWRDYFLPPTGTMDPSVKHKWAIPEEYHYNWIAERTNALLEQYREEEQPFFL

WSSFFDPHPDYLVPEPWDTLYPDPELTIPSVVEGEHDHNPPHFKLTQEENPDFGYLQE

TSHSIHGYQSHLTPENERKQLVATYYGMISLMDKYIGKILEHLDKLGLYDNTIVVFTT

DHGHFFGQHGLQHKGGFHYEDLIRLPFIVRYPGKVPADTQNDAIQSLVDLAPTFLSFC

GIQPPNEMTGLDQSKVWMGIDSMARDHVLCEFHHEPTTIHQKTYVDVRYKLTLYYRQT

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CDS complement(2463564..2465588)

/locus_tag="EFAGFIKM_02099"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTSKATITIDCSQKSEHVISP YLFGHFVEDIRDHMEAMLAYPLK

DMDFESDALIGTAVSGSWRPYTNGRNTKYALES PARGHSGRAQRIRILSDDEGHAGIA

QSAALKGPMEYSLKLVARASIELQYVVLEVVD RRTTEEQLGLVTIPIMNHNWEHYDAKM

FVTRACSDAEIRLYVPSEHPRWLDHVSTGMLWIDHVSMLPADSIGQVKPEVVEMTRGL

NAGMMRLAGNYISAYHFEVAIGPVLERPVMYNEAWGGWTC KYFGTDEFIQFCRELQVE

PLICINDGSGTPEEAAKWVEYCNQSVETPMGARRAANGFPEPYQVRYWEIGNEVWGDW
QVGHCSPDQFAHRSILFAEAMKRADPSLIILACGHTDQEWNRVLDIAGEHMDYLT
LYHGYGRFGMNRDTPAEERYKAMASFPEWTRDNILQTVEHIRKHEKHHHVKLAITEYN
TMYYPNTVRKGNPDEHTLGA AVANAANLNEMLRCS DVVHIGSFSDLVNGWLGGCIRVG
DNYADQYAGKVPGWSGHPLVVYGTPTYEV LKLYAGRDIQRLLSVDV VSGTFSVETLKS
APVLLDTLPDL DVVACTNEDGSLVTVFMVNRSLHAVKAELRLSAFSTDEETLLYEIIG
NSTDDINSVFDPEHILCRQSVIPTNAWQQGYLLRPASIIYALEIQT KQATG"

CDS complement(2465609..2466499)

/gene="araQ_12"

/locus_tag="EFAGFIKM_02100"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MIKRATTKG V WDEKVFDAIVYTIAAVIIVLVLYPLLFLVSASLS

DPAKVLSGEVWLLPKGFTL DAYTNILHNEKIWLGYRNTIFYTVIGTVINVIMTILAAY

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VMRTYFQTIPWELQEAASIDGCSNWRLRSIILPLSKPILAVMVL FYAVSHWNSYFNA

LIYIRNEALYPLQLILREILMFSQSDAMDSTVGLEDKIMLAESIKYAVIIVSSLPVWI

MYPFVQRHFVKGMIGSIKG"

CDS complement(2466517..2467479)

/gene="yteP_15"

/locus_tag="EFAGFIKM_02101"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system

permease YteP"

/db_xref="COG:COG4209"
/translation="MKKAGVVPTSGLP RARSKPGIGLLRQMARRYDLYLMLLLPIIWY
LIFHYAPLYGLQIAFKNFNPGKGIGGSSWVGLEHFVRFFDSYYFWRLWNTVSINLFS
LLIAFPIPIFLALIINEIPNKAFSKWLQNITYIPHFISVVVIVGMISLFFSPTSGPVN
LLIQTFGGTPIRFIEEAGWFKTIFIGSNIWQNMGWQSIYIAALSGINPQLYEAAKID
GASRLRRVWHISLPGIVPAIVILLILDVGHFMNIGFEKVLLMQNSLNSEASDVISTFV
YTTGILKGEYGYTTAIGLFNSVINLTLLLLVNRIARKTSETSLW"

CDS complement(2467531..2469117)

/locus_tag="EFAGFIKM_02102"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRKPWKQLTLRTMIMFSLVLSGCNSGIVATNEAVPGKHAADVSK
EGFPVKEPLKLMFTRIAPVNGPFKDMPIFQDYSKNSNVQVEFSEVPTDGFQEKKNL
LFASNELPDALFRTGLSPLETIRYGTSGQLIPLNLIIDEYAPNFKKLMEQYPEILPAI
TTPEGHIYSLPAVTLSSARMDKKWINQKWLKKLGLKEPETTEDLYQVLTAFRDKDPN
GNGKQDEIPMTARAGGGQGQGLPIVAMMSGSFGLDMQLGYNINLEDDKVNIWMGSERN
KELLYLNKLYQEKLLDPEIFSHTEAQYLAKQASGNTGFFFDQTNNPFLKIADQYTG
APLEGPHGDRLQSQGAPVPRDFGAFITSVNEYPEATLRWIDYFYSEEGSTLLRFGRE
GEHYELKDGIPIYKEDFLNSGNQSKITPYAGGGAPHLISEEVASYINPPQVQEAQKKL
DPYLPDIRYSSPMFDEETARKVEILRNDIDKYEEQTTKFIVGSLSFDQWNEFQDTLK
KMKIDELEKLYQDAYDSMKK"

CDS complement(2469228..2470082)

/gene="rhaS_15"
/locus_tag="EFAGFIKM_02103"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaS"
/translation="MKDYGHEYADIYYYPNEFEKLGGLWPLRTGHNVAKANYSVGAR"

IIECFSFHFVLSGAVTLSSMGETVTLTKGGIFCLFPNVKYSYWVSQYDPESPLRMCWL
AFNGTQAESLVRRIEITEQKPYLRNKLTSEMEELLKACMKQIGGRQRDGDQLQLIFY
RLFEMLSRPLHNVMEDKLKACMQYMEMHYAEGITVADIAEFTGMHRSHLSTRFKQCFG
ISPRDYLIKLRMERADEMLQNGALSITEIALSLGYTDLYTFSRAFGIYYGMSPSNFRS
RMLPLTKC"

CDS complement(2470284..2471351)

/gene="galM_3"

/locus_tag="EFAGFIKM_02104"

/EC_number="5.1.3.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39840"

/codon_start=1

/transl_table=11

/product="Aldose 1-epimerase"

/db_xref="COG:COG2017"

/translation="MVITHHPLTNKGETRLNTNTSAASASSEGDYQGEKAIYLRYS
YEAVMLPEIGGNLVAYRDHVQDYQFLHEPTPEEMTSFKARPMIHGIPVLFPPNRYKNG
QFAWNGEMLQLPVNEEATGNHLHGFLYNIPWKVEEYGHTGKESYVSVSITIDENHPVY
SFFPFSFSLTRYALSSDGLMQHVKIRNHGESTMPCLLAFHTSINAPFTADGSARDYK
LKLTVGDRWELDERMLPTTHFQPFVPEEEQMRDSGVYPFFAEMDNHYTAVPQNGRNRN
ELHDTKSGVSLIYDVGTSYKQWMIWNNGAQGGFFCPEPQINLVNAPNLDMKLDEVGLF
SLEMGEIWEETSRLYVRQSHK"

CDS complement(2471320..2473086)

/gene="uidA_2"

/locus_tag="EFAGFIKM_02105"

/EC_number="3.2.1.31"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P05804"

/codon_start=1

/transl_table=11

/product="Beta-glucuronidase"

/db_xref="COG:COG3250"

/translation="MLREDYPRPQFVRQNWMSLNGQWEFEFDDHHRGRSEKWSEGTQS
FSRRIQVPFAFQSQLSDIGDPDFHDNVWYKRTFEIPDGFIGNRLLLHFGAVDYEAFFW
VNGQLVVRHEGGHTPFHGEITDVLQEGTNVLTQALDYSKDVTLPKGKQFWQEESAQI
FYTRTTGIWQSWWLEAVDPIHLQKVRMTPDIDRNQINVTSYVHGTLDARDVRLRVQIS
YQGEELTADEYRISAKEESRTIGLHTFNEHGLGRLWSPEHPNLYDIHFTLLVDGVPSD
EVDSYFGMRKISIEQGRLFLNNRPYFMKLVLDQGYFPDGNLTPPSDEAIRQDVELTKE
LGFNGARKHQKIEDPRYLYWCDKLGLMVWGEMANAYEFSQEYVSRMTREWQEAIKRDY
NHPCIVVWVPLNESWGVNLTKEQYHALSMYYLTKSIDPTRPVISNDGWEMVQTD
LYNIHDYEWKRVLEERYSRNAVNLPGNRHLSVGGHRYDGGPILITEFGGIGYKK
SNWEGWGYSGAEDDKDFAERLHAVIQPLLDSPVVEGFCYTQLTDVEQEINGLLTYDRQ
PKMPIEQIRAIIDGHNPSSVNE"

CDS complement(2473137..2474903)

/gene="uidA_3"

/locus_tag="EFAGFIKM_02106"

/EC_number="3.2.1.31"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P05804"

/codon_start=1

/transl_table=11

/product="Beta-glucuronidase"

/db_xref="COG:COG3250"

/translation="MTTKFYSKDYPRPQFVRKDWLDLNGEWDFFSDDNQVGESEHWYD
QAQFPEGLQIKVPFTYETQASGIGIETFHPLVWYRKQVVIPQEVKGKRTILNFQGVYD
RAKCWVNGTVAGEHEGGYAAFSFDITPYITYGSENNIVLEVEDSQSAMQPRGKQRWVD
ENFECFYVQSTGIWKSXWLEHVSEARVEMVKMTPDIDRHMIRLDFQLNGIEGKNNLRL
ETRIELKGQHVQSISLSPDRPWMTVEASVKHEAGGPWKQSLWSPASPNLYDIEFVME
DGKEIDRVHSYFGMRKISIEGQILLNNAPLYQRLILDQGYWTESHLPSPSVEALIED
IDKIAEMGYNGIRKHKLEDPFLYWCXVKGMLVWSEMAATFEFNDEAVSRFTKEWLE
IVPQQYNHPSIITWVPFNESWGIPTIAHEVRQQFTQSIYHLTKAIDPYRPVITNDGW
EHTVSDILTLHDYVESGEAFSERYQDKDMIVNNKTASNRWKFAFAEGYHYKGQPIIS
EFGGIAFQSDKGWGYGNQVDSVEAFIERFRSITEAIKAVPYISGYCYTQVTDVQQEIN
GLLTEDRQPKVPLEVIRKINLA"

CDS complement(2474989..2475795)

/gene="araQ_13"

/locus_tag="EFAGFIKM_02107"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein AraQ"

/db_xref="COG:COG0395"

/translation="MKWLFRTGSALMAVMFAAPLVWMLVVSKEEGMKIITVLDWFKP
PYSLAYEIEILTTTKLSQWIANSLFVAVVVTULTVIFAAMAGFALSKVPFRYRTIVFF
FILGGLLIPGEATIIPLYQVAKDLHLLNSYSGLIIPALASPVAVIVLKSFFDGVPNDL
LESVQIDGGGFWRIFTSIMLPLTRPAMASMAILTFIGSWNNFLWPFLSITDDNLFTLP
MGIPTLMGQYSEDYVKPMVINAVASVPIIILFIIFEKQIVKGISMSGIKG"

CDS complement(2475795..2476658)

/gene="melD_5"

/locus_tag="EFAGFIKM_02108"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34706"

/codon_start=1

/transl_table=11

/product="Melibiose/raffinose/stachyose import permease protein MelD"

/db_xref="COG:COG1175"

/translation="MQALVFLLPFLIVYVLFTIWPMIKGIEMTFYKWTLIKKMDFVGL
DNFRKVLQDREVWEAIWHSTFFVFLSTPTMIVLSIVLALIANRKSVLQKFYRIIFFIP
SVLSVAVAAYLGLFVFQPYTGFVNSVLHLIGLLPQNSEIFWLTETSLAWIVITVITLW
WTVGFNFILYLSAMQEIPDEIYEARLDGASDTQIFWRITLPYLAPLTKTITMLQIIA
SYKVFMQIYVITGGGPLDQTRPIIQLIYQTGFKNNNLSYAATMSYILFVILLVLSVLQ
YWINNRRKGADS"

CDS complement(2476765..2478057)

/locus_tag="EFAGFIKM_02109"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKRRMGLLALTILFLLSMVLSACNGSDSGAGEGDSGDGKVTLSF
WTLFDGGDGANMQTLVDEFNKSHPDIVKNTKLAWGEYYTKLITAVGNGNGPDIGISH
SSRLPDLIDQGVVTELDTPATDADVDWNSYNQNLLDAVTVDGQHYAVPIDTHAFIMFY
NKKLLKEAGLLGEDGKPVLEQSADGFVSFLKTLKEKLPKATPFALSNNNDPFRLLWW
SLYTQLGGNDVVSDDLKSAIDKEKGIQAADYIQKLYTEGYIKKNDPDFYKNFQSGTA
AITMTGVWTTGTWESTKDFEFGAMPIPKFYNQEATWGDSHTIVLPLTQDEDEAKRKAA
MIFADWWADNGQVWAKAGHIPSKPSVLEKQEFKDMPYRSDYSEVASVVKFSKQSTKTA
QIREEVAFKFLNEVWVNKMTPSDAMNNMEAGIQKILSE"

CDS complement(2478246..2479187)

/locus_tag="EFAGFIKM_02110"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLELSFDDPKLVTVTHALSTRSRVDILRLILKLNIVEIAEA
LKLPVSTVASNIKVLEAARLINTELLPASRGAMKVC SRNYDDIHIALNTEKALPKG DV
QVYEVDMPIGHYS DCEVSPTCGMASADGMIIREDEPASFFHPKHIGAQIMWFRKGYVE
YLMPIEPTGARIESLELSMEICSEAPNYDHNWPSDISVWINGVDIGTWTC PGDFGDR
RGKLNPAWWYEWSTQYGLLKTWRVDREKTTLDMEKISTVTNLNLQDTHKL RMRVGI
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CDS complement(2479418..2480818)

/locus_tag="EFAGFIKM_02111"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKIMNYRKKLLLALCAFLIFPMGQISHAATTQNNFYNVVMQDGA

DPWVYKHTDGFYFTKTTGGNVTIWKSAQLTTIDAAPTTVVNTGCCGIWAPELHYING
AWYIYYAKDDGDNINHRMYVMENTSADPTQGTWQYKGQITDPTNKWAIDGTVLQSNQG
LYFIWSGWEGDTNVRQONLYIAHMSNPWTIDSNRVEIARPTYAWETNHSPNVNEGPQVI
VRNGVISLVYSASGSWTNNYCLGLITASTSSNLLSPASWSKRSQPIFQSGNGLYGPGH
HSFTKSPDGTEDWIMYHTAKFNNSGWNREIRLQKFTWNADNTPNLGVPVNPNAIALP
SGEKSVVRYEGEEGTFGGIAYASQSPSGSGGMKAGHIDTVDSYVEFNVAASAGQYIL
LARTANGTAGGNWSNLLLSVNGGTASPFHITNKGWENWGMSTARVQLNAGVKNIRFSK
GVGYGELDFFDIKPVN"

CDS complement(2480875..2482635)

/gene="lacZ_2"

/locus_tag="EFAGFIKM_02112"

/EC_number="3.2.1.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01687"

/codon_start=1

/transl_table=11

/product="Beta-galactosidase"

/translation="MKEQSSSMSSTPRPEYPRPQFVREAWTNLNGSWQFEIDHGKSGK

ERGYEQSGHQFYGTITVPFCPESKLSGVEYTDIEAVWYKREFTIPDTWMNGRILLHF

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QSERFHSHGCDYTRTTGIWQTVWLESVPDVYLSDMKVVADPDNACAHLEVKICGNAAG

AELSASARFEGRDVGSETAVIHGPSVKLTVP LSEIHLWEPGHAKLYDLELKIQGKSQA

SDTVTSYFGLRSVRLDGMAFRINEKSVFQRLVLDQGFYPEGIYTAPSDIDLKRDIEIS

MELGFNGARLHEKMFEPFLYWADKLGVLWGEHANWGLDITTESLARFLPEWVEGM

ERDFNHPSLIGWCPFNETWDRGGTRQDNDVLRIVYEMTKRLDPTRPVIDTSGNFHVVT

DIFDLHDYDQNPETFQARYEPMRNGGEVFNTFPERQTYGGQPYFISEYGGIWWNSDQQ

DEKSWGYGDRPQSEEFITRYEGLTNVLLDHPMMFGFCYTQLYDVEQEVNGLYTYDRR

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CDS complement(2482652..2482999)

/locus_tag="EFAGFIKM_02113"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYVILPLSKATLAVIFLYLVGNWNSWFNAMVLLQDRDKFPLQL
LMKEILVAKDSSATIMGSAGGVVIDSASSATAYRELVKYCTIVVSTIPILMVYPFLQK
YFVKGVFVGSIKG"

CDS complement(2483025..2483270)

/locus_tag="EFAGFIKM_02114"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTIMEAFVLSRRDLYFKNAIMIVITITMFFGGGLIPWFLMKDI
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CDS complement(2483267..2483545)

/locus_tag="EFAGFIKM_02115"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKYRKTMGNRMFDIFNYTLTLLTLACLYPILHIVFASFSEPAR
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CDS complement(2484248..2485201)

/locus_tag="EFAGFIKM_02116"

/EC_number="3.2.1.55"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q82P90"

/codon_start=1

/transl_table=11

/product="Extracellular

exo-alpha-(1->5)-L-arabinofuranosidase"

/db_xref="COG:COG3940"

/translation="MTNKTIFYNPVALQSADPWVYRHSDGYYYFMRTSRDKLELIQSS

RLSKIDAGTRKIVWTPPEGGPYSHHLWAPEIHFLNEKWYIYYTANDGGGDDSRICVL
ENESPNPMEGEWWWKGALHTPVPGLDGTVLMLGGQLYFLYAGYGHFPDYGSAIYIMRM
SDPHSLTGEHVLLTAPTFIWEKQGGMAINEGPVTLHRNGRIFLVYSGSTTWSEDYALG
MLTMNEWDDPMLASSWTKSAEPVFRKSLENGVYATGHNSFTTSSDGEEDWIVYHALPN
PGADTVLRATRVQKFGWNPDGTPDFGVPSDNEALQVPSGE"

CDS complement(2485363..2486211)

/gene="rhaR_13"

/locus_tag="EFAGFIKM_02117"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P09378"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MPNNGTSFIVSIERFKPNWFHLEQGEGLFKSHSHAYDELTILID

GEGYSSPEQNVKVVAGDLIMIPPGLYHGFVCTEPWQGISVHYHDHLPVHCRYLFNG

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RNCSLEVPHIVNDPTGQGIQEV LKEIHSAYTPTVSELASRYFLSASNLRKKFTET

VGVSPKQYIINLRLMEAKRLLQHTNKAVEMISSEVGFTSSSRFYDFFVKSVGLTPLEW

RIQNKH"

CDS complement(2486201..2487160)

/locus_tag="EFAGFIKM_02118"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLELSFNDPEKLVTVTHALSTRSRIDILQLLHANKLNIIIEIAES

LELPVSTVANHIRVLEAANLIHTEMLPASRGAMKVCSRNYDDIHIVLDLVSSLSTRDS

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YLLPMDIPTDATIEALELSMEICSEVATYNNDWPSDISIWWNGIEIGAWTSPGDLGDR

RGKLNPAWWPDGSTQYGLLKKWRVDNNKTM LDK EKISDVSLSDLNLGDKPKLRLRIGI

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CDS 2487425..2489908

/locus_tag="EFAGFIKM_02119"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKWRIFLSAALCFLMPTNIYAYNNPLNLSDSWHWSNSDFYGE
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NTIEARPMTSPTTFGAPITGLSMAGWTEGSTTFKRDGKYMTYTGNIHVVSTAYRVDY
ATGSSPTVGFKPTADLNPVLINTEGTNVLGLHNSIIKGPDLDSYIVYHSHASDGNIT
YPGRKMNMMDRIVWNGEKLIVQGPTIASQPNPELPDFEDRFNRTSIGNNWTNVGGGTWG
IYNQELMWQDTIGSASTYRQITAVNSASDYAEFNLKQIKQGTIENPVYGTVFSYTNE
NSYGVAVLNRNKNRLETNYVVEGVSQGWQYASLPAGYDYSKWHQIRVEKAGSSFTVYV
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YMDGIEGTAYHDLTPANIGGAYRKDAVDIRSSAAEGKNVVGWNQTGEWLKYRVNVAET
GYYDLDVRLATTFNDASFRVWDGATDLTGIIISAPNSGDWEKWTTASKKGLYLTAGNHE
LRFEFVQGEFDFSDMTFTRGEAVADMVDDFNDGNDNGWTRFEGNWSVIGGELDSAGNG
VFGKTTIGKESWADYTVESDIKLIDTSGDAGILFRVNNPSNGKVLANNPDYVQAYYAF
IKPDGVYLGKMNYGYEQLASVPLSIASGIWQHMKVVTSGTTIRVYVEDMNTSKITYKD
NSMNPFTHGKVGLRTMNNHTRFDNFRITP"

CDS complement(2489967..2491175)

/gene="araR_1"
/locus_tag="EFAGFIKM_02120"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P96711"
/codon_start=1
/transl_table=11
/product="Arabinose metabolism transcriptional repressor"
/db_xref="COG:COG1609"
/translation="MYNQPSLDEISCPSSSTHSILNMVIVMKNIPLYKQIQHAIKHQ
IWLGNLRSGDRIPSEKELAEQFHVSLITTKNAMAGLAEAGVVVRIKKGKTFVAGQASF
KLRIPITYQKTDESAAHHIPLPPKAKEMIGIIIPSMRTKVEQRLLDAIENAVNENG"

YTLVIRVSRGSSVKELLAIDELYELKVVLVLF SIGSEHERQTVDRATELGFPYVLID
RYYTDKPNVSVCSNNIEGAYKAVTNLVKQGFRKFALVTPPKAHSVIERIAGFEKAAA
KAHISPEHIIRLTLPYEIFIESIQHREQILDNWSQYYGRFTALVAVDVELARLAHYS
LIRTIGREKAKHIAIVTFDDPGIDGIAYVQQDEKMIGIQAVTLLLDQIHGIRTPKNL
FVPMIEWIPSS"

CDS complement(2491282..2491656)
/locus_tag="EFAGFIKM_02121"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDS DILINQFLRLFPEFYDCYIEHLDLNQEFLGHVFFGDEVATY
VEGLLRENDDELIEKFFNFFEWMAIQSDLYIVQVLSTILYDLGGQSDILQIAQSYM
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CDS complement(2491742..2491954)
/locus_tag="EFAGFIKM_02122"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLKIINFLLFLLIWWVIFYPFRFAWFEG LKQIPADLHGVYLLF
LFFGYLICSSAMGLIVGKMFFKRKEQ"

CDS complement(2492266..2493504)
/locus_tag="EFAGFIKM_02123"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSTSKKRVQFIDGLRGFSLAGIVLANMLAFQYGMYGQSKPQLFG
IGGADQAFLSFLLITVGSFMPIFAFMFGFGMVKLSESLKSRDLRPKCHLARRFLLLF
GIGLLHIIYLWEGDILAFYGVLGFFLLMFLNRKPKTLLIWAVLLLMGAGILGLPASNP
MNPLAIESIHMENYIIQSQDVYGNNGSYAEIRDFSNNGDPFGGDLEVSFALLILLLAPL

MTVPMFLLGMHAARIGTFSDPQTMRAMYLRRASLLIPVGLILKTYGVLAPQLGAEGWL
GIGIGGTLGGTLLALGYIYAFALLYAGNRRSSLMGRFEAVGRLSLTNYLMQSVICTTI
FYGYGLGLFGRAGVFIGAIIALAVYGIQLWLSPLYLKKFSNGPIEYLLRIWTYLSWKG
QPRKKKRSNLTTTHENAPGVQ"

CDS complement(2493669..2494409)

/gene="map_1"

/locus_tag="EFAGFIKM_02124"

/EC_number="3.4.11.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P99121"

/codon_start=1

/transl_table=11

/product="Methionine aminopeptidase"

/translation="MIAKTEEDFNGLKEIGKIVASIRDELVQRTIPGITTKELDLAG

ELFEKAGAVSAPKSEYNFPGFTCISVNEEVAHGIPGDRVIQEGDIVNIDVSGSKNSYF

ADTGLSFVVGEGAEVLTKICDVVKLAFEAGLKKAKPGSKKSGIGKAVFQTARQHELT

IKNLTGHGVGRGIHEAPDHIYNYNDPSSDELLKEGMVIAFEPFISTSEEEVDQTGDGW

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CDS complement(2494567..2495529)

/locus_tag="EFAGFIKM_02125"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPKNDNMLAILWMLNSGTKVTAKQMSEKLEINIRTVYRYIDALC

ASGVPIISDTGHNGGYSLNQHIKAPLLFDIDEKKALLQAAVFAKEAGYPLSEALDNA

TSKLKMYTNQDQENTLRRHLAGFNVINRMGDPSVQPILAELEQAVANDCSVEIDYLR

RDEQPKNRVIDPYGMVHWNNKWTIAFCHLRNEFRSFRADRILGIKLTPLRFKRSEAF

SAREFFLQNLLPDVGGKEGLISLVIEGRSEALDDLGLHWFMGHYLKERTSNQAIFLFD

EKSIDTYVPYFLLSYGKSIQVIEPQRLKDRLVAVVSELMEYYQL"

CDS complement(2495750..2499802)

/gene="cpdA_2"

/locus_tag="EFAGFIKM_02126"

/EC_number="3.1.4.53"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00905"

/codon_start=1

/transl_table=11

/product="'3',5'-cyclic adenosine monophosphate
phosphodiesterase CpdA"

/translation="MISHLYKKMLPILLSLSLVIGWFAGFGGANSQAASLSEPDILL
ERNANWKYFDQGGQNLESQWRASYDDSSWEFGLAPFGYKDNGNGISTSYFGPLKTEVSY
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IQYSTKATSSQDLPVMYEDIDLTEPLKAYLHDGNNEIAVEVHQSDSSSDLYFDMELK
ALAEAPSLDINKVTVTFYGDATTSKGFTWYTPLASTQSTVQVVPNQGSAADFSQAQSF
NGRSSVASNSPGEMVHKAATELTPDTSYYFRVGDQDLGIWSEVGTFTKTAPTNGAFRF
IDLTDQAKEEDEAILS GSTLSKALSQVPDAAFVHNGDVVENGTSEQEWNWLLGHSQ
SSLMNTTIAPSAGNHENKNYAFYEHFNLKQPDNAATVTGAYYSYDYSKAHFIVLNSNE
NSSEYANFSNEQVAWMKQDVEEAKAAGAEWIVNIHKGPYTTSNHATDSDIIGANGVR
NKIAPLMNELGIDLVLQGHDIYARTKPIKSDGTAEDVSKITETLNGQSIEYAVKPDG
TIYMIPATAGAKVYFKNQKPELGEAYFSLFERAEENHARQYGDTTSAARGQVQNFVSF
TIDGSKLTAVTYEIDQHTNNGEPFIVDQFGILKETDTPVPEQISKITVTFHGDPTKN
KGFTWYTSQQLQSDLQVVEKTEATPDFNQAKLFQGRSVQPANSPTERMHKAATDLK
ANTTYFFRVGDATKQVWSATGTFRTPAKGKFTFIDLADTQAKEEDEAILSSETLAKA
LTTVPDAQFVHNGDIVDKGVKEEQWNWLLGHSQESLLNTTIVPSSGNHEDENYAFID
HFNVQPPANSATETGAYYSYDYSNAHFVVLNSNEDSTEYDNFSLEQVKWLKEDVQAAK
KKGAEWVIVNIHKGPYTTSNHATDSDIMGVNGVRSKIAPIMAELDIDFVLQGHDIYA
RTKPIDQKGNARQPEMITEMQNGQKMEYSVNPDGTIYLIPATAGPKVYYKNQSTSLGE
AYYSLFERAEENHAAQYGPDPSPDNRRPKRSQVQNFVGITIDGSKLTAITYEIDQNVNG
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NGTGDGSNPGNETDTGSNNNGNSENTPPMKDTAGHWAKSAIDRALAAGFVNGYGDDTF
RPNQKVTRAEFITMLGRALNLNNISDNVQYTDENKIPSWSKPYITAATSLGIINGYAN
GSFGPSKTLNRSEMTMIVRAGGIPTDSNTKLNFKDAKDVPAAVAVSYVASAVESGLVG
GVGSNRFAPMQTATRAEAITLIIGLLDKVK"

CDS 2500096..2501220

/gene="yndE_1"

/locus_tag="EFAGFIKM_02127"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31809"

/codon_start=1

/transl_table=11

/product="Spore germination protein YndE"

/translation="MKQATTKINTSEVIIVVINSILGAGILTPRTISKAVGTPDVWI

SVILSGLIVTTISILLVTLRFRPGKTVFEFIPEITGHWISYLLGLLIIVYFVVLCSF

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VFLLSSKLFELNNLRPLLGDGFMPVLKGLKPSCLSYSGYEVLLIITAYMVDLKASNKA

AIYSILSCTIIVLTIVTVVGNLSLPGIQTRMWPTFDMVRSFEIEGFLFERYESLFIV

FWLMQIFATYAFKHYYFAAIGVRDLFRLKNITSIQFAMLPVLYVIAYLPKNLDETLALG

DFLGNMSIFLFGLLPLLLLIISFVRKKGGKQASSEALKAS"

CDS complement(2501308..2502576)

/gene="codA_2"

/locus_tag="EFAGFIKM_02128"

/EC_number="3.5.4.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P25524"

/codon_start=1

/transl_table=11

/product="Cytosine deaminase"

/db_xref="COG:COG0402"

/translation="MIIQNAKLRGKEGLWNIVVKDGKFERITQSLETTENEEILDVNG

SLVLPPFIEPHIHLDTTLTAGEPEWNLSGTLFEGIQRWSEKAFTHEDVKTRSKTAL

KWQLAQGIQHVRTHVDVTDPSLIAVKAMLEVKEEMAPYMDIQLVAFPQEGIHSPNGA

ELLEESLKMVGVDVGGIPHFEFTREYGVDSMKVAFDLAEKYDRLIDHCDEIDDEQSR

FVEVVAKEAYERGLGSRTTASHTTAMGSYNDAYTYKLFRLMKADLNFVSNPLVNIHL

QGRFDITYPKRRGLTRVKELQEAGLNVCFGHDDIFDPWYPLGTGNMLQVLHMGIHASQL

LGYDQIVNSIDLITKNSARTLHIEDVYGIEEGKPANFIVLEAENEYEAVRKQAGVLYS

YRGGRKIAESKPRDTSIIFEGGTEKVTFNK"

CDS complement(2502545..2503897)

/gene="codB"

/locus_tag="EFAGFIKM_02129"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AA82"

/codon_start=1

/transl_table=11

/product="Cytosine permease"

/db_xref="COG:COG1457"

/translation="MYNLTSSLFLLFLVSDTLVGGILMSKQDQFSWQAVPKSQRN

HFWKTL SVM LGFTFFSASMLAGGT LGVSLTFMEFIGIVLAGNLVLGIYTGALAHIAAK

TGLSTHLLAKYAFGA KGSYLP SFLLGFTQVGWFGVGVAMFAIPVAKAMDWNVYLLIIV

FGLAMTASAI FGMKSLVILGYIAVPAIAILGGYSMFEGAGSLGGLQGLLDYTPQTTLT

AAAALTICIGSFISGGTLTPDFARFSRTSKQAVTATVIAFFLGNSLMFLFGAVGAMAY

NLADISEVMFLQG LIIPAIIVLGLNIWTTNDNALYASGLGFANITKISKKFFVIVNGI

VGTVFAMWWMYNNFVSFLNLGA AVPSIGAI IADYFIVKRRNYKPFADMSFKNVNWVA

MVAWAIGVAFAQLAPGVTPLNALLGTAVAYIVLMLIVPAKESKEMGKINDYTERKIAG

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CDS complement(2504184..2504834)

/locus_tag="EFAGFIKM_02130"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRYSWWEFGFYLVLMFVLFMQINEYPLFLIVGVVVVTILIAFI

KHVFYPLVFDKRIDRLESFLSKQQNTPGTYYIIVLANRLDDEVELVMEQIMQKYKRKT

TQAQFKAAYGLYLKDMFAIRQAVAHIGLSDYRTYYETILLLEDGKSEDARERLQSIKK

QWMRSTLLAGLELKAENRDTAIQHAHEALNSSRGVNRVLYKEYERVLPEVVEHIS"

CDS complement(2505026..2506060)

/locus_tag="EFAGFIKM_02131"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRIAIVGAGSLGTIVGAYLADGGLDVELIDAYQEHVNALNQTGA
KVTGTTEFQAKVKAITPDQKSGQYDLVLLLTQQLYNNSILQELLPFLKEDSMVCSLQN
GIPEEKVASIVGEKRVIAGSVEFGATFIEPGVSSLTTEYTQFKQYAFQIGELNGEITE
RIQRVKSVLDLVGGTHISDNLVGTKWSKLLINNAFSGLSAALNGEYGDIIDHEAGIVS
AAHIADETIKVARANGVTLVKMNGFDIASLELNSEEDIPERVKTLRYVMEPSRLLKAS
MLQDLEKNRKTEIDYINGVSSRAEGTGIATPYNDLVVKLVKSAEETQTPDFDTNIK
AFEEILSAHK"

CDS complement(2506075..2506821)

/gene="adc"
/locus_tag="EFAGFIKM_02132"
/EC_number="4.1.1.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P23670"
/codon_start=1
/transl_table=11
/product="Acetoacetate decarboxylase"
/translation="MKIDVNNIKAKNLNTPLTAPAYPMPPYKFVNREYLNIIYRTDEKA
LRAAVPEPLEITEPLVKFEVMWMPDVSGLGAYTEAGQVIPVQFNGEEGDYVHSMYVDN
FPAIASGRELTAYPKKLGAPKLYTDSDTLVGTLTDYGTLRVATATMGYKHVEMDKEFAK
REICRPNFMIKIATDYTGNLRICDLIRTQITDIEVKEAWTGPRLQLFEHALAPLADL
PVLEVVSASHILTNLTNAAQPVYNYLEEK"

CDS 2506973..2507860

/gene="gltC_1"
/locus_tag="EFAGFIKM_02133"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P20668"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator GltC"

/translation="MELLQLKYFQTVAYTEHISKAAAQLNIAQPSSLTIKRLEDELG
TLLFHRRGRNIQLNPSGEILLKHVNRIFIEIENAEMEIKAEQQISNTIRISITNTRF
LTGLISDYINGSPETKLHQGIGTRSEITGLKKGDMHLGITGHPIQDEEIESVVLVEE
DIVLVVPMNHAYGGETSISLSVVANEPFISLADNKEYSRFTTMLCEKAGFLPNHAFEV
DSHTLLEIIRLNQGVALLPVSVCTRLGLRYAKIADDSAIYPISLSWVKQKWLSPAVRE
FRDFITSYYEDHAGLFKVE"

CDS complement(2507942..2509348)

/gene="melA_1"
/locus_tag="EFAGFIKM_02134"
/EC_number="3.2.1.22"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34645"
/codon_start=1
/transl_table=11
/product="Alpha-galactosidase"
/db_xref="COG:COG1486"
/translation="MNAKSTQHPKVVVIGAGSLFFGRQSIWQMVHSPYLNQGTALVD
TDEERLSKMKLAEMVAKENNVSLKIEGSVDRRQVLTGADFVLSFAEESVKYRGIDC
QISLKYGIRMCSGDTIGPGGIFRAMRELPVIMECAKDIEELCPDAWVINYINPSTVHG
IALHRYAPKLKSFALCDSHHMPHKKAYYAVRAGIIGDNSQFTEEINQEFDRIAGVNH
FTWLLKAEYEGTNVMPTIAEAMRKMAGDENNGGDRGAKALYNDAITYELYDIFGIPT
CTAHTKEYVRYWQGLGKTADTIPPLSIWETEDRYERHDEMWRQVDDFLAGNIPIADYM
STFGPDHATDIIENMVGNLGKKFFINTLNQGAVTNMNADSFLELLCDVDMDGVKPLHV
GEMPRGIRGMQELVLDTHELTVEAVLEQSYEKLRRAMLTDPVSSISDADKIIHELLE
LERKMIPDVWYKDRLQYS"

CDS 2509546..2510376

/gene="rhaS_16"
/locus_tag="EFAGFIKM_02135"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1
/transl_table=11

/product="HTH-type transcriptional activator RhaS"
/translation="MSIIDELSEYITLRMSSYLEQTHDSNWTEHKSHSDYDLWFITAG
SVLITIDGIEHMANPGDVVFFYPDMPYTASTTGELCRFVYMHFDFSIAEQKRILGEFQ
LPGIVLGNLIQEESTLFTSSYRRFKQSSGASASPLYLKASLLLVIAKILELHGQGLYH
GEFLKDRKPRKIEGSLEVLQNVFPYVDANLHRAIRVNELADIAGVSEKYFISLFFKIL
GITPGQYINQIKMNRARDYLYEKYTIQQIAGFLGYPDPFTFSKAFKKFYNVPPSKFE
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CDS complement(2510475..2511599)

/locus_tag="EFAGFIKM_02136"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MWTLHCGKPSRQCLLEEIIINFNEAVNISNTHLLTLVSELFHLE
GYNIQLIPPHEGGRNVVYICEQEGRESLILRVSFLPDRKREDYIAELEVVRYLFEHGA
SVSNVVSSKKGHLLEEITYDEHTFFVCMFVKAKGKLLVENHYQYREGVPLSEYYYNSG
KVLGRMHQLSKGYTPIHRRHHLIDNYSGEYIDNLVPESFPLLKEKMVELLNTLEGLDT
NQETFGMIHFDYNDGNYSIDFTGQITVYDFDNSCFGWYMYDLADLWTHGVGWIQFEP
NADKRKQFMDDYFQTALAGYTSETKIEDSMLEKLPLFIQVTLLLENILGQFEEMQRAGE
ELEANEELLYLIKCLEEDIPYKGFFHEMYSTEAPFEYEGR"

CDS complement(2511773..2513239)

/gene="bglH_7"
/locus_tag="EFAGFIKM_02137"
/EC_number="3.2.1.86"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P40740"
/codon_start=1
/transl_table=11
/product="Aryl-phospho-beta-D-glucosidase BglH"
/db_xref="COG:COG2723"
/translation="MTKTIKHSFPEGFLWGGATAANQLEGAYDADGKGLSTSDMAPFV
PHEERNKGKDFTFDVSQLEEYLSGNTNVYFPKRNGVDFYHRYKEDIALFAEMGFKVF"

RLSIWTRIFPTGEEAVPNEAGLAFYDNVLDDELLKYGIEPLVTISHYEMPVELTRKYN
GWESRE MIDLYLK FANTLFDRYKDKVKYWITFNEMNMMLTSLYTG GILEDKIKGSQE
QVAYQATHHQFVASALAVKSGKEKMPNAQIGCMICRLETYAASSKPEDVLQTMKEDQM
NLFYPEVQARGEYPSYMQRYFEENGIKLVKAPDDDAIRDNTVDFIAFSYYMTYIGKY
DPNDNSNSGMLVSQIKNPHLKATEWGWPIDPIGLRVALNRLYDRYRMPLFIVENGLGA
KDTLEEDGSVHDTYRIEYLRSHIEQMKEAVADGVELMGFTSWGPIDIISCSTSEMGR
YGFIVDQDNAGNGSLERTRKDSFHWYKQVIETNGEIL"

CDS complement(2513282..2515219)

/gene="bglF_7"

/locus_tag="EFAGFIKM_02138"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P08722"

/codon_start=1

/transl_table=11

/product="PTS system beta-glucoside-specific EIIBCA
component"

/db_xref="COG:COG1263"

/translation="MNHRELSKEIIQLTGGQENITQAWHCITRLRFNVREQNKVQLEQ
IKALDGV LGAQFQNDQFQVVIGNQVAAVYEQIEDQMKQSGIAKPETDAPRSKGINAVL
DTISGIFT PILPAIVGTGMLKGILALLVTLGAIQENSGEYQVLSSIANAAFYFLPFL
ALSSARKFKVNEYIALTLAGTLLYPTMLNAYLANQLEPIRFLSLRVSIVNYTQSVIPI
ILGVWLLSYVHRWVDRFIPGPVKVIFTSMIVLVITVPILLIAIGPLGNYMGIYLEMGT
SWLFAHSGPLTGII LGGFMPLIVMTGMHYAFFPGTLQNLSKLG YDVLLLPINLITNMS
QAGAVTAVFLKTKDKKMK SIALSSGISALLGITEPALYGVTLKLKKPFYASLIGGAAG
GGFITAVGLKCFGFAVPGLLSLPLYIGPNGGMSNFWYALIGIGISFTVSFVVTLLLKW
DETARNSDMSDSAQTLTEQE QDTTAFSQETVTPVTVHSIEEKKGEVFSPLTGELVP
LAELPDQTFAQEMTGKGIAIRPDGRVTAPFDGTVTLVAKSKHAIMLTSSSGIDILIH
VGLNSVSLKGKYFDVKVVTGQEVKKGDLLLEFDM DGIQGAGIDLVPVIVTNTPDYLD
VVPVQVKGVIPMNELLLLTVR"

CDS complement(2515378..2516226)

/gene="licT_5"

/locus_tag="EFAGFIKM_02139"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39805"

/codon_start=1

/transl_table=11

/product="Transcription antiterminator LicT"

/db_xref="COG:COG3711"

/translation="MRFKSLNNNIALAEDAEGCEVIVIGTGVGFKKVKGQPIEQSQI
QKMFRIGSNDKYQRVEQFLSDIPLQVIDITDQIIEEGKTMIGKKLNDILLSLTLADHIH
FALDRFKKGVDVQNPLHWDIRHLYPAEYRAGEWAVQKINDAFLVSLPSGESSIALHF
VNSQFDSGSMNQTIKITQMINDILGIMTEHFGMALNQESADFSRFITHLRYFIVRQLN
REVLSFKDQQFLYDVLSEYRYPVSFQCALKIKEAMEQQRGFVITPDEMYYLMIHIERVT
SRTDTD"

CDS complement(2516457..2517389)

/locus_tag="EFAGFIKM_02140"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMLGTDAASLLIYEALASEARLNIVRLLLQNREMHINALAQELF
LSKAIVSTHVSKLQKAGIVGSRMKRENGGTYKYCFIVREFMTINLSPEPVDAPYHEIS
IPVGQYTDYEAWPTCGIATTTQMIGQYDTPACFMDPDRVNAGILWMARGFLEYKIPNY
LYNDQHLREIEISLELSSEAPKVNENWPSDIRFTLNGNDLGTWTSPGDFGDRKGKHTP
LWWKLDVNQYGVLMKMLRINGEGTFIDGQRISDVVRVQDLELGASTYWTFGLKPEEGVAG
RGGLTLFGKGFGNYDQDILIRYYYDAQENKTPDE"

CDS 2517598..2519106

/gene="abfA_1"

/locus_tag="EFAGFIKM_02141"

/EC_number="3.2.1.55"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9XBQ3"

/codon_start=1

/transl_table=11

/product="Intracellular
exo-alpha-(1->5)-L-arabinofuranosidase"
/translation="MLTSKMLIDKDFQIAEVDPRVYGSFIEHLGRAVYGGIYDPGHPT
ADAQGFRQDAIEAIKALNVPIVRYPGGNFVSGYNWEDGVGPVAERKRRLAWWTIET
NAVGTNEFADWAKLVGTEVMMAVNLGTRGIDAARNLIEYCNHPSGTYWSDLRISHGYK
DPHKFKTWCLGNEMDGPWQIGAMTAYEYGRIANETAKAMKWVDPDIELVACGSSSRDM
NTFADWEATVLDLTYENVDYLSLHQYNNNKDNTYDFLATSLDLQFIDSVASICDFV
QAKKRSKKKLMSLDEWNVWKSIGTSRMEERWQIAPPEFEDVYTHEDALAVGCYLITI
LKHADRVKMACLAQLINTIAPIMTENNGAIWFQTTYPPFMHASNFGRGTVLRSITSSP
KYDSKDFTDVPYLEAISVHDEENGITITIFAVNRHLDEKLELNVDLRSFGETTFVEHIV
LENNDLKATNTKENPRNVVPHNGGYTTVDQGKVQAVLNKASWNVIRLTKQA"

CDS complement(2519690..2520262)

/locus_tag="EFAGFIKM_02142"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAKTNEIHVRVKRLKDRPVCVTLHNGETYVGYISGVNSEGVVLT
GGGKLTQTAITAPSSSEGSARKTKPKAGATRKTVSSRNRKRVNSTRKSQVRSRSMRSK
SRQAQVSSFMPMLGSLGGFGGAGSIGGMLGGGMRLFGMIQRFTPVVKMGYGMIKQIQ
PFMGAVQGLMTPASQAAQAETDGEIEEAQQG"

CDS complement(2520379..2521293)

/locus_tag="EFAGFIKM_02143"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31606"
/note="UPF0413 protein YjbH"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSNESMMCDLETGVCGVNEEEAMQEINLNHVEKRITLYYATDPI
CSHCWALEPVLHRFIEEYGHYFTLQIKMGGLLANWNGFSDGANGIHKPSDVAEHWKEV
GEHSRMPIDGSLWHDNPILSSYPPSRVFKVIQSTHPGKEQDFLRRAREAVFAFNRNIG"

EDDVLTDIVNQLGLNGKEVVEAAAEQSAQELLEEDFESVASLGVRGFPSIIIVNEENQ
GMKIVGARSLETYVQALQQVLGGDLKPKQITSLEQKINEGHLLFSKEIEGLYSIEKSD
IESYVKSELAEHTYRIGHILNEMYIEHI"

CDS 2521428..2521775

/gene="yrbR_1"

/locus_tag="EFAGFIKM_02144"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37486"

/codon_start=1

/transl_table=11

/product="putative HTH-type transcriptional regulator

YybR"

/db_xref="COG:COG1733"

/translation="MKYEFNFDQLCPATYAFQVIGGKWNLPILAILSEND CIRYNELK

RRLPGITGTMLTNCLKDLIHSGIVHREQYNEVPPRVEYSLTESGKELVPLIESMVIWG

QKNMTAGVKQQDI"

CDS complement(2521937..2522401)

/locus_tag="EFAGFIKM_02145"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MERKIRNSAKALIIKDGRMLAMKQDDNDEVIIYILPGGSQNAGET

LTDVAKREVAEEIGIDVEPLSLEFVIEGVYGEALHRVDFVFLCEYIGLMDQDSSILPS

DENQVEYEWLEIKNINELPLFPSKLRKQIIRLVEGEKTVMYLGNEEDDDLNS"

CDS complement(2522513..2523397)

/gene="glrR_3"

/locus_tag="EFAGFIKM_02146"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94501"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator GltR"

/db_xref="COG:COG0583"

/translation="MEIRQLKTFWTLASTCSFSQTAELLSYVPSTITMQIKSLEEELG

VKLLDRLGKKVVLTDAGQQFLPYATKILNDVEEAKCISSQHGELAGTVVIGADEVLCA

YLLPALFKRFRADYPGVRLFRPLSGQELKSSLREGHTDVVFLDEPINSKDLHSEFL

KDETQFMVSPDHMLASRSALVIDDFHKQHFLLTEKNCSYRTYFDQSITKKGADALTE

LEFHSVEAIKQCVAAGLGIALLPAMALKKELSDGEVVALPWDLSDVSFSAQMLWHREK

WISPSMAAFMEVAKSELI"

CDS 2523522..2524532

/gene="metXA_2"

/locus_tag="EFAGFIKM_02147"

/EC_number="2.3.1.31"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q3M5Q6"

/codon_start=1

/transl_table=11

/product="Homoserine O-acetyltransferase"

/db_xref="COG:COG2021"

/translation="MNDYETYNLGDTLLQSGQQLPQAFIAYKTYGNLNAAKDNVIVVP

TWFAGIHTDNEWLIGTDKALDPSRYFIIVPNMLGNGLSSSPSNTAPYDKNNFPLISM

YDNVRAQHQLITQKFGISKIKLVVGWSLGATQVYQWGTSYPEMVERIAPFGGTAKSSP

HTQLVFEMIAALQADSNYKNGRYERPPVAGLAAMGRAYAPWGFSQAYYLEKLYQSEG

YDSLKSYVEDYWDQVFLPFDANDLITMLRTGIYGDISDNPIDDGNFEQALSKITAPAL

VMPGSSDLFFTPEDSSYDAQHMPNAVYQPIESKWGHCFGIGANEEDSLVIDHHLKQFL

ET"

CDS 2524719..2526323

/locus_tag="EFAGFIKM_02148"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKKTKALVLSVCMSTLLLAACSNNGSGADKGSTTDTSNEAGTT

TIHTVTSEYSSAKYPKGDDITNNVWIKRYKEKFNIDVKTDWVSDEYDTKLNLAIASND
LPDVFRVNPSQLRQLVEADMVMDLSEVFDQHASDRLKGYMEADADSYESGKKDGKLYG
IPQMHWGGLIEQPDFIWIRNDWKEELGVQDPKSVEDIKNIALKFMEKHGGYGIADVQSL
DYLNLLAIAWNAHPDMWMEDSTGKLVYGSVQPEMKNALAEWSEWYKRGIIDPEFAIKD
FNAMNADIVAGKVGMQPYQWWGYNPGVDTVSNLGKDAIFYPIIPTVDGKEAKQSIF
FANNNYIVMKKGFKSPEEVIKILNDYAYIVDEGNGKESTETLSALLDNDIAHVGAFR
VLNPNSDYEQFEAVSAALQSKDTSGLTSGMWQKYNNSVEFIENATPGAVGDYLQQGA
PKNAYGLAKKVLDSENYTKTALWGVTPPEILSSYGTTLDDILTEGFTKIIMGSESIDYF
DVIVQNWRAAGGDDATQAVNEAYGKK"

CDS 2526414..2527304

/gene="yteP_16"

/locus_tag="EFAGFIKM_02149"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system

permease YteP"

/db_xref="COG:COG4209"

/translation="MLRKWKQQSPYHLMLIPSLVLVIFCYIPFYGLIAFQKYNPGL

GFNSPWVGWDNFTNIFNQPNFVRTIWNTLYMSVFKIIGGIIVPVIFALLNEVLHSGI

KRTFQTLVYIPNFLSWVIMAGIMLDILSSDGIINTFLSVFGIAPISFLGTPSIFPWTM

IVSDIWKGFGFGTVVYLAALTSIDPGLYEAAVIDGAKRWKQTIYITLPLLMPTIVLMT

VLSLGNVLNAGFDQIYNLYSPVVYQTGDIIDTYVYRLGIQQAQYSIGTAVGLFKSIIS

SVLVAVSYILAYRVAGYRIF"

CDS 2527323..2528213

/gene="dasC_3"

/locus_tag="EFAGFIKM_02150"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9K489"

/codon_start=1

/transl_table=11

/product="Diacetylchitobiose uptake system permease
protein DasC"
/db_xref="COG:COG0395"
/translation="MIYDKSMSRRVFLIINYTILLISLLCILPFINLLAVSFSSSAA
VSAGSVTFWPVEFTTKAYEFALTGGSFFSSLWVAIQRTVIGTLVNLVLIVLTAYPLSK
SKQKLMGRNIYMGFFIVTMLFSGGLIPTYLVVVKMGLIDSIWSLILPGALPVFSMIIL
MNFIRGLPEEIEESAIDGAGPVQVLLRILLPLLKPALATVGLFSIVAHWNSWFDGII
YMNNPDNYPLQSYLQTLLQSFEQIMLKSGSDYTQLLSMMNARTGRAAQMFLGAIPILL
VYPFLQKYFTKGLVLGSKG"

CDS complement(2528321..2530066)

/locus_tag="EFAGFIKM_02151"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKHVRPFRIKYKIMVICMTVIILPVLVMTINSYSSERLLAQNY
TLLNDLAKQTNIRIDEFLKEIEKISLLASNGLSDNLSATHEGSFPIQDFLREGDEQH
EIAAYNILMNYIMMKDRVFSIYLYNMNGGQDLFVSPHQPIDPNFKVANELWFKKFMHD
KDRTITLTRIDEQLENKILAVSHARKIHDTVSGKLLGVIVVSIDIKFIEIVNRNLQE
GLRSRFMIVDEDDKIVYNVNERLIGTLFRDNVRPPEALNVVVTSPQSQQKWTTYLYMP
LDELTADGKILGRNLVTLAIVIVLFAAVISIFLSHVITTPIKKLLRNIALVEKGQFEQ
VEPIGSRDEIGHLSIRFNRMSELKRLVERMQQEEIEKAKAEMRALHDQIKPHFLYNT
LGSVKWIASMQQADKIVEMTDALISMLRYATKSDGTLVTIREELDNITNYVTIQKVRY
YDCIQMRYEIEDRVLDYHMPKMILQPIVENAIFHGLAELEEDGIITIRIQLRVDTVVI
EICDNGVGMDHHTMQNLLEEKSSASTGTNGIGLHNVQRRIQLHFGKPYGIQVESKMGE
GTIFSILLPAIIEAK"

CDS complement(2530095..2531711)

/gene="cheB_6"
/locus_tag="EFAGFIKM_02152"
/EC_number="3.5.1.44"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00099"

/codon_start=1
/transl_table=11
/product="Protein-glutamate
methylesterase/protein-glutamine glutaminase"
/translation="MYKLMIVDDELLMRVGIRSM LNWA EYNFYVVG EAANGKEALSLA
LEVMPDLIITDIKMPIMDGLQLIQEASCVLKTCKYVILSNFDEFHYVKEALKLGASDY
LIKSEITESSLIDLLSTVGQKLQSEHVHPTNTPSITQDYSKSLRYLKDSFFQDIVSGF
ISEEDIVTKAEELHFIRSDQLVVMKFIVNYYE DAKRKYIEKGEKLLRFSILNIMEEI
IPSKWEKEIFVESSEYWWIVNVLPESQSVHADLNKLCNKLLSSIKDFMNLSLTAGVS
RMTSGFLHIRKACQEAETALQQGFFTGSNQVLYYDDMVQSPDRHEVKGALSPQQERDL
LKLWVSKDNQKAE EFLEGI RSNLEQLRADENSIRKQYIMVMETIHSHLSRATERGAPS
LTEKSPYEIVLKGEYWEDIHQDMLAHIAYYFQTDSQIKQESTYTDLATELIDKYAED
ISLQSIASQISVNPSYLSRVFKQERGENFITYLTRVRIEHAKAYLLSRGMRVYEIAEK
VGYHNYTYFSKIFKKS VGVTP EEYRELQQG"

CDS 2531899..2532174

/locus_tag="EFAGFIKM_02153"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNLYKFELTVNGYLLRVHFSASEESGLKWCKRVASEFQNNVANL
EIKVDIHKKQKQKHAREYHGKPYLYDRTL RKKPLAKKNKVSESSAVM"

CDS complement(2532366..2535026)

/locus_tag="EFAGFIKM_02154"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNRYTSLTQKYL LGQKKRSILTIVGIILSVTLLTAIGTIGLSFR
DKVVRQTVQEYGDYHVSFNGLPGEAVSRVNNNTSVESAGIISREGYSVISKTSEKEKK
ENPFAAPYRYLNLKGYDADAMNMLQVQLDSGRLPKNSHEVLLSTWSLDRFATKPKLGD
SITLSLGERTVASTGEIKPINGLGDFGWDLDEDFHPQKEREFTVVGFMKTGTNASWSA

SFILPAITYEDNEKIDADKNYFIYVKMKSMNHIKAKTEAMISSLKLEQVDQGSIALD
KDIQYKNIRVEYNNELLKLYGKSTYEGVNHSLLYAFIAIIIIIMGCTSAVIYNTFHIS
VLERTSQFGMLRCIGATPSQIRKLVLEATILSLIAPIGLLTGTVMKLLFYNISFL
ALGFLNDMQMVISLPILIIAGVLGLLTVYLSAIGPARLAAKVSPLEAIHSSGSTKVED
ITSVRKSKLLGKLLGIEGQFASRNIRRNKKRFRITAFSIVVSMILFIVFSGLAGLLGQ
TSQSGIDYSYSVIYEGPSKRIDDSVYSDIVKLDAVEHAYPYYINQVMATFPKEKVNPK
YYELRPGMYSVEEGEGYRTDNNYLESYGDNGLDALKSKLTAGKIDKEKMNRENGVIVN
QKLRMTTEDGRQIVMDQTQFKVGDHIKVRSLDSDEKGRGYTTMTVTGIVDQGLLSSNY
NESAVLEFITTPEVVEKVTGNDTYSRIFILAKSDISNKPITDYLKSLPQKDAGYSYTD
KVEQLAQAKNDATTAKIFLYGFIGVIVLIAFLNILNTVSTNLILRSKEFAVLKAIGMA
QRNVGKMILLEGVLYGLYAAVYGSILGTVLSYGIHHLFKGAFDVGWAIPWSSIVLACA
GAITTTLVATVWPMYRLNQTSIVEALRKET"

CDS complement(2535023..2535709)

/gene="lolD_1"

/locus_tag="EFAGFIKM_02155"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P75957"

/codon_start=1

/transl_table=11

/product="Lipoprotein-releasing system ATP-binding protein

LolD"

/db_xref="COG:COG1136"

/translation="MEILKTDHLCKIYGSAEARVEALRDVNLSVNQGEFVAIVGASGS

GKSSLLHLLGGVDQPTSGHVIIDGMDLYSQSENELAVFRRRKIGFIFQSYNLIPVLTA

EENIKLPMLLENKHVDEGYLEELLSVLGLSDRRQHLPSQLSGGQQQRTAIGRALINKP

SIILADEPTGNLDSKNSKEIVDLLTYSVRKYNQTLIMITHDLNVAQRADRVVNIKDG

LLQQTGVKES"

CDS complement(2535815..2537062)

/gene="sasA_6"

/locus_tag="EFAGFIKM_02156"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01837"
/codon_start=1
/transl_table=11
/product="Adaptive-response sensory-kinase SasA"
/translation="MFEVMRNPEWKSIKVLALQVLLSLMMFLYMQHQVDSINTTIV
NQNSALIGHLLMKNPQLESEVIHFVTQGAQTDEIAKGQRILAQYGYQEDMPIEEQPAL
SGRALPLKTATQVLLFLIPLMVLLLWEYRTFFVKIRTISHAAEQVVEQQFDKKLPETE
DGDFGALGRSFNAMAGRLTNSLELLRQEKTFLRNLLSDISHQLKTPLASLIVFNENLL
NDPGMKEEMRMTFLERSRQQQLDRMEWLIISLLKLARVEAGAIGFRKERIELREMLESV
VYSLRTVADQKRPNMSILGSENAFVQADEEWLKEAVMNLIKNALEHTPPEGEVRIHLE
ENALFDTHIIQDN GEGIH PDDMPHIFKRFYKGKNHNKPNSIGIGLALT KSIIEEQQGI
ITVESVLQEGTTFRISFFKKERT"

CDS complement(2537065..2537760)

/gene="regX3_1"
/locus_tag="EFAGFIKM_02157"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P9WGL9"
/codon_start=1
/transl_table=11
/product="Sensory transduction protein regX3"
/db_xref="COG:COG0745"
/translation="MNRLLLVEDDDNLVFGIQYTLSNEGYEVVWAGNLEEARQALQAK
SIDLILLDVTLPDGSQYQLCSEIRVTSQVPIIFLTALDEEANVVAGLDLGADDYVTKP
VRTKELISRIKAVLRRNNKGKQEVSLWISDNQVRILEGTVLKYNSEVTLTALEYRLL
LMLISHPKQICSRSSILNHLWDLSGDFIDDNTLSVHIRRLREKVEDIPAAPQYIVTVR
GIGYKWNVEVIGR"

CDS complement(2538001..2539728)

/gene="hepA"
/locus_tag="EFAGFIKM_02158"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P22638"

/codon_start=1
/transl_table=11
/product="Heterocyst differentiation ATP-binding protein
HepA"
/db_xref="COG:COG1132"
/translation="MNELTILSKAMIQELKDILLSILGGFIAGIAGVALFSASGYMIS
QTVFAPPLYTLIVLTSMVKLLGFLRAASRYGERLYSHRATFSMLSRLRTSFFAKLIPV
TPGILNKNRSGDLLARIVGDVESLQNYFLRVAYPPIMVVMVFLATMLFTSAFSIWIAC
LLVLGMLITAFVVPGIVLLGQRKIHGVRVQRALLSTEVTEVLYGFRDLKVYGGQLEQR
EQQLQQASAALATEQKQAASHLLRGQSMHVFVTYLVTWGVLALSAFLIVNGAFAGVFL
AMLILATQTVFEEAAAMAILPLYKLDSEHAAQRLAETVPTSDVQPVQPSGEVSADQSV
SIELSGVNFQYEGEWRPALRELSLQLAAGSKTAIVGPSGSGKSTIIDLLLKLRTPTSG
NIRLNDVPVQELNEESIWNANVVLQQSHFFRGITRDNLLLNNGEEHSDEQLSAVLDKV
QLSNKLLSDLVYEKGENLSGGEKQRLALARAMLRKGRLWLLDEPTSSLDYVTEQRLVQ
HLFAQAAEDTLLICHRLTGLEEMDRIVVMDQGKIVESGSFSELMEQKGYFYEMKQIE
RQMIGDAGA"

CDS complement(2539725..2541548)

/gene="cydD"
/locus_tag="EFAGFIKM_02159"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P29018"
/codon_start=1
/transl_table=11
/product="ATP-binding/permease protein CydD"
/db_xref="COG:COG4988"
/translation="MKRRAKSNLISQQMSLQRKNRLLLAISLALGVAIISQATLVAE
AVQRIFVEKASFSSVILLGLLLVMAVRSLLSYGNGKVGLHMAARAKTNMRASVLQN
LTRASMPSTLRGQTGGKVSVALDAVDEADSIFYSQYMPRMMEAAMIPILIVTFTQHA
NTGWIMLFTAPFIPLFMILVGLQTKNKSEEKQAQLAEFSGTFLDSLQGLVTLKIFGRA
KRQQQEIERSSLYRDATMGILKIAFTNTFMLESIVMLSIGIVALELAIQLLVFKSMS
FHTAFLVLLVPEFYSLKNTGTAFHSGRTSMGAIRKVEQMLADTSVKSTQTKPEEGP
DQSELTDVDAIAKTEELRTARAELIPMPPTIELNDVRFQYTPDSFGLETGQISIGPGE

QIAIVGKSGSGKTTLLHLLIAGLLKPDSGAVLVNGSQLSQHDEAAWFERVSYITQHPYI
FAGTFAENIAIGAGRNVSRAKIEQAAEEAGLAGVVAQLEQGLDTFVGEGGRGLSGGEK
QRLALARAFLLKRPVILFDEPTVGLDLHTERVLQQSIAALAKTATMITVAHRLYTIQH
ADNILFMDSGVLVDSGHHEALLARLPQYAEMVDVQRKGGLA"

CDS complement(2541563..2542576)

/gene="ythB_1"

/locus_tag="EFAGFIKM_02160"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34505"

/codon_start=1

/transl_table=11

/product="Putative cytochrome bd menaquinol oxidase
subunit II"

/db_xref="COG:COG1294"

/translation="MSYELIGISVLWFLYGYLIVASIDFGAGFFAFYARLTQDHLI
NRLISRYLSPVWEITNVFFVFFYIGIVGFFPDATYYYGSALLVPGSIIVILLAIRGSF
YAFENYGSKKSVYLFYLGATGLLIPASLSVALTLSEGGFILKQGDTVSLDYWALFTN
PLWSIVGLAIVSVLFISGSFLTIFYASRAEDHSALKLMRNYALFWSTPTIILALTAFI
YLGQHNERRHFQNMMDLWLLALSVAFFMIAMWLLYNGRRYGLAFICIMLQFLTAFFAY
GIGQYPYILDPIYTIQSSATSPAMGFALVVVFIGGLCLLIPSLILVFKLFLFDADYVK
GKK"

CDS complement(2542576..2543940)

/gene="ythA_1"

/locus_tag="EFAGFIKM_02161"

/EC_number="1.10.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SP90"

/codon_start=1

/transl_table=11

/product="Putative cytochrome bd menaquinol oxidase
subunit I"

/db_xref="COG:COG1271"

/translation="MAIDTVLWSRLVTGLTLGFHVIFATLGVGVPLMIAIAEFIGIRK
KDHYYILMAKRWSRGFVISVAVGVVTGTAISLQLALVWPNFMKLAGNVIALPLFMEVF
AFFFEAIFLGIYLYTWDRFKNPYIHWLLTIPIVAGAGMSAVFITTNGFMNQPEGFVM
EAGQFMAVNPVQAMLNTATFSKV FHLSSAYLTGAALLAGIAAFAMLRKGV SAYHKKG
LNLMMAVVLVFSLLNSLAGDVS AKFLAEHQPEKLAAAEWHFETESGADLIFLGWLNAE
HEIIGALHLPKLLSFLAFGDFNAEVTGLNEFP PDEHPPLL VHLYFDLMAGIGFALLAI
SSLYFLFVFWKKRNQFNKWMLRMVALSAPLAFLAVEMGW FYAEIGRQPWIIRGYMRVE
EAATSSPSVRILFFVFLLLYILLGVMCVVLRRLFN NNP AELEMEKWLKEKHDQSAKK
GDQV"

CDS complement(2544269..2545660)

/gene="ribZ_1"

/locus_tag="EFAGFIKM_02162"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q180E3"

/codon_start=1

/transl_table=11

/product="Riboflavin transporter RibZ"

/translation="MNV RNKGLMLAVGFGIMLNPLNSSMISVAISRLQQVYQLNFTAV
SWIILSFYIASAVAQPV MGKCSDLFGRRKIFLMGLVIVFVSSMLAPWSPSFSWLIVFR
IVQSIGTSM MVAVGMAIVRINVTEKQASALSTLAIFLSGAAAIGPFIGGVLIHWWDWH
SIFVNIPIFVLASFVFAWKTI PKDEQSPSISGHMSIRQWLALIDAPGILMFTVALVTL
LIGLLSVNSTGDISTWHLLTGGIGLIALVMFIRHELKAATPFIPLRTFSSYPEMTWVN
VQYMLVNILFYALFFGVPTYLKQVRHLNEVHTGMSMLALGLCSVIIAPIAGRWDGSG
SRPALIVSASLMTFGSILIVVMNETSPIIIIVALALFGISNGLNAVGMQAALFKSTP
KEMIGVASGIFNTSRYLG TILSSLLIGIVMGDTFNVTGFQKLGIIITVLAASLIIMSV
RREAGAVSPEKVK"

CDS 2545770..2546645

/gene="gltC_2"

/locus_tag="EFAGFIKM_02163"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P20668"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator GltC"

/translation="MELLQLKYFLTVARCEHVTEAAGKLHVTQSSLSKTIQRLEDDL
G
VPLFDRIGRKLRLNDFGRTFLQRTEKALFELEQGKREIADLSNPDQGTQLAVTTAST
LPGILREFRKNKPDIQFHVQMVLENMSRLLHRGEVDFCLSSPPIQGDDIECQILYDD
PIVVAVPMGHRVADRSSISQLTELKDERFVGVKQGYGVRDMVDSVCQSAGFLPKYVYEG
DEPARLTALVEAEIGLAFIPSTARNPHERIRYLQVEEHQLVREIALLSHKNNRYISKAA
LEFRSVVMDYFSAMP"

CDS complement(2546884..2547450)

/locus_tag="EFAGFIKM_02164"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIGYGLLLFVIVAIFINYNLQITPLILEKNIGTATNGSNIIAFI
GLGAFVAGFSFGKVYKTFGNVIVPLSILLGSSMFVTTISQSIILTTVCSMIIGFSFR
CIMPYLLHTFAQHIAKVAKLGTITVLIAYNLGATLSPYEGRIITQLQLDQTVQSLISS
NAMILLVSVASFGVVTLHRKKKNIQQT"

CDS 2547658..2547843

/locus_tag="EFAGFIKM_02165"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRWMRKHREQGEFGLMDQGRGRKEYLDQERYVQKLKRENELLK
KCLVIWKEEANKKDFRS"

CDS 2547792..2548676

/locus_tag="EFAGFIKM_02166"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISBth8"

/codon_start=1

/transl_table=11

/product="IS3 family transposase ISBth8"
/translation="MLGNLEGGSKQERFQIIIEKVAAYGDIQKLCDVFGVSRSGFYAYV
KRRKFRDRDAKAKKQVLQTYQRYEGKYGYRQLQLFLWQDQGIWMNHKKVLRLMQMLGIQ
SRIRRKRRSNSSYAPAQRVAENRLKRDFSAEKPNQKWVTDITQYRVGERWIYLSAIKD
LFNNEIVAYEIGERNDNELVLRTFSKAFKQTDVTGLVHSDQGFQYTSWAYHDMPLK
VGAQISMSRRGNCYDNASMESFFSHLKTEGLYPYHIRTLTEAQSKIEKYIRFYNRKRP
QRKLKKLTPVEYRRQFAA"

CDS complement(2548697..2549344)

/locus_tag="EFAGFIKM_02167"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEKLKTYSLLSVALLNSSGPVIAANIPAITNDFPEISVTHVGLL
TTIPSLFVILGVLIANRLELLIGKKATILTGLGLVLIAGVFPALYHDLFSLLFISRCL
FGLGVGLFNRLIIQMISDMYHKNPQKQATVIGLESAFEGLGIGICTLLVGQLLKMGW
TSFYVYALALPIFIAFLIFVPSDKKELNRREEVTTNPSHTNNKKALQVMIGQDPI"

CDS complement(2549476..2550900)

/gene="bglH_8"
/locus_tag="EFAGFIKM_02168"
/EC_number="3.2.1.86"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P40740"
/codon_start=1
/transl_table=11
/product="Aryl-phospho-beta-D-glucosidase BglH"
/db_xref="COG:COG2723"
/translation="MTRKDFLWGGAVAANQCEGGYAEGNKGLSTVDVIPAGKDRVPV
MRGQLKMLECDQEHFYPSHEAIDFYHRYKEDIAALLAEMGFTCFRLSLAWTRIYPNGDD
ELPNEEGLKFYENVFDECLKYGIEPLVTITHFDVPIHLVKTIGSWRSRKMVDYYERLC
ETIFTRYKDKVKYWLTFNEINMLLHLPFGSSGLVFEEGENEDAVKYQAAHHQLIASAK
ATEIARRINPAFQIGCMLAGANTYPYTCAPDDVWKAMTRDREHYFFVDVQSRGEYPNY"

AKKMLERMNIHLAMEDGDEECLKNNTVDFVSFSYYGSRLTSADPEVNTQTAANLFPTL
RNPHLKTSEWGWQIDPEGLRITMNSLYDRYQKPLFIVENGLGAIDTPDETGYVADDYR
IEYLRQHIQAFITAVEEDGVELLGYTSWGCIDLVSSSSGEMSKRYGFIHVDKDDAGNG
TLKRNNKKSF EWFKKVVSNGKEL"

CDS complement(2550929..2552818)

/gene="bglF_8"

/locus_tag="EFAGFIKM_02169"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P08722"

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/product="PTS system beta-glucoside-specific EIIBC
component"

/db_xref="COG:COG1263"

/translation="MSKKYEKLAQDIVEKVGSENVSTLTHCMTRLRFALNDTNKADQ
KALKSFDGVIDAVESGGQFQVVIGTHVEDVYKEVIKHLQPNASSSGEPTQARKVSILG
KLIDFVSGTFSPIVPAIAGAGMIKALLALLILFNWISKDSQTYVVSLMSDAIFYFLP
FLLAFSAANKLKCSPLALVLAGVLLHPNLTLRLDGTDSVFGIPLTLVSYSSSVVP
ILLIVWSQSYIESLFKRIIPNAVKVIFVPMCTILVTGILALTVLGPLGSFFGTYLAMG
FDFLGAGHSWLVI FLVATFWPILVMFGLHHNIVPLSIAQITTSGYENILGPGAMINCI
GQGVAALVGMRTKDKALKQISASSGITALMGITEPALYGVNLPKRYPLVAGMIGAAS
GGLFAGLMDVSRATGASGIPAIPLYIGENIWNLYNIIALVITTVTAVLTYLLSLK
YEKDAPSQNTVSNTNAGSGVADEVITIKDSVIATPLKGQLIQLQDVQDAAFASEAMGK
GIAIEPSEGKVIAPFDGMIVSLFPKKHAIGLLSDEGVEILIHVGLNTVKLNGKYFEAF
VEEGQRITKGQTLTFLDKIRQEGYVTQTPVIVTNSYSYSDVIAEISPQNIDFNNTL
LVVKA"

CDS complement(2552997..2553878)

/gene="hcaR_1"

/locus_tag="EFAGFIKM_02170"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q47141"

/codon_start=1

/transl_table=11

/product="Hca operon transcriptional activator HcaR"

/translation="MELRVLRVFLTVARVENITHAATILHVTQPTLSRQLADLEKNLE

TQLFIRGKSKITLTDAGMLLRQRAEEILTLADKTEKEFKDQNNLVGGTVSIGSVESLT

SNVILQLLKDFNMEYPQVKYHIYSGTGDDIKERIDKGLLDVGILLEPIHIEKYDFIRL

PQKERWGVLMKTSSPLAQKEYVTSTDLAGVPLLISSRSVVQNEIASWFADEYAHNLFV

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SQTEVRFLEHIRHAFQA"

CDS complement(2554007..2554762)

/locus_tag="EFAGFIKM_02171"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNRIEKSQETYKRLFGEGVPAAYATHPEFQDILSRFIFGEIFDQ

GALDDKQRELITLVVLATNQTLPLQLKAHTRAALNVGLTPTEIQEALYQCAPYLGFPKT

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KHIQDYLSAFCFGDFYTRGGDLKLTRELLTLCILSALGGADSQVKAHVQGNINVGNNK

ETMITALTHCLPYMGFPRTLNALACVNEIIEPK"

CDS complement(2554961..2555932)

/locus_tag="EFAGFIKM_02172"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNEEQFKQNYKKAVDHMKTNEQMKKRVEQSLNTQHQGPKRQRKP

LYIAASVVIASIGLAAPSVWQQFNGPAAPTQVAAVTPGASVDPIVIPKMELPSSQG

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SNIGEADIVAVNGYDKDFRIMSYTEIDGQVYAQLFDKNNGITIGTGADLIGKLHLEGN

IASAQWETFNSWNNGLQQLQLPADEALDNFISSLNAAKPIATSLELEENLYGKEDRK

IYLTLEDKTQVPLVLFGDGLVRYGNVPAFLEVEEGAFQSFWNSLGE"

CDS complement(2555932..2556423)

/gene="sigW_3"
/locus_tag="EFAGFIKM_02173"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q45585"
/codon_start=1
/transl_table=11
/product="ECF RNA polymerase sigma factor SigW"
/db_xref="COG:COG1595"
/translation="MQRSVPQLGDHVMKVYETYADTLFRIAMVHLGRREDAEEATQDT
FIKLIEKAPTFNDAEHQKAWLIRVITNHCKSLLGRGWRKREVKLEGVDPLTTDNPEDH
ALIELVLSLPVKYRSVVHLYYYEDYSIREISEILEISESAVKMRLKRGRQLLKLELEG
EEL"

CDS complement(2556575..2558155)
/locus_tag="EFAGFIKM_02174"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MMIKKIGISVASLAITSVSFVDVYGAGSKRMIEVSEQSANVVV
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TPQSRDQFIDGLKESLGDNKVDILASAFEEGKDPYLRPYDLATKYNEYVEDGDWVKLY
EDYVTQSTGTHYAKEVLLQFFSDDFYQRLNAEEFELKDEKGKVKLSNPTETASNLYEL
YIISNIKGEQDFEFGRYFTANQLKWYESVDNINDFYEKGPSLTSTDLPQNIIAPLVK
ELIVSTDQSIQQKDTAGIFRFAHAETIIPLSSFLDIAGANVSIDKPQDVTQNWNGSVI
SPMGANIQWILYSNGKDVLVKMLRNEEEIAFPIETKTPYYKWEDVKAYYQNKLQKVG
VSLDSSLEDNIELLQKKF"

CDS complement(2558397..2558816)
/locus_tag="EFAGFIKM_02175"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MKLEELFTVRVNIEESFDLQNSEDDSVMITFTGSVTGKYFEGI
VLGGGVDTQIIGKNGDPHTLSARYMLQGTDNTGNSCKIYIENNGNIDKTLKTALFRTS
PKMITDSKALSFLNRETLVGEGHPTESGIDIKIYRAL"

CDS 2558945..2560156

/gene="tetA_2"
/locus_tag="EFAGFIKM_02176"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P02980"
/codon_start=1
/transl_table=11

/product="Tetracycline resistance protein, class B"
/translation="MTYMSTLPKSVRFPLFILMLNLFIALLGQGMLIPILPEYLKLFH
AGGTVAGFLVAAFCAAQFFFSPLGGQLSDRFGRKKLIAGMFLSVISDIIFALSSSLP
FLYVGRFIGGISLGLMV PANLAYVADITTPETRAKGMGYFGAAMNLGMVLGPGLGGLI
AEMGIRMPYFFAAGLGLIAALMTLLLPETLPPEKRTVSIRLQKGDHLGKKIWSSFVKVP
YFKYLIVLLVMTFGLMSYETVFALFAEQKYGFDAATISIIITLGAIIIGIVVQIWLLDW
FVQRIGEVKLIRLSLIVTPIALLMLIKVNLVFLLFASALFFAFNSFLRPSVSTLISK
NAGDRQGYASGLNTTFSSLGTVIGPLIAGLLFDKNINFPYIFGAIMLLASLGLTLNAF
RSKKGQLYTSE"

CDS 2560149..2560793

/locus_tag="EFAGFIKM_02177"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MNENWHQQLGNKHRDDLIAAGKELFLKYGLLQVKIKDVCTKAEL
SRVTFYKHFQSMDELLAIQMQLIEHLTDEVSRASKDLNGREQLRVMLNAWVVYAEN
HPDYIRFIQLFDINYEMYDFSPELREEYDKFNQNGKENHFLMGALSQGVVDGSIKNPS
PPLDLAQFIFTMMGMLQRMVTIRAAHDNSLDMRMTEQFVKMLLHFVCSEEIPE"

CDS complement(2560885..2563146)

/gene="nagZ_2"
/locus_tag="EFAGFIKM_02178"
/EC_number="3.2.1.52"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00364"
/codon_start=1
/transl_table=11
/product="Beta-hexosaminidase"
/translation="MHVKWMTIIGAVVGSMLIGVGTAAAEETFVDLKYSKWAEDGITY
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REIMIAAKNGLASGFPNGTFRPDAPLSRAETA AFLTRAYALVEGKNAAKWTDTRHWA
AAPILIMSSNGLVGGYSDATFRPNQAVTRA EYAVF MARVIRFEREAAIRTQDWDKLIS
YMTVSEQVGQMLMPDIRQWNGKATTTVNEGLKRTIHDQDLGGLILFDKNIVDVTQLTT
FTHDIQREAGDIPLFLSIDQEGGVIKRIPGGTNLPGQMALGATGDATLAEAAGQLTGE
ELKALGLQINFAPVLDINSNPDNPIIGIRSFSGSEADLVTRLGLATIKGLQQSGVMAAV
KHFPGHGDTTVDSHLGMPVLAHNRRERLDAVELKPFRAAIKNDVEMIMTAHIAFPaidN
EHVTSLKDGERVPIPATLSKKVLTGLLRGELGYEDLIVSDAFTMNAIAEHFGENQSVE
RAVSAGVDIILMPKDSAAAHQTLVKAVNNGTIKDATHASVKRILEMKAKYGLFERSQ
TLAQKLTQLNGIIGSKAHRAVEQTIAERAVTVLSSREGVLPDPMKQGDRVVIVAAEQE
QAKQLEKQLLQAANNLSLKTEISLVGQGKTNETLQAIGKADYVILASYQFRNVASQFG
WSEYQTLINAMNKSQRYTLFSLGNPYEMIYLNVRSGLAVYGKQEPNTSAGIKVLLG
QLKAGGQLPVLTD"

CDS complement(2563245..2564165)

/gene="araQ_14"
/locus_tag="EFAGFIKM_02179"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94530"
/codon_start=1
/transl_table=11
/product="L-arabinose transport system permease protein
AraQ"
/db_xref="COG:COG0395"

/translation="MRKGNTSRLRNSSTGDRAFTFNIIFMICLMIVTIYPFVNMIASV
SFNNANDAIRGGIYLWPRVWTLDNKYIFGESDIYHATLISALRTVIGTVVSVFCTAM
LAYTVSRQEFVLRKFTVMFFVFTMYFSGGIPGYLLIRDLGLIGSFWVYIIPGVIGVF
NMIVIRSFIEGLPEGILESARIDGAGEFTTFIRVVLPLTIPAMATVSLFVAVGQWNSW
FDVFLYNSSNKLSTLQYELMKILQTSTTSATSSASDAYQSAESNATAVTPTSIRATM
TIIASVPILMVYPFLQKYFVQGMTIGGVKG"

CDS complement(2564181..2565152)

/gene="yteP_17"

/locus_tag="EFAGFIKM_02180"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system
permease YteP"

/db_xref="COG:COG4209"

/translation="MEKPNVSLNSMPPASSPKGTRAHSFFKRLVQQRTLAWMCIPFVI
WAFIFKYLPLWGWTFMAFQNFKPARSFSDQQWVGWHHFSILFEDNTFYRVLRLNTLMSS
IKLVLGFVTAITLALLNELKNVIFKRFVQTVSYLPHFISWVWASSIVLTVLSPDGII
NLLLMLKLHLIDSPVLWMGKGEYFWGILGATEVWKDVGWNTIYLAAITDPAQYEAA
EIDGASRFKRMLYITLPGLKPVIVILLIMNMGSILESGFEPQYLLGNGMNMMDYSENLD
IFVLKYGLGMGNFSLGTAAGIFKTVVSFIFLFSANYIAKKMGESRLF"

CDS complement(2565444..2567120)

/locus_tag="EFAGFIKM_02181"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIKPKFRTVGLAVLLTALLAGCSQNSSSSAPSATGDDENSPVTF
SYYMFPSPGKKDVLASETTIGKALQEQTGVDWKMEYLVGDSATKAGVMIASGDYPDVIS
SSGEMSKLLDAGAYIPLDDLIEEYGPNIKRVPYFDKMKNAEDGKIYALPYTANQGE
YSGSPNVGGGAFWIQRSVLKEFDYPKITTLDYFDLIQDYKEKHPTVDGADTIGFVSL

AGVANNFFTLQNPAMHLAGYPNDGSVMVDMTTHEAKVVAGTDAQKKWIQKLNEINAQG
MLDPESFTMNKDQYLAKLTSGRVLGYFNYGWQVGDASKNLLSAGIDEKRYAPLPIVFD
EGIKDQYVDPGPFVNNYATGISVNAEDPVRIIKYFDNLLKEENQVLVQWGIKDETVSV
DEKGRFYFANEDQRKVHDDLELSRKFGFTYFGSDWPRYGGESTLTDGNAYSPGNQPEV
AAASYTEGDNKFLEAYGIQTFSELFNKPEERPWFPAWSIALEQGSPEQIFTTKSDDLQ
RKYLPEMILGAPSNFDKLWDAYMAELNKLDKAGYEATITKVVKDRVAGKW"

CDS complement(2567163..2568824)

/locus_tag="EFAGFIKM_02182"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFRKKNIITGLAILLAVTLAGCNKASPEASYPDSNDNTPVTFKY

FTFGGGKKDILASSTIGKKLQEQTGVDWKMEYLVGDGATKAGVMIASGDYPDIIDSS

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PNFQTGFYIQRAVLKEFNYPKIKTLDEYFDLIEQYKQKHPQIDGKETIGFATLAGESG

SFFTLNPNAMHLAGYPNDGSVMVDMQSHKALVAGSDYQKQWIQKLSEVNTQGMFDPE

SFTMNQDQYLAKLTSGRVLGYFSYSWQVGDATNNLKKAGIDDKRYVSLPIVFDSDVKD

QYVDPGPFVNNYGVGIVNAKDPVRIIKYFDNLLKEENQILVQWGVENETYSVNDEGR

FYFENDDQRKAHEDPELSRKFGFDYFNYSWPRYGNNSVLEDGNAYGPGNQPEVATFSY

TDGDKLLLEKYGVETFTLSTPDERPWSPAWSIALEQGSPEQIFITKAEDLQKKYLP

KMIMDSPSTFENTWNEYMSQLNQLDKKTYEATITQAVKDRVAGKW"

CDS complement(2568946..2570685)

/locus_tag="EFAGFIKM_02183"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPRWNLNYMKLRDKLLLMYVLSVFIPIVVTNVVFYNVTSANIRS

QKTRDAGMALNNLKNDLRVITDQGVGLSYSLYTDPVFNDTISRFSHFYIDAYNSY

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SSDQMLSLVQRLDNLDTGGREQLLKIDLNMDMIKQYFHNSGFDGKVYLLDPGGYIQFS

NDPTAEEAQIGKRYSEIQFPNKMIPFELTYTGINYLEGWSLQGVMDEEIVLKEVRKSR
SFVWWLACINFLPSIIIAAMSRTIHVRILKHKMKVKTQNFQTIPPEDARDEIGQ
LTMEFNRMETETIHNLIEVYLADIQKKDLELKQQQAQLHALHSQINPHFLFNTLESVR
MRSLIKGEKETAKIVHNMAKMFRRKSSWNQNDVTVKEELELIESFLQIQKYRFGEKLQ
YTIEADPAVLMYRIPKMVILPFVENASIHGIESSPGVGIIQLFVSMENDQLHIRLTDN
GIGMSHAKLEELLSYLDQNTDMGEHVGMKNAYSRLKLCYKNHFTFDIQTWEGEGTRIQ
IKLPLDPSDMPGD"

CDS complement(2570667..2572253)

/gene="cheB_7"

/locus_tag="EFAGFIKM_02184"

/EC_number="3.5.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00099"

/codon_start=1

/transl_table=11

/product="Protein-glutamate

methylesterase/protein-glutamine glutaminase"

/translation="MLKVLLVDDEMYVRKGLYELINWMDLNMEIIGEAENGAEALNLI

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EMLGINRNSLLMTLIELQTGLDAIKITIEQLREAVHSLESNLCKMFISEQQRGTFAL

LLLWPDHHQGGSALQDKLHSIHITMSKRFLNDIGLYAGTLVKKIGDVPQSLVAAEEAA

KHKYAETSSVRYTEIKDKPLFVFNQYQDEVDQLILSLEEGNRPAYHKIVEEKFILFH

MNRFSPQAVSGSLLRYITGILAVVNEMGGNDEGLQQLKELAQSHDGWNLRLLKNAFL

IALEEAEYVSHLRMERSKGDISKIKRYIDANYTENINLKSIAALFYMNPVYLGRFR

KSYNQYFNDYLLNRIHEAKLLRQTDLRMYEVAARVGFQNADYFVTQFEKLVKLSPT

EYRNLLMGNEQRGAQCQDGT"

CDS complement(2572359..2574341)

/locus_tag="EFAGFIKM_02185"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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DIQIYNEGQNAWAGVIHVEMPLDKQNPFFLP AFMYGRNRGEAPQNPNEFPRLREGS
PSRPSSPWWMVRSDRLSHPAALIYDEGRIVGLSASPYWINTGNQKQWYPGMEGTFVQ
YGGFTCSIEKGTVG YTLGYENAPLLFIKSRLVHERAALGENCFELAAGESVGLTLELY
NYQSESELGINPALETIYKRYHEKPREGSDIQTTVTDLSNAIYEYAWLPEDRHYSTFV
YEDAAETGGYRYNKIISISWTNGMTIAAPMLMAALRLNNEPMRQQALSCINNIIENAM
NPESGLPYDAYQDGIWGVKGWWFDGMRTPGHSSYLVAQAMFYILKSYDYEKHIRNVRH
DDWLAYVKQVLDRLECTKNTDGEYPTILSERTGAGLEYDAFSGVWCLA AKAYYCWLTH
DESSLDELRRSEAHYYNTYVQHMECYGAPLDADKAVDSEGILAYIKAVRFLHALTGDE
LFLDHMRDAISYEFSFKFCYN SPIKIPPLSILGWSSSGGSVTSVANPHIHPMSSNLVD
ELLYYVGQRDENYVRQRMMDTIGWGCQTYNRYDQEFGYGKKGWMSERFCHSEGLVTEK
YADGTPASTWFCLMPWASGSII EGLVGDYWDYARHE"

CDS 2574501..2575352

/gene="rhaR_14"
/locus_tag="EFAGFIKM_02186"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01533"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaR"
/translation="MNETSEYLFDP IQNELLYLHRTTTYNMGT FYHRHNAYELYFLR
GNVNFYIENHCYHLQRG DLLVLSPEEMHRSFALDKNEYERITINLKKS YLNRLSTSST
NLSACFDYRPKGKGNIVHLEEEELQRVLQLTDELEQCLSSSDYGADILGNILITQLLL
LTNLT FQNTDFVATDIMPELVRNTMDYIECNLTRQLTLEQLSEAMFTNSSYISRQFKK
HTGLTIRAYILSRRIELSKSYLMEGLSITEACYQSGFGDYANFIRSFTKQVGTSPGKF
VKYGRLL"

CDS complement(2575471..2577789)

/locus_tag="EFAGFIKM_02187"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MKTKNIGFNQPAGTWEEALPIGNGLGGMIFGKTQIERIQLNED
SLWYGGPMQRNNPQALESLSQIRSLIFDGKIREAEELAADTLVGVPDGGQRHYEPLGDF
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GKLSFSTIFGRGTVLESTKYSDILKHPVGFQSYLDRIEKRGTDNLIIRGRSGGEEGIR
FCCAIRLISEGGQVHYSSGQLSLKDGNSATILITACTDFRVPKEQLEVECLRRIEAAS
AKPYSELLADHVSDYQSLFKKMDIHLEDENKDVICSELPIDQRLERLRAGKHDPELMS
LYFQFGRYLLISSSRPGSLPANLQGIWNKDMPLPVWDSKYTININTQMNYWPAESCNLS
ECHIPLDFDFIDRLQVRGKETAETMYGCKGFVAHHNSDIWADAAPQDVCMTSTFWTMGG
AWLSLHLWDHYEYNKDAQFLKKVYSTMKDAAMFIMDYLIEDPSGNWWICPSSSPENRY
ILDDGESGALCFGASMDNQIIRELFTRCIESTRILQEDQEFGEVLRSAITKIPETSIG
KHGQIQEWSNDYDELEPGHRHISHLFALHPGTQITLQSTPDLAKAARVTLDRRLEHGG
GHTGWSRAWILNMWARLEESELAHDNIVELLRSSTLPNLFCDHPPFQIDGNFGGTAGI
AEMLLQSHNEVIRLLPALPAAWPKGYIRGIRARGGFEIDLEWENGRLNTRIRSAES
RVTVSYLDQKIELTFPGPNAMIELKGNKWNNK"

CDS complement(2578076..2578501)

/gene="slyA_2"
/locus_tag="EFAGFIKM_02188"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01819"
/codon_start=1
/transl_table=11
/product="Transcriptional regulator SlyA"
/translation="MTNTVDCEIRQSLDRISSQMRRNYSESLRELNLYVGQDNLLYRL
WLGDGVTQMQLSEHMKCEPPTVTNMVKSLEQNGFIYRKRVDQDARIMRIFLTDKGKEL
EKPVEHKWREQQEKLQSISSDRLILRQFMQQMERNIL"

CDS complement(2578709..2579470)

/locus_tag="EFAGFIKM_02189"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MKLTGNTIFITGGGSGIGRALAEALHKLGNKVIISGRRKERLEE
VLSANPGMSAVELDIQDLSSIEATAKQLIRDFPDLNVLFNNAGIMLFDEAAGVIDEEV
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YTLSQRYLLKDDTTVKVLEIIPPGVQTELMTDLSNDQHAMPLEAFIEGTIRLLGTDAEE
VLVEQAKMIRDNQGPNEGAFVTQLNDMASQAAKGH"

CDS 2579710..2580255

/locus_tag="EFAGFIKM_02190"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGLKVRNIRTTTRTRESIFESLFELMEEKDFDKITIQLTERAQI
NRATFYAHFQDKYELLDEIRKSAEELIQHTNGVCAFTKNNMMQLVFAAFEYHQVK
KKCRRNYNKIIPLLSSKLVIALKHYLDLCMQNIYSDERTLYVQIYANMINEAVTLHTA
EQTKLTERSIAEHIVQMIILD"

CDS complement(2580424..2581164)

/gene="nfsA"

/locus_tag="EFAGFIKM_02191"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P17117"

/codon_start=1

/transl_table=11

/product="Oxygen-insensitive NADPH nitroreductase"

/db_xref="COG:COG0778"

/translation="MNHTLELLHNHTSFRSYTSQPLTEEQINAIQFQAANQTSSFSLLQ
AVSIIRITDPVIRNKVRKLSVNQPYIEEAAEFWIFCADFNRSHQIAPEVDIEYIEFLL
IGSFDAGLVAQNALTAESMGLGGVFIGGVRANINELSEVLNLPKYVIPLVGLCIGNP
AGDKPELKPRLPQSMVLLNHYHSLDQEKLATYDETMLKYYENRPTAPFTVKKVKGW
SDHIQDHLQRSIQPMMDYLNKQGFACK"

CDS complement(2581238..2582341)

/gene="iolG_4"

/locus_tag="EFAGFIKM_02192"
/EC_number="1.1.1.369"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01671"
/codon_start=1
/transl_table=11
/product="Inositol 2-dehydrogenase/D-chiro-inositol
3-dehydrogenase"
/translation="MSKKIRTGIIGASINNGWASGTHIPAIEHLDEFELTAVGTSNMA
SAKKSAEAFHADHGFENIEELAQHPDVIDMVVVSINVKEHYNVAVKTIAPAGKPIYCEWP
LGSNTDESIEMQKWVASAQLPNAIGLQARQAPAVQYVKDLLAEGYVGKVLNLSANLKISI
DGMGGVGDKSTAYLYDRKVGGNLLTIVGGHNLDFTYMLGDFTELSALTAQQFPEVEL
VDIQKTIKTTDDQILIAGKLTSGAAASIHIQGGVKHQTGLTLEIFGDKGTIVLSAPA
SIQFGSHQLRGAGATDNELHELTIPDAYYWAPHSLYNDSGFVLNMAQAYRKFAQDIQE
GTTLAPTFADAVKLHQLLDAVEKSAQTGERQYF"

CDS complement(2582385..2583512)

/gene="moxC_4"
/locus_tag="EFAGFIKM_02193"
/EC_number="1.14.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34974"
/codon_start=1
/transl_table=11
/product="Putative monooxygenase MoxC"
/db_xref="COG:COG2141"
/translation="MAARKLKLGGIIDGVGWNHTGWRHPDTPADASENIEYYVQKAIQ
LEQGKFDLIFLADVSHIGPGMIPHYLSMFEGISILSALSMVTHSIGLAATIATSYADP
FTVARQIASLDKISKGRAGWNAITSNPGGLANYSRSHLTAKADLYPMKKEFLEIVEGLW
DSYEDDAFIRDKERGIFYNPRKMHPLDYTGNYFSVEGPLNISRSRQGRPVPVFQAGTSP
AFMDIAAKHAEVIMAPGHDLEYLKAFTAEKLRKVQNNQGRSPHDLLMMPSHNPVIGRTE
KEALEKLREMESWMPQGYRMTKPGLIGSAEHVAEQIEHWYRAGVMDILLIRQDHPAGF
KDFIKLVVPIQDKGIFRKEYEDDTLRGNLGLPYPENQYTK"

CDS complement(2583542..2584072)
/locus_tag="EFAGFIKM_02194"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVPDMFMLGSSEGGLHFALEKGLGFVFAAHLAPQLAIPVLRAYH
ANFKPSSYLTEPQSMLATMVITAETEEEEAKYIAGPAELMWAQMSTGTRNLTFPTPEEA
KNHRYTPHEELARERNKDRFVIGSVGQVADQLTLAKASLVDEIMIADFYPNQESRKK
GHELLAKELGLSQGNK"

CDS complement(2584125..2584574)
/locus_tag="EFAGFIKM_02195"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSTANGIKLSILEFVHIYAGYEASESLQNVTEMVQLAEQWGFNR
YWFAEHHNTKNLMSTSPDLLSMHAAAHTKNIRVGSGGIMLPNHSALKVMENFTLLEGL
YPGRVDLGIGRASGTDGRTMWALLRSQELMEVNDNFPEQLDNAFLLCF"

CDS 2584826..2585170
/locus_tag="EFAGFIKM_02196"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRVCNEGFEQEFIDGKSDMYAIAFTQNVLSGRWKYFILWYLKNE
TRRYTDIKKFLGDLSSQSLTKQLKELENDGVIQREVYPEVPPRVEYSLTDKGMKLLPI
LEKMEDFGKEYG"

CDS 2585222..2585437
/locus_tag="EFAGFIKM_02197"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFFFFFFLLGMIGLFFGVRALRRPNSWPFNRTKDELHEYDMMG
IKFRGVFLLAFGTVLTIASVRLLLIDK"

CDS complement(2585473..2586444)

/locus_tag="EFAGFIKM_02198"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDNLISQALNKAHMGIMIVDRHLKVVVWNAWLERFTGKNVEEVV
GLNLLEVCPRFKSNMYLNILQNALYHGQSRFCSSALHKAFILPNEGEDEQLFRQNMHV
EPLYHEDRSYALIQTDMTNTNTRVYKLKNLIKELEYAKIKISEKISKHLSLHDPL
TGLPNRLAYNDRLAWAISNAKRHNHKLAVMFVDADGFKQVNDTYGHHVGDQVLLEMAK
RLSETIPSADTVARLGGDEFIILSHLKDDHDAEVIKRLEAAFSTHFKIAGNYINLSM
SIGISLFPKHGQEPSELLRHADGAMYKIKKNGKNGYGIYEPENAEEI"

CDS complement(2586437..2587072)

/locus_tag="EFAGFIKM_02199"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLNDLQKDLLTELNVVYVGQAANMLSEIVDKRIVLNIPEVELIS
ISDVDPGDRRYNIFFSEGHLFRSSLQFGYEFQGKAFLMFPVEQAKVLANICLGELGES
VIPNDPNLMDTDLDVLKEVSNVLLNAIGELGNFLEIKLEYVLPDIELIYVTNSDQQI
LLQNEVYVLVLHTSFLLADTDVTGIIVIALSMNSISSLLAKMDALLEADNG"

CDS complement(2587062..2587436)

/gene="cheY_1"

/locus_tag="EFAGFIKM_02200"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q56312"

/codon_start=1

/transl_table=11
/product="Chemotaxis protein CheY"
/db_xref="COG:COG0784"
/translation="MKVLIVEDSIFVQKLLTKLIVDHIPGCEIQIANNGEQGYNLFKE
FQPDFITDLLMPGLNGQEMLRMIRETDSNVKIIILSADIQKTRDEVEMLGISGFLN
KPLTAEKATTMIQLIQAAAYHAE"

CDS complement(2587720..2588622)

/gene="araQ_15"
/locus_tag="EFAGFIKM_02201"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94530"
/codon_start=1
/transl_table=11
/product="L-arabinose transport system permease protein
AraQ"
/db_xref="COG:COG0395"
/translation="MGINKSRLEPIVFHTLNGILMIAIAIVTLYPFVNTLAVSFNAGN
DTIRGGIYLWPRVWTDQNYRAVFAGGTIFSAGFISVARTVLGTVLSLFLTSMLAYTLS
RKDYILRKPIITVVLTMYSAGLIPTYFLMKDLHLLNNFLVYIIPGLISAFNMIVIR
TYIQTLPGLIESAKIDGAGDFRTFISILPLCQPVLATVALFIAVGQWNSWFDTFLY
ASSKQNLSTLQYELMKLLSSSMNSNSSAAVANGADLGAARNMVTPVSIRAAITIVAAL
PILVVYPFLQKYFVHGLQLGGVKE"

CDS complement(2588635..2589600)

/gene="yteP_18"
/locus_tag="EFAGFIKM_02202"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:C0SPB3"
/codon_start=1
/transl_table=11
/product="putative multiple-sugar transport system
permease YteP"
/db_xref="COG:COG4209"

/translation="MANTPGAIP EQTTRTVVPKAPLLKRLRGQRQLMFMSLPVAYIL
VFSYYPWGWVMAFQNYSPAKSFTQQEWVGLKHFLLTDDAFLNVLNRTIAMSVINM
VLGFATAIIFAILLNEIKHKLYKRTIQTISYLPHFLSWIIVTGIVASSLSVDGGIVNV
VLMKLIHQEPIMWLSVPEYFWGIVGASHVWKEVGWNAIYLAITSIDPSLYEAAEI
DGANRYKKMLYVTLPGIKSIVILLIMNMGWILEAGFEVQYLLGNGVVVDWSQTIDIF
VLKYGLQIGNYSLATAAGIFKTVVSITLIFAANSISKRLGEDRLI"

CDS complement(2589713..2591368)

/locus_tag="EFAGFIKM_02203"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGGLKKKKLWGSVSLVLALSLALAGCSGDNEKATTKDGKEVLNI
TAFIGTPNQAPAKDNRIYKKIQDELGVNLEMEFLVGD LQQKLGVM IAGGDFPDLITAD
TKLVSAGAVIPLEDLIEEHAPNLKKHFGKDWNRMKDSSDGHYWLPNYGVYTGEFISN
YYSGPAFWIQKSILKDAGYPTPKTLDDFTKLVRDYAAKNPTIDGQPTIGFTTLASDWR
TFPLLNPPEHLTGHPNDDGGVVDDSGVATVFADKDISKRYKELNNLYNEGLLDKEAF
VQNYDQYLAKISSGRVLSMFDQHWNFQAGEDPLVAQGKIGQTYVGFPLVYDTSITDHY
LDRPVINLNNFGISKDAEDPVALIKFLDKLMDEKYQKLLSWGEEGVYQVNEEGRFY
RTPEQRTEQDDPAWRLVNKAEGFYAAAPKLEGTFEDGNAIGAINQPEEFYDNLKPEDK
ELLDAYGFKTWSDFPAPENPVYPAWQVDLKEGSDAAVANKQMTDTS LKFLPKAIM
SKPNEFDNIWIEYVDAYKKIDVKSIEDRINEQLKWRIENWSVK"

CDS complement(2591508..2593049)

/gene="cheB_8"

/locus_tag="EFAGFIKM_02204"

/EC_number="3.5.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00099"

/codon_start=1

/transl_table=11

/product="Protein-glutamate
methylesterase/protein-glutamine glutaminase"

/translation="MYKVLLVDDEPYAIEGLQLLINWEKYGFEIRGVCANGEEAIRMM
EQDRPDLVVTDIRMPVMNGLELVEEARREHESVLFVITSGYSDFNYARQAIRLGVS
N
YLT KPVD TTEAEDMLVRLRMQLQERETQERIREHANEQRIKAFLSALIKDKQNISEEE
MSEIRPRLNKSHWAYLRIAFQGGDIQEVCSVVEQTAEETCCYVIDRTRDSLGLVWGEE
TND RNETFEAIKFTQRLMNNMQHNGCEEIHIAVGLTVNKLHLSSESFRSAQEVGRYL
FFNQERLLFAKDIQLENWQFDPETLSEVDHICDLENGSVEELSSAIRSAFELFVQMK
AAPEIVHIFSTHIIIFRGLSLCRELGGEPNALMNELASGILEKGHRNIEEVANNLEHFC
LQCKSALAI FRERQMGGIQATVAEYVQMHYRETFTIQELAERFYVNPVHLGQSFLRKY
GKG VIEVVHDLRMEEAKRLLQQTNTSSAIAEQVGYRSYQHFLRHFEKRTAMKPVEYR
QKYAN"

CDS complement(2593063..2594844)

/locus_tag="EFAGFIKM_02205"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRHKFWMFskVNDIPLRSKFLLIYVLSILLPVITINIFFYERTS
ADIKIREQENLRKSIDRAAGELLGMIDESVALSRIIAADDSLYEALDRTYHSPVDYYN
VYHAFRLDKLTRYMSANILEVRIYTDNDTIQTGSHYIVMKDKNVLPGLKQLKSTSGGI
LVVDYIEPSGFNAGRRISVIGKMDTYTSYANYNKYSKIDLELSRVYSILNRESDSLQL
RLVDSNNRTVVSSGEFSETDLSPLDNESMLKESGDSAYTLEKSLGNLAYLKGWKLIGV
ADTRHLDHLLQEAFKSILGLLALSIVVPSVLIYIILRSYHYRIRKLSRHMEKVRNERF
DLIEIHEGRDEIGGLIRTFNIMIGKIHTLINDVYKLEIRQKDLELDQVRTELSMLQSQ
MNP HFLFNTLNALLVVSTKNGYTEVIEIISLSKLMRQLLSHSDNLIPLQEELQFTNL
YLQIEKFRFGELFDYTFEVDPAASLLIPRMSIQPLVENACKHGLQARKNGREIKITA
RRNATELVIQVIDNGIGMDAGRLTELLRDIRSERPRNGEHVGLRNVYRRLELFYEGNA
IFDLSSVPGKETIAGYRIPISKLEQRK"

CDS complement(2594849..2595964)

/gene="rhaR_15"

/locus_tag="EFAGFIKM_02206"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaR"
/translation="MYKVIVADDEPFMLEGWRTMIDWRACGYELCGTATDGEEALALF
NSVEPDLVVTDIQMPVMDGLGLIHTLREDLAYTSKIVIVTGYSDFNYAKQAIRYQVDQ
YVLKPLVP EEIHQILMDMIEPLDKRRNEQKQKNGVTVTDEAYENHLNEYRIGEEYDLE
QMMNISKEILALIEAENTYSIDIAVSALLEKSEKAEVSLEWIIHHVIRYIHGELLRKYG
KREGCREILCEKDWHEAASWSSGTLQDLCVRLSKQLFQSELKQKTGTGGLVAEAVIEL
KQHYRSKIKLQDVADRIHVNSAYLGQQFKREMGVSFSDYVHQLRVEEARKLLRRTNMK
ITDIAFRLGYHDAEYFTQKFRAHTGELPSVYKNKNQG"

CDS complement(2596315..2597154)

/gene="pkn1"
/locus_tag="EFAGFIKM_02207"
/EC_number="2.7.11.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A0A0H3MBJ2"

/codon_start=1
/transl_table=11
/product="Serine/threonine-protein kinase Pkn1"
/translation="MKKLVWLTLIAIVVSLSACSASNTKLSDDLVFVEGGAFKSSKPS
QIDRNETLDSFYIGKYEVTQKEWMEVMGENPSGFKGDDLPMVMVSWYDAVEYCNQKSI
KENLKPYYNIDKDNQDTNNHNENDTIKWNVTINEDANGYRLPTEAEWEYAASGGQKSL
NYTYSGSNNPDEVAWYVWNAGENILTGDWSWTAIESNRNQTKKVGTTQKANELGIYDMS
GNVREWCWDWYSDSESPNQTWVRVVKGGGWIGGVNNNEISFRGKFDANGFGPDQGFRIV
RGE"

CDS complement(2597288..2597923)

/locus_tag="EFAGFIKM_02208"
/EC_number="3.2.1.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:V9TXH2"
/codon_start=1
/transl_table=11

/product="Endo-1,4-beta-xylanase Xyn11E"
/translation="MFKFSKLLTVVLAASMSFGVFAATSSAATDYWQNWTDGGGTVN
AVNGSGGNYSVNWQNTGNFVVGKGWYGTPNRVVNYNAGVFSPSGNGYLTFYGWTRNA
LIEYYVDSWGTYRPTGTYKGSMTSDGGTYDIYTTMRYNAPSIDGTQTFPQYWSVRQT
KKPIGVNSTITFSNHVNAWASKGMYLGNSWSYQVMATEGYQSSGSANVTW"

CDS complement(2597995..2598768)

/gene="xynZ_2"
/locus_tag="EFAGFIKM_02209"
/EC_number="3.2.1.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P10478"
/codon_start=1
/transl_table=11
/product="Endo-1,4-beta-xylanase Z"
/db_xref="COG:COG2382"
/translation="MELISPAVTGYDQYRENIPRGVMETVEYPSTTVGNSRKAMVYTP
PEFSSTMYPVLFLLHGIGGDETEWHTHGSPQIILDNLYNDHLLPEMVIVFPNGRAMS
NDRAEGDLFEPEKIKAFKRFESDLLNDLIPYMESNYPLHKSRDKRAIAGLSMGGGQSL
NIGLSNLDHFAWIGAFSAAPNTRSPELLVPDLKAPSSLSLLWISCGEQDNLIEISLG
VHQYLAHHGVPHIWHEESGGHDWPVWKNDLYLFSQRLFK"

CDS complement(2598810..2600093)

/locus_tag="EFAGFIKM_02210"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLQDSGDAGENTEFTAPRDPVGVGTASAVKPAIDFESHRYRDMIG
RSLLNKGNNVRLKRAIEKAKNGEPVVIAYIGGSITHGAGAVPIHLQSYAYRSYESFKF
MFALSKDSPIHLIKAGVGGTPSELGIVRYDRDVL RGGAVQPDIVIEFAVNDADDETQ
GKCYESLVLKALTADNKPAVILLFSVFENDWNLQDRLAPVGWHYDLPMVSVKDAVVDQ
FSKTRGEGNVISKKHFFHDIYHPTNIGHRIMADCLEYLFDVTNRSEWDEKDHDIEKAP
LIGNEFVNVKLLDRKNGNHIARIDAGSFCKTDTDLQMAEMDAHDYGTPQFPNNWMRTG"

EGKEDQSSFRISLQCKRLILIFKDSGNDEFGTAHIKVDGVFVQKVDPRQVNWTHCHAI

LLLNEEHVGEHSIEIEMAEGHEHKCFTILGFGYVD"

CDS 2600382..2601524

/gene="rex8A"

/locus_tag="EFAGFIKM_02211"

/EC_number="3.2.1.156"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0A0S2UQQ5"

/codon_start=1

/transl_table=11

/product="Reducing-end xylose-releasing exo-oligoxylanase

Rex8A"

/translation="MNITGQGAWDTGTYTNLFLKLGYDENEITNRLEETWNELFYGDD

NTRIYYPMGEDKGYLLDTGNLDVRSEGMSYGMMAVQMDKKEEFDRLWNFSHTFMQHK

AGRYKDYFAWHCKPDGTRLSQGPAPDGEEFFAMALFFASNRWGDGAEPYDYKAQARKI

LHACIHQGEDGEGDPMWDPETKLIKIPETPFSDPSYHLPHFYELFAKYADEEDQSF

KEAAAASRAYLHTACHPVTGLSPEYANYDGSPAPIQPHGDFRHFYSDAYRVAANIALD

WEWFRKDHQIEQSNRIQSFFSDIEMSDYRRYTIEGEPFDEPSLHPVGLLATNAMASL

AADGPHADTFVHKFWNTPLRQGERRYDNCLYFFSMLALSGRYRMY"

CDS complement(2601747..2603387)

/locus_tag="EFAGFIKM_02212"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKAGFIILACMLFTSLVLAGCSSSDKGKGEGSDPSGKTAINVF

AHQGSDTNLSTNKFTKKMEKFDIKFNWTTVPFDGAAEKQISLASGDYPDLYLLIPW

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LNECFHCSYPNKMWWNTKWMEQLGLTEPATTEEFKEMLRAFKTKDPNGNGKADEVPLS

GSTENFGVHIIPYLMNGFIYDDDRNYLIVNQGVETVVNKPEWKEGLAYIKSLYDEGL

IDPGAFTQNVGAFKKIGDNADAQLLGAGAAHPSLFVTTAEGSPYGNNDYNPIPLKGP

HAAYATYNPIDPGASVLTNKASEETQIAAIKLLDYLTQEGTMASYLGEEGVSWRK

PQEGEVALNDQIEPLYKAIPSPGEEPRNDSWAALSQYNHYQAYRDSEVQGGTDIYAND
GGERRLYEATLLMEGKEPKEIFPHWALWVDPSQADEASMMQTNLKDYIDQNALQFITG
AKSLDKDWDEYVKGLEGLNINRYLEIMQSSYDTSSVSK"

CDS complement(2603425..2604354)

/gene="melC_3"

/locus_tag="EFAGFIKM_02213"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34518"

/codon_start=1

/transl_table=11

/product="Melibiose/raffinose/stachyose import permease
protein MelC"

/db_xref="COG:COG0395"

/translation="MPNTQTNAGRSRIKSSSTIRESWGDRVFITVVYFMLTVVLI AVL
YPLIYIVSSSLSSPAAVSSGKVLWPIDLTFDGYKSVLRNDQVLTGYANS LFYTACGT
FISVALTIMIAYPLSKKTFVGRSSLMMFITFTMLFSGGLIPTYL VVKTMGLIDTRWAL
LIPNAVWWVQVIIARTFFQNSIPEELSEAADIDGCSDIRFIFS IILPLAKPIIAVL SL
MYAVGQWNAYFDALIY LKSQSLYPLQLILRSILILNSSTGSM DASEMIKQQQMAELMK
YSLIVMASLPVLIIPFVQRYFVQGMLIGSVKG"

CDS complement(2604382..2605356)

/gene="yteP_19"

/locus_tag="EFAGFIKM_02214"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system
permease YteP"

/db_xref="COG:COG4209"

/translation="MILRTTMTSESKSVEKPSKAFALKQALSRSWRRHWQLYLLILPP
IAYFIIFKYVPMVNAVLA FKDYNVIKGIWGSPWAGTKYFELLFKNPAFVMLIKNTLYI
SFYSLIVGFPIPILLALALNEIKNIRFKKTVQMVTYAPYFISTVVMVSIIMLFLSPRL

GIVNTIAGALGFEAVNFLGEPGLFRSIYVFSDVWQGMGYSAVIYLAALAGVDPSLYEA
AKVDGANRIQKIINVLDLPGLLPAAVILILSVGNIMAVGFEEKYLLQNPLNLSASEII
STYVYKIGLLNANYSFATAVGLFNSVINLILLIVNAVAKRLSNTSLW"

CDS complement(2605512..2607863)

/gene="rhaR_16"

/locus_tag="EFAGFIKM_02215"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MQLLWSKFSPVFRFLISYLVILMIPQIAGYASYRASIEAARSS

SIENSLKSLSLGKEIERNLLQVEAFTRQLAVNPDLQNLIAGPKPHDLYNVYGMNRMQ

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KQPHFNEIPLRNYKREILGTVLADVPAITFLQSLPLNSFNKPQATIGVMIDQDQMAS

LTQNIVDQYGGWTLVTD AEGQIIFSHGIEQAEAEQMAQSRQREGNDAKTELNVQNVQP

GSDGRLLISMQSSQNGWNYMAGIPEKALMTKADQIKQVTLVFTLATIALGLLFGLVLA

YRNSAPVYRLLASFREQITDSPGRRGNEYDFLASHINNLIANNDSLKNAMNEQIPLLR

DGFIKRLLTGEVYTSLELEVISSQAHISLHSSKGLAGLVKVNGYANPDSEETIHELGV

ARLLIKQVLTEWNAQLLITDWGTDQIAFACPLDENSLNEAIGRCEKELNTLMEVIYRE

HRISTTIGTGAAYEVWNDAGRSFDEAKQALDYAIHMGTDHLVRFEDTMKENEMFYYP

ESEQRLLNTIKVGEPEEAVRILEQLFLRNLEERELSYEMTQQFIMELKGTFLKLDEPK

FKLDASLLEEKTRVTSIQMTETITSLRAKFKRLTEDICGDFQRRRAGAHADTVSEMI

CFIQQHYGDANLTIYRIAHEMSKSEKFISQLFKEHTGENLSDYVERVRIDAASNLLHS

TGQTIDEIAEATGYNSAHSFRRAFKRVRGISPSVFRKMDVHSG"

CDS complement(2608157..2609863)

/locus_tag="EFAGFIKM_02216"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKFMTSCKLVLILALLITIAPWGGSR AEAWVGMPMGKLHVNGK

NLVNSNNQPVLLNGWHQPSGAYWTYQDSNYLNLHGNNRHAATLAYLKDITDTFADTS
AKYGSNHGWNMNQVRLFIDRQDMGDVAAGTYNFAGVQTVTQNVIIPIQYAKTKGVYV
VLGLDFTLKDDQATTPANLQKFNEIWGYLASRPEIKSADNVHFELINEPVKSYANGHW
GGYNGENDFVDHWNDLRNFQNSMISTIRSKGADNVIWAAGLGYNQFYSLTASHPLTDP
LNNYGYAVHWYPGYGAYDNFSILQDQWNTNVKAAADKYPINITEVTWFKNKP GD SAYW
NLFNGSNEGFGTNTKTIFNASGNVSIAAHMNGFILSEGPRSSFADPTAGLKWDGDASR
SAMGRFLFNWYHERAQTPGSGQGGGPTTGLVSGATYKIVARHSNKVVDVPGGQNN
LQLQQWSDLGGNPQKWVLTSIGNGNYLTLSVNSPDKVIDIRNGTLTNGEAVQLMSNLN
TTAQHFKVNDLNGYWSIVNVNSNKAIEVANASTSDGALLQQNTYTGATNQQWKFAV
SN"

CDS complement(2609946..2610080)

/locus_tag="EFAGFIKM_02217"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQHSICEKGACNDLMNVCSQQNRDPSLRRIPLLVWNGLRERAPT

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CDS complement(2610139..2611086)

/gene="dasC_4"

/locus_tag="EFAGFIKM_02218"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9K489"

/codon_start=1

/transl_table=11

/product="Diacetylchitobiose uptake system permease

protein DasC"

/db_xref="COG:COG0395"

/translation="MTTSRLLSLEHWKGWLWAMIRFVLITGLSFVILFPIFQKVSTSI

KAKGDLYSAVVVWIPQNFSIDNFKEAIRVMDYWATLFNTFALSATTTLLTTASCALAG

YGFARLKFRGSNWLFAGVILTILVPPTTILIPVYLNLSFDLMGLMTLIVGKPVNLLN

TYWPFILTAITANSLKAGLYIFIFRQFFRGIPKEVEEAAYVDGAGIGRTFSRIMLPNA

IPSMVTVMFLFSFVWQWNSFYTTTTLTSSKVMSTQLSSLPYNLAQQVTDGAASQADPF
YLSMIQDTGILLAILPLIIYLFVQRYFVESVERTGIVG"

CDS complement(2611104..2611949)

/gene="lacF_2"

/locus_tag="EFAGFIKM_02219"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29823"

/codon_start=1

/transl_table=11

/product="Lactose transport system permease protein LacF"

/translation="MWGVYIVLPWLIGFVLFFFIPLLASLRYSMTIQANAEGIAIQF

NGVANYIQALTVNTSFNRALIEAITDVLINVPLIVIFSLFLAVILNQKFRGRAVARSI

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AVDRIYQIVSQSGVQILIFLAGIQTISPQLYEASKMEGATGYEAFWKITFPMVSPLIF

VNAIYTIIDSFANNAMTELIRDTGFVKFDFGLSSAMAWVYFLAIAIILVIVNIIFSKR

VFYQD"

CDS complement(2612003..2614579)

/locus_tag="EFAGFIKM_02220"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNYTVAKKITGMLLAGSLLLGGCQFSPTPLAHETVTAADSTDFP

SLPPGEKLKSSFSDVRLPGMVGIAQNAALQLFINEETAIEIAVIHTQSGQIWRSNPADR

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FGSTERSIEDLPMKISKERFEQRLLAQLDKAGQRALKVGYAEDKDEGAYVRIDKAMQG

LQLSRALKAFDTAGYTSEDLAQDHAIEFGIEEERSGPRLFMLTMEYELDGEDLLVRVPS

SGIHFPEEYPINSISVMDYFGAGGSEEEGSILVPDGS GALIHFNNGKLQYPAYQQDIY

GPDMTMKLREASSNEARARLPVFGIRKEGAFLGIIIEGDAVAVVNADISGKLNSYNN

VYPSFYVWNKSDVTLQASDMVRTLPKFQKNPTVSDFVRYAFVGADKASYSGLASLYR

DYLMQNGGLPELNASKEQSNVPFYLQLFGGMTTRQHMLGIPYDSTEALTTFDEAKNIL

SALTEKKVSNIQVRYAGWLNGLHHRLPDSIQVDGAVGGKKGLRDFSTYTQEAGIGFY

PDIALINVQSKKGFKPSKEASRTLTQEPVLYPMNQAIQRRDRDRSPSYVLSPNMLED
VTADMLDELRLSLQKDGLSLSLNDLAAQLNSDMNPKKLVDRTQALGSVKKALEQIGQQA
GSLVAEGGNAYALPYVTGLTDAPMTSSRFKLEDEEIPFYQLVVHGSIGYTGTPYNLST
YTNAHQYVLKLEYGASPYFAWFNAPNHVVKETDYDDLYAANYEQWIDLAAEIYNEVN
QVNQPFAGRSMMSHESLEEGVFRTTYEGGGFVIVNYNDFPVEVDNDTVEAQSYVTGGE
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CDS complement(2614597..2615232)

/locus_tag="EFAGFIKM_02221"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQASSKQLYQYPLHLIFHPFDGYWELKYERNQRNSLLIAFMILV
LLVITKILHAQYSGFLINLSNPKYLNSLLEMLYVIIPVLFWCVANWSLTTLMDGEGKF
SEIFMSTCFALVPLLLIHFPWIWLSLVISAQETAFYYFSNALAVAWTVYLLFVGNMTV
HQYTSAKTVLTMLLTLVAMAFMAFLCLFFSLVQQIVSFVVTIYQELVLRG"

CDS complement(2615216..2616679)

/locus_tag="EFAGFIKM_02222"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRRSTWKKRKSIIMGMICLLLFVQEAPYVNADGKTDAYHYSFWG
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VRTIDSFQKQEGKEDHFKNPQGLYVTEKGHLLVADSDNHRVVHLDEQGKLVKIVSEPKS
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LWKRFATREQRSQMVMFTPTFTNLDMDEEGFIYATSGDRGKDPVKKLNAQGTDLRR
EGYQTPQGDLTYQEAGPSRLIDVDVGSDMYSVLDSSKGRIFTYNGDGYLLHIYGGI
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REHFSWMMSGIFLAVAAIVTVIIVRRQKRRTTNAGIK"

CDS complement(2616695..2617570)

/locus_tag="EFAGFIKM_02223"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTSKVRAVFGMPKRLNRSFTVSLMLFALLGVFGSFMVLPLIYAV
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IVPSLAFSLGLFLMKQFMEQIPDALLEAAKIDGANeyRIFWSIVMPNVKPAWLTLML
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QSSVMQTMATSGMKE"

CDS complement(2617573..2618529)

/gene="araP_3"
/locus_tag="EFAGFIKM_02224"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94529"
/codon_start=1
/transl_table=11
/product="L-arabinose transport system permease protein
AraP"
/db_xref="COG:COG1175"
/translation="MQAKTTKTAAPAVHTRQVGWWSLLKRDLYLSRHYYVLMAPFML
IFFMFTVIPVGISLGLSFFHFNMLELPRFVGWQNY SRLFLNDDVFLIALKNTLLFAVI
TGPLSYVACFLFAWIINELSPKIRAVMTLVFYAPSIGNVFFIWLIIIFSGDSYGYMNG
FLMRLGVVLEPIQWLADeKYVLAIVIIVQLWLSLGTSLAFIAGLQTIDRSLVEAGTV
DGIKNRWQELWYITLPSMRPQLMFGAVMQITASFAVAEISIALAGFPSVNyAAHTVVT
HLMDFGTIRFEMGYASAIATVLFALMLGTNVFTQKMLRKIGE"

CDS complement(2618549..2621446)

/locus_tag="EFAGFIKM_02225"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
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NREDNVRQDDRGNELRPRQVEQPEWQLTSFKDSAGYFEPPFQFYFEKGSQKLSLTSR
ESMAIDYIELYQESEVPSYAELEQTYASLGLKQSAPVMLKVQGEEAVSKSSPTLAPIS
DRSSPSLEPYNVSKIRMNAIGGINWKLPGEWIEWEIDVPEDGLYQLALKVKQDQLRGI
YATRSLTINGEVPFKEMKRIRFNYSAPWQTQVLGSGEDQPYQFHLEKGKHRIRMTVTL
GDIAPLLRTVESSVLELNEMYRKILMITSNSPDPLRDYQLERRIPEMTEVFERQADTL
RSVADYLEKATGEQSDKVAVLHAMVLQLEDMAARPETVPKRLDTFKINVGGLGTWILS
VREQPITLDYLVSPPGESLPKAEASTVQQVKHELGAIVASYTEDYDSIGNVEQKKDA
ITWITTGRDQAQVLKGMIDDSFTPDVSVQLRLVPPNILLPATISGEGPDVAMQMG
EDIPVNYAMRNATADLSQFPDFEEISGRFRESGLTPYRYNDGVYALPEQQHFPMLFYR
KDILNELGLEPPKTWQDVYNAIAVLQKHNMIFYLPIEDTLNNANLVPNSTFAMLLYQN
DGTFTYEDQKKSALDSEISMDAFKRWTQFYTNKYFPLKADFPNRFRTGEMPIGIADYT
TYNMLTVMAPEIRNLWDFTIVPGTQLPDGSIRHEVASATSAVMMLNADNKEAAWKFM
KWWTAEQTQIEYGREMEGLMGAAARYPTANIEALKQLPWPVKDYQNLEKQWEVWVGIP
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CDS complement(2621552..2622907)

/locus_tag="EFAGFIKM_02226"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRKNKFMLLSLVFAVLLVIAACSSAPTAQPEPEKTPQEEQKPA
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YVSIDFGEYQEKVVASLMAGEPLGDLVRLGKNYAIPALTKQDLLWPVDDYIKNDKVFN
QKTTKEYMQYEGKGYGFTEDQSSFINGIFYNRTLQELGLKPLQEYVDADEWNWDTFI
SVAKQANKDRNNDGKLDTWGLAQTLLEPILYSNEASLTKEKQNLDPKTKEALNFL
SKLATEKVGRASEGGDWTEPSTFFRQGNTLMYSGAMYVEGIMTDMQDYDIGFVFPFK
GPSATAYHSGESRYQAITIPKAIVENPEQLMYIWEKINEIESIYEYPGQSTLETHLTDE
ADINNAREVAEGMLVLDHNTFPSLPFWDFDGELKEGVSSTLIEKYKAPFQAAIDEVY

K"

CDS 2623182..2623949

/gene="rhaR_17"

/locus_tag="EFAGFIKM_02227"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MYDILLVDFSRRLCGELQQMLLRSKAQYTIANCVFSSAEALTAL

SERDFSLVMVHTERFDTAGLWLCNDIRKKSQIPILLMGGRDHFRFVRKALTYQVNDYL

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HLSDEITLKKISDMLHFNCAYLGGQKFKLEEKMSFNDYMLQQRMEKAQQLSSTNLRIY

EIAIEVGKIDIDWFYKKFKAYAGSSPNAYRRQKIHTA"

CDS 2623915..2624130

/locus_tag="EFAGFIKM_02228"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLIEDKKSTRPKGGLPNRFVYQLDINHKKTQDVFFFLRFFVWW

VWSSKGFTINVPKGIPGILGESFPLFS"

CDS complement(2624072..2625697)

/gene="rhaR_18"

/locus_tag="EFAGFIKM_02229"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MYRLLIVDDEEITDSLYETFARHIPEQLDVCKAYSATEALSWM

QRSRIDIVLDIRMPGMSGLELTERIQASWPNCRVIFLTGHSDFDYAYQAFQMANVRY

LLKTEGYDKVMSVVEDVMEEIRRSMSVELLEHSHKVNSQLALIQQKEYLRKLLQDCT
AVIDSTMDMQDELFRDIRLQINSPVYLILGRFNNPPEKGSDLTQVQESVRIIGSSLM
NERTVCTSVTDHYGDTIWLLQPKQEEEMTNDKLVRFLEGTLELVQEACMVSLGVSIAF
SLSSRSCNWSLTKQYERLRLQWMKIGDGVSMVLTDRNELSSDVPKESMRISNRIE
IMSGYLETGRIQPFYDIFEELAGELLQQDITMERAMETYYNLALLHSTINRWGLQK
IPDQRSLLHLGEYTCMKDAVQFLYRAADELVRYKRSNEQERANVVIHSLCSYVKENLE
KDLSLVRLAELHHFNPSYLSRFFKQEMGINVSEFIDDCRIRKAKELLQNTNLMVREVA
LQVGYEAAHSFTRLFKKITGMTPQEYRESLLVR"

CDS complement(2625682..2627439)

/locus_tag="EFAGFIKM_02230"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIKIPAKSWFNSIFARLIITYLVFVIPLILLGVYLYHWSYDNAS

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TVKEDALNLSAVRLTGTRGEPPLFVIQVELDTYHFQNELTRLNLYPESSSTFLIEDKTG

HAITDKHQASVILANYREHSVKGTLDGFRMKVGDTRYHVSQHLHVDLSGLSVATYLPEA

IVTKPLSKFYHWAWLFAITSFVAISAYLYSSYKLIHIPLLLLVRFKKMEGGMLDVPI

AHNRKDEFGFLYTRFNLMIENLQSLIDRDFKKTLMMQRAELKQLQSQINPHFLYNSFF

ILNSLARTGETERIEQFTNMLGEYFRFITRNETDHVKLKVEVEHSRIYTEIQQLRFSR

RIKVDFGSLPAEMEHKVPRLIIQPIIENAYEHSLEKNTDSGLLIIGFNMEGSYAEIT

VEDNGNELEEQHIQTLQQRFHKGDDGDEM TALINIHRRVLTYGEGSGLFLSRSELQG

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CDS complement(2627497..2629182)

/locus_tag="EFAGFIKM_02231"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYKRCLDITRWTFILFLAVSIPAGHTEGNTKQHHPQQDGGQIQQL

PATFERYSPPIVVSFVRETGDDLERMISQLPGETILDNRWTRLYEKELGIQIHYDWT
KGDVYNQKLGVSLAAGRFPDVVKVNPYQLRQLSNAGMIEDLTHVYQEYASPLTKSILE
AEGRGAFDAATIDGKLMAIPESSSSIETAQYLWIRTDWLEQLGLRPPETMEELLQVSK
AFTEEDPDGNGEHDTYGLALTNHLWDPVMGAAGFMSGYGAYPNIWVKDAEGNLTYGGI
QPEVREALKVLQTLYREGQLDPDFGYKSGNKAFLVQDGKIGMLYGEQWTSFMLQSTR
DKDTDIDVEWQAYPIVAKSDRSLFVPLRSNTGQYFAVKKGFSNPEVVVKLMNLHLDIN
WGDQAQYETYNDSDRAVWMLSPVTPFPGNKNIDAYKQIRDARSTGDFSALQNEALAI
HKRIVAYELENVESGWGWKQTYGPSGAFSIADSYEKNQQLLYDQFTGGITDTMVDRQI
ILRDLQLEAYMNIILGRSIDEFDQFVENWRKLGGDQITSEVNAWFRASKPKER"

CDS complement(2629313..2630857)

/locus_tag="EFAGFIKM_02232"

/EC_number="3.2.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:T2KN85"

/codon_start=1

/transl_table=11

/product="Beta-xylosidase"

/translation="MYPNPPIIWADYPDLDVIRVDDTYIMVSTTMHMMPGCVILRSYDL

IHWEVATYVYDTLDDTPAQLVDGHHVYSKGMWAASLRYHQGMFYVIFVANDTRKTYL

YTSTSISGVWKKQIVEGFYHDCSLFFDDDERAYLVYGNTEIYLTELSSDLSGPKPGGV

HRLIVKDKQPHHLGYEGAHFYKINGKYIVFLIHITKASGRRTQAFYMADSLEDVFTGG

EVFNDDMDYFNSGVAQGGIVDTPDGDWYAMLFQDHGAVGRVPVLVPLHFDQGKPIFAS

KAPKQIDIPSTRPEHRYNPLVGSDSFNYEPEEDGSIRLRDFWQWNHTPNHELWSVTEK

SGVYRVRTGQISPNTFAVNTLTQRSMGPACEAIVTLDGSRLNDGDYAGLCFLIGSYG

MIALTKQDNKFYLMHARDSSEDSTIFGNLIDQKPATEHERIPVSDPVVKLKAFGNFEN

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VINPVE"

CDS complement(2630865..2632382)

/gene="xynD_2"

/locus_tag="EFAGFIKM_02233"

/EC_number="3.2.1.55"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P45796"

/codon_start=1

/transl_table=11

/product="Arabinoxylan arabinofuranohydrolase"

/translation="MNHSTPQAGEQKQDQAANLERIPGEIGKLRPNGNPLVAHKFGA
DPYALVFNNRVLYMTSDKLEYDKDGLPQKNSYSSINRITVISSDDLINWTDHGEIRV
AGPQGAATWASQSWAPAAHRILDGKDCFFLYFANNASGIGVLSAPTPIGPWIDPIGK
ALITRETPGVVEEVTWLFDAVTVDDNHQAYLYFGGGIPHGKAEKPDTARVMRLGDDMI
SVVGKAKVIQAPYMFESSGIHKYNNSSYYYTYCSNFVEGDRPEGSPPPGEIAYMTSVQP
MGPWTYQGTLLQNPQHFFDIGGNNHHAIFQLADQWYIAYHAQTLQAMNIEGYRSTH
LNRVEHDEATGKIKKVHADYQGVDPQKCFDPYQHVSGSTIGWSSGVSTEQYLDSELS
SSDSNIISAKLQNDSWIAISKVDFESEGPTTFTATIANQGTEGTLELRLDRADGLLIG
EIIVPPATGSLQWMELTNTVTGATGVQDLYIKFSSTDSSTILLREWKFNRKNEV"

CDS 2632545..2633414

/gene="rhaR_19"

/locus_tag="EFAGFIKM_02234"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MSGSSSECFYDPIQPELLYLHSVTTYKLETIYHRHNAYEIYFLR
GNVHFYVENRCYQVQPGDLLVMSPEEMHRAFILDESEYERITINLKKTYLFQLSTPST
NLSSCFDHRPKGTGNIVHLDDYNLQMLQCTKELEGLLASDAYGTDIKINAABAQLLV
MINVWFHNNNSFVPNDIMPELVRETMDYIETHLNQDITLRKLAEVFYMNSTYISRQFKK
HTGLTIRSYILGRRIERAKFHLSEGMSITDACFQSGFSDYANFIRSFTKMVGISPGRY
IKQRRDVIEALPR"

CDS complement(2633531..2635225)

/locus_tag="EFAGFIKM_02235"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MRVSKMLGACLVTSVVLVSAGCGNAGENSESNTSDPNSPITFT
FFGADASPNWNKMQDAVGKKITEETGVSIDAEFDISSGGGNDRISLMAASGDYPDLIF
PKGNLTRLVDAGAMIDLTDLIEEHAPNLKKIYGEHFNRLKYSNDDPSIYWIPTNGAID
QVSFDATNGTAIQHRVVKELGYPEIKTLNDFENVLREYYEKHPTTDDGQPTIPLTSLA
DGWRRMITVTDPAVMSTGGPGDGEYFINPDTYEAVLHYKRPEEKEYFRWLNKMYNEGL
LDKDSFVQKDDQYKSKIASGRVLSLLDPSWGFSDAENALKSAGKDDMTYGFYPVTLDD
NFQRKDFQNIQFDGYGIGITVDCEDPVRAIKFLDWMSSSEGQVLRNWGVEGEQYNVED
GVRTIPADVQERKNKDNNTFTKETGVGLYYIFGAHYGDGVKDSTDNYYTTNYPEQIQQ
SYSDEEKEALKGYGITTWKDLFPSEEKFPVKEWGAAYNMPIPSDSVDYNVYQKTQDI
IQKRIAEAITSSPSAFEDIYDNMITELDNAGAVAMEQQYTEWIKDRVRLWTGKEIN"

CDS complement(2635501..2635776)

/locus_tag="EFAGFIKM_02236"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P11540"
/codon_start=1
/transl_table=11
/product="Barstar"
/db_xref="COG:COG2732"
/translation="MSIIQINGNDFHSKEELHQILQNQLELDES YGGNLDALWDVLTG
AVSMPLTVQWIGFEKSKEILGDYADQVMELLRDVEGEIQGFTLELYY"

CDS complement(2635791..2636225)

/locus_tag="EFAGFIKM_02237"
/EC_number="3.1.27.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P00648"
/codon_start=1
/transl_table=11
/product="Ribonuclease"
/translation="MFFRKFA YTLVIILAALLFSGCTSESLRDLGSPQVSEDMGFDEV
ADYISEHNELPPNYITKKEARDLGWEPSEGNLREVAPGKSIGGDVFRNREGLLPNKKG
RIWYEADINYSGGRRGSDRILYSNDGLIYQTTDHYKSFEQLK"

CDS complement(2636483..2637244)
/locus_tag="EFAGFIKM_02238"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKTAERTNKWKIIMWTILSIVIIVAGVYVYLNSVTYSPSERAE
TAMTSDAQVNVAKIKDGYRFEPVGTEITKPNIIFYPGGLVEPESYSPLAREMAEQGHR
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LASYADEGGSVKNTDLSILQITGSDGVLNWEDWENSKANLPEDTTYVSIEGGNHGQF
GSYGMQKGDNPVITEEKQLEEVVIALENWMGKLGK"

CDS 2637383..2637994
/locus_tag="EFAGFIKM_02239"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTEKSPKRLPGRPKHGNDDISIQQTIIQTASQLFMEFGYETVTL
QQIGKTCSVSKPTIYYHFTSKPELFKVAFTTMLQNVSRSLTSHILDQAENLESGLVRLA
EARLGNPHAEIETMLREAEPFLEPAQIQDIRNAEQIHEVLASHFQRAMDENRLRTDD
PFFLAETFSTLMLMGNREDNLHKYGSNFSLSGQKLVDIFIRGAQ"

CDS 2638022..2638903
/gene="rhaS_17"
/locus_tag="EFAGFIKM_02240"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaS"
/translation="MNIPRGTYGFRFAEDKELQLCVLYAAGCDSITDPSYHWDGLERS
DGPLLLFQYTISGEGVFESNNRIHHVTAGQAFLAEIPGPHRYYYHSASKEPWEFLFL
FRPTLILSHWRKFLREAGEVPYLPADCTPIRLLRMIVTDAAAGRITDPLIASSSVYQF"

MTELTRLQKTTLRNRENWSENIQIAVEYIENNYSKMISIDHLAEHVSLSKYHFIRRFSS
SSTGLTPGAYLTRVRTEKAMELLRGTSLSIEVIAEQVGYSYFIKAFRSITGVTPG
EFRSGGESLVYRKLFDD"

CDS 2639012..2640292

/gene="agaA_2"

/locus_tag="EFAGFIKM_02241"

/EC_number="3.2.1.22"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:B3PGJ1"

/codon_start=1

/transl_table=11

/product="Alpha-galactosidase A"

/translation="MNHTLAASTPPLGWNSWDCYGAATEDEIRGNAEYMAEHLKDFG

WSYITVDIQWYEPLANSSQYRPFVPLIMDEYSRLMPAENRFPSAAGGQGFKPLADYVH

SLGLQFGIHIMRGIPRQAAHAGTPILGTTATARDIAHPNSICPWNTDMYGVDSKEGA

QAYYDSLFEYLAQWGVLDLVKVDIAASRLYDTHQPEIEMISKAIERSGRPMVLSLSPG

PAPVEYSEFLADHANMWRVTDDFWDLWPLLLDMFDRCRTWQSVPKAGCWPDCDMLPLG

HIGIRSDGGGADRWTRFTPDEQLTMMSLWSIFRSPLIFGGELRDNDWTLSSLTNRE

VLRMHRESYGAREALRKEDLIVWTAQHADGSSYVAVFNIGENTLPVDLSIDEVGLSSI

TKGTELWSGEATEFTENSLVTTVPAHGVRLYRFS"

CDS complement(2640351..2640707)

/locus_tag="EFAGFIKM_02242"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MENVSQEDQLQSIKAFQSTIRKSENALVNMTQKRNNNTLLQKRL

QALYIGLALLDKVWNQKSHPYTEEDIAEARLVLMGLFPSLESMYANSKEVSPQKTLLE

RRIKAFHLAVQAMDTY"

CDS complement(2640829..2641557)

/gene="artM_2"

/locus_tag="EFAGFIKM_02243"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54537"

/codon_start=1

/transl_table=11

/product="Arginine transport ATP-binding protein ArtM"

/db_xref="COG:COG1126"

/translation="MAKIKVEGLKKSFGSNQVLKGIDVAVNEGEVVCVIGPSGSGKST

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LFDEPTSALDPEMVGEVLGVMKDLASEGMTMMIVTHEMGFAREVADRVIFMDGGYIVE

QGTPEEIFGNPKNERTISFLEKVL"

CDS complement(2641550..2642995)

/gene="mltF_2"

/locus_tag="EFAGFIKM_02244"

/EC_number="4.2.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_02016"

/codon_start=1

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/product="Membrane-bound lytic murein transglycosylase F"

/translation="MKTTKISFFILSLMLLLVSGLSGWVGNAASDSGKTYVIGTDV

TFAPFEYEDENGDFVGDMDLLDAIAKDQNFKYQIKSLGFNAAVQALEANQVDGVIAG

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IASKYGFTVVPFDESYQMYDDVKTGNSVACFEDEPVLRYGVKQNNGLKIVTAKEDGAS

YGFAVSKGKNQELLEMFNAGLVNIKANGEYKRIIEEYVGENAQVANLGRWELIQKSLP

ALFKGLGKTLTYIVSLFFAFIIGLIFGFMKVGQNKFLRGVATVFVDIFRGIPLIVLA

FFIYFGIPQAMGFTMPLFLAAITLSLNAGAYVTEIIRGGIQSIDRGQMEAARSLGIP

YRKAMIKIVIPQAVRVMIPSFINQMVITLKDTSILSVIGLVELTQSGKIVIARTFSSF

DIWLTVAVMYLIVITLTKIADYLEVKVRRG"

CDS complement(2643339..2645438)

/gene="yfeW_1"

/locus_tag="EFAGFIKM_02245"

/EC_number="3.4.16.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01034"
/codon_start=1
/transl_table=11
/product="Putative D-alanyl-D-alanine carboxypeptidase"
/translation="MTRKKRTSIAAITLVFAMMSPMSAMATPATSNDSSPKYDLTKKA
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ILFRDNDTHAHDTLLEQLATQH LKADPGAYSVYSNDGFTLAEILVERVSGMDFTTFMH
RYITEPLGMEHTKTPQDIVDFSQMAATYSPSDEEQLPLETTNMIASGGIYSTAEDLVQ
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QAVSKGGNTITYHSSLIVLPEYNMAAAVTSSGGHSSTDQLLATELLLSALEEKNIPE
RKPEKSHDAPMKTTMPKELTQHTGMYAGGANMLMKLDVKDDGQLTSLNLSSPNSSDQT
YTYTADGSFVNDAATEKLKFVQEVNGNTYLWSRSYQSVPLGQVASSEYKAEKLETNE
LSEEVKAAWQKREGKAYVLVNEKYTSTLYNAAMPMPHPIHTFNELPGYVYTNKIVGANQ
AVNQLQIPGLAGRDTMEFN FYEENGVEYVKAGGNVYAAQDIKPIYAGKQSKTTIQAN
GHATWYSIPASAAGKEMTVKMSANSFAVYNQAGVGINHTVVSGQNEIVLPENGTVF
AGEAGSKFEIVLTTRAN"

CDS 2645730..2647160

/gene="gabR_3"
/locus_tag="EFAGFIKM_02246"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94426"
/codon_start=1
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GabR"
/db_xref="COG:COG1167"
/translation="MLKVN RNDQRPIWQQLLDQAIHNITTGKWQPGELLPSRELAQL
IGVSRSTIQIVYEELFSRGYTVTSRRAGTRVSDWTYAPRSSEGVTMQGPIPPDLPTLN
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RGLLALREIQRYLSLERGIHIDVDQILLTSGAQHSIDLIAQALLSEGDTVSVEDPGF
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MHLAAHHRYWIVEDDYDSEFRYRGDPLPTIFSQQPQNTLYMMSFSKMVAPGIRLSAIL
GPKIAIDRLTQVHELTYRHLPIMEQLTLTHFIERGHFMRHMRRVRNIYRRRHEVMTKA
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CDS 2647206..2647826

/locus_tag="EFAGFIKM_02247"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKILVLGATGRVGSHFVSNALRSNHHVTALVRSPDKLQINDDNF

ILHQGNALVKEDIHHAIQGVDLVSSLSTDGTTTLSQSMGHIVEVMAQERIKRIITIG

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SLGKYRVERDYLPDGGTSSIVIDTAEFAYQQLMSDEYVQSRVGIAY"

CDS complement(2647922..2649166)

/gene="glyA_1"

/locus_tag="EFAGFIKM_02248"

/EC_number="2.1.2.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P99091"

/codon_start=1

/transl_table=11

/product="Serine hydroxymethyltransferase"

/translation="MKHLEKQDKVIGMAVQQELGRQRDTIELIASENFVSQAVMEATG

SVLTNKYAEGYPGRRYYGGCEHVDTVEEIANSRFKALFGAEHANVQPHSGSQANMAVY

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KYRPRMIVAGGSAYPRTIEFELFAQIAAEVGALFFVDMAGIAGIVAAGLHPNPVPHAH

FVSTTHKTLRGPRGGAILCRESWAKAIDKAVFPGTQGGPFMHVIAGKAVALGEALQS

DFTTYIEGVLNNANVLAETLMNEGLTLVSGGTDNHIVLVDLRTMGLTGKEAEALLDEV

GITANKNAIPHDTASPLVTSGIRFGTPAMTSRGLGAREMKEIAQLIGLAFKNPKNSDV

KNQILGSVREITSQFPLYEGLK"

CDS complement(2649192..2650397)

/gene="ydcO"

/locus_tag="EFAGFIKM_02249"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P76103"

/codon_start=1

/transl_table=11

/product="Inner membrane protein YdcO"

/db_xref="COG:COG3135"

/translation="MKTASPSLRGRDLISPVIAALISVIVNYGGTFILVFQAAKVAGL

SPEMTASWIWSISIGVGTGIWLSYRYKEPIITAWSTPGVAFLVSALAVTPYPEAIGA

YMISAVGFILGLSGMFERFVRLIPPGIASGLLAGILLQFGISAFGGAKVDPLLIVL

FAGYIVLRRFTSRYAIVGILAIGLIYLICMGKTDFTIQLAVASPVFVVPFSLNALL

GVALPLFIITLTGQYMPGMLVLRNDGFKTSANPILAVTGLGSLLAAPFGSHAFNVAAI

TAAICTGKDAHEDSTKRYIAGIACGVFYIFVGIFGVTLAALFLILPATFIATLAGLAL

LGTIGGSLANALTDPKGRETALITFLATAANVTLLGVGGAFWGLFAGMMAHLLMNSKF

PKKQLGTNK"

CDS complement(2650417..2651160)

/locus_tag="EFAGFIKM_02250"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P44506"

/codon_start=1

/transl_table=11

/product="Pyridoxal phosphate homeostasis protein"

/db_xref="COG:COG0325"

/translation="MKHLVEENLQAVRQQMALACQASGRNIEDIQLLLATKTVPLEKL

QIAIQAGEVLFGENKAQELRDKFPLMEQSKQVEWHFIGHLQTNKVKDVKYVTLIHSV

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GLMTIGKLNATNEETRHCFRLLNQIRTQIKEKNIPRVDMDILSMGMSGDFQVAIEEGA

TMIRVGTSVFGQRYLPDEYYWNENTRIDD"

CDS complement(2651485..2652417)

/gene="rbsB"
/locus_tag="EFAGFIKM_02251"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A2C5"
/codon_start=1
/transl_table=11
/product="Ribose import binding protein RbsB"
/db_xref="COG:COG1879"
/translation="MKKWTVTLISMLMIIVLAGCSLEPPEWAKPNPNKNNGQKKIGLS
ISTLNNPFFVSLKDGVM AEAKKQGIQVIVVDAQNDSAKQTNDVDDLIQQGVSALLINP
ADSAAISTAVQSANSVGIPVITLDRSADKGEVAALVASDNVKGGRMAAEYFVEQLGEG
AKVIELEGVPGASATRERGKGFHEVADKQLDVVSKQSADFDRSKGLNV MENLLQGNPD
VQAVFAHNDEMALGAIEAIQSSGKDIPVIGFDGNDDAIKSIQDGKLTATVAQQPILIG
QLALQAALDVLSGKQVDSSIPAELKLVTKENVNE"

CDS complement(2652432..2653403)

/gene="rbsC_2"
/locus_tag="EFAGFIKM_02252"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AGI1"
/codon_start=1
/transl_table=11
/product="Ribose import permease protein RbsC"
/db_xref="COG:COG1172"
/translation="MTTMQENKTAKSGFRFSNVIQKLGPLLGLIILIVSVLNPSFL
EPLNILNLLRQVSINALIAFGMTFVILTGGIDLSVGSILALSSAFVANMMLSGLDPIL
SIIIGVALGGVMGMVNGLMITKGKMAPFIATLATMTIFRGLTLVYTNGNPITGLGDNL
LFQLFGRGYLLGIPVPAITMLITFMILWIVLHKTAFG RKTYAIGGNEKASIISGIKVN
RVKIMIYSLTGMLAALAGAILTSRLNSAQPTAGTSYELDAIAAVVLGGTSLAGGRGRI
VGTLIGVLIIGVLNNGNLNLEVNSFYQM VVKGIVIAIAVLLDRKKTA"

CDS complement(2653405..2654886)

/gene="rbsA_2"
/locus_tag="EFAGFIKM_02253"

/EC_number="7.5.2.7"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P04983"
/codon_start=1
/transl_table=11
/product="Ribose import ATP-binding protein RbsA"
/db_xref="COG:COG1129"
/translation="MHIQMQDIHKAFGTNQVLSGVDFELKDGEVHALMGENGAGKSTL
MNILIGLHQRDQGTITIDGEENYFASPKEAEKLGTLFIYQELNVWPEMTVLDNLFIGK
ELTSSFGLLNTRQMKALAKEQFAKLSVDIPLERPAGECSVGQQQMIEIAKALMTDAKV
IIMDEPTAALTERIEQKLFGVISLKEGVSIVYISHRMEEIFTICDRITIMRDGRTV
DTQAIPQTSSDEVVRKMVGRELTERYPVRNPSYGEVVLEVRNASSKGLFENINFTVRA
GEILGFSGLMGSGRTEIMRTIFGLDTLDSGEIFIRGKKANIRKPADAVKHGIGFITED
RKDEGLVLDFSIRENMALPNLFSFSSKGFISTSKEQDFVDTLIKRLQIKTSSETAAR
NLSGGNQQKVVIKWWGIGPSVLILDEPTRGVDVGAKREIYELMNELTDRGVAIMVS
SELPEVLGMSDRIAVVHEGHISGEVAREVATQEHIMTLATGGQ"

CDS complement(2654901..2655302)

/gene="rbsD"
/locus_tag="EFAGFIKM_02254"
/EC_number="5.4.99.62"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P36946"
/codon_start=1
/transl_table=11
/product="D-ribose pyranase"
/db_xref="COG:COG1869"
/translation="MKRNGMLNSHISKILSDLGHTDMITIADAGLPVPDGV LKIDLAL
KLGTPSFREVVEAIAEDMVIEKVIVAEIECEGNPVAMQFITEKFGVEAIDASVSHEQF
KALTRQVKAVIRTGEATPYANCILQSGVHFG"

CDS complement(2655302..2656147)

/gene="rbsK_1"
/locus_tag="EFAGFIKM_02255"

/EC_number="2.7.1.15"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A0A0H2WZY4"
/codon_start=1
/transl_table=11
/product="Ribokinase"
/translation="MDLVVTSSRRPGAGETVLGDSFKTVPGGKGANQAVAAARLGGEV
TMIGRVGDDAFGKDIVENFRANAVNTQNVKPVTHLESGTAHIILAEGDNSIVVVEAAN
REVTPAYVDEAAEVIRDADIVLIQQEIPEETVHVVSALCAEFGTPLLLNPAPARTLPQ
EVIDNAAAYITPNEHEAEILFQGMSPAQALRQYPNKLFIGSGKGVRYFDGTDEILVPT
YKVEAVDTTGAGDTFNAAFALAEGKALQESIRFANRAASLSVTKFGAQGGMPTRDE
VEESL"

CDS complement(2656173..2657162)

/gene="rbsR_1"
/locus_tag="EFAGFIKM_02256"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0ACQ0"
/codon_start=1
/transl_table=11
/product="Ribose operon repressor"
/db_xref="COG:COG1609"
/translation="MTTIKDVAQLAGVSVATVSRVINDRGYVHADTRKKVEDAVKALN
FSPNEVARSLYKRKSKLIGLLLPDITNPYFPQLARGVEDRMQEQDYRLIFGNSDEDER
KEQDYIQTFIQNNVGVISSTNYPHSSIIYENLKIPVVFLDRTSLDRPSVYADGREGGR
LAAREIIKGRSRRITVMQGPSQIRPAQDRFEGAIESIREAGLDYRVIQTTSFSINEAS
MWAEELFRKYADTDGVIASNDIAAMAVLHEASRIGRKVPDDVQVIGFDDIPMSSLLSP
ALSTIHQPAYEMGREAAGLLIQLVEQAAIENKNIQLPVSFIERGTTTRKVRSDG"

CDS complement(2657474..2657881)

/locus_tag="EFAGFIKM_02257"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MAKHEEVKDGVIFPVG EKNEAFS QYFIGQSYLQSLVADPKVNVG
VGNVTFEPGCRNNWHIHRGGFQLLLVTGGEGWYQEEGKAAQFLKAGDVIVTHDGVKHW
HGAAKDSWFEHIAITAGTPEWLELVTDEVYVKL"

CDS 2658058..2658651

/locus_tag="EFAGFIKM_02258"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MCNYSLERMVITIVSITDRKDRRIKSQEAIKSAFIKLMNEKPF
DTITMQDISDHANVGRRTIYHHYSDKFDLLDKLIEEHIDELRRLCKEASDLDFIESNV
LWFDYFEVHYSSAMLLSKGAPFFRNRLALVIEELEDEVNVTEGKNKGLTKEVILT
FFGTAIVGIVESYFTNGLPRQPHIVAEQVGILLERNL"

CDS 2658812..2659780

/locus_tag="EFAGFIKM_02259"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIERNLTLEKPSKFSDPIFVMLVASLCCLLWGSAYPSIKLGYIAF
NILPEDIASKYVFAGYRFTLAGMLLLLLSRIVRKQKLQTKPQWTGLIMLGILQTGLQ
YMFFYVGVANTTGVKGSIMNATTTFFSVLAHFIYKNDKLSRNKIVGCLLGFVGVIIV
NFHTDLLAFSFSFTGEGFVIAALVFSVTALYAKRLTATIDVLIITGVSLFVGGLVLT
MLGLSLGGRVTHFTLESTSNLIYLALLSSVAFCLWNMLLKYNKVGRVSVYNFLIPVFG
ALLSALFLGETILELKNLAALLFVSVGIYLVNRVRSVQSSNDTPIK"

CDS complement(2659884..2661026)

/locus_tag="EFAGFIKM_02260"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MIHPKHTAKWASLALLTLIAYVLSALLLLPPNAAAKGEQISAKQ
LESMSRSLFTLRDAKQTAYTVYIFAYDEQKRTLTEENGWTNNKKGDKSYSGTYRAALL
KKGAAYGTVQAAKLDLNTIILPQTNFVVKSEASTPDMLMITDWGTSNFNEVKTYIV
RSGELRRVTYVDNKGKKIDDSYSASRDDGIRTLGARGVQFKNYNNLQFVYGVDTFKLN
VKNSELRLDTRNLRSDAWPNSGVGDRAYLKSLEAALKGALPGRTDIKIGMTLQNAQ
KKLGKPTSRSNEEWGAFYYYSKFGVGFDSYMHELTNKSRIAVFDLYNEKQNLSPWNVK
IWMGKPSSEYYNEVGGYEMVYQLGNHAIVFNYYYYEEDLIDFTSIY"

CDS complement(2661324..2662457)

/locus_tag="EFAGFIKM_02261"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WLZ3"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/db_xref="COG:COG1680"

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EIRLEKATRAITVRDLFTMTAGFSYDVGCPISIQEAVKSTDGTLPTRDFARALAKEPLL
FEPGTHWNYSMCHDVLGALVEVVGKRFGTYL RDEITGPLGMNDTAFNLNDEQQTRLI
PQYAYNDELEKAVRLDGNGFRVGTELESGGAGLLSTVSDYARFLNALTGHGTSPEGMR
ILSQASVELMRTDHLNEMTRSDYSWDHMYGYGYGLGVRTHISKAGSGSLSPIGEFGWS
GAAGCMAIIDPDSELTVMYAQHLLNSQEPYVQRRLRNVVYSCL"

CDS complement(2662788..2663372)

/gene="ydjA_1"

/locus_tag="EFAGFIKM_02262"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ACY1"

/codon_start=1

/transl_table=11

/product="Putative NAD(P)H nitroreductase YdjA"

/db_xref="COG:COG0778"

/translation="MKTSVVEKLIRERRTIRQFNGKPLAKETIMHLLAAVWAPVHSR
KEPWRFILFVEEGRKQFADAVLHTFSKDERERWTEKLQKDYCESIQAHLLVIEADPR
QRVWEDAVGASAAALIQNIQLLAWEQDIGVWKTNEYNFDPDFYSKTGVKAGERIIGTL
HLGYFDTNKVPKPRPRTPEELMTFVSTARAEVQ"

CDS complement(2663400..2665370)

/gene="rhaS_18"

/locus_tag="EFAGFIKM_02263"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MHVEEHVKLWNLASIKIWDVRHVVVVRAGEPIHAYRFPISGFIYT
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QALLRQHVPFHVQYAFAPSYPIELYDKVQRIEQHWERTDAFSKFQVKTLFYQFINELM
RQLSAQGIETAKPDLVAQAVRYLQENYMLPVMVDPLAELLDCSAGHLSRTFKKETGSS
LITYLTRIRMYKAKELLHTDASLQKIAEAIGIPDVIYFNRLFKKYVGLSPGRFKQKC
IALPTGQNNAIQESELSIVSPMHRGYDPIDDDNYYQYNSKGESLTSMRSRKPVALLLM
LSLTLISACSPSQSSATSSNGTSGNNAPTTEVAQSTESAVQERVVKHPWGETVIKG
DPQHIISLFPVATDYLLALGIVPQAASSNEEGSDQFPTYLSDQLQGKENLGWQVDPNY
ESILAAEPDLIIGQDFMSDAYDSLKIAPTLLAEKLQDEQGIIRMKTSLLHMGDMLGK
TDQAKQVIEEYEKKAAEAREKIKQSIGDETMFLRLSDKEVRYYSKRNYEVLYDDLGL
TPVSSIPDPTDSMKVISMESLPSINPDHIFLLSSDENETTELQKTAVWKSLSNAVKNNN
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CDS complement(2665552..2665746)

/locus_tag="EFAGFIKM_02264"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTKQDPQELLKQKHELDDQKRQFTNFSRNISGHGEVEAGQEFSV
DRVPDDQNRMKSVENRRGEV"

CDS complement(2665885..2666199)
/gene="gdx_1"
/locus_tag="EFAGFIKM_02265"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P69937"
/codon_start=1
/transl_table=11
/product="Guanidinium exporter"
/db_xref="COG:COG2076"
/translation="MSWFFLILAGLFEVGGVIFLKLSDGFTKLKHTLMFAMFLALSFI
FLSLSLREIPISIGYGIWTGIGASGSVLLGMYVFKEPKNAKKLAIVSGIISIVGLKL
VS"

CDS complement(2666202..2666543)
/gene="gdx_2"
/locus_tag="EFAGFIKM_02266"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P69937"
/codon_start=1
/transl_table=11
/product="Guanidinium exporter"
/db_xref="COG:COG2076"
/translation="MAWLFLILGGILEVGWALGLSFSDGFSKIEIVIPTVILMIGSFY
FFAKSTKVLVPSTAYAVFTGLGSFGTAIVGMIFLGDSVSAIKIVLVMILISCIIGLKF
VSNEPKPKAGV"

CDS complement(2666794..2667666)
/locus_tag="EFAGFIKM_02267"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MHQNRKQKSNKLIKLSKVLLIIIGGFITAYGLEAILIPNNVSDG
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HHVPTIIEGDTLLVTVVGGIIIGFGMGLALRNGGALDGIDMLAVLLSRKVPFGTSDLI
LFLNMFVFIVVSTVFLGLQGAILSGLAYFIASKVIHIVEEGLSGSKTFKIITNQPEIMV
ETIRDRLGRGATYTEAYGGYSNEQFKEITCVINRMEESKIKDIIHEIDPTAFVVVYDV
AEVRGGNFKKKDIH"

CDS complement(2667757..2668113)
/locus_tag="EFAGFIKM_02268"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P44558"
/codon_start=1
/transl_table=11
/product="putative HTH-type transcriptional regulator"
/db_xref="COG:COG0789"
/translation="MYTIGEVAELLHISAHTLRYEKEQIVTPLRDASGDRRYNESHL
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EMLEHKISSYRTLIGQ"

CDS 2668225..2668980
/locus_tag="EFAGFIKM_02269"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKYTVITGASSGIGYEAALAFARGKNIILAAARRTDELDKLKAK
VAEINPALDVVIRTVDLSIAANVHEFYDSLQAYSJETWINNAGFGNFASVGEQHLPKI
EQMLHLNIEALTILSSLYVRDYSVDVGTQIINISSGGGYTIVADAVTYCATKFYVSAF
TEGLAQELKGKNAAMQAKVLAPAAATETEFKHSFNVDEFEYGRVPKFHTAEQMAGFL
LELYDSESVVGIVDGLTYDFELREPLFPYAARR"

CDS complement(2669065..2670192)
/gene="nspC"
/locus_tag="EFAGFIKM_02270"
/EC_number="4.1.1.96"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A8FNH9"

/codon_start=1
/transl_table=11
/product="Carboxynorspermidine/carboxyspermidine
decarboxylase"
/translation="MRFEQLPTPCFVVDEALIEKNLKILNGVMQRTGAKIVLAQKAFS
MTAMYPLIGEYLSGATASGLYEARLGHEEMGKENHVFAPAYRAEEIDEIISICDHIIF
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EGVSGLHFHTLCQQNSDDLETTLNAVVEKFGQWLPQMEWINFGGGHHITREDYDIPRL
EACIKRMQNDYGLEVYLEPGEAVALNAGYLVTSVLDFHKNMGMDIAILDTSATCHMPDV
LEMPYRPPPLIGSGEVGEKAHLYRLGGQTCLSGDVIGDYSFDQPLQEGDRLVFEDMAIY
SMVKTNTFNGMPLPAIAVKRKDGDCEVVREFGYQDFKMRLA"

CDS complement(2670194..2671432)

/locus_tag="EFAGFIKM_02271"
/EC_number="1.5.1.43"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0DPE4"
/codon_start=1

/transl_table=11
/product="Carboxynorspermidine synthase"
/translation="MGKALIIGAGGVASVAVHKCVQNSEVFEEICIASRTKSKCDELK
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IEYIDILDCNGGDHGYPFATNFNPEINIREVSANGRYWENGEWIETKPMEIKRVYDFK
EVGEKDMYLLYHEELES LAKNMPGLKRIRFFMTFGQSYLTHLKALENVGMTSIEPIEY
EGQQIIPQLQFLKAVLPDPASLGPRTVGKTNIGCIFKGKKDQGDKTYVYVNICDHQECY
KEVGSQAISYTTGVPAMIGAAMVMTGKWNKPGVYNVEEFNPDPFMEELNKWGLPWVED
FNPVLVDELPEEVKESELVR"

CDS complement(2672285..2673538)

/gene="pksS_2"
/locus_tag="EFAGFIKM_02272"
/EC_number="1.14.-.-"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31785"

/codon_start=1

/transl_table=11

/product="Polyketide biosynthesis cytochrome P450 PksS"

/db_xref="COG:COG2124"

/translation="MNNNQTSKSEFNLFSEENVKDQFAIFEQMRARGSIVVPNPMPG

GSEQTWITRMDVAMEVLKDHRSFTVDMNSIDSDNDIRKNLSGELGSSEPQTFFTGKS

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FPINVISEMLGVPQEDRPQIHVWSEAIKGLGFGKQDPEVEQHLSFAEYTAQLVANK

RVEPSDDLISQLIAIEEEGDRLNEDELISMITLLIFAGHETTSNLIATGSYLLLTPE

QLEQLKQNLNLVPSAVEELLRFNGPATSSGPRYATQDTELDGQPIQKGDVVIPLKSA

NRDELQFDQPEELDLERKIKRHAFGHGHIHMCLGAPLARVEGDVAFTTLLSRLPGLQL

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CDS complement(2673745..2674638)

/locus_tag="EFAGFIKM_02273"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSSRKQSLLETALALFLEHSYANTTIQMILDQSGVSKGTFYKFF

SSKEDCLYSIIDQRMQEDVFIRKELEQNHYSYDIALLDQIAIPMSGPDKERWWELYW

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NTKKPVWNEVVPKVLTYIEVILRTMHQRNEHIFDVQSLYFLNADERNHDMGLDIDNVL

IEFDEFNNVCVQKSKESASLKQLSKGLLTLLQDQEDLNIPVIEVVLQAFHKEYKSSAFQ

SEANRLTEACWWYLELVKHRN"

CDS 2674876..2675523

/locus_tag="EFAGFIKM_02274"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIKRNLRLHLKKEATEKALASAAFELTLEHGLDGFTVEDIVHQVG

CSRRTFANYFTCKEEAVARGAISVQNTTELEELLTEMPDNVSLDDVLYNLIKMQLTTE
LIGRLHQLLSLSQTYPVLEPHYLGAMHRMQTQAQDTLLDLSNGKYDEIYTYLLINALY
GSILPLIDGRLNVLLPGQVITEDTKPGVLTFDQFLETTFNHLRAGFEHANHPHSS"

CDS 2675543..2677867

/gene="ydfJ"

/locus_tag="EFAGFIKM_02275"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P96687"

/codon_start=1

/transl_table=11

/product="Membrane protein YdfJ"

/db_xref="COG:COG2409"

/translation="MSTLLYRVGKTAFSKPAYFIIGWVLILGIVISMISINGIHISSE

MKIEGTESQKVLDQLAKELPAASGGQGSVVKAPDNERLDTPERLAAMMKGVNEVYGL

DKVINPADYAAEAGNSGAQAEMAQNAQATDMAQSAATPPPYGPLMVDGVPVPGMLIS

SDGSIALFQFQFTIEQSAITQDVFDSDVIQSVTTVEQGTNIKVLPGETLKTVSIGVGSA

EIVGLVIAVIVLLITLGSVVAAGLPLITALLGVAIGVGGAFSISKFIEMPSVTSVLAL

MVGLAVGIDYALFIVNRQRRMIIDQGLSAKEATARAIGTSGSAVFFAGLTVIIALCGM

LVIGLTLSTMALVAAATVLINVFVALTLLPALLGLVGERICSAKAREKSTKHPKATN

HGVADRWVKFVIKNRWATIIAIVILGFAATPITKMEMGIPGASSANLDTTARQSYDA

ISEGFGEGFNGPLILVAEPNQSSTKVTPELLGGLVMELQGQNNVAQVTPLGMTEDLAI

FSLIPKTGPNDNLTKTLVTDLRAADSSIAQTYDVKLGVGTGLTAVNIDMSAKLAQVFPI

YVGIIILLSLIILLVFRSIVPIKATIGFLLSILATFGITTAVFQWGWLHSLFGFDT

GGPLLSFMPPIIVTGILYGLAMDYQVFLVSSMRESYVHGHRTESVVGYNQVSRVVVA

AAVIMVSVFAGFIFTDDVMIKQIGFTLAVGILIDAFIIRMGLVPAIMAIFGDKAWALP

KWLDRIIPNLDVEGEKLIASLNAAEEHANTKSGLK"

CDS complement(2677976..2678731)

/locus_tag="EFAGFIKM_02276"

/EC_number="2.4.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O33341"

/codon_start=1

/transl_table=11
/product="Putative glutamine amidotransferase"
/db_xref="COG:COG2071"
/translation="MKKPMIGVLPLYDTDKKSYWMLPDYMNAIEGAGGIPIMLPLTTD
VEILATLAHEFDGFLFTGGHDLNPELYHEYAEVTCGELCIERDLMESILLQKVIEDK
PAFGICRGLQLLNVMLGGTLYQDIPTSLQLHGNKIVNHKQSPPYTNLVHDVHIEEKNI
LYDILQTDTIKVNSYHHQGIKMLSDKLTAVAVAEDGLVESVVMNRSFVLAVQWHPEY
SYKVDDYSQKLFAAFVNASKSPRYTIHIEDITA"

CDS complement(2678947..2680146)

/gene="sotB_2"
/locus_tag="EFAGFIKM_02277"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00517"
/codon_start=1
/transl_table=11
/product="sugar efflux transporter"
/translation="MTRNRENLLILTTLVSFVLGTTEYVIVGVLKEIESYMKVSLAA
AGMLVSGFAIAYAVGTPFAVAFLAKISRRSSILIGFAIVLALNLLTVFSTTFSSLMAI
RIVSAVACGLTISLSISIVSDAVNRERRGEAIAWILGGFSIANVLGVPLGTFIGQHLS
WSMTFVVTACIGVVPLVFMFRILPRQTTTIAGSFNDQMSLFVKPRILLACLIPVLGNS
CIFVVFTYITPLLSETMGVPVHWISAILLIYGACSIILSNWIGAKIAKGDFLPKLRFL
VIQAILFLGMSFTVSNVWLGLAFLFLIGCLSSSMSAASQYLFDVSGSIAPGSKAFAS
TLLPVAANVGIALGSGVGGIIVNMGGVHWVPPVAVMLALLAFVITLICQRSIQLNSDE
ATTVKAA"

CDS 2680391..2681263

/gene="rhaS_19"
/locus_tag="EFAGFIKM_02278"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaS"

/translation="MNTHHEFGQLHPNRNCTIIYVGKLADNPHWSFPTHKHDDLHEII
YVTEGKGVFTIDGTKHWAQKGDMLIYNKGTLHEEKSNAEFPLSTFYCGFRFAEGTQSL
EDWWIPPSNNPIIRANRYSDELHSLMQTLFNEFSIREHGYESISGHV LKAILLIIDRQ
SRQQLPSGEIVGSNTLAESIKDYLD TNYRQNIKLKELADQFHIDFYLIHMYKNHYGT
SPYHYLIQRRMGEATRL LVSTNKKVWEIAKLVGYDNP NYFTILFTKTVGESPRSRKK
NQKDMFGDKVSHSY"

CDS complement(2681356..2683350)

/gene="mcpA_1"

/locus_tag="EFAGFIKM_02279"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39214"

/codon_start=1

/transl_table=11

/product="Methyl-accepting chemotaxis protein McpA"

/db_xref="COG:COG0840"

/translation="MRLMSTRLIAAFLAVLIPTALIGYFSYDSAKDQVQQKMTDPIN
TILMTGQHINN LVGEKAALLSYIDSMYGTTPSQTNNEAVQVGIDQLADTYPDILAIT
VGNDQGDVISSPAIEDATYDPRSTEWYAKGISNNGSLYFSSIMKDPVSGKIYVEISKA
LSNEQGVASIKDLERLANEISIVDVGGNGSLIVVDSNR TIVAWSGAIVKGGGGELGG
ALIEGIPVHPNTASSSDEPMAFSQFVRTDLAYDLEVHSGVNALTGWNVIALMGHEDFI
AAAKPILVTSFTVIIISVLIAGVIIFFILRSFIVPMQKLRKATRSVSEGNLSERVNLK
TENEFGILANDFDQMTSSLQSVVAELHQTSSLLSHSSQMIQESTEQTTSVQHVAETM
QQTAE SAIVGAENSEQTANAVEEMARGISTIAESASAIVHSAEETERAVAKGGKTINQ
VGEQMEHILGAVEETSALINELSSLSAEANRMNEAIADISRQTNLLSLNASIEASRAG
EHGKGFAVVAGEVRTLSMQSKQSADEIGATIGKMLDLIAKSTSLMNDKVRNQVGEGMR
ISQEASATISNIEQYTTTHIVDQIQDISAVSEQLSASTEEVSATVAAMSHISKVSADSA
QTTSAAAEQMAAMQEISASSAQLSKTAENMQELVRRFKL"

CDS complement(2683585..2685111)

/gene="rssB_5"

/locus_tag="EFAGFIKM_02280"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00958"

/codon_start=1
/transl_table=11
/product="Regulator of RpoS"
/translation="MYNVMIVEDSKPILRNIKMLLETLSFPIRVAATATNGEEALAAI
KQSPIDLLLTDIRMPKMDGLSLIEQAKLANPDLKVILISGYSDFEYTRKALNLQVFDY
LLKPVEREALEEVMGRVIDQLDQQMSKELLDLQEIIHPQCETALKQGEAFPLFSQMM
IIMSKQPFTAGHERWWQVELEGIVQDFFAFHPCRVTSTPYQFIQFVFNKSALEVYSS
VHECLESRLRRHLVAHDIDAIIGGQLLFAESGNLPELYHRMSSILSEQRLKQGIVLDT
GNPVSMARSETGCLDPVQESAFVQMTQARQKERFALKLSELLNRWAEKNVHMTEVERF
IGLIVDTFAHLYEEQGAGMRLGLELRSRQFAQAQSYADFCRELTEWTGQCFDMLQSHV
RKSKAILFEQIDDYVKLNKYSQLSINDIAMKFHVSPSYVSRVIKNATQITFVQYYTRL
RIQEACRLMESQPDMKFKEVSDLLSFSDQHYFSKVKEYTGLSPTDYKQQMSGIKTQS
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CDS complement(2685128..2686891)

/locus_tag="EFAGFIKM_02281"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAKLIHKATQFSLQTKVFLTFLTLLLFVLGCFIVYVNVIVVRPL
KLKTEQDTLVTATKVREQVDLYVEQQNQMSQRILSSKNIFAAMDKSSSAHSNYERLKQ
IRIIKDIMFQAIGPSMNIKDMSIYDNHGVLLTSYLGSGNPPAILNTMMESSQVGRDWT
ESGFVLLRQDDTISFVRTINDQNGKVYGYLSIQMEQAYIQNLTEGITAGEVYILNEQG
EQMTGSEAGVTFANWTKPSSDEGLDVDKNDNYITHSTSPSTGWITYIITPKKSVLGS
HSVQTMISILLITALLVSVFYIFLSTRNLLLPIRKLRGQIWRMNYSNMNLKVDETPKN
NDLLLLNEAFQDLMERLQQSIDREKSALHEEVKARNALQAQIAPHFIHNVLYLISIA
AQEGKTKVSDMCKHLSDSLRYIVSSPYAHVTAEELQHTRHYLSLVQQKYEEDLEWD
ICADELANDIRLPRLVIQPFVENCIEHAFANTPPWRIQITVKQYNGLWALEIKDNGE
GFPPDKIQEILANIQASGSGMNQTADCGTALGNMGIINSVNRLKLMYNNRLFINIFNN
HAEEQHGATIQIIGSLTKDFY"

CDS 2687098..2688411

/gene="msmE_3"

/locus_tag="EFAGFIKM_02282"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q00749"
/codon_start=1
/transl_table=11
/product="Multiple sugar-binding protein"
/db_xref="COG:COG1653"
/translation="MKTIKRKKAISILASLLSVSLTACGSGGTDSGTAAGGDSKSGK
VTLELAISKSSQDSAFIQDILDAFEKQTNIRVNLQLIPAEQTTTVLQTKLAVDETPD
IIQYNLASAVTDLNLERNFEILDNESWASRIVNKDVLSSGGHLYSFHVSQDTGMQGVV
YNKQIFEELGLSLPTNYEEFLAICEKIKASGITPVFMPYKDAWAANIWPAAAFADFVA
KNEPTFFDELNSNKKKWSDIPEFKTFLEQQYEIYTKGYTNTDVLSDSYDMAVGKFLNK
EVAMMFMGDWLIEGVAEQDPNMELGVFPIPSSDNASLGASPLGGQLFIPKKSXHLEEA
KQFLDYIASKDVAQQIVDSKGYVSNFSDVTTPELPAYKQDIVDNYITPKKTVLTDAF
MLVDRSELYRLLQDQFAGGLSPEEVLKSWDEKFSQLMQDKGVEGF"

CDS 2688479..2689351

/gene="melD_6"
/locus_tag="EFAGFIKM_02283"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34706"
/codon_start=1
/transl_table=11
/product="Melibiose/raffinose/stachyose import permease
protein MelD"
/db_xref="COG:COG1175"
/translation="MKRTKNLYSYMIFPALIIYSIFFVVPALAAFYYSFTDWRLDRL
ELKFIGWDNFEKIFSDKTLILALKNTAIFAIVTVVGKNVIGLLLAVGLNMRLRKTNLL
RAIFYSPSILSILVISILFTPMLRTEGTINNLLSVGLHLSLQAWLTNPSIVIWTIAI
VSIWQSAGFQMAIYLAGLQSQISQEYYEAAKIDGASSWRSFFKITPLLLPAININLML
TLIGGLKVFSEVYVMTGGGPGNASQVVGTIILRSFGEGNWGLGTAVNTLLFVVVTIIA
IPLLIFMRRKEVTE"

CDS 2689353..2690183

/gene="melC_4"
/locus_tag="EFAGFIKM_02284"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34518"
/codon_start=1
/transl_table=11
/product="Melibiose/raffinose/stachyose import permease
protein MelC"
/db_xref="COG:COG0395"
/translation="MGYTRKLAIRNYIVEGFLILASLIVLLPLVILIFGSFKTSAEVL
SFSLSFPKTWQFSNYVRVFQEGGLSRAFFNSILITGVSSIINIVASSAAAFILARRET
KLSGTIYMYFFMGLIAPMSIITTIRVVQGLGFYGSITSVILIYAALNTAFSVFLYSGF
IKTIPRALDEVAFLGASVFGVFFRIVTPLILPVNATVAIMVFMSVWNDITIPVYFLT
DSSTWTMPLSIYNFYGKYSRDWNLIIFANLVLTSPLVFILYLFQGQKYIVSGLTAGAVKG
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CDS complement(2690302..2691006)

/locus_tag="EFAGFIKM_02285"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNISKQVAIVSGANRGLGKELALELLARGTKVYAGARNPESIDL
PGAIPQLDITDPQSVMAAAELASDVTLLINNAGSATGASLLTGELNDIHLEFNTHVF
GTLSMIRAFAPVIEKNGGGSILNLSALSWLSLGNMSGAYSAAKSAQWGITNALRLELA
PKNVSVAGLHVAFMDTDMTAGIDAPKTSPTDIAKIAIDSIEADLYEIIADDTSRNVQQ
GLAGGVAALYPQLFQK"

CDS complement(2691228..2693642)

/gene="helD_2"
/locus_tag="EFAGFIKM_02286"
/EC_number="3.6.4.12"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32215"

/codon_start=1
/transl_table=11
/product="DNA helicase IV"
/db_xref="COG:COG3973"
/translation="MDKTNEWKLEERLVQVRNKLQARLDELEPKVAGLHEQAAEIRK
RFWEDVTINTSSYTD FEDAFYTINQQSRVLAERERGHKLLTQQWKNTKRLPTPYFGR
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IEGKMELKRQFQIQHGGQLHSMFDSTETIGDELLQQVLAKGADSQMKSIQKEQNA
IIRDDRSRMLIVQGAAGSGKTSALQRVAYLLYKHRQTVKADQIVLFSPNPMFTSYIS
TVLPELGEENMQQTTFQEYLNWLDSSIRPEDAFDQIEYVLTQNDPGYEARMEAIKY
KASETFLQVLQNYGKWLGREGMRFNGIQFRGREFITSNRIKTQFYSLDQNLTLNRL
LLQEWLLRELVSLERLEREADWVLEELNYLDTDEYVEAFRMLHKEKPVFDVAEKYAAR
EDGNNKVVQDEGAFNFAVREEELLRQKLVKDMFKPLRKSVRKFQFVDVKGIYEQLFVN
ETAYREQTNGAIPPLHWPEICKQTKAMILQNKL FHEDATPYLYVKEMIEGVRTNTEIR
YVFVDEGQDYSAFQYEYLKKLFPRARMTVLGDFGQAIFMQATDLAASNSPLVHLYGEG
ETTLIRLVRSYRSTKEIVEFTRQMLPGGEEIRPFERGDQKPLLTRLKDDKLRGAQILT
DIAALKAEGFDSIAVITKTAAESRDAYERLQSQGGEGQLITKDTQVFEKGIMVIPVY
LAKGVEFDAVLVYDASSVAYSQEYDRKLLYTACTRAMHRLHLYTVSDWSPFVQALPAN
LYDIKS"

CDS 2694011..2694328

/gene="yybR_2"
/locus_tag="EFAGFIKM_02287"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37486"
/codon_start=1
/transl_table=11
/product="putative HTH-type transcriptional regulator
YybR"
/db_xref="COG:COG1733"
/translation="MNIEPVEDRCPVEFAVNMIGGKWKLLIINRLIRHSTIRFNELQK
MLDPITHRTLTRQLRELEEAGLINRVTHPVVPPKVEYSLTEKGQSLTSILFQLGDWGS
KHM"

CDS 2694476..2695354

/locus_tag="EFAGFIKM_02288"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTQNDRFLVYGASGSQGGAVAQLLVQHGCEVRTITRNEATAKTL
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LIVVNTGTYPDPITHSKGIELKREVIHELQQSGLPYIIVEPIVYLENFLIPGILNNG
VLAYPVPADKPISWISLNDAAQFHYYALHSELAGSIIPAPGLEALTGAQLAEQFSAV
LGEKISFMSLPFDHFEAAIQPLLGSETAAGLKGLYQWIDGHTDLLPRYQELDDNIKAN
LKLTQISDWIHQTMIK"

CDS 2695586..2696566

/gene="yajO_1"

/locus_tag="EFAGFIKM_02289"

/EC_number="1.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77735"

/codon_start=1

/transl_table=11

/product="1-deoxyxylulose-5-phosphate synthase YajO"

/db_xref="COG:COG0667"

/translation="MEYTKLGNTGLDVSFCLGCMGFGDASKWVHEWVLNEENSRPVI
KKALDLGINFFDTANIYSLGTSEEYLGRALKDYANRDEVVIATKVHGMHQPNGSGL
SRKAILSEIDKSLKRLETDYVDLYIIHRWDYNTPIEETMEALHDVVKSGKVRYIGASA
MFAWQFQKALHVAEKNWTKFVSMQNHNLNLIYREEEREMLPCKEEKIGVTPYSPLAS
GRLTRDWSVSTLRSETDQIQKSKYNATSDADRLVVERVASIAEKYGVPRTHIALAWLL
QKDTVAAPIIGATKISHLEDAVGALSVNLTSEDVTFLEEPYVPHPVVGAQ"

CDS complement(2696642..2697013)

/gene="fra"

/locus_tag="EFAGFIKM_02290"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q797E6"

/codon_start=1

/transl_table=11

/product="Intracellular iron chaperone frataxin"

/db_xref="COG:COG5646"

/translation="METFAEFIARIDNPEHQARTEEVLNWITEKFPNLKQKIAWNQPM

FTDHETFIIGFSVSKQHLAVAPEKAGINRFSEEITQAGYDHTKELVRMKWKQEIDFSL

LERMIEFNIADKAECSTFWRK"

CDS complement(2697142..2697624)

/locus_tag="EFAGFIKM_02291"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRKMTASFHQPEGYECPCRIWGIEQPDQGTKQRDIYQNEKV

TAFIAGKWWPNKGHALIVPNQHFENIFELPADYAVEIHRAAQLTAFAMKSTYGCDGI

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CDS complement(2697803..2698843)

/gene="adhA"

/locus_tag="EFAGFIKM_02292"

/EC_number="1.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPA5"

/codon_start=1

/transl_table=11

/product="putative formaldehyde dehydrogenase AdhA"

/db_xref="COG:COG1064"

/translation="MIIAKARAVDGPDQQFKSAEIKRRDLDTNDVLIEIKYAGICHSD

IHTAHGEWGPPVNYPLVPGHEIAGIVTDVGTGVSKYKVGDRVGVGCMVDSCGECVNCRK

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ITTYSPHHWGAGPGKKVAVVGMGGLGHMAVKIAHAMGAEVTVLSQSLSKKEDGLQFG

ADHYFATSEPETFELAGTFDLMINTVSANIDINAYFSLTLDGTLVNVGAPAEPLAV
NVFSLIGHRRSFAGSMIGGIRETQEMLDCAEHDIAPNIEVISADQIDEAYKRVLASD
VKYRFVIDISTM"

CDS 2699035..2699448

/locus_tag="EFAGFIKM_02293"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P44558"
/codon_start=1
/transl_table=11
/product="putative HTH-type transcriptional regulator"
/db_xref="COG:COG0789"
/translation="MTYSIGEVAKKLDLTVYTLRYDKEGLMPFVERTTSGTRLFKDS
DIDFLKIIQCLKLTGMPIDIKDFIEWCSEGDSSLKQRYDMFTERKAIVEAQMEELRR
TMEVIEHKRSYYETALEAGTEEIHKIKPMENAITN"

CDS complement(2699542..2700120)

/gene="comR_4"
/locus_tag="EFAGFIKM_02294"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P75952"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional repressor ComR"
/translation="MARSKEFEVNEVLDKAMKIFWEQGYEKTSMSDLVEHMGIIHRRSI
YDTFDDKHSLFLQAMDRYRGKVSTLLAEIKASKTAVEALHKIFDVMISEAEETPSGC
LIVNSAVELGTRDQEVDNRSLESFNEAERMFEQIIQWGQREGESFDHDAKEMAEYLH
NISVGIRAMARTSMDKGKLNRIIHVTMKLLEK"

CDS 2700410..2701333

/gene="rhaS_20"
/locus_tag="EFAGFIKM_02295"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1

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/product="HTH-type transcriptional activator RhaS"

/translation="MSDQIHEQQNELATLIDRYSDKDGVHPTAIPSLFLIRESVVTEP
IFRVNEPSFCIIVQGEKEVLLGQDRFRYGPFSYIVATVDLPVSGQVIQASSEAPYLAL
KLEFTSSEILEVLNHSDFPARPRKTRRAMFVSQAEPSELLDAVIRLARLLEDHSEDIP
LLAPLFKKEILYKVLKGPFGIALEQATMEGSHTYRIRDVIEYIMNHSEQNFRVEELAD
LANMSTASLHRHFKEVTAMSPIQFQKQLRLQEARRLLLSKSTDAADVAFQVGYESPSQ
FSREYSRMFGFPFPREDIKRLRGRADETTTIS"

CDS complement(2701467..2702489)

/gene="namA_1"

/locus_tag="EFAGFIKM_02296"

/EC_number="1.6.99.1"

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/inference="similar to AA sequence:UniProtKB:P54550"

/codon_start=1

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/product="NADPH dehydrogenase"

/db_xref="COG:COG1902"

/translation="MTDLFSPYSFKSLELKNRVVMAPMCQYSVERKDGIATDWHYMHY
VSRAVGGTGLIIEMTDVEPDGRISDYDLGLWSDEQIPALKRIVDACHSYGAKVGIQI
AHAGRKAEDAIEVPVAPSAIAFDENSKQPRALTDEVKGMVEKFRSAVARAVKAGFDAI
ELHGAHGYLIHQFHSPLTNKREDEYQGDLTLFGREIIQAAKAEMPEDMPLMMRISAKE
YVEGGYGINESSEFAKAYKEAGVDVFDISSGGEGPIAAWGRPGTHAAYQVPLAKAIKE
ALDVPVIAVGRLDDPTLANAVIGNEEADLVAVGRGLLRNPYWALEAASALRKTTDVPK
QYTTGF"

CDS complement(2702601..2702945)

/locus_tag="EFAGFIKM_02297"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MIMLMLLTIFILGIFIVVRQFWPVRNLEYIDYQVFLRQERDFRQY

KVIDIRDATDYMANPTPDTINISLGRLAFTWEKYLLREDNVIIMSPGMLQSKKAVRIL

RKHGFECIYVMK"

CDS complement(2702997..2703152)

/locus_tag="EFAGFIKM_02298"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MKVFVVGSYGQIAREDVAHVILASLSDKNTYKRSLDLIAGEDITI

SEALSGL"

CDS complement(2703290..2703694)

/locus_tag="EFAGFIKM_02299"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNVWLAFSNIHTQLNEKLEQALLQQYDLSLKEFYVLNFIYNAEG

KELRLQQQLQELVGLSQSATSRLVVRMEAKDCGALERHACEDDRRGYTRITELGENKY

KRALQTFNQVLQTELEQDGFETRLENLTKELF"

CDS complement(2703902..2704930)

/gene="fhuD_2"

/locus_tag="EFAGFIKM_02300"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37580"

/codon_start=1

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/product="Iron(3+)-hydroxamate-binding protein FhuD"

/db_xref="COG:COG0614"

/translation="MRKQIKSIWIMMALILLIVLSACGQSATTNSTTGDSTNAATETE

TKTNSDSASSAESTATAEEELVTYQSDAGEVQVPKNPKRIIDLTSFSTGYFVALDAPV

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PVVQITFGKRDFKDLMEMGKLTNREDAAKAWNAKWEAKINELKPKVQEAVGDRTVSI

LNPYAKGLFVFGHNYGRGGEIYGEFDLKAPAKAQAEIDSGTGWASISMELLPEYAG
DIIFTSPWSGDTPKIVYDNTLWKNLPAVKANDVFQLDPTSDSYNDPLTLEGQLQFI
SDSLLTAK"

CDS 2705142..2705954

/gene="uppP_1"

/locus_tag="EFAGFIKM_02301"

/EC_number="3.6.1.27"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WFF9"

/codon_start=1

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/product="Undecaprenyl-diphosphatase"

/db_xref="COG:COG1968"

/translation="MEEIILWLKYLFLGIVQGATEPIPVSSSGHLIIAQKLMGIKQNG

LSFEILTNTASLIAIIFREDIKKLIIGALGYLRTRKEEYRADFMFCLYIIIGTIPA

AVVAVLFKDRIEEIFSSVYTVSIALITGVALWLIRNLRGRKQDGDLDLSTKDALLVGLA

QAAVALIPGISRSGATVIASIAVGMKQETALKFSFMLYIPISIGGLIMGVSDIANDPNR

SQLAIPYLIAFITTLFVTYFSMRWFMGIMAKGNLKYFSYYCFAAGTLLLIFL"

CDS complement(2706042..2707220)

/locus_tag="EFAGFIKM_02302"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVTLLLIILYLAFIGLGLPDALLGSAWSVMKNDIHATTEMAGYI

SLIISFSTVSSLSASRLLHRFGTGKVTLSILSTTIALLGFSFSENFVLLILAIPL

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VALILLGIVVVLLSTLSLWKIFEKGRVEGSGDEKKRVSNRETIRIPGVKMSMLAMLCY

NGSETAAGLWMASFFIVSKGVSPGTAAALSSLFFIGIILGRVISGFLSTHVSSKNLIR

YGGIVGCFGLVILVMPYPIYWIAAGALFIVGLGGAPIYPSIVHATPERFGEKASPSVIG

LEMASAYTGSTLIPLGMGLIASQWGMSPVPLILLILFSVMFAATELVNRSNKATRLTV

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CDS complement(2707365..2708222)
/locus_tag="EFAGFIKM_02303"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTQKTIRLLMPQWQGGDNPYSGAELLAWLAPDNDQPLIHVPV
EAYDGTSLVSENGIKGRAQLLQQLQAAQHIIQAHQPDRIVMFGGDCLVEQAPFAYLNE
RYGGELGLIWIDAHGDLVRYEGYDNGHTLPLGNLLGEGDPEFARHVRVPLKPGNIFMA
GLTTPTEQETEVQIRLGIRTAGTEELTHGMDSIKKWIKETGIKHLAIHLDLVDLPNM
FRSLLFAKPGEPYVLSPAGTMQIPHLLHLIKELSEATDVVGLGITEHMPWDAINLKNL
LGEIPILNQ"

CDS 2708325..2708693
/locus_tag="EFAGFIKM_02304"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MMSMAEYHGKVKNIQDTPFGYTLVIGGKWKMVIMYLLADNQPV
RFNELKRQIGAITYKTLSSQLKELEADGMVERKEYPQVPPKVEYRLTAKAETLLPVLE
GLCEWGVQHQEPSINNSATD"

CDS complement(2708835..2709305)
/gene="ysnE_1"
/locus_tag="EFAGFIKM_02305"
/EC_number="2.3.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94562"
/codon_start=1
/transl_table=11
/product="putative N-acetyltransferase YsnE"
/translation="MTHIVHAAAEDIRSEDSLLLIKELSEELGLLYGGDGTAGFQLSD
VEVPRAAFIVARIDGYPVGCALRPLDETSVEVKRMYTRSGYRRKGIAQAILAEAERL

ANELGYTNLKLQGTGPLQPEAAALYERVGYRIPVFSGNWDRVLAYQKDLVHEKV"

CDS 2709513..2710178

/gene="yflN_3"

/locus_tag="EFAGFIKM_02306"

/EC_number="3.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34409"

/codon_start=1

/transl_table=11

/product="putative metallo-hydrolase YflN"

/db_xref="COG:COG0491"

/translation="MEISKGIEMQLDFEGNIIHPVLIWDEEMVVLIDTGFPQYDDL
CIALEKIGVPISRLKAVILTHQDVDHIGCLPEILQECGSQVKIYAHELD KPYIEGQLP
LLKDGHLEHPPMGKVD ETVTDGQELPFCGGIRVIHTPGHTPGHISLYLMDSKTLIAGD
SMYSVDGMLGGIHEPTTLDTEIARISLKKYIELDISSVVCYHGGLTHRNVNEQISGLY
KMN"

CDS complement(2710409..2711032)

/locus_tag="EFAGFIKM_02307"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNLYHIQSNVHGINRVASFLEDNYIGIAWSGTGDLEHTPPELWK
EQLVQHYPLDEAELASTLATLHMFGNLMQDGDYVLISDDEWTVYVDIGDYDDDSAGS
EEDLICHRRGVTWLGRIPLAELNDKVQALQND SAILAKFEYPISQAQLDRGLAVSITA
EATNSLSTGVDEATIQTALQVLREALHSEEEELRIRAATAILQYAKQ"

CDS complement(2711049..2711444)

/locus_tag="EFAGFIKM_02308"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGIQKRLFHFILAATLMINSVSLSTDVTYADPESIQEQDYKAIA
LTMLNPYISREITNYYQANHMPVPSYGLYEIHVLELKRHTQGGYSFRTVLEVRTFDGP
HNPPYGKEVITFEIDPANVTMVNYVHTND"

CDS 2711712..2714006

/gene="metE_1"

/locus_tag="EFAGFIKM_02309"

/EC_number="2.1.1.14"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80877"

/codon_start=1

/transl_table=11

/product="5-methyltetrahydropteroyltriglutamate--
homocysteine methyltransferase"

/db_xref="COG:COG0620"

/translation="MTKSSVLGYPRIGADREWKKALEAFWAGKLEEFHARLQEIRI
DHLRKQQAKGIDIIPVNDFSYYDHILDTAVMFGIIPKRFSYDGGSVPLSVYYGIARGT
KDAAASEMTKWFNNTNYHYIVPELDGASPTLTENKPLLAYREAKEKLGIEGKPVIVGPL
TFLKLSKGYDKSETDAWLDRLPLYTQLLQELASEGVQWVQIDEPILVTKLSDEDVQR
LNKIYKTFAAAVPGLNIMLQTYFESVENYSIDVALPVQGVGLDFVHGLSGNTQSIRTS
GFPADKVLGAGIIDGRGIWKASLQTKLNLLNELTEFVTPERIVQSSCSLLHVPVTTD
REAKLTSELKNALAFADKLDIVLLTTALSSPSAEITAKIDEAELTLLALQQSEDRN
RTAVQKAVASISVQQPERSRPFAERHEAQKAWQLPLFPTTTIGSFPQSAEVRKARQL
WRKGELNNEQYAAFIREQIDIWIKIQEEIGIDVLVHGEFERTDMVEFFGEKLAGFAFT
QFGWVQSYGSRVCKPPIIFGDVAFTGEMTVEETKYAQSQTERPVKGMLTGPITIMNWS
FVREDIAREQIAYQLAYALRQEVEALEQAGIGMIQVDEPAVREGLPLKENEQADYLAW
AVKAFRISTCTVHETTQIHTHMCYCEFHDMIDSIEAMDADVISIETSRSHGELIHSFE
ENTYELGIGLVYDIHSPRVPSVDEMSSMIERALRVLDPKLFWINPDCGLKTRGQEET
VASLRNMVDATRIARNNHASAAVL"

CDS complement(2714180..2714737)

/gene="resA_2"

/locus_tag="EFAGFIKM_02310"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P35160"

/codon_start=1

/transl_table=11

/product="Thiol-disulfide oxidoreductase ResA"

/translation="MKVSLLQKKSFKSRRTLILIGVIALITGTWAIFENVSTPESQR

GNAIEVGAVAPEFTAVNSAGEQVKLSDYRGKAVMINFWASWCTPCVREMPVLVHQAED

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GEFRHILLGELTEDTPLQQWLKDSI"

CDS complement(2714734..2715447)

/gene="lnrL_4"

/locus_tag="EFAGFIKM_02311"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94440"

/codon_start=1

/transl_table=11

/product="Linearmycin resistance ATP-binding protein LnrL"

/db_xref="COG:COG1131"

/translation="MDKMGLEVMGLCKSIKKQPIVEDISFRITSGQVLALCGGNGAGK

STVLRMIAGILRPTSGEVAVNNVRWLKERKRYSEQIGYMPDDYQFNQGLSAEEMLLFW

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NGLDPFWMQELTQLLKGIKQEGHMVVFSTHQLEIADDIADQVIFMNHGRNVGEGSTHD

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CDS complement(2715440..2716222)

/locus_tag="EFAGFIKM_02312"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGFRNPWAYSFLILFCTFSLLLLLNSQNLVEGYSGTTGSMLNL

ILYLLPLMTLFLGSFSLTSEKEDGSWQLLSTYPIGTMSFIVGKYLGLSIVLITIVAFG

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WFFAVIGWPTLLLSVLGLMPYLWVKPLLVMLTLINPAELVRLFVVIKLGGSILGPEY

YRWVEWVQQPSGSWIFIGICLFWIAFSVLTVYAIWERGRSHG"

CDS complement(2716290..2716835)

/locus_tag="EFAGFIKM_02313"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVLMMFGMVLLTACGTKYAALPINEDVDICAICKMQVKDDAYATQ

LTTKDQGQNYKFDDIGCMNQWKTENGTDNIGMDYVRDYNDKEWIEYSKATYVYDASLRT

PMAYGILNFKDKPSAEAFIAEQVGTIMTAEDLASHDWKQNTENMDMMGEHGHDEHGH

GEEGDGNEMHQEGEMKEESGH"

CDS complement(2716868..2718169)

/gene="nosD"

/locus_tag="EFAGFIKM_02314"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P19843"

/codon_start=1

/transl_table=11

/product="putative ABC transporter binding protein NosD"

/translation="MLLLSLPHGAVMASSGHRDLIPLQPMIDRSAPGEVIELASGRYS

GPVTIDKNITIQGDPTVIVVNAEATSTIMIRSDGVKLSGFTIEHDTNEQTAAIQVEGK

NSEITDLHIQTQGYGMIIRNSSQATIQRNNITWAGSDSASSGQKGNGIDLNAHDSYI

EANEITGMRDGIYLENSRKSNNVQNNRLLHTRYGIHCMYIDGSSVMDNTGEENMTGAMI

MGVKNTVISGNSFRKQSTNVHSQGILLYDVHQSSVHNNVVEGNRVGMNIAESSGNEIH

GNAVLRNFVGIQLVLAEANEFTRNQLVSNVIEASALDSPNNVLMENYWDSFQGLDLNQ

DGISEISYAINPFYEQLVSRNSAYQLFFQSPGMVFLSGLFTEGREQWTTDKSPRMSMD

TESDLNMSVERVAGSKMVWMFGLVLLGMATFIIYMGVLRK"

CDS complement(2718574..2719248)

/gene="bshB2"

/locus_tag="EFAGFIKM_02315"

/EC_number="3.5.1.-"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q81AU5"
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/product="putative N-acetyl-alpha-D-glucosaminyl L-malate
deacetylase 2"
/db_xref="COG:COG2120"
/translation="MNTTHNEHERILVVYPHPDDEAFSVSGTLAKYIDGGAHVTYACL
TLGEMGRNMGIPPFANRVTLPGIRKQELIEASEAIGIQDLRMLGFHDKMLEFEDPQLL
EDPIMSLKELNPTLVITFYPGYSVHPDHDATGAAVIRTIKLPVDERPIVHCVAFAN
NQEYIGKPDVFVDVSEFLDRKMASIRAHRSQFQAAELVGNRELNNEEIKRFGRET
WTFPFE"

CDS complement(2719272..2719616)

/gene="yofF"
/locus_tag="EFAGFIKM_02316"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31858"
/codon_start=1
/transl_table=11
/product="putative protein YofF"
/translation="MQPIKPQDIQLRINNADQDLYVHLELTSGAYAQHMDSTKHPAS
AFITNAAIRYTQGSISGTGPYRVGLKTTQGWLYAEGLTIDEQEERLILAGHDSQGK
LVVALQLSREMF"

CDS 2719882..2720667

/locus_tag="EFAGFIKM_02317"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MKSLLQLLHFGYHQAMSCIFPVAIFGTLALSSVIPFLHRYDA
ILLVLLAVQYLMYRSGLETKDEIKVICVFHIIGLVLEIYKVVWMSGWSYPEQAYSKILG
VPLYSGFMYASVASFMCQVWRRRLRMDMTGWPGFAPSMMLLGAAYINFFTHHFMDFRW

WLTALVFIVFWKTIWYRVRATTYRMPLSLAFIIVGFFIWAAENIATFFNAWKYPDQH

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CDS complement(2720849..2723329)

/locus_tag="EFAGFIKM_02318"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLLKYPSSWWQGLWREALPSGNGKLGASVQGGIQTETVLLQHSE

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TVEMKCNNAFRKYRRELDMDTGEVQVRWQDGSNDYTRSLFVSRADDCVVYEIETHRVK

DGASAQGTGAAEHSLLSGTIGLQFPQGDRVREDDEFNVLKSSITIRIDRDDAGEYLCY

GGQNDGQDYGAVLRILQLNEIPGASHDQKKESETNEDMLSRQLHFHTSGKVLVLVKM

FATGRRAQEWTRLKQELASLESEYNTLLDRHISLHQPLFSSAELDLDDKTDDGRCNED

LLLEAYEGEAPTGFVRKMWAYGRYLFISGTSEYSGLPFGLYGLWGGDYRLIWGHNMAN

ENVQMMYWHTAVGGLSKLNRSLFRYYNGLMDDFRDNARKLYGCRGTYPAGTTPGIGV

PNQIVPVIINWTGAAGWIARHYAHYQFTGDKQFLLEEALPFMKEALQFYEDFLVLGE

DGKYKMYPSVSPENTPENFMPKHGQPLAHPMPTAINATIDIAIKELLQHVIAASRLT

GVHTTKIPCWEAMLEHMPDYLLPEGAVKEWLHPAFEDRRDHRHLSHLYPVFPGQEV

REEQPELFQAFETAVDQRRLLGAQSGWSLAHMSSIYARLGNGERALESLDILARSCVLS

NGYTLHNDWRNMGVCMSMPAAPIQLDANMGWVNAVQEMLLYVSEQWIKLLPALPERWV

RGSIHGWRFHGGSLSCTWNRSTGFFRAELVADRRINTKLYIPEWVKGCEMPSSRRACLC

ELEENGIYELEIEAGGELVLEQTAVFDA"

CDS complement(2723383..2724528)

/gene="yteR_2"

/locus_tag="EFAGFIKM_02319"

/EC_number="3.2.1.172"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34559"

/codon_start=1

/transl_table=11

/product="Unsaturated rhamnogalacturonyl hydrolase YteR"

/db_xref="COG:COG4225"

/translation="MVGTSKSVTQERRMSVKIADTLLSECQNGNHPKIAGKWGYVGG

MTLMALERAAEWNQESRYAELVQRHMDDLIENDGTIRTYRLNDYNLDMINEGKNLNFQ

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TFDHPESFDEVARQILLIERMTRNPSNGLLHHAWDESREQRWCAQDTGRSVHVVWGRAM

GWYAMAVVDALEHFPVDHPQRGQIMGIFERMAYAIAHVQDHDSGLWYQVMDQNGRAGN

YLEASASCMLTYALAKGLRLHYLAELDREVVDHAYAGILKRLVTEDEKGVHLHHICHG

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CDS complement(2724596..2726653)

/locus_tag="EFAGFIKM_02320"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDRQSVVTRNHPVLTQLEPRSPSVGNGEFAFSADFTGLQTYPD

LYEIPLGTSQSNWGWHYTGHHVFGDEDIVYQAFETYGRKVAYPMKPEDKEEAYHWLRQ

NPHRLQLGRISFRLLGEDGQETGVTHVVPVRQELNLWTGILHSEFTVQGEEVRVETAC

DPRLDCIAIRVQSELIRKQRLQLFVVPSPDMTHRSWSKSVFPDWKQHDRHSTVLTSV

TSTSASLKRVLDEDEYTLIEWDAGQLEQTGTHEFTLSPKAVPDLDIWSCSVSFAAHK

PETLPADTVLRSSSVHWNQFWNDGGVIDFDGSSDPRAAELEERRVLSQFLSAVHSGGS

MPPQETGYMYNSWFGKMHLEMHWWHAAHFPLWNRRTLLCKSMDWYLTMLPEARELARS

QGYVGARWPKMVGYNHGHQTPSPVAPGLIWQQPHPMALAEMCYLSRLDPAMLTRYKDIV

FEAADFMVSYAHWDEKRQAYVLGPPLIPAQENHAMNDSLNPPELEYWKFGLEIAILW

AERLNHPANPDWRRVASHMAKPRHENGVLAHENCPTYTVKNHDHPSMVGALGLLPG

SLIDPEIMRNTLLKVKECWDWESAWGWDFPMCAMTAARLNEPELAVYFLMMDATKNTY

LPNGHNYQRAGLWAYLPNGGGLLTAVAMMAAGWTGAGEQANPGFPRDGSWTVKWEGLN

PLM"

CDS complement(2726697..2728991)

/gene="yesS_4"

/locus_tag="EFAGFIKM_02321"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31522"

/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator YesS"
/db_xref="COG:COG2207"
/translation="MTLSFLKWLFNVTNTQTRLLLILTVVFMIIIIVGMMTTYSSK
SVLQQELSEPQHQMRLISMNDIDEVIRESDQIAVKIALNSNVYRFLTNEVQGSYRNIT
ELVQFLETLSSTSIKSAIFDMNRESIVAFPQGYSSSKVNFPSDWVSVADELEER
PMLVKQREISTSSGVSMPTLYRKIMIALGELKGIIVNFKTEKMFEHMLLSSVSDLD
SHRFILDTNNQPLYDLGNYAVGEEAVSHVLTQLDGEKLGEFKHEGKLLLASQTISPYT
GWRYLSVISQDSLLANAQKIRNIVFIVSLLALVAGAVTITVYNAAAFRPVRRMRQLLS
GYDQERIHPEQIDLEKITGQLLDHAQQAINLRQTLPEASSKFLTDIYNHMTGSREI
SEKWCRYFKDWSDEPLSIAMLSIDNYKAWCERFTKSDHSLKFAIGNIIAELLSGQWR
VLSADLGRDRMLVMLQPIHSGGSKSVATAIRETIGMIPRLLKFQVSSGVSGGHDGFMRL
LQRAMHEAESALDYRFYWG YERVISFEEISGLQPTENTSEEHEIMTQLTETVEAGRGE
EALRTFDKIVGRMTHEQWHPSSALAFLEAVAATIDRIRLKRETEGCGLEMVDMRTMHL
EAVCEVLRSQLIEGLADWFGSLMLSKDFILCQQMITFMNKHLEDPVSIQEIAEHAGIGS
SLASQLFKQEMGDTIHGYFTKLRMERACELLDDTDYRISEIATMVG YQHENSFIRVYR
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CDS complement(2729079..2731310)

/locus_tag="EFAGFIKM_02322"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSSHVYFEPEESMAYQSGEDVMHALMSIAGRYIGANSPPHPPVYR
VSRPGLVRKCDDHRYVFPLGDLFPNMSKGQH VYTWAKLWSDSDQEFVFHITCFGPVRL
YHNGVLIYGSAPEEEEYPAIPVLKLCGLVRGWNHVFLEFKSGENG GGGQFGTGSRK NK
PLHFIVPSLERDGE EWLYSEPLDFPLSEIPSGPMREKATGVNWLPREEDHEKASPYG
QLARMYGLTSGMSAYAWTKISGTKCGKEAMLISGEAYSPIEFSVEGKVVFHQEQAGR F
RFELPLSAAVQDLTANCVGGDRDWGFRMDATTDKMLTPALDVKGHRGKWLYLGPFQAE
QEIDLASCQKMKRTARSGTGEDVYWRTELPEGEVRPFLENEWFGRWNYPLGVTLYGLL
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ATMLLADRERKLDGVSETAAHIADYILHQQSRLEDGTLRKIGVSRMDNTMWCDLY
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RGNGWVLFSELTALPQEHSSYTVLIQFYRELCEGYLALQGRNGLWHQVLTDPESY
EETSCTSMFIYAYARGVRMGWLLDPKPYAQSAQGWKGLSERTIDKRGNVYGVCRGSS
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CDS complement(2731307..2732635)

/gene="yteT_1"

/locus_tag="EFAGFIKM_02323"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34371"

/codon_start=1

/transl_table=11

/product="Putative oxidoreductase YteT"

/db_xref="COG:COG0673"

/translation="MKKRYALCGVSGRALGQFAKPIHELFSHNSEVVALLDSDPARFE
VYRARFPEHTEVAVYGASDFGVMVDETRPDCIIVAGRDDTHAHYIVAALERDLDVITE
KPMTTTGADARRILEAEARSKGNVIVTFNYRYMPIHMRIKELIQEGKLGRVTSIDLNW
YIDTHHGSSYFKRWNRRERAFSGGLSVHKSTHHFDLVQWWINQKPVEVFAYGALNYYGA
EGEWNPAQEDGRHCRTCHVSEDCAYYSRWTSRSRQIRVPDDHLNQLGIASQQEFPYTS
YRPDQCIFDSTIEIEDTYAATVKYSGGALMSYSVNFSLPYEGYRLAINGTKGRLETLE
YHMPDRTPFPPTPVQTIDYFPLFGSKETIHVVHREGGHGGDPLLLEDIFLGEDKRRPY
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CDS complement(2732632..2734170)

/gene="lipO_7"

/locus_tag="EFAGFIKM_02324"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37966"

/codon_start=1

/transl_table=11

/product="Lipoprotein LipO"

/db_xref="COG:COG1653"
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VKVKVFKSHMGVGS LPTADNPHVKYIAEQTGVQYELITTPPGSEPSEYLNLMIASDEL
PDILRPIGGIEQTLIQGGALPLDELLPEYAPHVWESIPQEAWDIVRSASPDGKIYYV
PKVFLVPERAPLIRQDWVDKVGMEPKTTDDYVELLTAFRDKDPNGNGKTDELPTSGR
EFGRWMDHLFAMYGVAMWEGYPEWDEYDGKIQYAGTTDNMREAIKFIRMLYVEKLLDN
ETFLNKGEVWQAKINNNLVGSWYHLPANVRDRYNAMLTQAPDAYIAAMPLPKADGFEA
FVTQKSMGEPEWMIPATKQDNAPNALKLLDFFYNPENDEFGRFGLEGEQHEVKDGRKV
ILPPADNKPLALGMKNLTTAEDMNKRIEETYPEDQQQMVKDMFEVSTADARQIAGDGL
PASVYEGFPDIQSHKLFQEVLT KIVIGELPIEAYDEYVKKWNASGGEVVTQRVQEWYE
KVRK"

CDS complement(2734194..2735066)

/gene="melC_5"
/locus_tag="EFAGFIKM_02325"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34518"
/codon_start=1
/transl_table=11
/product="Melibiose/raffinose/stachyose import permease
protein MelC"
/db_xref="COG:COG0395"
/translation="MIKQTIGEKL FQTANYIFLTAAFTMLLPLLHLLAVSLSSPIAA
DSKEVFLWPVGFTFASWKHILQSSGLWQSFGVTVFITVVG TALSMLFSVLTA FPLSRR
EFMIRKQVMLGIVITMIFNAPMIPFFLT VRELGMMSIWSLIIPGVIGTFNMVILRTF
FMSLPKELDDTARIDGCHDFRILFQIYLP LSKPVLATVSLFYAVGYWNTFQRAVLFLR
DPGLWPLQMKL RAYLTSPEELAQVNMFLGDYNFNTTTLKAATILFASVPIILVYPYLQ
KYFVKGSLLGSLKE"

CDS complement(2735066..2736025)

/gene="yteP_20"
/locus_tag="EFAGFIKM_02326"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1
/transl_table=11
/product="putative multiple-sugar transport system
permease YteP"
/db_xref="COG:COG4209"
/translation="MAELSETSTLQPGVKVNKPKPSYLRNIRKHWMLYVMILPGILF
YIIFKYIPLGGSVIAFQNFQIMKGIWSSPWVGLDNFKFIFTYQDFYHVLNRTALIALY
KLVIGFPAPILLALLFNEVRKMIKRFLQSLFYLPFLSWVVGGIVFEVLASGGFVN
AVRGWFGFEPILYMQQEQYFRPIVVLSSIWKEVGWGTIIYLAAVSGIDPTQYEAAMD
GANRWKQTIYITLPALFPTILTLLNIGNFLELGFDQIYNLLTPMTYSVGDIIETV
YRSGVLQGQYSVTTAIGLFQSVIGFILLWVFNRLARKSGEGLW"

CDS complement(2736256..2737146)

/gene="murB_2"
/locus_tag="EFAGFIKM_02327"
/EC_number="1.3.1.98"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P61431"
/codon_start=1
/transl_table=11
/product="UDP-N-acetylenolpyruvoylglucosamine reductase"
/db_xref="COG:COG0812"
/translation="MNIFEHQIPILEKVKFNEPLKNHTFIKIGGNADILIHPTTIDEIT
KIVEIANLHQLPLTVIGKGSNVIKDGGRGVTISLSHFDQIEVNEDSMIAQSGVDII
DVSRLALEHSLTGLEFACGIPGSTGGALYMNAGAYGGQIADVVERATVITKDGAVLEI
PREEMKFGYRNSLFKMDHYIILEAEFGLKKGNKEDIASKMKELTFLRESKQPLEFPSC
GSVFKRPEGHFAGKLIQDCNLQGTRIGGAEISMKHAGFIVNVDHATAQDYMDLIQFIQ
KKVYDTFQVELETEVIFLGE"

CDS complement(2737413..2738393)

/locus_tag="EFAGFIKM_02328"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MKQENNIRTLQHKMGSGFNHNSTAEDVLRDLDSLGLAIVTGGY
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LASDRNIDMLILNAGIMACPETRVGPGWEAQFATNHLGHFALTNLLWPALTSQGGARV
VSLASAGHHFSPIRWDDIQFEHGYEKFAYGQSKTATILFSVELDRRGAEHGVRAFSV
HPGGIMTPLQRHMPKEEMIALGWIDESGQVANPAFKTPEQGAATQVWAATSPQLEGKG
GVYCEDCDISEMAPEDGGFYGVKKY AIDPEQAIRLWELSAKLTDMDMPTT"

CDS complement(2738565..2739227)

/locus_tag="EFAGFIKM_02329"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MFQPRSIMMSISLVVIVLTLAACSGSNEPLPSPQPSMPVGEPAP
APSTGNEQPSETDGTEEANETERPQTASFEMLTADGNQSLEATLQQGEGFSLYVFEKF
TFDAAQGRLSLTNSDYVDIEPLPSDYNLAELETAGKEELVKAGKVSDYSGELVEHP
LGYAELYLQASGEEGSDYMWVKSEEEEAFLFRLHNPKGEEGSDFASPVLVSLSTVQGD
S"

CDS 2739427..2739570

/locus_tag="EFAGFIKM_02330"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSASIERRKVDINATLEDQLVWLEEAGFRVADCMYKYLDFAVFY
AQK"

CDS complement(2739640..2739864)

/locus_tag="EFAGFIKM_02331"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MVMPRFLRLMLYGKGMYRAQRNGTLLALNRMTGQPAFRVATGGD

LHNTTLKTNGMIIIQAEGKLLGVKLPASLK"

CDS complement(2740054..2742105)

/gene="yfeW_2"

/locus_tag="EFAGFIKM_02332"

/EC_number="3.4.16.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01034"

/codon_start=1

/transl_table=11

/product="Putative D-alanyl-D-alanine carboxypeptidase"

/translation="MKKLISLLCTAVLVITPLADVSAEANNSGTIEARAEQIAKEMVQ

NYGVTSVQYAIMDEGEYILSDSVGLHDKASQKPIDKDSMYGIGSVSKMVVTAAAIKL

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HDELLLKLQSEKLKSKPGAYSVYANDGFQLEILVERVSGLSYSEYIAKFISEPLKLE

STKTPLDSFDRAQLSETYWPTLEMKMPTENANIIGTGGVYSTAEELSQFGEVLMGNRP

DILSESAVKAMQSHEYRKGIWVSDEQNTINYGLGWDSVDLAPFSDYGV TALAKGGDTM

LYHAVLITIPHDISMAVLSSGGSSIYNQMFASKVLLEVLADQGIIDKVKPDQTFSP

VKVKMPTELNSYSGLYGTVGETLDITIKDGEMQLPALLGGIIEQKYVYTGDEHFTSA

DGSVKASFVKERNKVVYVKVQGMITLPGIGQTMNTYDYQKLEHNALDAATKEKWTAR

DGSKYYALDEKITSIFYLLPSMLIKNLSVDAKNGYANGTQIMDANNAENIAEIPVMNG

RDAFDLKFYTKNGAEILLQDGQEYIAEDAITPIFGGKKGITTIPANGQARWYAIDDRS

GNKSITVDSPKTGGYAVYNDKGEMVDFSVATNQESTKLPKSGFIVFGGDSGDVFIQ

LK"

CDS complement(2742216..2743514)

/locus_tag="EFAGFIKM_02333"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDTYMIFSIIFVTLLMAFQANFYFDSVLGKSRRKPRRAIYFMVF

VMLGYFYLVSSFSDIVSTAVALLLIFSLAQSYEVEFKIKLVFTILYAVLITMANTIAV

YILGVLESTDFISWEQFNGEDHWILSKVMLVGCSIMFIVIQIVRLVAKRRSFAVHYRY
YLLFLIVPIITIYQINVASIYSEKNIFYVFSVLGSLFLNVFIVYVFDNMVEKVQLAHE
NTQLQRQMDYQDANYEKTVHSFKNIKSIIHDINQQFLYIDECIQRNELAAAGDHIKST
LDTIEGAYQRVNSGNLVIDALVTNTLAMGQANGIKIDTKIQLHSQHIQIDRYDLCVWL
GNMLDNAIEASKKVRQAEDRYILIAIHSTSSALVIQIMNHVEQPIVDLKSDKPNPEYH
GIGLTNISRMCEKYGGHMSIEHQHRKFNNMVVLPFHTDNP"

CDS complement(2743516..2744256)
/locus_tag="EFAGFIKM_02334"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MFNIAICDDEEQQRERVKTMVLSLSLKTNFDQISLFTSGEQLL
SHYREVGDTFNILILDVEMGGMNGIQTAKAIRIMKFLDVQIMFLTSYPEYMVESFDVI
TFQYLIKPIQPQVFEEKMIKLCQYFQALDKKYVLIKSDYDELLLKYDDILWIEVVKSL
TIKNKLNFTQENVHETKGILSSYASGLKDHGFLQIHRSIIINLMHVQKFSGTQVIML
NGTELPIGRSKVKEIKDAYTKYMIMRIQ"

CDS complement(2744455..2745219)
/gene="yheD_3"
/locus_tag="EFAGFIKM_02335"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07545"
/codon_start=1
/transl_table=11
/product="Endospore coat-associated protein YheD"
/translation="MGVDKLQPLRSKWLTKLIINNELIKPFIPDTQKYNKTNLKSMI
SKYGMVYVKPERGTFGMGVKAEMESQQHFVYQIEQKRLTFDSFESFYNSLTRLVNKR
SYLIQRGIHLLKHNNRRFDIRVMIQLSPTKHWEATGIIGRLGHPKKIVTNYHSGGTPM
DIHKLLKSHASTKRRNELVQEMNELSLRIARHMKKKYPHLKQIGVDIGLDHSLKPWII
EVNVKPDPIYFNQLKDKTMYRKVIRYYRHAVPKKTK"

CDS 2745422..2746231
/locus_tag="EFAGFIKM_02336"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSVQPGIRLNNAPKIDVLIPAIEKDLATLPLVIDNIRRYVKHPI

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NGDSIVKAKYFLVMDADTVLIKPHSFLVEGKTVFYCRDWSQPEYFNTYRKLLGMKAPR

PRSFVTHYMLFDKSKLAALKQKIEAVHKLPWYKAIISNINKKKQFGFSEYETYANFMY

TKNPGSMVLRSSKNKSLNVNASSLKEQQIRNLALKYRSLSFHKRKIYSKAP"

CDS 2746249..2747622

/gene="rfbM"

/locus_tag="EFAGFIKM_02337"

/EC_number="2.7.7.13"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P26404"

/codon_start=1

/transl_table=11

/product="Mannose-1-phosphate guanylyltransferase RfbM"

/db_xref="COG:COG0662"

/translation="MHIVMLCGGSGKRLWPLSNELRSKLFIDILPSPAGGRESMISRV

CRQLDSSSLTDSTLIISHQDQANITARHTQGKIPVIGEPYKRGFTAAALATLYLQSF

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PGGEERNAYAPITQFIEKPEATIAETLLQRGALWNCGVYAFTVAFMISHIKKMGLPVH

YDQLSSLYEALPERSFDKHVAEKVQRAVVLPHYKGVWQDIGSWDTLCAQLDTHVIGHGG

ISGSSSDSYIINELPYPIQVIGVPGIIAAASPDGILIANKNNSNEIKAQLGNWPLKPM

YGEATWGSYRVIESSLDDENTTVTTLNITVLPKGHIGLNWHRTGCRAWTVLAGSGQVL

VNGKVMQVSTSNQFVITKESLFSILAETRMVILEVRIGVTEKDNILFEEEDWNVILK

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CDS complement(2747729..2750548)

/locus_tag="EFAGFIKM_02338"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MIAALNLEGVWKLQLDENKVETGLNFSDVITLPNTTSHAAGKK
NENVLIGALTDEYLFEGYAWFSREIEIPEHLAGKRCFLHLERTRVTTVWIDGVEWGTQ
NSLNTPHQYEIETGLTAGHTITIRVDNTDYPTKGGHLTSEDQTQTNWNGITGKLELQF
FERVFLDNVQVYPFLATRSFDIKAALVGDLQGVRIVVSAAVVSADPVYTTEEQVFTPD
SQEIQLTYKIGEDAMLWSDDEPNVYQLHIHLQDQDGEVLDSTEVWTGLREFRADGDKF
TINGRKTFLRGKHDGLIFPLTGYAPTVDVWVRILATSKSYGINHYRFHTCCPPEAAF
IAADLLGIYMEPELPFWGTITDESSDGHNQAQDYLISEGFAMLRAGNHPSFVMMMSM
GNELWGSKDRLNSILKAYKAYDSRHLYTEGSNNFQFVPDILEESEEFCGVRFSKERLF
RGSYAMCDAPLGHVQTDLPNTLKDYDSNIVPEQGSADADPSGQTGDKEIQYGTGSKT
VQAEAGSDQLVSHLPIISHEIGQYATFPNFEEINKYTGSLKAKNFEVFRERLNAKGLG
HLAEAYFRASGKLAVACYKEELEAAFRSQQLAGFQLLDLQDFSGQGTALVGVLDAFMD
SKGMITPEEWRTFCSDAVLLARFPKYNQAGELFQARIELSYFRRQALDGLQLKWELE
REQIEGSVLMEGKADLPAFHGEHYVSITDLSIRIPEVSNMSKAELRLSIPGTDIRKSY
DLWAYPSQLDVELTGLNLFTELSEVALVLEQGEDIMLFPNPDQLQHAIQGFYSTDFW
SYPMFRSISENMKREVPVGTMGLLIQQDHPAFEHFVTEEHSTYPWWSIVSESSSIILD
ELDKDLNPVQTIDNFERNHKLGLLMECRVRKGRVLMGALNLERLMTTLEGRQLLYSF
QRYVQSSAYQPVARLEVEELRKLFN"

CDS complement(2750735..2751529)

/gene="bdhA"
/locus_tag="EFAGFIKM_02339"
/EC_number="1.1.1.30"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O86034"
/codon_start=1
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/product="D-beta-hydroxybutyrate dehydrogenase"
/translation="MDMGLKEKTALVTGSTKGIGKAIAIELAREGVHVLINGRNDEEV
ERTVREIKSTFPETSPQKATADLVDREQRQALFEKFPEVDILVNSMGIYEIMSYEDVN
DEWVERYFRTNVLAANGLSQFYLPKMVKNNDGRIIFIASEEALMPSGQMPQYCMTKSM
LLSLSKSLSKLTAGTEVTINTILPGPTLSENVREIIEGIYPDEALTFEKENDFMKSN"

LPQSELQRFIKPSEIGRLATFVCSPYAPAFRGSPIRMDGGMVPTIF"

CDS complement(2751661..2752659)

/locus_tag="EFAGFIKM_02340"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQPQPNDRIKVHPGFWAGLHQLGIGADDIARAAQLSLETINQPV

VTQSQYFAIWQAYSDLIGDTAEGIIKLATRYEISKYPPPVLAMYPHARDYRDALNRMVR

YKQMCPPESLQITEAGEEWFIELEWLHKEQPGPPLLVGITLAFLIELGRRGTGQPLIA

KRVEFSQPMGDVATLEAYFGCRVDTNSNYNRLTLERKDLSLPFLSYNEELLEILTPAL

DRSLDEQESNRSVTEVVKWIMKRSLIGKRPDIQMVAKELRMSDRTLQRRLTEENTNFK

QLLTEARREQAREYLADPSLDIKEVAFLVGYEDQNSFYRAFRNWEGDTPSNWRVRQ"

CDS complement(2752863..2753468)

/gene="estA"

/locus_tag="EFAGFIKM_02341"

/EC_number="3.1.1.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37957"

/codon_start=1

/transl_table=11

/product="Lipase EstA"

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IVSPVLSRLNGANNVSVSLVSHIGLLFNSRVNALIKTALNE"

CDS complement(2753622..2753930)

/locus_tag="EFAGFIKM_02342"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNQRFRI TRSMQDSNTEQSSISLEECKLYFESQPDFTYSPVLNIV
GAESTMTIEGDFFMWDLEGAQIAFRLYMGDLYVAISNEAIVPKMIEIATDLRADIVEG
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CDS 2754094..2755329

/gene="rcsC_6"

/locus_tag="EFAGFIKM_02343"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00979"

/codon_start=1

/transl_table=11

/product="Sensor histidine kinase RcsC"

/translation="MLKTEFIDVLSIVSHKLYDSAANVMDTASRLIPANTFCIAQLDH
LSTKVLNVYNRDKLILGEGLVVDNAESYCALVTEHSQGPLVIKNNLTHPLTRHMDATE
FVGGCSFVGVPPIHNENGEIYGSLCSFDQDFYSYQQKDVDLLLSLSSFFTSLLEMETTL
QQLKQAEETAAKVLEEKNLLAVLSHEIRTPMNGVLAMANLLQSTKLNEDQSLYVNV
ESSGTSLLSMMDQILDYSKAEAGAISLEINPYSVIKTVDHVLQLFSSEAQKKGIRLYA
EYDINDHMLIGDQQKVRQILINLVGNALKFTEQGEVCISTQVSADPEGTLHASYEII
DTGIGIPQDRQDLLFKSYSQIHGNSGKYGGAGLGLSICKQLAELMGGIVWLKETSHLG
SRFAFNISASPTSMQISE"

CDS 2755372..2755797

/locus_tag="EFAGFIKM_02344"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTQFLDARSSQNAALFNSISIPVINTPQLFAQIGLQTVGAGA
NPRVSLKGTITVRLPLALFQVRITIVRGTVATDPIVYSANFTYGLSGLLNPEVIMFSA
NDYNPPISAQITYTAFISTNLLGTVRVGPESFDGFIVSD"

CDS complement(2755876..2757108)

/locus_tag="EFAGFIKM_02345"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVVVNITGALAGNQFEPsIAVNTLNPnIMCVVAVDTSTGPTLTG
FYRSIDGGSIWSTTVLPQPVEYSGAEAPTIDYTFPSTFIVTVHLFNGINDGTIASYTS
FDDGVTWQPPVIVQAGFGTIVHNDEPYIAVDRSPGSPYRGNAYVGYTPLATTSSAIFT
QRSVSQGLTWEPPDRQSNPRGIHDRAALAIGFSGEVYAGYIITGPASPSALLRISYDG
GITYQPPIERQATFISSVVPAPSPLPVPNYAFRVQTNLSLGADISVGPNSGTVYAVWN
DARAGYTDVLLCESPDGLLWSDPISITGAPPGTQNFPSITVSPFAGTIRVIYYSNRI
DGFLLDVFVAESFNGGASFTNRRITTSFNPNNGNSPMPTILIGDYITAATVSPDNLAA
VWMATTPPTGKLDVYFGN"

CDS complement(2757127..2757495)

/locus_tag="EFAGFIKM_02346"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MPNSTGFIYNPTTGATQSTQLIVTCINDSLNAPVNIELEVFRWD
TTQTARIAIGHDLFELLPQATRTLIIYPLINAAFYEVQSDYFSATSTVIHVYGVNSTGQ
IIQRVLQSEMTLIDRFTNIP"

CDS 2757677..2758951

/locus_tag="EFAGFIKM_02347"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MFIKRVGKIAAVTVITLSVLGSTPNIGGAYAAPASVHLDDVPL
KFDAAPRIDRGVTYVPFRTVGEALGIDITWNSKSQTVKATNTVKGQTTEVLLQVGSTT
ATVNGKKVTLAAAPVQREGRVLIPLSSFSNQFGVQVSWNQATKTVSLVSPQREMHLRA
FYALQSFQEKLITSMNSVAFGWSRIDREGQFTLQGDEYRLPAAAGDITPQSIVADAA
DQQIQPQLMVYALDGNGELTKVLSDSLRLQKSIEGITAABAEGFGGVWLD FEGLGFK
LDAVEQQKLLNAYVKQLKSSLPQDTALSLAVPPLNSAYKGYDYKTLASIADDLIIMAY"

QYNPVGTKSQVPEPNSLVDQAIQLAIQAGVPSKLLLGISLSSETPSSVDDKLGLAKR

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CDS complement(2759039..2759257)

/locus_tag="EFAGFIKM_02348"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLGSILGILLLATAIVYGEWKSSKEKRARIVSAGITAVAAVIG

IILLFQPRLPGPTQIVKLVFGSVDFKMK"

CDS complement(2759301..2760476)

/gene="gerAC_1"

/locus_tag="EFAGFIKM_02349"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P07870"

/codon_start=1

/transl_table=11

/product="Spore germination protein A3"

/translation="MRIYRVLLMPILCCVLLSGCWDRIEINDLAIVLATGIDYEDGKV

QLTSQIFIPRKASAGDSSGSGGSPSGVTMIRTAEGRTIAEALNRLQRKVPRNMFWGHC

EVIISEQAGKRGIREYIDFFLRYPQFREHAYVFSSEKAAKDILALLDPLERSSAESL

REMANLKLGTRVTALELAKSIEGPSSSAILSRMLILPPEPDQDKLTTTPYVKGLSMYK

KDRYVKTIKEPLSVGVLLAKELNSIIMPVEFEPLSGSFSIRLIENKTSCLKPRIVNQQ

WSMKVDIQTRGEVVLNTTDANLTDPAVLTKLEKEWSAKLTSLAHDALVMSQKELRSDF

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CDS complement(2760495..2761688)

/locus_tag="EFAGFIKM_02350"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

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/translation="MVASIPKEQTTLEQSTFRANKGAGLHMLTDKGKISVTQLAFMVF

PAILATAILSVPGITMHYAGHDMWMTPIIGSIVGLAAIGISVGLDRLYPGKTLIQSSV
LIIGRIPGKLFGLIYIAFLPHLTGLIIREYGEFIVNNALPRTPLFVVMGTMVVCAIN
VRLGIEVVGRTAQVFVTLIVLLALIFILLIGELNPAELFPFMEKGPIPIITGAAAPA
AWFSEYIVLAFLLPYVNEKKRITRVMLGSLVFTTTAMVTNLFCLFLIGDLTDTFVFP
VMIAARYITIADFLQHIESLIIAIWIFGIFVKISVFLYIFATSTAEWFGLRDYKPVVG
PLSFLCMVFAYWVVSGSGVSSLVSASANLYTISILLILPAMIYGVAWLKKGWAHFRK
NRANT"

CDS complement(2761652..2763061)

/gene="gerBA_3"

/locus_tag="EFAGFIKM_02351"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39569"

/codon_start=1

/transl_table=11

/product="Spore germination protein B1"

/translation="MDTSAITQQDLPLTGQLVIDQEMLRSVFAGCSDVVFHTFQTACL
TSALCVYCVGVC DTERLERQVLTPLQEMGIKTAQVPLASVKQVETTTQAVQAIFEGEA
LLLLDGSIGGTTYPLYLAANRSTEEPLAESTVRGARDGFTESLTMNMSLLRKRLKTPV
LKIHTRNMGERTNTSISLVYMEGIIDPKLVKEVQTRLGDLKLRDVLESQYIEEGIVDQ
RYSFPQMATERPDVVVSNLLEGRFAILVDGTPFTLIAPVTIFSMQLQSPEDYYQNVF
MSVFVRWLRYSEFFVLSMMLPSAYVAITTFHQEMIPTVLLLSIARAREEIPFPALVEAL
IMEIAFEALREAGVRLPKQVGSAVSIVGALIIGQAATSAGIVSAPMIIIVAITGIAF
MIPRYAASIATRLLRFPMMFLAGTLGLTGVM LGVILVVIHLSSLRSFGTPYLSPVAPT
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CDS complement(2763261..2764142)

/gene="araQ_16"

/locus_tag="EFAGFIKM_02352"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MQTAKSVEQPNAAIQYATTRRLTAGKIIYLLLIGLAVLCIIP
FYLM LIYSTHNNASTFTFLPGSFLVDNYMNMVSKINIWRGFANSIFIAGTSTVLS
LYIGALTAYGFAKFKFKGRNGLFLFLLATMMVPGQLALIGVYRLFSIMGLLDSYAAII
LPAAANAFNVFFIKEFMESSIPDEIIESARVDSAGEFRFTNQIVLPILGPAIAALGIF
TFIGSWNNFLTPLVLFFSLDKYPLPVLVALVQGYYGMDYGLLYLGVAISILPIIIVFS
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CDS complement(2764157..2765047)

/gene="lacF_3"

/locus_tag="EFAGFIKM_02353"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29823"

/codon_start=1

/transl_table=11

/product="Lactose transport system permease protein LacF"

/translation="MFAKTIRKDHYGYYFIAPFFIIFTTFLYPIYSLYISFTNFDG
ITTPDFVGIGNYVAVLQDPLFYKTLFNTLFIWGVSVVPQLTISLVLAFILNDKLLKGR
DFFRAVYFFPNIVTAASLGLLVSLIFDWQSGGLNHFLVQTGIIQDPINWKNDPWFMRL
IVSSILFFQYFGYSMVIYLAGLQGIDPSLLEAAQMDGAKKKHIFIHIVPMLRPIILF
QMITSIIGGIQIFDQPFTLTNGNGGPDRAAMTSIMYLYNVAFQSTRFGYGAAIAFCLF
IIIIILLSVASFIMTKRKSRS"

CDS complement(2765102..2766367)

/gene="lacE_1"

/locus_tag="EFAGFIKM_02354"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29822"

/codon_start=1

/transl_table=11

/product="Lactose-binding protein"

/translation="MKKWFKPTIVLVCAAMLLAGCQFSPSSQTKQQEITVWSFTDEAG
YAIKFEQKYPDIKVN FVNIPGNFYITKLKSALQTTSKAPDVFM IENANIRELIDVPY

LENLSASPYNANELIQEQYAFVQANEQDSEGNVRAIGYQGTGGIYYRRDLAKKYLGT
DDPEKVGSQLNTWEKIFEIGEKVQQLSGNKVHALANWNAISNSYDGIPWVKDGKLVID
PTYLEVLDLVREARERNVLAEYEDGSAGYAASMQKGEVMFYPGATWGLQYTFKANAPD
TEGMWGLAQGPSAFSSGGTYIAMYSKSEKKDLAWKFIEFYNFDHDFLSELAKEQDYFT
SNMVVNDKLAPSLSSSYLGGQKHFEFFSEAAKRPVYERTKYDATINNDIYKIVLQLY
LNKDIQTKEEVVKRIKRDVTLRFPELEV D"

CDS complement(2766453..2767337)

/gene="rhaR_20"

/locus_tag="EFAGFIKM_02355"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MGVPTFLETGHMQEGFPIRVIHTGNQFNAAHWHDEVELVLVNG

KSARIGVNDHVCELEKGDVLLIKPGDVHCFPGTEHLTIILFRLELLTGSFTTEAEIQ

DLGQLFNRTTVIPS NKGSQSNLTQYIDDIITEKKNQKPGYRWLMVSRLYDLIIILLRT

IVPVTDESTSSGWPCTSSKFEFLESVCEYLEEHYAEPICLEQVAEHIKFSKFHVCK

LFKEIKGVTLMEYLNHFRIKSEWALLFRQDTILEIAIGHGFNNVNSYNRLFKKYNDC

TPSEFRKKHRANMTKYGG"

CDS complement(2767455..2768453)

/gene="rbsR_2"

/locus_tag="EFAGFIKM_02356"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ACQ0"

/codon_start=1

/transl_table=11

/product="Ribose operon repressor"

/db_xref="COG:COG1609"

/translation="MMTTIKDVAKMAGVASSTVSCVLNDKGNVSEPTLRVLEAASQL

NYVRHGPASELKRNSTQTIGIIVHDMSSPYFSDLVNGIETVVM SHGYDMIVCSSLGGE

KSTAHRYIRERRIDGAIVIAQNIQDQLLIEASEAGFPIVVM DRDLDAQHIVKVLMSDT

QGGYLATRYLIDKGHRTIAYISGPSQSECNLHRYQGYLKALKEAGIEENPEWKIGGQY
MKQDGYNAANKLLEGELPSAVFFANDEMAIGGLEAFREHDISIPEQLSVIGFDNIPAS
QYMNPLTTFRQPKRDAGQLAGHVLFLQLLNGEIVETLYTLDIQCVERDSVRLLNLS"

CDS 2768615..2769040

/locus_tag="EFAGFIKM_02357"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRFSEYVIGQSYETKSLALSKSDIIEFATIIDPQYMHLDEEKAK

QGRFGSLIASGMQTMNISFKLWIEGVGYGEHVVAGTGMNNIQFLKPVFPDDELHVIAE

VIGLTPRRKGNGIVTVLLSTFNQKNQKVFQAELSALIDN"

CDS complement(2769110..2770300)

/gene="lysN_2"

/locus_tag="EFAGFIKM_02358"

/EC_number="2.6.1.39"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q72LL6"

/codon_start=1

/transl_table=11

/product="2-aminoadipate transaminase"

/db_xref="COG:COG1167"

/translation="MNYSFSNRIAALQPSIIREILKASSGQNVIPFSAGNPAPETFPI

EAIRFTFTQSILEHDPVTALQYGITEGYVPLREALTQHLKTGFDTGKPSDQLFIVSGAQ

QGIELACKVFCNEGDTIICESPSFIGSLNSFRASGAKLAGVPMEMDGMIDIEKLEQALQ

TEPNVKLIYVIPSFQNPVTGVTSLAKRKAIYELAKKYGVMILEDNPYGELRFNGDDVP

TIKSMDEGLVIYVGSFSKILSAGLRVGFVQAPHEVVEKMVVAKQGEDVHTAMLPQIL

AYKFMTEYDYAGHINSIREVYRRKATLMMDKLQEHMGESITYTQPDGGLFLWCDLPAH

VPMLDYAKTAAQGVAVVPGNAFLVNEHPCNAIRLNFSTPSDEQIVKGVEILGQVLK

GYNA"

CDS complement(2770480..2771628)

/locus_tag="EFAGFIKM_02359"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSKSIDVIVIGAGIAGSTCAMQLAGKGHRTLLLDQRQEFPRHKTC
GEFMSPETKEMLEVLDIHLLDQSKKPSTMDHAKIVMPQGGVIEAPLPGFAYGISRYEL
DQILHQKALEAGAQIVTKATITSIEQLEDASYEVQVKQGDERISYRAKAVIGAHGTTK
PRGMASAPDLRDQTVYVGKSHFSGIEIPARVELYFCEGGYVGISPIEDGIVNVAALL
TLDTVQGSQSVNDILQAASLTNVSLAARLAEGMPVDGTQVSIAPLHLSNVPEPWSQY
PHIGDAMLMIPPLCGDGMSIALRSSLLCARWTDKYLQGDIEHADWQSNYTLASREFT
QLLRARRRIQKLAFKTNKFYPGLARMIPGLAAYVVKATRLSEMNAAR"

CDS complement(2771635..2772354)

/locus_tag="EFAGFIKM_02360"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSFFRTLIRAKEDELMDDFS LGGEELREALRHLRRLNKIFAAP
GPTLAGVEKLWNSVGKPNKLTLLDVGAGSGDVNQKLLQWADRQGVQLEITLVDLTEEA
CEEARQLFRDEPRVRVQRADLTQLPDASADIVTGSQFVHHFDGDQLVDMVSHMLRASR
YGVVINDIHRHPVSYKAVWITTRIISRNRIRHDGPLSVAKGFTGRDWKELKQRLNHD
TMTYEWKPLFRYSVVIPTKGR"

CDS complement(2772341..2773498)

/locus_tag="EFAGFIKM_02361"
/EC_number="2.3.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P9WPF1"
/codon_start=1
/transl_table=11
/product="Alpha-pyrone synthesis polyketide synthase-like
Pks18"
/db_xref="COG:COG3424"

/translation="MNQYNPSDIALGMGTALPAHPVAQSDIAELIASSLQDRPDLA
RFARRIFKSCGVETRYTVEPSYLSLEECRYLPSGERSDIPTTEERMSTYKREALPLG
IDAAEKALED SGVSPKSITHIITVSCTGQYLPGLDVMLIRHLGLSARVNRLLIFQGC
AAGLKAIQMARDVVQGAPGSQVLVVCVELCTIHFQPVQDREALFAASFFGDAASSCVV
GTPEPQHKNYLSLGTGYSVLLPDSTEDMTWEVGNLGYDLYLSPRIPKLLGVHLEEEELR
LLLQSEQLPELWAIHPGGRGIVDSVQNVMKLRDEQTKYSRDVLRTYGNLSSNTILFVL
NAMREDMKAQVQSSTDGVAMAFGPGLTAELMKFTYVPSLSSVMEEHDHVLV"

CDS complement(2773728..2774612)

/gene="aes_1"

/locus_tag="EFAGFIKM_02362"

/EC_number="3.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01958"

/codon_start=1

/transl_table=11

/product="Acetyl esterase"

/translation="MDQQQQLEMVQRMQRNVVGTGAALQPGSTYAVTVKEVMIPPTKG
DTRVLVYTPDRDQSASMPVFFNMHGGGFILGQAEMDDPWCRLIADRSDCVVVNIDYSL
APEHKFPTAVHECYDVVQWIHANPQSLSVNPSLFAIGGHSAGGNLAAAVCLLNQQRGS
ELPIVLQVMDYAVLDVATDTAEKPSFAEAIPADIARTFNAMYLDTSEDAQDPLASPV
ATSLEGLPEALIITA EKDSLAEARTYAASLKASGVKVT LKEYKGAAHGFT HFGDLQM
AEDAWYLM SDKIREAFTK"

CDS complement(2774775..2775461)

/locus_tag="EFAGFIKM_02363"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKTYLKTIWFHYLG NKQDR TALFNVASLVINAVTGIGKLILGIY
LFSGWFITNAVYYLILCVAKGQVLHKYTVTKRMESPLERYRLELT VYKRGGLFLCLLG
ASYSMVCLRMYLIGDAFIYEGIIYIVATVAFTKL VFAVYGTWANRHLHNPIISTLKM
INFTDAMVSIVVTQATLLTMQGSPLALKTSSLFGMGCSVLFCLMGVWMMFHKKKETST

DPNRSPGTEC"

CDS complement(2775573..2775926)

/gene="yjbR"

/locus_tag="EFAGFIKM_02364"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AF50"

/codon_start=1

/transl_table=11

/product="putative protein YjbR"

/db_xref="COG:COG2315"

/translation="MKDTMIEYSLKKKGATKDYPFGDPVTIKVGGKIFALLFEDKEE

NGLLNLCDPPIAENLREQHEAVRPGYHNMNKKHWNTIMLDGSLSEDEVYVMIDHSYDM

VIQSLPKSIRESLAE"

CDS complement(2776069..2777475)

/gene="rhIE"

/locus_tag="EFAGFIKM_02365"

/EC_number="3.6.4.13"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P25888"

/codon_start=1

/transl_table=11

/product="ATP-dependent RNA helicase RhIE"

/db_xref="COG:COG0513"

/translation="MTFKDLNIIPSIMEGLSKANYTNPTPIQEQAIPAVLAGRDLLGC

AQTGTGKTAAFSVPIIQLLSERSKGQGSKSARHIRSLILTPRELAIQIADNIKVYSR

YTDIRCTAIVGGVSQKVQERALNQGADIIIATPGRLNDLINQKRIDLKMVEILVLDEA

DRMLDMGFIHDVKRIIAKMPNKKQTLFFSATMPPEITKMVKTLVDPVKVEITPV SST

VDRIEQSIYLLENGKKQHMLNQILEDKSIVTALVFTRTKRGADRVTRDLAKANVTAQA

IHGNKSQNERQRALNNFKSGATRVLVATDIAARGIDVEELSHVINFLPNIPETYVHR

IGRTGRAGKSGMAISFCEKDELPFLKDIEKVIKKTIPEVKGHPYPMTGVPVFDKTSKA

SGSKPSFNKSAAGKPAKSKANPARKPKSEWFAKSGKSNSSRSNDGRPNSSRSNSSSSK

SNHGSFSRSSKTRNDRAN"

CDS complement(2777592..2777906)

/gene="gdnD_1"

/locus_tag="EFAGFIKM_02366"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P49857"

/codon_start=1

/transl_table=11

/product="putative guanidinium efflux system subunit GdnD"

/db_xref="COG:COG2076"

/translation="MNWVFLILAGIFEMIGVLMINKLHKDRNLISLVLLVAGFGLSFL
FLSIAMETLPMGTAYAVWTGIGASGGAILGMVFGEPNALRILFIAMVLGSAVGLKL
VS"

CDS complement(2777906..2778244)

/gene="gdnC_1"

/locus_tag="EFAGFIKM_02367"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P49856"

/codon_start=1

/transl_table=11

/product="putative guanidinium efflux system subunit GdnC"

/db_xref="COG:COG2076"

/translation="MNKTWMSVVI AALFEVGWVIGLKHASGLLEWGFTLVAIMISFSL
MIAASRTLPGTVYAVFVGLGTAGTVLAEIVLFNAPVQAGKMVLIGVLLLGVIGLKML
SKEKNKEVQL"

CDS complement(2778518..2779147)

/locus_tag="EFAGFIKM_02368"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKMDKPKIQEQLLEPETIAFLESKVEYKHKLIENITLDQQEASK
VSFENVVFRHVTISESALEQFEFTDVRFEHCDFSNNL SGA FMHRIEWHNCKFVGTD F

SNSRLQNVSFHLHGLGDYSNFRFAHLKQVSFSECTLIGADFAYLALQKMEFSQCNIDQA
SLTGTKMKDLDLSDCEFDLSVLTMEDLNGCVISPHQAATFVGLMGLIIK"

CDS complement(2779159..2779923)

/gene="tam_2"

/locus_tag="EFAGFIKM_02369"

/EC_number="2.1.1.144"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00560"

/codon_start=1

/transl_table=11

/product="Trans-aconitate 2-methyltransferase"

/translation="MSNGHSSGQTNESWSGHSAPFATLQETPIISLLQPSQGERILDV

GCGNGDLTAKIAAAGALPTGIDFSEETIRQAKQKYPDMNIQVANACHYRTEEPFDAVF

SHAVLHWIKDAPAVVQSIQLALKTGGRFVAEFAANGNTAILITAVQEELDARGYKWEQ

RNPWYHPTIGEYANLLEQHGFRVSLAQHVDQFTPFGKPGARKWLTSFAEYLFSGIKPAE

QDVIMEAVEKVRPQLMRDGQWYLDRSRLRVVAIKE"

CDS complement(2780058..2781044)

/gene="yajO_2"

/locus_tag="EFAGFIKM_02370"

/EC_number="1.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77735"

/codon_start=1

/transl_table=11

/product="1-deoxyxylulose-5-phosphate synthase YajO"

/db_xref="COG:COG0667"

/translation="MEYVKLGRTGLDVSRCLCLGCMYGVPERGMAPWSLNEEQSRPFI

QKALDAGINFFDTANMYSDGTSEEIVGRALKDFARRDEIVLATKLFFRMNEGPNGAGL

SRKAIMNEIDNSLMRLGTDYVDLYQIHRWDNKTPIEETMEALHDVVKAGKVRIGASS

MYAWQFMKAQYTAERHGWTKFISMQNHYNLLYREEEREMPLCQEEGVGVIPWSPLAK

GRLTRDWNEQTARSGIDPAGKAFYENAMVDADRQVVVERVLKVAEQREIPRAQVALAWL

LHQEAVTAPIIGATKIHHLDAIAALTVKLTVEEIGFLEEAYVPHPVGTGNLS"

CDS 2781413..2782330

/gene="rhaS_21"

/locus_tag="EFAGFIKM_02371"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MTEELFQSKQELSDLIKRRHSNHNGAMETAIPSLFVYHHSKISEP

AYRVYKPSFCVIVQGLKEVLLAQERYEYGPSNYLIASMNLPVIGQIIKASADAPYLSL

KLEFTPNQILEVLNECNIKVTFNENARRAMFVGQMESSIQDAILRLVRLDTPGEIPF

LAPLYVKEILFRLLQGPYGGELAQIAVEGSSTYRIREAIEYIVHHWEQPFRIEDLAET

ASMSVSSFHRHFKEITAMSPLQFQKQLRLQEARRLLMAESADAADVAFRVGYESASQF

SREYARMFGAPPRADIRRLKEKYDMALSE"

CDS complement(2782508..2783587)

/gene="ltaE"

/locus_tag="EFAGFIKM_02372"

/EC_number="4.1.2.48"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O50584"

/codon_start=1

/transl_table=11

/product="Low specificity L-threonine aldolase"

/translation="MIRFECDYNEGAHERILQRLMETNMEQTSGYGTGDGHCERARMLI

RQACDNEQADVHFLVGGTQTNTTVIASILRPYQGVIAATSGHIAVHETGAIEATGHKV

LTVPSEDGKITPEQVRAVYDAHMNESPEHCVQPGMVVISQPTENGTMYSKAELQALH

TVSRACGLPFFVDGARLGYALASRDCDMTLADLARLCDVFYIGGTKIGALMGEAVVIL

NDALKPDFRYMIKQKGGLLAKGRLLGIQFETLFEDGLYLDISRHAVIDMALRIHDSLEQ

QGVRFLYDSPTNQFPILPDRLLEKLRRGGYTFTFWEKVDDTHSAVRFCTSWATRQENV

DALTRDIAQLLHGEIHVPERVEALV"

CDS complement(2783584..2784006)

/locus_tag="EFAGFIKM_02373"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRRFNRFYTNILGVLDKHILGTGYSFAEVRVIEIGIRGESIAN
NLVDTLTIDRSYMSRIVNKLSKEGLLVKVNAAADSRVSLIRLTVKGEELYAQLNDRSD
QQILKLMQELNEEEIQEVYTSMMNIQEKLNNKAGETTR"

CDS complement(2784461..2786179)

/locus_tag="EFAGFIKM_02374"
/EC_number="3.6.3.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q99T13"
/codon_start=1
/transl_table=11
/product="Putative multidrug export ATP-binding/permease
protein"
/db_xref="COG:COG1132"
/translation="MIRRRFSYYRPYKKLFLIDFGCAVLAGLLELAFPLAVSKFINEL
LPGQDWPLIMLACVVLLSIYALNTVLNYYVWYWGHLGINIETNMREKMFAHLQKLSF
RFFDNRKTGHLIGHTLNDLNDIGEVAHHGPEDVFIAIMTLIGSFWMANINLELALLT
FIIIPIMAWVIIVFGGRMTKTYRRLFGDVGNFNARIEDNVGGMRVVQSFANEEHEKEL
FAVDNQNFRTKLLAYKTMAKSISVSYMMMLVTVFVMISGAWFYIDGRINMGEFMAF
LLLSNIFFRPIEKINAVIESYPKGIAGFKRYLEIIDTEPEIADSKNAVEFESVKGDIR
FENVSGFYESSRRILNDISLSVRPGETVAFVGPSPGAGKTTICSLPRFYEVEEGRITV
DGVDIRDVKLESLRKHIGIVQQDVFLFSGTIKENIAYGDLSATDEQIWDAARRASLEE
LILTLPDGMDTVIGERGVKLSGGQKQRLSIARMFLKNPPILILDEATSALDTETEALI
QQSLAELSVGRITLVIAHRLTTIKNADRIIVVNTDGAIEQGNHEELVAAGGIYSRLHQ
VQYSHS"

CDS complement(2786182..2786556)

/locus_tag="EFAGFIKM_02375"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MRDRPIEEMDGSVRQGERPRRDMSDNEQRSERSRRGRGHGEHEG
KRGRGAQTFRRGRILVFLEQMQRRTTLVRQLGQEEYEHIRPVISGELKAIDQVIDEY
IHLFELQNEDVNPKNKDLESESE"

CDS complement(2786732..2787673)

/gene="rutD_2"
/locus_tag="EFAGFIKM_02376"
/EC_number="3.5.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00832"
/codon_start=1
/transl_table=11
/product="Putative aminoacrylate hydrolase RutD"
/translation="MMKKILILLKIFGAIVIAFALFIATVFIVNVFSNKSEEGKIKP
YGQTVAVDVGKNMNVLIQKGKEETVLLPGYGTPAPALDFKPLINELSPFYKVVVIEPF
GYGLSDVTEKERTPENMVSEIHEALQQLNIHRYTLMGHSISGIYGLDYVNKYPNEVTA
FVGIDSSVPTQGGNDDPFPTETYKLLKKSGFYRLLMKLAPDQLIAPNVDDETREQIRI
LSLKNTFNPNNLNEGENFGPNFKAVENLSFPKDLPVIFFLQANDTETEGWIPLHEEQV
KDSVHGKVMTLEGEHYLHHTRSKEMVQEYRKFMSEIK"

CDS complement(2787731..2789854)

/gene="yfeW_3"
/locus_tag="EFAGFIKM_02377"
/EC_number="3.4.16.4"
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/inference="protein motif:HAMAP:MF_01034"
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/translation="MIQQEKMDVVKRTVKKRTSIAALTLVLTMLAPLSAMAAPTAMNN
NSNLTYETTKKVIEKAKLLTETYGTSLQYALIDGGEIVVSGQTGKNDINDKVPLTS
NTVYGIGSTSKMMLTAAVMKLVDEGKIDLDAPVVNYMPDFKMKDTRYKQITPRMLLNH

SSGLLGSTSNATLYGDNDTYSHDTFLEQLANQNLKADPGEYSVYSNDGFTLAEILVE
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GGLYSTAEDLVKFSRIFMGEVDGILSSKSVEAMAQEEYKRGMWPEDSDTLMSYGLGWD
SVNLFPFNEYGIKAVMKGGDTLSYQSSLVVLPEYNMAAAVISSGGSSLTNNFIANELL
LSALEEKDIITERKPEKSFGVPVKANMPKGISKYAGIYGGNNSIMEIKINKAGQMTVS
SLTAPSNPAQEYTYTADGTFVNNEGTDKLFVVENNGKTYLWSRSYISVPGLGQLAFS
EYNGEKLANKLSKEINAAWAKRDGKKYYLVNEKYTSMVYLNASSILPIHMNKENPGY
MSNHKIIGANEATNLLQIPGTAGRDTMDIQFSKKNNGGEYLTALGYVYASEELVKPIYS
GKQSATTIQADGYAKWFSVPATAKGKVMTVKMPAKGAFAYDQTGICINHTVVSGENE
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CDS complement(2790071..2792158)

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/locus_tag="EFAGFIKM_02378"

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ATLYGDNDTYSHDTFLDQLASQNLKADPGAFSVYSNDGFTLSEIMVERVSGMSFTAFI

HQYFTEPLDMKHTKTPQDVVDTAAMAGIYSPMYEGQLPQENYNVIATGGIYSTAEDLA

KFSQIFTGEVQGILTDKSVEAMAQEEYKKGMPWPEGGDTSISYGLGWDSVNLYPFSEYG

IKAVTKGGDTISYHSSLVVLPEYNLAAAVTSSGGTSAKDQFIASELLLSALEEKGIIT

ERKPEKSFGVPVKADIPKEIATNAGIYGGNNSVKKIEMNTAGQMTVSTPSAPSDPAQK

YTYTADGTFVNDEGTEKLKFVKEKNGRXYLWYRSYISLPGLGQLAFSEYKMEKLEANE

LSQDITASWEQREGKKYYLLNEKYTSTVYLNAPILPIHLDKETPWYVSNTKIIGANE

AVTELQIPGLAGRDTEIYFAKKNGVEYITAVGSIYASEEMVQPLYSGKQSLATIQAD

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CDS complement(2792191..2793648)
/locus_tag="EFAGFIKM_02379"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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LFVEGYRWQLLLVYIMTALFIIIVLFRHSEKMMNLKIGKFLKYSLSLIVILLVGSTV
LSVYLPVFNLPKLDGPEKVGQTQFHLTDQNRDEIFTEDQSAKRELMVQVWYPTENSNN
NKRDTLFPKDKEMFKKYIQSFSNSLKLPEFLLDYLYKYSQTNSYENVEILPSTSPYPVV
LLSHGMGTSRVLHVSQAENLASHGYIVVTIDHTYSTFATLPDGRVTDYKKSTTTLDE
RTKTGSIWTKDVEFVIDQIEKLNSGAIESQFKGKIDLDHIGAMGHSFGGATAFNATYL
DQRIKAGVNM DGSLEYENRDDINKPFMFIRSGSFEDWFANFEIDRNSEDEVTKSLSD
ELHIMKNVMNHGGKVIYVEGTQHFNFDTLQFYSELVKLSGITGDINGKRGSNIVNQYV
LDFFNKQLKGTGGDLIQGPNDLYPEVKFVDPEEIK"

CDS complement(2793688..2794671)
/gene="rutD_3"
/locus_tag="EFAGFIKM_02380"
/EC_number="3.5.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00832"
/codon_start=1
/transl_table=11
/product="Putative aminoacylate hydrolase RutD"
/translation="MTQPEEKTKNRSRAKKVRNMILKIVGAIVIAIILFLGIVYITN
VISSNSEAKKIESYGQHVSVDGKNMNVLIQGEGKETIVLLPGYGTATPALDFKLLIDE
LSPYYKVVAVEPFYGLSDETEKERTTENIVSEVHEALQQLDIHQYMLMGHSIAGIYG
IDYVNKYPDEVTA FVGIDSSVSTQPSITDAKFPLKTFALLRNTGLLRLMMKVNADPYE
GLAFDDQTVEQMKNMKNMYPNPTSLNEMDHIYSNFQGAQGLTFPKDLPLLLFVQANN
EGVEGWIPLHEGQIKDSVHGKVITMDGEHYLHHTLFKEIAEDVRAFMNEAK"

CDS complement(2794897..2796267)
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/locus_tag="EFAGFIKM_02381"
/EC_number="2.7.13.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A6QJK4"
/codon_start=1
/transl_table=11
/product="Heme sensor protein HssS"
/translation="MIRSLYIRVVLTLFLSVITGTIISFFMSTWIFEDQLNENAQINI
RNFGQDVVQIYKTLPADEAESFVSRMKQLDSYHIRIYDATGKFQSYGKLNEHKSSPVS
TDQLKKVLNGGVVQDTPKGIATVLLGLPIKTETGIRAMFLETLPSPSASFVVQFGLIF
ASCSLIVGSLLIVVASVYLVRPIKKLTATKRIAAGDFNVKLNKQTTEIGTLARSFE
EMMHDLLQLEQMRREFVTNVSHEVQSPLTSISGYASALKQVNLSEHERNRYLDIIIE
AKRMSKMSDSLKLSLLESQSQQLRLSSLSLDEQIRRVIVALQPQWSERNIHFELELE
NVKVTADHDQLNQVWTNIIGNSIKFSKDGGMIKVSIEEDFKNVTVRISDTGIGIPLD
QKRIFDRFFKADRSHSRKYDGSGMGLAIVKQIVSLHQGDIRVESEPGQGTTFMITLPI
HPPTDS"

CDS complement(2796264..2796938)

/gene="hssR_1"
/locus_tag="EFAGFIKM_02382"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A6QJK3"
/codon_start=1
/transl_table=11
/product="Heme response regulator HssR"
/translation="MATILVADDDANIRELVCLFLKNDGFTTVEAADGKEALTIYGET
PVDLVVLDIMMPVMDGWALCKELRRANPDLP LLMLTARGETWEKVKGFE LGTDDYLT
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PFDPLELTARVRALLKRYKIGSTHTIQIGNVILDRQTYKVMRGTESLTLP LKEFELLY
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KLAGTPGQVYTREQLIDQIWGIDYAGDDRTIDVHIKRLRERFATPDFRIETVRGLGY
RLEVYE"

CDS complement(2797012..2797545)

/gene="rimJ_1"
/locus_tag="EFAGFIKM_02383"

/EC_number="2.3.1.267"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A948"

/codon_start=1

/transl_table=11

/product="[Ribosomal protein S5]-alanine

N-acetyltransferase"

/db_xref="COG:COG1670"

/translation="MKYSAERIYVRFWNVDDASLLLGLQIRNRAEIEKISASDREESF
YSSEGQRSLIESWNKKREEGNRYSFGIFLHTTDELVGEISLFEILDSTPKWIVGYVT
DTLHQKGKGYMSEALQCVMEFAKHETAITRIEAGAVPDNTGSIRVLQKAGFKENGSQLV
PIQGTLEHTMFAVDIL"

CDS complement(2797591..2798196)

/locus_tag="EFAGFIKM_02384"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKDEKKSAVDPRIVRTRQLIRGAFVELLQEMDIEKLSVNKIAER
ATINRVTFYLHYRDITDMMMEKMADEMIENIERIVDEYAPHFEKQRTEEAWPVLVKLLE
HFAENASFYQVVLATKRTPIFTERLLKLLSTLVKAKIDRVEMEDELEESGIHKEIAIW
YGSSALIGTIVAWLRNDMPYSPHFLAKQFSLIRSYSYNDLI"

CDS 2798419..2799918

/gene="emrB_2"

/locus_tag="EFAGFIKM_02385"

/inference="ab initio prediction:Prodigal:002006"

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/codon_start=1

/transl_table=11

/product="Multidrug export protein EmrB"

/translation="MSQVRVQEELSVKKGPILFIMILGAFLATLNQTIMSVATPELMG
DFNISAATAQWLTTGYMLVNGVLIPITAYFMQRFSTKQLFQASMFIFLIGTIVSALAD

NFGTLLTGRMIQAAGAGIIMPLLHVILTLFAPEKRGSAMGMVGFALFAPAIGPTLA
GYILENYSWQTMFYGMIPLTLIVIAFAFVYLKNVSERVNTKFDTISVVLSTIGFGALL
YGFSRAGSLGWSSAEVLICIAAGIVSLALFTWRQLVSETPLLDLRAFKYNMFSLTTVI
SIAITMIMYADMMLLPLYLQNARGYTALESGLLLLPGALVMGFLMPVAGKLFDRFGAK
WLAVIGMVITIVTTIGFIDLTDSYGYLVLMSTGRRIGMALLMMPIQTAGLNQLPPR
LGAHGTAISNTVRQVAGAVGTSLLVSVMTSRTSAHVQDMMATGAANGLSQQLATESM
IQGINDAYVVIIGIAVVGLVLSFFIKRTKQAKEEEIKQVVRQKVSMNSN"

CDS complement(2800017..2801252)

/locus_tag="EFAGFIKM_02386"

/EC_number="1.14.14.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P14762"

/codon_start=1

/transl_table=11

/product="Cytochrome P450(BM-1)"

/db_xref="COG:COG2124"

/translation="MYKEVIRVEDITGFQSRSEEFFPLHWFRKMlsenPVYYHEDTDT

WNVFRYDDVKQVLSNHEYFSAEGTRTTIAVGAKNNEGTPDKLNISSIDPPLHQKSRS

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TDSHRFKNWVDILFQPINPKTAEESLKKQTAAQEYYQFLYPIVIHKRTHPGEDIITD

LLNVDFEGEKFTEDVVRTTMLLLGAGIETTSHMVSNTFYSLYDDPSLYDQLRQNPE

WVPLAVEEMLRYRFHNAKRHRVTKQDNQLLGVDLKKGDVVISWMSAANMDEQMFEDPF

ELNIHRRNNKRHLTFGNPHFCLGAPLARMELSIALTAFVEKIARIEPVESFDLENNL

ATSAPGQSLTHLPVKIVAE"

CDS complement(2801469..2801756)

/locus_tag="EFAGFIKM_02387"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTYSQRVSDGANSSDIYLEHQIGTTKEKLRIALEKQETYKSEL

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CDS complement(2801753..2802895)
/gene="thiO_2"
/locus_tag="EFAGFIKM_02388"
/EC_number="1.4.3.19"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q88Q83"
/codon_start=1
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IICPWLSQRRNQDWYQLAKAGARFYPGIIAELKAEGTETGYAQVGALSIHTDEDKIN
KMEERAHLRKEDAPEIGDITPLDAKETRDRFPLLDERYQSVHISGAARIDGRALRDAL
IRSAQRNGAEVIHGDATLQFEADRVIGVSVNDQSILADEVVVCAGAWANELLKPLRIH
FKVHYQKAQIMHLHVTGDGTGRWPVIMPPSDQYLLAFDQQKIVIGATHENDVEGYDT
RVTAGGMQEVLNKGLELAPGLANSTFQEV RVGFRPFTPGFLPVMGAVPGWQGLITANG
LGASGLTMGPFIGSQLAKLALGTELDIDIEPYTVGKAMDEIERGES"

CDS 2803192..2804007
/gene="rhaS_22"
/locus_tag="EFAGFIKM_02389"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaS"
/translation="MPKPSMGNPLDMDPLMITGQNQLTVDELMNWSDHSRDYSIVQC
IGGTGRIAAKNHEFSIKKGTALILFPEVTYRYHNLSDSLRFDCLSFNGYLLPRFLHTL
QIGELRAFKPDGMLHILLREITLALQSRHKDQIWHVSALLYMLLVRLTIEGERYSAYE
RSDARLRLDELITFIKQNYHQDISLPMLAEQMDVTEQHLNRIFKKEFQMTPLEYLMRY
RLLKAKEMLIENNATTAHEIAKAVGFNSASYFGSVFKKYEGISPIELRKQYLD"

CDS complement(2804004..2804645)
/locus_tag="EFAGFIKM_02390"
/EC_number="3.1.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9X0Y1"

/codon_start=1

/transl_table=11

/product="Phosphorylated carbohydrates phosphatase"

/db_xref="COG:COG0637"

/translation="MVKAFIFDFDGLIVDTETPWYYAFRDIYEEHGVELGLELWSKNV
GTSFEEFHPFLYLEQALQKKIDHDHIKLLSEQKYEVYLGQAAILPGVYELLQSAREKG
IQLAVASSSTRDWVHGYLQKLGIFDYFTVVHTSEDVKRVKPDPELYLLALQSLGIEAS
EAIVFEDSPNGLKAANAAGIRCIIVPNEVTRGLEFAMHELRLSSLAEIDMEAL"

CDS complement(2804685..2805278)

/locus_tag="EFAGFIKM_02391"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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AGKHIRATAPFLSMPVPGDFEITTQLTVDMKNQYDSGCLMVMADDLNWCKICFEYDGK
VPTIVSVVTRDGSSDDCNSVEVSVPNPYLRIKVEGCISFFYSPDRDEWKLIRYFGMP
IQGELRAGLVVQSPTGTGCTCHFSLSVNVTHPDLTARF"

CDS complement(2805360..2806604)

/locus_tag="EFAGFIKM_02392"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLLQDLPKNPRYSILLEPVWAIPGTIVLFYAPLYMKEAGLSDI
EIGLINSVNLIFYAFIFQLFAGSITNKLGRKRTTLIFDLLAWSVPMFIWAFSQNFWLFL
IAYLLNATSKFVTVAFNCLIIEDVEEHKRSKVFAILNMIITGAGVLTPIAGVVIADYG
IVPTLASIYFVGGILMTAMFFIRNRYTDETEVGKELMGLHSKTRVLQSLGSSSLRLFGK
SFYKRRLFPIILITVLSNLILQLNFFQVIFKEQLKFDDRVISFIPVVTAVTVMLLYL
VIIPRLKRRSEEKYVGFISIVLSTAGAILFLLIPVGSIGMLFTLIVLAAGNFILQTYR"

DSLLMNRLGTHEKADMFSAVQTVMTLTAIPSGYLTGLLYHHNPTLLFSVILGLYVLM

VIMFFLPDPQKHSQVLEPYKNM"

CDS complement(2806697..2807728)

/gene="gutB_2"

/locus_tag="EFAGFIKM_02393"

/EC_number="1.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q06004"

/codon_start=1

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/product="Sorbitol dehydrogenase"

/db_xref="COG:COG1063"

/translation="MKALVYQDLKQVTYQEIEEPTIQKPNQVKIKIYGSIGCGTDLNI

VKGKVPANKGTIIGHEGVGTVEVGDDVRGFKIGDRVLVDPTQSCGTCSYCREGLFIY

CENFDDYQVGMTTHGTFAEYFVGDEKYIYAIPDSMSWETAMMIEPLGCVLQTFMKAGT

KPSDSVLVLGSGAIGSLCQLVSKRLARLTVGTEVDPYRKEFASGIADHVFYPQDLTLD

KVYEINNNKKFDIIVDAVGNQLHVGFEIAKGGKIIPMGYDDSYEVTFKSTAVINDGI

SIIGAVANHSMISTALKFAQSIPELEQMVTAKELLSDYEQAFNGTIGYDMHTGEKLPM

NSVKTALIL"

CDS complement(2807771..2809078)

/gene="kat"

/locus_tag="EFAGFIKM_02394"

/EC_number="2.6.1.111"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:B0VH76"

/codon_start=1

/transl_table=11

/product="3-aminobutyryl-CoA aminotransferase"

/translation="MKEKESTLDRAVRFRNLEWLEQVEKVIPSGCSTLAKAPERLFP

GHTPVCCAEAYNSRFTDIDGNEWLDCEMAMGTAPWGHARHEVQLTVIHQLKKGTSFSL

PADIELECAELILERFEGRYPSLRFTKSGADAVSGAVRLARAASGKSKIATAYHGWH

DWSAYGYYGGQTKERGIPVDIERSTIWWNKPTTERIEAQITASPEDIAIVLCPNEWK

KDALEKAVNLCRSLDIIIFDEVTSGIRMGKQATAGEYDIWPDLLCISKGMANGLPLA
AVMGPEHLMSLSGQVRFSNAHSSETTALAAAIACERLMKNAKVWPTWREPATRIMDRL
ESELVLLGLTDQLEVRGTYASFCIQSLAEDNFQTDPFREFMVKRMAHFGIFTKGYFIF
SDAHTREELLWVEEALLQILSDWKEIQKQEHLHAMQLSKTFEA"

CDS complement(2809116..2810270)

/locus_tag="EFAGFIKM_02395"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLYTIIPVNQDYNILNLFTDSLRTVSPSTQIIFINDGSGSAV

FQHLDKCLKQEVREGVTIEILQHDFPLGCAVSINSALSLAKGEYIFFLSDTILQPNWQ

PMMKETLDSITIGMIGGVLLYPQTGGVQHCGIAFADTIGRHLFLNASPDDIPKETFS

VQLVVFAMFGMKREVYETIGNLDEKFFNGYEDFDYQMRARAAGYDTVINPNIQAYHWE

RSSGIHRNFNRKNNLARFWKKWGGQIEADVWPVFVSHLKAQLESQEEYQHLPIVGIDL

AEVRSDADTFWTKLEEAEFANVAEVRDYSNRFNSNGAIWLPQVLGKELIHSENRLFL

VDNFARLLENRYWIEMRHAHRAKDLIIDLYGNVITMDRIYDGCWPGTKVR"

CDS complement(2810623..2811189)

/locus_tag="EFAGFIKM_02396"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKEMTTIKQTRLHSILDEATKLLIEKPNASMNEIAESAKIGIA

TLHRYVESREQLMVHLGLRAIEVVSETMQQIQLDEEHCEKYIPELIEALIPLGDKIYF

LAHDTTINYNPEIEGADLKLREPVLHAVGLLQQKGYFRSDLEKTWIVDVLYSIMFLTW

QQVVSQHIARKAAPALVVDTFYHGFQKS"

CDS complement(2811397..2812875)

/gene="expZ_1"

/locus_tag="EFAGFIKM_02397"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39115"

/codon_start=1
/transl_table=11
/product="Nucleotide-binding protein ExpZ"
/db_xref="COG:COG0488"
/translation="MSLINVTNLTFAYEGSYDNIFENVSFQLDSDWKLGFTGRNGRGK
TTFLNLLLGKYEYSGHISANVSFEYFPFQVENKGAMTVDVIGEIHPEYLHWQVREFN
LLKVSIEDVLYRPFDTLSNGEQTKVMLAALFLKDNRFLLIDEPTNHLDLHARQIVGDYL
RSKSGFILVSHDRSFLDHSVDHILSINKSNIEIQKGNFSAWWENKRRQDQFELASNEK
LIKDIKRLSDSAKRTGGWSHEVEKTKNGTRNSGSKVDKGYIGHKAAKMMKRSKNIEQR
QQSAIQEKSLLKNIESAERLQIHQLDFHKQELVELEHVSISYGSNTVFKDVSITIEK
GDRISLYGKNGSGKSSILKLICGEDIAYTGLFRKDHQLKISYVSQDTSDLGGHLSEYA
ATQGIDESLFKSILRKLDIFSRLQLEKDISTFSAGQKKKVLIKSLSEKAHLHIWDEPL
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CDS complement(2813251..2813787)

/locus_tag="EFAGFIKM_02398"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MELIKTYDVDLSEEWSTLLQELLVTSFPEVYPKDRLFFKQIPHG
RVLAFTPDNQLVGHVGLDYRMMNLNGKPIRVLGIIIDLCVSPAIRSQGIASLLISEVER
LATGRVDFVLLFADHEELYSKNGFETVNNTCKWLKIDHETLTTVGVGTTQAVEGLMIKE
VGNMPWGEGELDFLGYYL"

CDS complement(2813800..2814657)

/locus_tag="EFAGFIKM_02399"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTGHHAAQHFTTSEFAKICGVTKHTLFHYDEIGLLKPEYTNAGY
RYYGMQQTYYVLDVIHVLKKAGSSLQEIKSFIQNQNTPLLIELFEQKLKALELEQQRIK
RMQKLLSGAIEMTKQATDASPEGLHIEQCELEYFITVQLEQGDGDKEFFRKFIEYRTH"

CDEQMIDYEFVWTLTQEHYEAGEYYPDYFGNKKIKAPISGETIWIKPKGMYAVMNR
GSYESMPETYSMLKKEIEKEGLQVCGHVYALDLLTYFAESNPNEYIIKIYVEVCKPEN
TSKKQNGLI"

CDS 2814798..2816303

/gene="smvA"

/locus_tag="EFAGFIKM_02400"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:D0ZXQ3"

/codon_start=1

/transl_table=11

/product="Methyl viologen resistance protein SmvA"

/translation="MSKFKRWMILVIVSSALLLIVMDMTILYTALPSLTHDLGASASE

KLWILNGYSLVMAGLLPAMGTLGDRLGHKKIFTLGLVVFSAASLAAAFSPVPAMLVMS

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WWGSVFLINLPAAIAFVFALKMIPKHQGDASKKWDFTSIQIMIAMVGIIYSIKEFT

RREGSLTLAIAAVIGVLSLIIFIRRNNSPNPLDLLSLFKIPRFSTGFITALVGLFA

QMGVQYMVTQRLQLVEGMSPLQAGLFTVSIPVAALIAGPVTGAIMHRVDVVYIKSFTL

FIAALGMGTYLMYFNAGFTGQIIGLALLGAGLGSGMTAASHSIMSYAPPHKAGMAASI

EEVGyelGGASGIAIGSMSTLFYTLAMKIPVGISVPANAKDSLDEALIAAESLPAAS

AESLKNAFAAFDQSFVVIAGVTVFLFIAALIMSWVAVRLKRAQKHSVKA"

CDS complement(2816532..2816915)

/locus_tag="EFAGFIKM_02401"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTVTLIIIVAIIVFGLITGTVITIVAFKLLRNNKEKHHLRKSIL

MDGIPTeAIIHDIVQTSSSRDGRPGVRLDLTVTQVDGRTFPTIVETYIPITHIPHQK

GNVINVRYIAMGNERKVEVEDAYLP"

CDS complement(2817059..2817664)

/gene="mfpA"

/locus_tag="EFAGFIKM_02402"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:I6YBX3"
/codon_start=1
/transl_table=11
/product="Pentapeptide repeat protein MfpA"
/db_xref="COG:COG1357"
/translation="MYQYKDQEYEAVHFEGRDRLRYGELISCVFKQCTFMNASMEEIET
SNCRFIECDFKGASMNGSIHTESAFENCTFGGANLFASKFSSCKMTGSDFSGAQMDGI
TLSHGDWSYTNLRHTRLGKQDLRGIRFFEADFTDFTKADLRDCDLTRVVLSRAKLQ
GADLRGANLEGIDLKSLDIKGVRLDREQAVLFVRSYGAKVD"

CDS complement(2817916..2818524)

/gene="wecD"
/locus_tag="EFAGFIKM_02403"
/EC_number="2.3.1.210"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_02027"
/codon_start=1
/transl_table=11
/product="dTDP-fucosamine acetyltransferase"
/translation="MNKISITKASPQSLVGGQLNQMALEYMAYSLAGTKDKGIIIEKTF
NKLWRSNQNRFSHQYAYEAKMGNQTLGMIMCYPTTIMNKLALPTFSKLFELRKWSLIK
YNLQHWKEFYSMVTLKEAENDEYHIGTLATLPESRGLGVGTQLIHFAEEQAITQGLSK
SSLTVKKENLLAIKLYERLGYQRVGEINKPSLSLYRMSKKLV"

CDS complement(2818557..2818919)

/locus_tag="EFAGFIKM_02404"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSIQNVFGKIQISDDVISKIVGKIANTTSEISSMSTGLIEGVTK
KWSGKSLQNGIDIRKVESRLEINLKIIVCYGTKVHEVCRELQNNVRLHVEQLTGLTID
TVNVIVEGLSFNQPAAKL"

CDS complement(2819086..2819562)
/locus_tag="EFAGFIKM_02405"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSRTQLSIPVGLLENVLTSGESKEVII ECLQRRDYSRLLPLVK
ESAMDFDERLQTADDIGDDWEKAIRQGYEFKFLHINGLKRLLDFRFDKVD RDYVQDE
LSLKHIHLTSQEIELLQSLGRQWIVQAEETEQAEEGSKESGLSSRIPVRIQLKFP"

CDS complement(2819559..2821580)
/gene="dpp5_1"
/locus_tag="EFAGFIKM_02406"
/EC_number="3.4.14.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:B2RIT0"
/codon_start=1
/transl_table=11
/product="Dipeptidyl-peptidase 5"
/db_xref="COG:COG1506"
/translation="MNQRPIMPEDLSHYRWISQPVISLNGQVAYVEQTIDQDKNEYNT
QIRGISLDGDEDIALSDGTDSSPAWSPDGTQLTFIRSV DGGKGLWTLHSDQKEPVML
ISPARKILSYIWSPNGEYIAFTSKVQPEDQQKKKADLQQEPVPVLRGKVFERTTPKAE
GSGWWDGQYSHLFVYVIKSGEITQVTSGLWNISAPAWSPDSLQLSFISKQVEDEELDA
DLLYFTDIYSVRLGESDLFKVTDSSLAISQFSYSSDGQQLILIASDREYSGSHNSLY
AVPVQRGVPRIIAPQLDMQMGNAA LGDMKSAGASPSISDNKHPERGVYVLGTQNGNV
DVYRIQDNGNCQSVTGAGEKD VYQYTLAPDGSSLVIAALTAEHPGELYRVYIDSGEMF
RLTRRNDEFMAELAVNVPVRVEFKSSDGWPLQGWLATPAIRDTNGKLPLILQIHGGPH
AMYTGTYSHEMQLVAQGYAVLWINPRGSMGYGQEFARACRGDFAGGDYRDLMEAVDY
ALATYDFLDASRLGVAGGSYGGVMTNWIVAHTHRFKA AVTQRCISNWLSMYGTSDIGI
SYVEGVIGGNPAENAEFLWSRSPLAHAHHIETPLLIMHGEQDYRTPIAQAEELYTTLK
RYGKKTKLIRYPGSNHSLKSGKPSLRIDSFEQVNAWFNQYLGNEEGEQ"

CDS complement(2821602..2822531)

/gene="gsiD_3"
/locus_tag="EFAGFIKM_02407"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P75799"
/codon_start=1
/transl_table=11
/product="Glutathione transport system permease protein
GsiD"
/db_xref="COG:COG1173"
/translation="MTGSNEMPIPGTEQEQDNGRAPTGFRYIWQQLIISKTGMFGAVL
VLLVVLIAIGAPLLTSHDPAAVNPLGRLKPPAWLEGGTAEYWLGTDNLGRDMWSRIVY
GARVSLIVGMGAVIVSGIIGAILGLVSGFYGKWLDVIMRVGDAFMAIPTILFMLVVM
AIVGPGITTILFVIGVTNWVPFTRVVRSEVLSIKERDFVHAARSIGAKNGRLILKHIL
PNILSSFIVICGMNVGTIIMEASLSFLGLGIKPPDVSWSGGMLSDGRQYVATSWWWAT
FPGLAITFTVLGVIFLGDWLRDVLDPRTETTHK"

CDS complement(2822548..2823465)

/gene="gsiC_3"
/locus_tag="EFAGFIKM_02408"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P75798"
/codon_start=1
/transl_table=11
/product="Glutathione transport system permease protein
GsiC"
/db_xref="COG:COG0601"
/translation="MGKYVLKSLLQIIPVLFIIVSLIVFILVRVTGDPVALMLPETATA
EDRAVLTQALGLDQPLYTQYVKFLGSAIQGDFGQSFRYNQPALELVLERLPASFELAV
AAMFFAVLMAVPLGVISAVKRNTFTDLISGISVIGKAMPNFWMGIMLILFSVMLGV
LPVSGRGGLSHLILPAFTLGVGLAAQMTRLIRSSMLEILNQDYIRTARSKGLGRMVVI
VKHAFRNGLIPVVTIMSLQFTSLIGGTITETVFSWPGLGQLLVAVNTHDMAIVQAA
VFVIAFIVVVINILTDVAYRLLDPRIKYD"

CDS complement(2823567..2825132)

/gene="gsiB_3"
/locus_tag="EFAGFIKM_02409"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P75797"
/codon_start=1
/transl_table=11
/product="Glutathione-binding protein GsiB"
/db_xref="COG:COG0747"
/translation="MKKRQWTGLWITLLAVVMVLSACGGKSTSTNDGSATEGTGSGSA
STTLTVAAATDIESFDPHNNNTSSEAVLVNVFDYLIKNDSEQKKVAGLATSWDQVDD
TTWRFKLREGVTFHNGDPFTSADVKYTLERVAKDETLKQNSYFKNIVEVKVDDYTV
IITDGPDPLLLNRLSKMGAGILPAKYIADKGFDAFLKQPVGTGPYKFSKWKDDRVEL
VKNENYFDGEPKWNEVVFRVIPEASTRVSELLAGGVDVASSIPSTDIARIEGEADKKI
VKAPIQRVLQLIFRQTEGSITADPKVREIDLAIKQGIVDSIAGGAGIVTRTSVTPG
NFGADPSLYKTSLYDQEKAKQLLQEAGYAEGEAEMTISVSAQYKEQAEVVAAMLEQAG
FKINLDVLEASAFSERYSSKSFEIFMIGIGNSLFDASNNYNRYMLEEAKGESDYN
NP
EVEKLLQSALVNMDPASREKEYQQVQQIFSEERPAVYLYQMEGVYGTNAKVNFA
PRSD
EMFYADEITPVAQ"

CDS complement(2825129..2826340)

/gene="scmP_2"
/locus_tag="EFAGFIKM_02410"
/EC_number="3.5.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54955"
/codon_start=1
/transl_table=11
/product="N-acetylcysteine deacetylase"
/db_xref="COG:COG1473"
/translation="MNRSELIQLAQPLQAQLSAWRRDLHQHPEIGYEEHRTSAIVAEH
LESQGLEVTRNVGQTGVTGLLRGETDGPTFALRADMDALPIQDQKAVEYRSQVEGKAH
LCGHDAHTSILMGAAQLLTGLGRPKSGNIKFIFQPAEEGLAGARAMIQDGVLENPKVD
AIAGLHMTPGQNTGTLGVSQGVAFASADPLIKVFGKGGHAARPHEGIDAIIVSAQVI

TALQNIIVSRMVDPLEPAVVTIGKITGGYMGTAIAPEVEMIGTVRTLSPAIRERMPALI
EQVVKGVCDSEFGAGCEVYGDGYPVVNDLGMVDLLTETCDQVNAEKGWYIKPSTGG
EDFAFYCEQVPGVFFRLGSGNDEERTRYPLHHPMFDLDETAMPYGVGMLSAVALEFLA
RNTTSEGEQSQ"

CDS complement(2826337..2827089)

/gene="nanR"

/locus_tag="EFAGFIKM_02411"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A8W0"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional repressor NanR"

/db_xref="COG:COG2186"

/translation="MSSTFSFRFEKVSTKKVSEFIREQLEEAILKELMSEEQLPAER

DLAEIFNVSRITVREALSSLEEKGLIEKRVGAKGGTFVLPTANSHKRTREEIKRDWS

QMLKVFEYRTIIEPEGAFLAAERITAGELELLEGYMEQSIEPDCTREWFRALDVKFHL

TIAKASGNPYCERAVRQIRTKINPALDLMPYDDRIRTVNHGVHMEILEALKAHDSTKS

KETMKRHIEFSADAIYARLVSESDKNEGNDSE"

CDS complement(2827277..2827990)

/locus_tag="EFAGFIKM_02412"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTKHKTGHGVSVIVCTNRPQFFDNILQNYSRQRYKSKELIIVLN

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YLTEQVGELRRTKSDIVGKHSCLVYLGASKTLLVRSPAENKPKVEFVQGGTILFKREI

LKKVRFTDRSIGEDVTFLRQCRKKGFKAYATSPYNYVYHRRQNKKSHWTRADDSFYLE

GSKKLAVTEDFRPFANKKL"

CDS complement(2828141..2829238)

/gene="gfo_2"

/locus_tag="EFAGFIKM_02413"

/EC_number="1.1.99.28"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q07982"

/codon_start=1

/transl_table=11

/product="Glucose--fructose oxidoreductase"

/translation="MSKVYRIGIIGCGGIANGKHLPSLSKLDNVELVAFCDIVQERAD
EAKQKYGTTEAEVYTDYQELLKDESLDIVHVLTPNISHAEISIAALEAGKHVMCEKPM
AKTSAEAQLMLEAERTGKKLTIGYNNRFREDSQYLKKVCEAGDLGNIYFAKAHAIRR
RAVPTWGVFLDEEKQGGGPLIDIGTHALDITLWMDNYQPKVVLGTTYHELSQLRENA
NAWGPWDPKQFSVEDSAFGMIVMENGATIMLESSWALNSLDVDEAKCSLSGSEAGADM
KNGLRINGEKFSRLYTNEIELSAGGVAFYDGKSESAPDVEMRKWIEAIENDQEPVVTP
KQALVVSQILEALYESARTGKAVYLNNGSEA"

CDS complement(2829251..2830174)

/gene="rhaR_21"

/locus_tag="EFAGFIKM_02414"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MSLYPYEKMLERQDLLERLDILMVWGHYEIRVMRFHLTSFPAGR
VVDFHNHAEFEFHFI PRGKGKVILDDQTHALSEGMLYLTGPGVVHYQEADAKEDMDEL
CLHVDIVHKPREHVPWEAAESEETMEKLRTLPLTPVNDYHRAMHCFLEAYEACDLKL
LGYYSIKQLVISILLKTVRAYDTGGRPEAPVRDMSVYRYEYAVQYMEANHTTVTL
EHVAEKLHISSRQLQRIFYQVQPEMPFSRVLEDIRLRAVCRNLEESNVSIEQIALASG
FNNANYLHAVFRKRLGMTPSAFRKMKPILK"

CDS complement(2830199..2831203)

/gene="iolG_5"

/locus_tag="EFAGFIKM_02415"

/EC_number="1.1.1.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9WYP5"

/codon_start=1

/transl_table=11

/product="Myo-inositol 2-dehydrogenase"

/db_xref="COG:COG0673"

/translation="MTIRIGKISLWHVHAWDYIKQAQEHEDTVIAAVWDEDAKRGQEA
AERLNVPFYASLEDMLAKDDIDAVIVDAPTRIHEEVITAAAKAGKHIFTEKVIASQV
ESNRILNEVKANKVKMTVSLPRLNAGYTLKIQDVLNQGLLGKVTYVRARLSHDGAISN
WLPEHFYDLKDCQGALIDLGCHPMYLAFLGQEVAVNANFGYITGKEVEDNAVAT
LFTDSGAVGVVEAGFVNESHSPFTIEVHGTESTILYGTPEEKLLIRTKAAQGQYQEWTE
LPLADQRESAFNQWVAHIQNDTDATENVQIAMELTRLMEANLSAKEGRRITLKELKG
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CDS complement(2831492..2832025)

/locus_tag="EFAGFIKM_02416"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKMSWIALFLVLILYFVSMYSLYSHMNNKWLVSPPNYLILILS
ILVLAIAILGFKDNLNKSTKVRSWISTVLSVLIFILLGALSFTSIFSGYKQLLTTH
SPDKHYTISFYKTDAGAMGSFGVMGELKGPLWFKRVFYYEGKTDQVDLEWVDNHTISI
NDQNVNLLNSETVRRSP"

CDS complement(2832118..2832765)

/locus_tag="EFAGFIKM_02417"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNYILFVLFFVLIIVLSLWLSLTRKHKRSAYLYEENYDLKAIT
IADIDRMEDGSGFEMYLYRLLIELGYSYGYKTLGSRDFGADVFTDREGVRNVIQAKR
YSIEYPVGISAVQEVFSCMRYKAKKAIVITSSNFTESCETLAGINFVKLIDRTDLIH
VIEAFRDGDMIEARDIIEEPRMILESWSEANSNTLHEVRKDYKAEKYVKKVMSK"

CDS complement(2832979..2835780)

/gene="mngB_2"

/locus_tag="EFAGFIKM_02418"

/EC_number="3.2.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54746"

/codon_start=1

/transl_table=11

/product="Mannosylglycerate hydrolase"

/db_xref="COG:COG0383"

/translation="MTTKKTAHLISHTHWDREWMPYEHVLLIELMDKLLDTLDQD
PEYRYFHLDGQTIREDYLQVRPEQQERLDRIYREGRIHFGPWYVLQDEFLTSEANL
RNLLIGHRDARPLGVISKTYFPDSFGNMGQAPQILQQADIHNAIFGRGVKPTGFNNA
VVDADSYESPYSEMIWRSPDGSEVLGILFANWYCNGMEVPVDPEKAQSYWDKNLEDAE
KFASTPHLLFMNGCDHQPIQTDMPALRTASALYDVEFIHSNFDDYIEAVTKDVPEH
LATIEGELRSQHTDGWGTLVNTASARVYLKQLNQGGQTLLEKVAEPLAAMAHIAGVKD
YPHLLTHAWKMLMQNHPHDSICGCSVDEVHREVMVTRFAKSRQLAEKLVSSAQAIIE
SIHVQSAETWGEEAVLFTVFNTSGWNRNGIEMDLIVDKAFFPEGPNPQALAQKMEKD
ALPVYQLVDSSGGRTYSAEIKDLGAHFGYELPKDRFRQPYMARKVRVTFQAVDVLSTGY
KTYALIPVEKQAEFAEIVEVPDTRVVIQVQGMMEENGQLRVTVENGATIEDKVSST
VYKGLNSYENTGDIGNEYVYRQPEGETTLTEHLKADLRIVEQSPYRAVMESVLRWDI
PAGADELFEELEKQRMVPFTEKRVQRVENTVPLVITTYTLEAGSNMVVKVKSDFNNQAK
DHRLRALFPSGLVTDHYADSIFEIAKRSNTPAKEWVNPSNAQHQQAFVHVTDGAHGL
MIANKGLNEYEILQHEEGSTVAVTLLRASSELGDWGVFETPEAQCLGPQSVEYAIIPF
AGDAAQSGACATAYTYPIPWTTVQLGALAYTFEQEGHAGADGHKVELPLSKQWLAWNA
QGSSLAFTLKIAEETGDLIARWYNLNSEPVENVQPGFETASVYESDVLERVKDTLE
GQSQTVSGYKIVTQGYTLR"

CDS complement(2835798..2836622)

/gene="sugB"

/locus_tag="EFAGFIKM_02419"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WG01"

/codon_start=1
/transl_table=11
/product="Trehalose transport system permease protein
SugB"
/db_xref="COG:COG0395"
/translation="MVKHGLQRKIQYGILVFLGLCFLPLWILASFDPNAAQQGIKM
PSTWTIQNFKDVLGDSSNLRSGVGLILSGGQAILVVLVSVLAAYPLSRYEMRFKKSF
LLSILFMTALPITAVMVPVFQMFLFFKMQNSIIATMLFLTASSLPYGIWMMKNFMDSV
PIDLEESAVIDGASVWSSLRRIVAPLMLPGIATIAIFTSGSWGNNFFVPYILLQTPEK
LPASVTIYQFFGSHGMVEYGRLAASFLLYTMPSVVLVYIFSQRYMSKGFMSMGGATKG"

CDS complement(2836645..2837511)

/gene="melD_7"
/locus_tag="EFAGFIKM_02420"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34706"
/codon_start=1
/transl_table=11
/product="Melibiose/raffinose/stachyose import permease
protein MelD"
/db_xref="COG:COG1175"
/translation="MKRKAPGSFLFLMPSVLLLLVFFIVPIILTICFAFTNMALTGAA
AKSLEFVGFGQNFNMFHDPDFRISVWRTLVLIFSAVIGQVLLGFILALLMKEKNVTF
RRVIGIIVIAGWVTPEIVVAFCMVAFFSDNGSLNQILGWFGANPVSWLFSFPMVSVII
ANIIWHGTAFSMMVYQSALDDIPKEVEEAAIIDSATGFQIVRHITIPMVKGSIVTNMML
VTLQTLGVFTLIYTMGGPGTSTQTLPIFMYNQAFVNYQFGYGTASLVLLFIGIIA
SLFYMRSMKVKV"

CDS complement(2837579..2838958)

/locus_tag="EFAGFIKM_02421"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MRKISLKMPVAAVMTSLLILTACSGGSSSTGTTSDGKKEVTVS
FRSSGSEDTLTKFFQSGLVDFEKENPDIKINIAPVLASEGDYTSKMVLQMKSPDTAP
DVIAEDTSIIKSDAAAGYLEPLDTQVQGWSDWTEHIIDNLKAGVTGEDGKVYGV PATS
DTRGIWYNKELFEKAGLEVFPKPASWAEVLEAARTIKQLPGVTPLNMIVGKANGEGV
TMQTLEMLLYGTADTLYNESKKWVVNSPGLLDSFKFIDQVFNTDKTGPTMQVALNGQ
AGSIAFQQQFPQDKLAMAVDGSWAGSTWAENGAAPIANVEEKIGFAPFPTQNGEEPGA
TTMSGGWAWSVPAQAKNKEEAWKFIEFLMNKENATARVVAEGSLSPRNDSTEVEGYTD
RPYTKEAQELLNVAHFRPANDQYAAVSAQLQSIVESIASGKLTPEEGVTQLKDNVSR
LGADSIEEK"

CDS complement(2839037..2840338)

/locus_tag="EFAGFIKM_02422"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLTPRDNQEISPSIYDMIDQVNKRMPDHPELNQMFKNCFNTMA
TTIQRKEDGTTFVITGDIPAMWLRDSAAQVRPYLVLADEDEDIADMIAGLVERQLNYI
LLDPYANAFNETESGKGHQEDLTLMNDWIWERKYEIDSLAYPIQLSYLLWKNTGR TTQ
FNDTFRKAAQIIMQLWQVEQHHETKSPYTFQRLDAPETDTLSREGRGTETAYTGMTWS
GFRPSDDRCEYGYLIPSNMFAVVALRYLQEIAEAVFEDETLAATAKQLEEQINKGIQD
YGTVEHPEYGTIYAYETDGKGNHNLMDANVPSLLSLPYLGYVDENDEVYQNTRRFIL
SSQNPYFYEGTAAAGIGSPHTPEGYIWHIALSMQGLTTGDRNEKLRLQLIHKTDADT
GLTHEGFSANNPHEYTRPWFSWSNMLFSELIMDYCGFRVQK"

CDS complement(2840564..2841727)

/gene="araR_2"

/locus_tag="EFAGFIKM_02423"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P96711"

/codon_start=1

/transl_table=11

/product="Arabinose metabolism transcriptional repressor"

/db_xref="COG:COG1609"

/translation="MGKDSASKPMYEQIFESLRERIQLHQYQVGERVPSEKELCDEFG
VSRITTKKALEMLASEQLIVRQPGRGSFVADTADVLQERPNNRPAPRAAVKDPEKKLLI
GLVITNFSDMYGTELLYGMEEASREHDCFLVLRRSFGIPEQEEQSIQELLELGVDGLI
IFPAQGEYFSDEILKLVVNKFPFVLIDRYLKGPASSVSTDNVGAAREGMNYLFDLGH
RHIAFLTQPPANTTPIEERIEGIIEAHHDQGVLVNRELWLESFLSTLPSVFDPPQVEVR
DVETLVEHLQKYPQITALFAAEYHIALLAEQAADRLGLRIPEDMSIICFDSPNAAEGS
RVTHMRQSQFDMGKQAFEMVLQSMQNNEMAVNRVVLPARLVKKGKSTSMVKQKG"

CDS complement(2842065..2847311)

/locus_tag="EFAGFIKM_02424"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIKINRLRKPISMGLSLLAFSIIHPVSAENSTSSKLDMKSGLA
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RNSVSSSLRETASRTQYPLETYLEKEVDLGKVKEYKSYFIVNSLAVTSTKEVMEQIAL
LPEVEKILPNETRYLQAEVSKEPANAASGKDVVQTPTKDSSVGVDKEPAAKDKLAT
ENVEWNLDYINAPAVWDRGIDGTGIVVANLDGVDYTHPALRSKWRGLDASGNIVDPE
LSWYDPHSNASLPADGDGHGHTMTGMTVGSEADGTNQIGVAPGAKWIGVRIFNPETTD
AIILDGGQWLIAPVDAEGNLHPELAPDVVNNSWGGGAGLDEWFRPMVQAWRDAQIFPE
FSAGNVRLGNPGGPGSVANPANYPESFATGATDINGNLASFLLGPSYGEIKPEVSA
PGVNIRSSVPGGVYEGGWNGTSMAGPHTTALAALLLQANHSLTVDQLEQIITDTATPR
TDSQYPTSPNNGYGHGIINALDAVGSVLEGITVSGRVVTAGDDLEEPVLAHTPVNSA
FTGIDIPLTAHVTDNVAVVSVEAFAKTTGTNQYVYLPNNRIAGDNKDGTATATIPAF
IEPQGVVEYYIRVNDYGNNGFESQVYKVAVSNGVQPGYLQDFEEDQLGFTTGGTGSTWV
WGAPSSGPGSAYS GDKVIATNLQGTIVANSNAYLLAPPIDLTESPEGALLSFKHWYDL
ENNIDFGKVYIASEDSDYVFEELLTFTGTGGNWKTQYVDLREYAGQQVFIKFNLTSDN
SLQKAGWYIDDFAVEELDEIAPGAPAEISATADILGNVALSWTGPSDEDELSYIVYRS
TTAGAGYESIGTATGTTFTDTATVTDSTYYYTVAALDYSGNESDKSNEVSITVEVPQD
IYIDHFDGSDDNWTHSGTKDEWERGIPVTGPASAVSPPNVWATDLNTYESGSNYSL
VSPVIDLTDVSEGTLTFNHWYIEESGYDYGVEVTKDGGTTWSELGKFSHSTNGKQWT
PVFYDLDTLTGNEVQFRFRLTSDNSVVKTGWFIDDFRVLGVAAETVTEDSAVVLSNDK

PKPSYDNPWYKISRTDKAEFNKTKQQQPEVEKPETGSVNPQSLPASATVTVLETGRSV
KTDSATGKYSFTHVAGDYTLKAEAYGYYPRTQQVTITDGS GAKANFNLEAIPHGQIEG
VVT DERTGQPLADASVLVVEDANVGEVRTGSDGSFVIQVLEGSYTLSIRAADYYSKTV
TVTVPGNGTAEANVALKPFIFGPEIAYDDGTAENARAFNAADNAWAVRMTPELETAQ
LTGASFRFWNTEWPVPGGTAFQYAVYDASGAGGAPGRQLAGPFDGTALRNDQWTTVEF
PEPVIVTGDFYIVYVQSLAGTSAPGLATDEDGPNAGRSWQRVGGAWSTSPDEEGNYMI
RAVVRYPVNAPVLTAPANTYTNQSTFTVSGTSPASGAQIKIYNGKDLAGTTTVANGKF
SYGVKLRSGINAITAEAVVDGKTTDRSLPVVIILDQTKPQLTILTPAQGDRINAEVVH
VTGNVVEQFLDKVTVNGQTVQVGKDRSFSHRVLVNEGENTITITATDIAGNKTTVTRT
VYVETALPELTNITPAEDVRITSGESVTVSFDSKPLQASFRIQLPLNLNAQGAGEIP
LVETEPGRYTGTYTTPSSLVLDGGVIVIRAQDAAGNKVESEAAGRLFVSAAQEQSVPE
PDSSPEETETEEAPPSAESLQP"

CDS complement(2847965..2849605)

/locus_tag="EFAGFIKM_02425"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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TAALALVGSTVTITAQLFSSPTPNNAFTAVPGAVVTLAPPLTGIIALGSISNGITTGL

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CDS complement(2849889..2851349)

/locus_tag="EFAGFIKM_02426"

/inference="ab initio prediction:Prodigal:002006"

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DWLIRCCCELVDQYQPKVIFYFDWWIQTVAFKPYLKKFAAYYYNKGEEWGVPAINYKHE
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CDS 2851472..2852305

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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A9E0"
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CDS complement(2852333..2853685)

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/inference="ab initio prediction:Prodigal:002006"
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LDENNGPTVPGFGRSTCRGIIQVNQQTKELTYTLDYYALAHFSAVIRPKAVRIESTSS
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CDS complement(2853708..2855351)

/locus_tag="EFAGFIKM_02429"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS complement(2855388..2856275)

/gene="ngcG_3"

/locus_tag="EFAGFIKM_02430"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O50501"

/codon_start=1

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/product="Diacetylchitobiose uptake system permease

protein NgcG"

/db_xref="COG:COG0395"

/translation="MNGKVAKEDLDSRIFDTLNMILLIICTVVILVPLWNVIISSFS

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CDS complement(2856291..2857280)

/gene="yteP_21"

/locus_tag="EFAGFIKM_02431"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

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/product="putative multiple-sugar transport system

permease YteP"

/db_xref="COG:COG4209"

/translation="MDKLAVETSTGKNAISPNGKKPIGQRIKEFIVDYRRQWEIQSMI

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YYEAAKIDGASRLRQIWNITLPNMKSIISLNLITVSGLLGSNLDQTLVLMNSQNRDK

AEVINSYVYRMGMSQGDFSYATAVGLGVSIISVILLVTANKITSKLNDNQSVL"

CDS complement(2857396..2858418)

/gene="exuR_1"

/locus_tag="EFAGFIKM_02432"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9JMQ1"

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/product="putative HTH-type transcriptional repressor

ExuR"

/db_xref="COG:COG1609"

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VAAEATKYLIGLGHKKIAYISGVDTMFDSVQRMGYLAALREYQLPIDEDYIIQGYF
EEESTYSAIKSFLRLYPCKRPDAFLAGNDLSAIGCMHALKSEGFEVPQDVSVVGFDI
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CDS 2858605..2863695

/locus_tag="EFAGFIKM_02433"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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GGVVGTLSPDPTSNHAGWTLAVVYQNAALPLRNMSIRVTADVILSTSGPVNLIIDGF
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PAGSSFVTD SITINGVPQPGANPITGVPIGALNSGASVTVTFQVLVTSVPTPPRLFNQ
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VNVVSQPLGLQLVNQGTASYTFQPPDGRVIPGSVTSNTVIIPVSLPMVSIVKSTPSTD
AVVGDITITYSLVTNQTAAVTNVLLTDPIPNGSVFLPGSVTLNGVPQPAADPVTGVA
VGTLLPGASATVTF SVSVTF LPPQLTDQAQVSFDSGSFSGISFSNMVVVPVFQAI
TVNKSAPVIFAVGGEVITFQFMVTNTGNIGATTTLDIISADASFVAGSVLVNSIPVP
LADPNVGIALGLIPAGSNALVSFQIVVTS LPAALQIVNQAIASF TFTP DGR IIPGSS
NSNMVIIPISPDDLTVVKSASELQAVVGDIVTYTLVVQNNDPVDATNVTLSDPIPVAS
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CDS complement(2863699..2864547)

/locus_tag="EFAGFIKM_02434"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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HMPQFWSSQASDISMDDKSPLYMSERLGLQKEDMESNIDFRLNTEFFYFPSYHGLYN

ETELLELRQSQLNVAYQIMYHLLVVKQPISDAEVDGYQSSELLEPDYIKEQRIQFQA

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CDS 2864776..2864913

/locus_tag="EFAGFIKM_02435"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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CDS complement(2864993..2865295)

/locus_tag="EFAGFIKM_02436"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MDFMKTVTGRFRIAGKWEGVSLLLIFIAMPLKYFADISSAVAV

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CDS complement(2865492..2866460)

/gene="ccpB"

/locus_tag="EFAGFIKM_02437"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37517"

/codon_start=1

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/product="Catabolite control protein B"

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SDGEEAMRRMAEGPELPQAVLCSNDYAAIGILSEARRRNIQVPEQLAIVGFDDIELSR

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CDS 2866804..2868228

/gene="bglH_9"

/locus_tag="EFAGFIKM_02438"

/EC_number="3.2.1.86"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40740"

/codon_start=1

/transl_table=11

/product="Aryl-phospho-beta-D-glucosidase BglH"

/db_xref="COG:COG2723"

/translation="MSNHTYQFPENFLWGGAIANQAEGAYNQGGKGLSTQDVAPKGI

MGPITEPTEDNMKLIGIDLYHRYKEDVKLFAEMGFKVFRTSIAWSRIFPKGDELEPN

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KRYKNKVKYWLTFFNEINSILEAPFMSGGIYTPKEKLSKDLYQAIHHEFVASASAVKL

CHEIPTAQIGCMMLSMPTYPLTPNPDDMIKVMFEHSNYFFGDVHVRGRYPGYMKRY

FRENGIEIQMEAGDEEMLLNTVDFISFSYYMSICQTADPEKQIAGEGNLLGGVPNPYL

PASEWGWQIDPQGLRYVLNMFYDRYQKPLFIVENGLGAVDELITGADGEKTVEDDYRI

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ERYRKKSFFHWYKEVISSNGKSLQR"

CDS complement(2868409..2869014)

/locus_tag="EFAGFIKM_02439"

/EC_number="2.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5HCZ5"

/codon_start=1

/transl_table=11

/product="Putative acetyltransferase"

/db_xref="COG:COG0110"

/translation="MMTEKEKSQGLLLYNANYDQELIEERLHAKGLCYDYNQLHPAKI

NEREALIKLLGKTTDRFLIEQPFVCDYGYNIEIGENFYSNHNTVMLDGGKISFGDNV

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GSVVTKSIPSGVIAAGNPCRVIRKITEEDKTKYSRDVVKNK"

CDS complement(2869249..2870412)

/gene="pbuE_3"

/locus_tag="EFAGFIKM_02440"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q797E3"

/codon_start=1

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/product="Purine efflux pump PbuE"

/db_xref="COG:COG2814"

/translation="MNKKVYVLAIAAFVVGTVELILGGILDLIATDLHLSLAKAGYLI
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AAGSLIFVLSLTLAARIVEPQYKGRAVGII TMGGSASLILGVPLGIFVGNLAGWREVF
MLIAILTAVVMVAIWIAMDRVQPIPAVSLKKQLTALWNPKM LAIHATTLLVLAGHRTL
YAYFTPFLQETLGASATMVTFIYMMFGIAAVAGGGIGGMLS DRLHPAKAIIIVLIPFI
VSMVIPFSVGLPLIAFLLLLSIWSALSWTVTPVQNSLI IKTSPETAETLISTNSGIA
HAGIALGTYIGGMVIDHSSILNTGWVGSVLILLGLVSAIY AISVKEKTVQAVA"

CDS complement(2870539..2871291)

/locus_tag="EFAGFIKM_02441"

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/codon_start=1

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/product="hypothetical protein"

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ETSLNRIYSLIPLDDAPEPSQLLIVDHAYLLFAGVEHDSWRAIKTMSKPIVKAMTDYF
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CDS 2871498..2871626

/locus_tag="EFAGFIKM_02442"

/inference="ab initio prediction:Prodigal:002006"

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/product="hypothetical protein"

/translation="MESTQDFVKKVNENAEKERHKNNGKGT PGDKLPSKQHSTNK"

CDS 2871722..2871982

/locus_tag="EFAGFIKM_02443"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MARVNAVQPQDLVLIYWSRNPLIPGSARRIQSVRVIGNTSPCTF"

TLVPGARLINALNCLLDNDIGFKVVYRYKTSEISGVLLLLKRK"

CDS complement(2872065..2873708)

/gene="lipO_8"

/locus_tag="EFAGFIKM_02444"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37966"

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CDS complement(2873828..2875507)

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/locus_tag="EFAGFIKM_02445"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MQRMLIVDDEPVILDGLYAFFQKANFQDMEIIKAYSAFEIDWL

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DRQDIVSLQEELDAVQLPFESDQLVIPVIIRVEEWNQYQSQADRSLIRYAVANVAEEL

LQDKAKVKAIDLDTQVIACFIQSQETYPSTTQGERGSQLESWVQTLRFVYGTLES
VQQSCADCLNLSVSIMVSEQAVEWSRVNQAIGQLRLSIHEGPGLGMEKLLRVNIQDEL
PYTPSIMNQQGVVTLHLDQIKQRITAGDREWIDSFHKWTEAAKEGLPDPFFRMKTYTG
AASVLIEVLHEMGLYESAMEEISLSRMLHFDIHTAWTDLVIFYQSAYEWMISKRSDAR
LNDQSQILITIHYYIKHHLEDDLSTRIAQKVSLNPSYLSRWYKRITGKGISDYIHDR
RVERSKELLGSSCKMHEISAKVGFSDQHYFYRFFKKATGCTPQEYRDQKS"

CDS complement(2875512..2877314)

/locus_tag="EFAGFIKM_02446"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAPFLLLMREREERRREILRFIRGRWRESSIVVKLMIAFVLVIL

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AEIDHALVYASIQKIRFGSRIQLELEDLDARYKMISIPRVIIQPIVENVFEHALAKRS

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CDS complement(2877356..2878246)

/gene="dasC_5"

/locus_tag="EFAGFIKM_02447"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9K489"

/codon_start=1

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/product="Diacetylchitobiose uptake system permease

protein DasC"

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NFFRGLPKLEEASWMDGAGHFRTLWSIYLPISLPSIATITLFALVGHWNWFDGMIY
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VYPFLQRYFVHGLVVGSVKGG"

CDS complement(2878262..2879167)

/gene="yteP_22"
/locus_tag="EFAGFIKM_02448"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:C0SPB3"
/codon_start=1
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/product="putative multiple-sugar transport system
permease YteP"
/db_xref="COG:COG4209"
/translation="MRSNYKQFIRNVPLHLMILPGLLIIVFGYIPMAGLSIAFQNFS
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FPYILVITDQWKEFGFGTIIYLAALTNIDKSLYEASVMDGAGRWKQTWHTLPGIRPI
VILMVTLSLGNVLNGGFDQVFNLNPLVYESGDILDTMIYRIGLQDAQYSVSTALGLI
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CDS complement(2879316..2883056)

/locus_tag="EFAGFIKM_02449"
/inference="ab initio prediction:Prodigal:002006"
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EKGPYFLTRQLLGTLYAGDNLVVHPSGGVASGEWLHIALSVAGSQGGTLSSAGPIVY

VNGEKAADGSISQTSSGNYAKLREWFDSFTDPENYSQNYIARSQYAADVDFAGSLSDF
RIYGAALTMDEVIEVMCESLTDEAIVKLAADKYLSFPNRIITKDVSLPADLLGGKVS
EWSSSAPEVLSENGEVQVITSAQEVTLRALLNRGDRKLSQSFDVSVVPAHLPPYVTI
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GRNREPLFAWSGDTEKMRVQHTDGLNVHFNVEDPEVNAYYVTVQDGATIRNRGFSDSN
QHCAMSIKQGesyDFTVWAKAELAGTITVQLQDGS DTSISDSVTLHVEGGNTWKKYGL
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RKDLIQALADLHPKFLRFPGGCISEGSFIWDNVYDWKDSVGPVELRKENYNVWGYMMT
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LSTDFEHNEWA AVRSQM GHPEPFDLRYLG VGNENWGTEFFANFEVFKRSIDDYMKQNY
PDHELHIISTVGAQADDDAYQEGWKFLSGNLTGSAQVAFADGAEVIEETVTWYENQDN
YMDTIADEHYRSNEYLLNNVD RYNNYDRAYLEDGSIDWKETSKV FVGEYASTDKNTL
AGAVAEAAIMTG FENNADVRLAAYAPLFNKVLT DGTyrWTPDCIWFDDET V WYTPNY
YVQQLFAKYVGDQVLETSFSTYNKGKPLSLIPRGGIEIATGHADIVVKRVT VTSNVDG
SLMFDEDFRERTEPSETWNQIPGSEGYTLTEGKGLILKAQSSGLNGLYLLNDEWTNYK
VHVEAERISGEDGFYIGVGLTDISPENKDVIEY AISYGGNATGVKVYKQGIEGYTLGD
YSSSSAAGNLRAANYEPLNGTDYTITVNYGGDTGKNLVC SYTDGRNTSKVLDYKLEA
YNREVFH SVTKDARHVYVKLVNADGV DKSTRICLQDLKVNSSAKLITLTGEDHLVHVP
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CDS 2883442..2885859

/locus_tag="EFAGFIKM_02450"

/inference="ab initio prediction:Prodigal:002006"

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EGPYKDQGILLKSGMWDQISEDGTIYDATIHPNVVDPDVFYDKNGKLWMVYGSYSGGI

FILEMDATTGKPLPNQGYGKKLTGGNHSRIEAPYMLYSPETDYYYYLYLSYGGLGADGG

YNIRVARSQTPDGPFLDAEGNDMINVKADKDKPLFDDRSIEPFGVKLMGNFLFERQIG

DPGTGLGSGYVSPGHNSAYVDPETGKQFLIFHTRFPGRGEEHEVRVHEMHMNADGWPV

VSPYRYAALGEDTTQLTTQEIAGQYHVVNHGKDITADIKPSQTVQFTADGQIHGAVTG
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QDIVDAVKKDLISNTDHVFFNLTLPTKGTSDAEITWKSSNTSALSTTGVVQRPRAGK
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FGNGLTRHMFLLTPSQHNGALQFTIHNEGRDQSLIAANPLPSKEWVHVAVTLQGDDVGT
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CDS complement(2886000..2886554)

/gene="sutR_2"

/locus_tag="EFAGFIKM_02451"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77626"

/codon_start=1

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/product="HTH-type transcriptional regulator SutR"

/db_xref="COG:COG1396"

/translation="MKNINSILAQN LKQLREQRKLSLDKVAEMSGISK TMLGQIERGE

SNPSIATVWKIANG LKTSFTALIHEPKSDTTVVTGDDIQV LMEDEGRVRIYPHF PFEE

GRRFEIYMMEMD VDSLSAEPHIEGTEEFITVFEGEVTIRVGAE EYTVNQGESIRFRA

DKPHAYINPGA KTSRLNMVIHYSK"

CDS 2886685..2887266

/gene="eamB_2"

/locus_tag="EFAGFIKM_02452"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P38101"

/codon_start=1

/transl_table=11

/product="Cysteine/O-acetylserine efflux protein"

/db_xref="COG:COG1280"

/translation="MNIIPLVTYAIIASFTPGPN NIISMTHARNQGFRKTL PFISGVA

AGCLLIMFLSS YFNLILHQYIPRIAPVLNV LGCVYMLYLALKIMRSKP ADSQENKVN H

YSFLFGFTLQFINPKVILYGLTAISVFLPLGQSHVQLIVFSLLLTFIGISANMTWAF

GGMLFQSFLRYERPVNIVMGMLLIYSALSILM"

CDS complement(2887320..2888297)

/locus_tag="EFAGFIKM_02453"

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/inference="similar to AA sequence:UniProtKB:P9WKP3"

/codon_start=1

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/product="hypothetical protein"

/db_xref="COG:COG2220"

/translation="MTKYENQLPTSAGMNFKSLISILRDSMRGNVERRPSGMMMPMEIC

EPAETFASDNPQVTWFGHSAFLLEIEGHRLLFDPM LGNRPSVSWVGTKRYSTNLPI

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HNWWDELSFKGLTFACTPARHFSGRGLFDRNSTLWCSWWVIVGQHTKVVFFSGDSGYGPH

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YHAWNEPVERIMKAAHALNVKIATPKIGEKVVLHTEQYPTHPWWRPELG"

CDS 2888497..2889474

/gene="rutD_4"

/locus_tag="EFAGFIKM_02454"

/EC_number="3.5.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00832"

/codon_start=1

/transl_table=11

/product="Putative aminoacrylate hydrolase RutD"

/translation="MKKWRKRLVKFLIFDLAIVLLLLGTGVIIYQQVGLRQDAKTLVPP

GKLYEVHGDNMHLYTGGECDVTVVLASGWGTANPYVDYIPLYEKLAPNTKFAVYDRFG

YGYSQDQDKKRDVDTVAEELHELLQVSGQKPPYVLVGHSLGSLETIRFAQKYPDLVKG

IVIIDGGSPEYYSNDDDSLADTIGGFANKFRIQTGLFRLSMQSDMVVETSNANRNELK

LVPDDLKKLDTTALLHNYGNVNTLDELREIAANAKVVVDHKQTLPPPLTILTADYLGA

SEPEWDKSQVEFKSWSDSKQVTIKDTHYIHQYRPDLVAEEILALVKK"

CDS complement(2889562..2890209)

/locus_tag="EFAGFIKM_02455"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIIINPISNNIEKMLLHYEKNHGLTLQASLISNSSVYRLQNYC
LKVYASRARLDGEMESEALRELQSNPYAPKLYAHSPGEYTLTEWIEAFKLKEYRVTYG
HIPPNLIYDMFTTELQQIHAGYWDWDVIRYENLLWTKTGDVKRTNFWLCEPVNSRREN
LYNQVIRRIDNIYNGDRTEAMEAMKQYFYRHQLTSLEIEQAFSDFRSQRPRLAIAQ"

CDS complement(2890516..2891997)

/gene="emrY"
/locus_tag="EFAGFIKM_02456"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P52600"
/codon_start=1
/transl_table=11
/product="putative multidrug resistance protein EmrY"
/translation="MKADSAQNQQETKQYKVPILFAMLLSGFIGLFGETALNVALTP
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LAPSFEILLVARVLQAIGTALLPLMFNTILVIFPIEKRGAAAGLIGLVIMFAPASGP
SISGLILANLSWHWIFWISLPFFLISLVCGLLFLPNISKLTCPKIDVLSIILSTLGFG
GIVYGFSSAGGHGETGGWTSPPVVATLVIGVLSLLLSIRQLRMKQPMMDLRAFKYP
MFTIGLILIFICMMMLSSMLILPMYLQQGMAVTALTAGLVLLPGSLLNGLLSPVMGR
LFDKFGPKWLVIIGLAVVTVVLFMYTGITPTTTLAKIITLHVFMVMVGISMIMMPAQTN
GLNQLPREYYPHGTAIMNTLQQVSGAIGTAVAVSILSAGQSRFLSGVANPESPENQLA
GFTSGVQNAFVFALVLSIIGLIASLFVKRVKVGSTPGQQGPMH"

CDS complement(2892066..2892653)

/gene="yxaF"
/locus_tag="EFAGFIKM_02457"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42105"
/codon_start=1

/transl_table=11

/product="putative HTH-type transcriptional regulator

YxaF"

/translation="MSEKSNARESIVSTAARLFFSQGYHATGLNQIIKESSTPKGSLY

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MEGALIISLTNQDKQPLLTAAYLSVVTKNKQIQ"

CDS 2892778..2892891

/locus_tag="EFAGFIKM_02458"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTRATAHGQIIITAANLETKLQIKRLFVSLRIVY"

CDS complement(2892915..2896169)

/gene="cypD"

/locus_tag="EFAGFIKM_02459"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O08394"

/codon_start=1

/transl_table=11

/product="Bifunctional cytochrome P450/NADPH--P450

reductase 1"

/db_xref="COG:COG0369"

/translation="MSDATSIPQPKMYGPLGNLPLIDKDKPTLSLGVLAEQHGPIYRL

TVPGYSGLIVSGPDLVAELCDVSRFDKYVYNELENVRAFGDGLFTSRTSEPNWKKAH

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NYRFNSFYRQDHSPFIESMVRALNEAMQKSSRLKIQNLLMVKTKRQFQEDIQTMFSLV

DQIIIEERKASSAPEEVDLLARMLNGKDPETGEMLDDENIRYQIITFLIAGHETTSGLL

SFALYFLLKNPNSLQKAYDEVQILVSDSPQYEEILQLSYIRMILSESLRLWPTAPGF

DVYAKEDTIIGGKYPLKKGESCSILLPQLHRDREAWGEDAELFRPERFEDTTKVPHHA

YKPFNGNERACIGMQFALYEATLVLGMLVLFELIDYSNYELDVKQTLTKLGDFRIQ

VKARAASQTRNKSTVSAKEKPAPVVHKNIASDSQRGEILAVEADAKPSLLVLYGSNLG
TAEGLARELAEKGRSYGIPSEAAALNEWMGRLPRQGVVLIVTASYNGKPPQNATAFVD
WLKGTESSEARDVNYAVLGCGRWSWGTYSIPRLIDEKLEELGGKRLLSRGEADAGG
DMEKQVEAWQHMVWPQVLSVLGISEETIKSSKPSASRLQMEFVREKTDMLPARTYDAS
YATVVVNKELQALGSGRSTRHIEVLLPEGMNYREGDHLGVLP SNQKQNVDRILSRFGL
RGDTPIQLTSDVSHLTHLPLNRPVKIHELLAYCVELQTPVSRTQLQELANHTICPPHK
RELEGMLDENSYRDYILANRITMLDLLERYEACELPFERLLELLPPLKPRYYSISSSP
SLNSEQASITVSVVREPAWSGKGEYQGVASSYLAGCQSEEDILMFVRTPESEFYLPKE
ADVPMIMVPGTGVPFRGFLQARAVMKQKGLPLSEAHLFFGCRNESDFIYRHELEQF
ERERIVKLHTAFSRADGKPKTYVQHLMKENSEQLIHMLMKNKGKLYVCGDGSQMAPAVE
ETLQQAYQEVQGATMQQAKDWLIQLQAEGRYVQDVWAGNNRTGETPKAVHEEVH"

CDS complement(2896469..2897437)

/gene="trxB_1"

/locus_tag="EFAGFIKM_02460"

/EC_number="1.8.1.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P56431"

/codon_start=1

/transl_table=11

/product="Thioredoxin reductase"

/db_xref="COG:COG0492"

/translation="MIRDIECLERVYSMSNMNQLLDVLIIGGGPAGLNAALVLGRARK

NVVVIDDETPRNWWTRETHGFVTRDGASPREFRKAAKEQIAAYPSVQFASDTATAITG

SDGD FEVKTQ GASYRTKKILFAVGKKDLPLDINGLTEVYGKSAFVCPYCDGWELRDQ

PLVIIVSGDKALHMAKVISGWTERYTICTNGSDSLTDEQREELKRHNVTVFDAPIQSI

NSEEGMVQQVVLNDGTEIPCTGVFFQPKLFTGSELPKAIGCEITESGTIVVDVSGKTS

VAGVYSAGDAASEMYQAITAASLGALSAVSINNELNFEKWDEPSHR"

CDS 2897852..2898781

/gene="ctaB2"

/locus_tag="EFAGFIKM_02461"

/EC_number="2.5.1.141"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P24009"

/codon_start=1

/transl_table=11

/product="Protoheme IX farnesyltransferase 2"

/db_xref="COG:COG0109"

/translation="MKTLNNGSQTNISLEYSSIPKVFFDTIKIGIISNLIAMFAGLS

LALYVFDASILANIVPIILSFIGSSLIIGAAGVFNNLYDRDIDAIMERTKKRPTVTGL

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SLSGAVPPLIGWAAISPGLGHFEIWALVVTMLLWQMPHFYGIAIRRFDEYKAAGVPML

PVVKGIRRTYIQTNVYLVLLLISSFLFWPMSPFVAIVAFLVSLAWLILSVATFDKKET

EKWSKRMFIFSINHITIIFLVIIAYSLIAQMMR"

CDS complement(2898898..2900667)

/gene="yhel_1"

/locus_tag="EFAGFIKM_02462"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07550"

/codon_start=1

/transl_table=11

/product="putative multidrug resistance ABC transporter

ATP-binding/permease protein Yhel"

/db_xref="COG:COG1132"

/translation="MTVAGFIGRLFRFRPLLIVINGLLWCIFHSLPLAIGIGMQWFFD

RTTAGSNDYMWLSVPLIFIALVRMARVGTFFVAFYAWVTYLYHVQAILRTNMLAAIMR

WPGRNLPASPGEAMSRFRDDVDEVVEYVESWVDFWGRLVFAVVSIVIMANINWQITLV

AVLPLVVVTLNLSGNRARKYAQVNREATGRITSFIAETFGAVQALKLGQAEENVAS

RFNQLNEDRRQAALRDNLFKQWMRSMNQHVLSICTGLILLMCAEMKAGNFTVGDFAL

FTSYLANIGFSISLFGYMFQHKRLKVSYDRMRKLFRPGEEDQIMDSREIYLYEDPPE

LVSEQRDPKEKLQSLEVNKLTYQYPNSENIEISFRLKRGQFLVITGRIGSGKSTLV

RTLLGLLPKQKGDHWNAAVDPATFLMPPRAAYTPQVPRLFSDTLKENIVQGKQGNT

EQALEKAIRLAVMEKDIKHLDDQGLETPVGPRGVMLSGGQIQRAATGRMLMTEADLFIF

DDLSSALDVETEQQVWEGLFQEPDVTICIAVSHRRAALSKADHIIVMKDGRIEAEGLA

ELLATNEEMQLLWQGEQTPAKVG"

CDS complement(2900664..2902409)

/locus_tag="EFAGFIKM_02463"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9WYC4"

/codon_start=1

/transl_table=11

/product="putative ABC transporter ATP-binding protein"

/db_xref="COG:COG1132"

/translation="MPKTEKRSMWLLRYLKPVKGRLALLIMLLTSTGLQLLNQII

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VPIALVMTVFTLLSILFMVFIRNLGVDSSKNERAASASLFGLEERIAGIEDVQANGH

VPYVMNRFYRTMRTVFRKGRKAWLLRVIPWNTTVVLFALAVTAVLLLGVHYMEGLIS

IGTLFLIYQYTQMLNDPIEMLGDQVQEFQKAKSGMLRSRELLSMHSVIEEGTEEQLPE

GPLGLEFSQVHFSYNQDKPVLQDITFAIKPGERLGIIGRTGSGKSSLSRVLLRLYNLD

RGTIRVGGTDITKLSLQALYRRVGMVTQDVQLFDGTLRDNLTLFNGDVSDQMIKETTD

RLGLSQWINSQPEGLNTYLAAGGASLSAGEAQLFALTRVFLTEPSLVILDEPSSRLDA

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HYARLLITGREEELA"

CDS complement(2903028..2904263)

/gene="mdrP_1"

/locus_tag="EFAGFIKM_02464"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0A1C7E424"

/codon_start=1

/transl_table=11

/product="Na(+), Li(+), K(+)/H(+) antiporter"

/translation="MKQYLRQIHPLAWTIIIGTMFGRLVTSMSIPFLSIYLTRVLDA

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SESTFPFVISGLVYIAYGLVLFLQFKLQHANLPERHQATAPRLREALMTTGRDRVFLP

VLIGTTCVVLGYGHFSSTLAQYLARSPIFENGSMFTYMLSLNAVTVLIIQYPLVRTF
RNFPPPLVPLIAGNLLVATSLMMVGIAEGVLMMSVILFTIGEVLFTMMDMLIDRIA
KPEWKGTYFGTIGFNNIGSVIAPVMGGLLSQFGAENGLAVFLPIALTTALGVPFLLI
AHRRLVVREKQTEPTSLSM"

CDS 2904593..2906359

/gene="sgrR_1"

/locus_tag="EFAGFIKM_02465"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01449"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator SgrR"

/translation="MDTLHTHFIRLAGAEQLSFKLHEPVAVTIDSLSAALCCTPRNVK

FILRKLEEQGFIHWQPGRGRGHHSSELTMLRSMNEALEASFTELLAKGKMKDAIELIGT

VQMDDTLREQLMSLHQQMGFHHGHDETASGQDILRIMRSRQLGGLDPAFVYTAFTYL

LSQVCNTLITYDAKTESFLPALAHMWECSHDRLWTFYLRKGVRFHNGRIMTSRDVQA

TLQRLIDMHSPSIWLYRDIERAEVAGDYCIKFLHRPNRFFLHLFSCIRMTILPYDYN

VANTLVGTGPFQISELNEDVLELTAFDAYYGIRPHLDQVHFWFVPDLSPNDRIYELPG

TDRLSLATGCDQTNISINYPALGCQYMLFNHFKEGIHHPHPLFRQALRIVYDSVALVRDL

GGNRITPASSFLPWRSAQDWTAASLEHARELLRNCGYQGEKITLSYKYNKDADVAEW

FQCRAASIGLNISMQAVVDYFNSEETTNAQLILAEIILEDWQYGMIHFFKNLSNHFH

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IFGMQIAEFGYLDISKLWIKNP"

CDS complement(2906439..2909066)

/gene="rcsC_7"

/locus_tag="EFAGFIKM_02466"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00979"

/codon_start=1

/transl_table=11

/product="Sensor histidine kinase RcsC"

/translation="MQVQKVDHHELFEQIYNQAPIGIALVAPTGQWMKVNPAFCCMLG
YTSELMDSLQDITHPEDSPQDVICSYELLEGENSKENQYEKRYINKNGDILWTSLHV
SLVRSEITDEPLYFICHIVDITDRKMSEQKLLHTEEMFKLITDHAQEIIYIADQEGVC
RFCSPSVQGLLGYSPEEVIGQNNNAYFHPQDLERISQMDLTGKGNLLNIRVRHKEGDYL
WFETTYKVFGDAEHGQQILSIGRDVSRKKQKDISAEAERIALIGSWEWDMVKDHITF
SDQIFEIFELEERTCKPYRVSDVFDVMDSEDLASLQKHITGVKQGEPLDFEYKHISSDG
NEKYLHLRGLITLDENRQPVQLNGTIQDITERKRIEFKLQESVERYTSLKKYNHDAII
SFNMDGNIMNANPVAVKMTGCPVAEMIDTSISRFIGASNGLGLILGSNYEMAEKEINAV
RHTDGSETEVLATLAPIIINKSNVGFYLIAKDITEQKKLLVAKETAERMNKAKEFLA
MMSHEIRTPMNGVIGMTDLLDTPGLSGEQKEYEIIQKSGDSLLAIINDILDFSKIE
SGKTDLVEDPFDLVEIVTETVQIVKPLAREKKLDVRMCVEDAIPTPVYGDAYRLKQVL
TNIIGNAVKFTSEGGVEVKVGVKEQCGNNVQLYFQVKDSGIGIPAERKQQLFEPFYQL
ENFMTRKPQGTGLGLAISKKLVELMQGEIWIEESDEPGTIFIFTAQFKLNNGEESNRL
DQQQKKSRTSALRILIAEDNEVNQLVLSRIVEKKGHFVDHVADGVEGVEAVKHTSYDI
VFMDVHMPRLNGFEATKAIKNALHPESCPFIIAVTANAVRGDMENCLKAGMDAYVSKP
IKIESIMQALETYYIKNNL"

CDS complement(2909335..2911716)

/locus_tag="EFAGFIKM_02467"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNNVLTEQADAGYRLAEQKASQYFTSLMQQLNDNTYTTALTQDI
HVWQKKHIHRFAWLSLLSPSKRKPDPRDVHRYIHWLNTTGKLLDDYLDRSISYIYMRDL
GQALDSPGTQTRIQNQQNTKKYFMGSATGRKGQPDYISLAALYRWGQKEHIETAVIW
VMNKLKNVASNIPKELDAEQARKLIIKLVVHLVDDMNEQTPPEERARRFDAAIR
LGYSYGLTYPFVDDLDSQALTVQEKEQYSMMIRDALLTGVPDLGEWKGSNLEVIEY
VHSELREAFEYIKNYQHPEKQRTFLEQSYVFFQSQEIDRNKKLANANYSNEELYIPII
IKSSSSRLIVRSVLSAPVDEGFDLRTFYGIYNQLADDFADMFDMEEEAVTPYTYYL
KYRDLRPDLINPYELYWAVISHLIHDVYNSDAKTREVILDRAINGLKRCKERLGQQKY
DEVMTIFASGQPEFNQLVQQMVRKADDVDFDKLLRDQVVLQLKNDKQEKEEFKQTIR
TVREQINVELQIAKPGGLHEMKETLIDAANYSLQGDGKRLRPILTWVMGVREYGLPES

SIVPLLRSL EYMHTASLIFDDLPTQDNASTRRGRSTLHHVHNSATAELTGLFLIQKAI
GEQSSLDRFDAATVLKLIQYSAEKAEDMCMGQAMDLSK GKALTLEQLNMICFYKTI
AFEAAALVMPAILAQVKEPEMATLKKFAYHAGIAFQIKDDLDFEGNHLLGKPAGQDE
RNNNSTFVSILGDEGAKKEMWEHYCLATDALNEMPKPIFLRHLLDYLVGREH"

CDS complement(2911904..2912701)

/locus_tag="EFAGFIKM_02468"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDLLLFVIMFILGLVGSFFSGLLGIGGAIINYP LLLYVPSWMGL

EPFSAHQVSSISM FQVFFASLAGVIAFRRKVRTGRSGGAIVHRGLVLYMGSSILAGSL

IGGFISGHL DGRVINLIYGILAIMAIVLMLIPGKGKLDTSAPLVFN RWIAAGTAFVG

IVSGIVGAGGAFILIPIMLTILNIPVRTTIASSLAIVFISAIGGVIGKITGGDIPMEP

IITYVIGSLLGASLGSRVSSMINVRVRLRYALIVLIAITAVK VSSIL"

CDS complement(2913188..2913943)

/gene="linC_2"

/locus_tag="EFAGFIKM_02469"

/EC_number="1.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:D4YYG1"

/codon_start=1

/transl_table=11

/product="2,5-dichloro-2,5-cyclohexadiene-1,4-diol

dehydrogenase"

/db_xref="COG:COG1028"

/translation="MTQHNGKVIIITGGASGIGKETALQLSDQGATIVVADYNEDGAK

KLAAEIETAGGTAGAYKVDVSKGDEIKALIDWTVEQYGTLSGIFNNAGIGLVKPFLEM

DPESYHRVIDVDQHSVYYGMYYGAKKMVELNVQGTIVNTASIYGSVAAVGSFN YNAAK

AAVVMMSKSGALELAEHGIRVVG VAPGFIETPILGDDQAMKDALATQHMRGELIQPEK

VASVVTFLFSDAASAVNGTTVAVD DGFLSFKTK"

CDS complement(2914193..2916697)

/gene="uvrA_1"
/locus_tag="EFAGFIKM_02470"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9WYV0"
/codon_start=1
/transl_table=11
/product="UvrABC system protein A"
/db_xref="COG:COG0178"
/translation="MRDAIRIKGARENNLKNISLSIPKYKLVITGPSGSGKSTLAMD
TLQRECQRQYMESMGLTSDSISKPKLESITGLSPSISVGQHVTNRNPRSTVGIVTDIY
TFVRFIFSR LGERLCPACNGIISPTVEPAGHLAEDEYMDHATMNCPHCSAVIEKLG M
SHFSFNKPEGACKQCSGLGHVATINEEAVFNPELSVREGGVASLNGVHRDIQIRILVA
ASKHFGFEFDADLPLKEFGEIERDLLYGV DSEQFKRHYPPIKPIQGTKFEGVIPGLW
RRYKEKEGEAGTTEKDGGFFHQQRCPECKGARL KKEVLSVHVADVSISEVTNWSFSNV
LEWTLGLQEISPEAHLLNPILHEL PNKLQRIMDVGLGYLSMDRQTVTLSGGETQRL
RLASLLGSGLTGVLYILDEPTTGLHPRDTVGLIRVLQELRDLGNTVLVIEHDIEMMRA
ADHVIDIGPGAGLNGGLVVGESLEDLMISEHSVTGAYLRNESVASPSYNRRRTGTGQH
LAIRRAHLRNIDIPVVSFPLGTLISVTGVSGSGKSTLVFDILAQGMESGQKLTGCEEI
TGLEHVGDIVFDQTPMGRMQRSNVATYTDVYTHLRQLFASLPDAKARKLTAKHFSFN
TPGGR CETCQGLGVLSVDMNFLPDLEVTCHDCRGKRFKEEVLQVQYEGFSISDLLNMS
VAESLPLLKIQT KIADLVEMLCEVGLGYLQWGQSVKTLSGGEGQRIRLAKELSKKTNK
HTLYLLDEPTTGLHPSDIKQLHVLLDKLVESGNTVVVVEHSLELIRESDWVIDIGPEG
GAAGGELVAAGTPEQVAEVQASYTGQFLKRILAEGL"

CDS 2916848..2917342

/locus_tag="EFAGFIKM_02471"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSRDQQQQPTALQENFTLRMRSLGTRTVLYQQHVAASLGLYNND
FISVDILREKGPITAGELSKLTGLATGSVTTLIDRLEKNGFVRRENDPNDRRKVIIVP
LYENKEEVSNTYLTLSAMVDLASTYTEEELALITGFLSKAGNVLDQQIDDLSSKIRS

KSSS"

CDS complement(2917471..2917947)

/locus_tag="EFAGFIKM_02472"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIMFIRKRKHTLMMTGLIASSILLISACSVVEQANQSLNYVSGA
TDYIEQVSNAGADLQELASSAANNPEITTQIQEKIDLIQAEASEFSQLTAPAIGESIH
ENLVSyntQLTEVVDNFENTIAEQGFTAENWEKTGIPELITNINNLLKDPLSGLGNE"

CDS 2918077..2919051

/gene="panS"

/locus_tag="EFAGFIKM_02473"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8ZKL0"

/codon_start=1

/transl_table=11

/product="Pantothenate precursors transporter PanS"

/db_xref="COG:COG0385"

/translation="MIMLQALNQRLNRIMPLITPISIIIGVLCGSFLSSYTFLSPWLF
AFMTFAGSISLGIRDFVNVLLKKPFPLFVCLFILHLAMPLIALGMGHLVFPTDAYTITG
LVLA AVIPTGISSFIWVSIYRGNIALTSLI LIDTMLAPFVVPGVLSLLIGTSVTLDT
AAMMSSLFWMIVVPSLLGMLLNEWTKGAIVPVWGPRLNPLSKLFMASVVAINGSV VAP
YLADFNWKLAVIIIFLASFGYALSFIARLLGWNEADQVALVFNGGMRNISAGAV
LAVSYFPPPVAVPVVLGMVFQQMLASLTGYLLGRRSQLLQKSDKTSAA"

CDS complement(2919154..2919414)

/locus_tag="EFAGFIKM_02474"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQAAPNQAVHKPGSQPVSGSWMLTLLLLAIPLVNIIMLFVWAF"

GNSNPSKANYAKASLLWLAIGIVFYILILALGLTAAFSGTDY"

CDS complement(2919702..2920787)

/gene="asd2"

/locus_tag="EFAGFIKM_02475"

/EC_number="1.2.1.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P23247"

/codon_start=1

/transl_table=11

/product="Aspartate-semialdehyde dehydrogenase 2"

/db_xref="COG:COG0136"

/translation="MSAKLKVGIVGGTGMVQRFVDLLDQHPWFEVTAISASANSAGK
TYEESVQGRWKLAVPIPEAVKKIVVQDASQVEAFASQVDFIFCAVDMKKNEIQALEEA
YARTGTPVVSNNSAHRWTADVPMVIPEINPGHLDVIEAQRKRLGKTGFIAVKPNCSI
QSYVPALHALREFKPTQVVASTYQAISGAGKNFTDWPDMLDNVIPYIGGEEEEKSEQEP
LRIWGSIIENNEIVKASAPLITTQCIRVPVTDGHLATVFVNFEKKPSKDEILERWLQFK
GRPQELALPSAPKQFITYFEEENRPQTKLDRDIERGMGVSTGRLREDSLYDYKFVGLS
HNTLRGAAGGAVLIAELLKAEGYIQPK"

CDS complement(2921313..2922158)

/locus_tag="EFAGFIKM_02476"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNESIIRDLIK YMDVEDNAAIQYIQTEHRMKLGLFWGIQEGSRV
LEIGCGQGDTTAVLAHLVGNGYVHGVDIAPEDYGAPLTVGEAAKLRRSPLGDRIRM
DYDFDILSDQAQFAENEFDVIVLSHCSWYLSFDELAQILSKVRTWGHQLCFAEWDAR
VTDVSQLSHWLSVLIQSQVECYKENSFSNVRTLFTPEDIQELVSAAGWTIKEETSIHS
PELQDGRWETEMTLQEAPVELQMLPIPKVKTLLLSELKLLKTHHVSGPGSPLGTYAM
VAKKQ"

CDS complement(2922310..2923182)

/gene="gtaB_1"

/locus_tag="EFAGFIKM_02477"
/EC_number="2.7.7.9"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q05852"
/codon_start=1
/transl_table=11
/product="UTP--glucose-1-phosphate uridylyltransferase"
/db_xref="COG:COG1210"

/translation="MQIKKAVIPAAGLGTRFLPATKAQPKEMPLIVDKPAIQYIVEEA
VQSGIENILIVTGRNKKSIEDHFDKSVELEHSLYAKGKQSLLEEVQAISEMANIHFI
RQKEPLGLGHAIGCARQFVGDDAFAVLLGDDIMVSDPPALAQMVHLYEKTGNQIIGVRQ
VDAANVSKYGIIDSNGAEDRVHRVTNLVEKPSLAEAPSRTAVMGRYILKPSIFILDQ
IERGAGGEYQLTDALKEVSQVEELLALELEGRRYDIGDQFGYIQAILEIGLMRKELQP
MLTPYLQKLATQWA"

CDS complement(2923240..2923632)

/locus_tag="EFAGFIKM_02478"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTKRLVTLFKFGIVGVANTAVDAVVFALLAVVGVPVLMQAQVISY
SCGVANSYWLNGRWTFRDAARGGNDRAKLVRFLITNLIVLAISALILMTLHDVLGWSL
VMSKILATLMGMVLNYMASRYWVFRIAT"

CDS complement(2923625..2924611)

/locus_tag="EFAGFIKM_02479"
/EC_number="2.4.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q55487"
/codon_start=1
/transl_table=11
/product="putative glycosyltransferase"
/translation="MAHAYRYSIIIPMYNEEAVIEETYRRLKKVMGSTGESYELLFVN"

DGSVDRSAQMIRDYARWDESVKLIDFARNFGHQIAITAGMDYAAGDAVVIIDADMQDP
PELILDMIKWKEGYEVVYARRTRRSGETRFKKWSASLFYRVLRASDTDIPVDTGDF
RLIDRKVCDEMRLPEKNRFVRGLVSWVGFRQTAIEYERDERLAGETKYPLKRMLKLS
LDGITSFSYKPLKLAGYVGATLSVGGFIYMLTVIISAIFTDSTIKGWPSIVSIMLMFN
GFILIMLGILGEYVGRIYDETKARPLYIVRDVVQAEGQQAQSRLTSRVAHHD"

CDS complement(2924850..2927024)

/locus_tag="EFAGFIKM_02480"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNNTKRRMDLVLLPIVLLAAFLNGYGIWNDQYANSYYTTAVGSM

LSNFHNFFYASLDSAGSVTVDKPPVFWIQTAFAFVFGHLHGWSVILPQVLAGIGSVLL

IYFMVKPTYGLAAARISALAMATVPVVAASRTNNIDSMLVFTLLLGSWFLFKGSKQG

STWRILVAFGLIGIAFNMKMLQAYMILPAFYLLAFQAKWRRKIILLIGSTAVLAV

VLSWAVTVDSIPEDERPYIGSSETNSVMEAFGYNGLARLTGQQNTAGNAGMPNGVG

QGNNRDNRGDSTSGPNQTDGVPGAGQDVNAPDNDNMNGSNGLNAMGGMNGPNGNFPN

GQMPNDMEMPNGRNFGGGMGGMFGTGEGKPLRLFQTELSGQASWLLPVLLGCIALFA

GLRRRNITNKHKEALFWLAWLLPVAFFSVAGFFHQYYLIMLAPPIAALTGAGFVAMW

KSYRDRNGWQAWLLPVSVLLTTQFGWYIMQAYNDTIGAGWSISELIVGILVTVILVVM

LHRTHRWKQGFIAGFMVMLIGPIYWAFTPITYGGNSMIPAAGPTGSNGMFGGAGMGM

PMGNGAGDIEMPTMGGRGGMGNRNEEVDATLNYLKEHNTGETYLFATTDYNQAAPYI

IDERAAVITLGGFSGSDPVYTTEELEQLVKSGQVKYFMVGGMGGRGNGNSEISDWIKEH

GTEIPMSEWQTGTDSGSTDNGDTGNRAGFGFGGQTTLYEVKL"

CDS 2927229..2927912

/gene="copR"

/locus_tag="EFAGFIKM_02481"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q02540"

/codon_start=1

/transl_table=11

/product="Transcriptional activator protein CopR"

/translation="MKLSSGIKILLADDEPHILQFLELGLSNEGFDVRTAPDGAAALE
LALEFKPHMAILDVMMPEMDGFEVVERLRKTGAEVGVIMLTAKDEVENRVKGLWLAD
DYMIKPFADFELLARIQARLRNQFPLLIGAVTHGPFRIQQRKEITYQNVLELSPTE
YELLKFIVLNHGIVLSKATILSRVWGYDFGGEENIVEVYVRSRLDKLGDKEHKLIRTL
RGVGYRVDL"

CDS 2927912..2929429

/gene="sasA_7"
/locus_tag="EFAGFIKM_02482"
/EC_number="2.7.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01837"
/codon_start=1
/transl_table=11
/product="Adaptive-response sensory-kinase SasA"
/translation="MNSLPKKNKLRIIRLHHWIWPRSLRSQLLSRSLFVLAGLLLLIG
ILQFWIMESFLYRNQAKTMEEQLMSMPVWLGIQSRNGSSNNPFGGQVGNNGSGNRVLF
IPDRSLALFDNEGTFEDVFGEDGLKAPQLSSAEYQDITDELKEQKHIPYRIVTDSQGN
EQLIVFASPGPRNRGLPMVQMGATKPLRDLIIKQLLIFIMLSLLAMVAGLVLYTKVL
RRTLVLPLSNMVNKVQQIDAGSLADRLPVVQGQEEVDQLAVSFNGMLERLENSFEAERE
SKEQMQRFLSDASHELRTPLTSIHGFIEVLQGAATNQDQLYKALDSMHGESVRINKL
VEDLLLLTKLDQAPKQEREVIQLDSLLEMQPQLAIMAQQRSIHLDLTAHVHILADPY
KLKQVVLNLFHNAVQHTDPEHGAISITLYATHHKAELSVKDNGTGIEPEHLPHIFERF
YRTSSSRSRKQGGAGLGLAITRSIVESHGGKITVQSQVGLGTEFMILMPLHKNDV"

CDS complement(2930048..2930758)

/gene="fabG_5"
/locus_tag="EFAGFIKM_02483"
/EC_number="1.1.1.100"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P99093"
/codon_start=1
/transl_table=11
/product="3-oxoacyl-[acyl-carrier-protein] reductase FabG"

/translation="MKKTVFVTGANKGIGYEIVKQLGEAGWKVILGARSVERGERAVS
ELTSRGLDVEFVQIDMCDSKSIEQAADTIHKSYYAAILLINNAGMPGAFSHSFTDTKE
EDLRNAFEVNFFGTFRNLNQRLFPLIKDNEGTIINVSTDMASLDHMQNAEFTLNAFDYN
SSKTANSAMTLSMAYEVKNSRAQVFAVTPGFTSTDNLNGNAEGGKSKEAGAAIIVRYAT
DGKPHNGEFLDENGVPW"

CDS 2930861..2931220

/gene="adhR"
/locus_tag="EFAGFIKM_02484"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O06008"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator AdhR"
/db_xref="COG:COG0789"
/translation="MLTIGEVAKKVEISIGAIRFYERKGLLKPAARNEQNNRLYLEDD
LNWLVIKCLRETGMSVEDIKKYDQVNEGTLKERSKLIEDQKQKLLNDIEEKKAQ
LVHLDNKLERYRGENY"

CDS complement(2931403..2931984)

/locus_tag="EFAGFIKM_02485"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MYQPKQADELIIDCKDIYLRERYIEDLEKLQEITWQPEVYEFLP
GWNATIEERALWLTEYEIPENQRFKQAVMAGGDIGELCLRMAIVLKENDEFIWWCCSG
IKDELPAPNREIMYGISKHFRNRGYTTQAVNGMTEYLFEHTNVEVLNAIALTTNQASN
KVIQKCNFERLNLIEIEDEPYNHYQLCKGEDHF"

CDS complement(2932030..2932605)

/locus_tag="EFAGFIKM_02486"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MREIDYSQYFWQDDKIRLRALREEDWKDHYYNRFDTPARRLLEC
AVELPPTHVEAKSFTENFSDFLAKGRIMFTIVNMDGENVGGVNLNSIDERNGTFSIG
IQIDRDHRGKGYGTRAVRILLKYAFFERRLNKFNDVLEGNEPSAAMMRKLGCIQEGV
RRQVIYTDGKYQDMILFGLTKDEFIEKEGLV"

CDS complement(2932773..2933072)

/locus_tag="EFAGFIKM_02487"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKDKFLREERQEYTDVSTVESQRNDITLEEFPEGPYGSSLLSES
LGKSSPWRVDQRSABRFDYENHELHEGDVRDYPGQDVFDVTPDNVSKPQYTEES"

CDS complement(2933232..2934995)

/gene="ecfT_1"
/locus_tag="EFAGFIKM_02488"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01461"
/codon_start=1
/transl_table=11
/product="Energy-coupling factor transporter transmembrane
protein EcfT"
/translation="MEIELTNIRIEASDLSKRALLEDVSVQLNSEEITLLLGCTGSGK
TLLQTLAGLRPPDAGSITLDGTAFWKEGKVPQSILLQMGLLFQFPEQQLFARSIQRE
FTYSLRPYRLLKQQQEITKALNQWDPPVSSELDRRFHLDRSPFALSGGEKRRRLGLA
LGSVTNPHWLLLDPSAGLEAQSVGLLLDVLEQHRLAGGGGVVATHDLDTFLPCADRV
LLLQEGRLIADLTPRELHKRPELLEQTGIGLPPSMRLAQQLRAAGLELPLTAMTPEEM
AESIVQSTSFEVGIQNGSKEASGTITMEVKS DVMKYEKEALMRSSFEAEDDPKLLPNT
LTHSGGLYGVM DPRLKWILYILLVTAAMLQQRWLGLTLVLPVLAALAVLPRQTLAGC
MKLMKPLLFFFIISTALSGTTLSTEGGGLHFGFSLGQAEGTLLNVYRLFIVTLASLWF
SLTPYGRMVEGLNWWVLGIGKKIRLPVASFALAVSLIFRFIPMIWSEWQRFSLIVRAR
GKAALRPNTVRIRDLGPMVIPLLMALFQRAEDMTIAMEMRKVREHSM LGGRSSLLVWS"

KRDTWISMAGLIVFVLLIWIR"

CDS complement(2934980..2935834)

/gene="ecfA1_1"

/locus_tag="EFAGFIKM_02489"

/EC_number="7.-.-."

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q03PY5"

/codon_start=1

/transl_table=11

/product="Energy-coupling factor transporter ATP-binding
protein EcfA1"

/db_xref="COG:COG1122"

/translation="MQGNLPIITLEDVRVHYASEGSQVRKALDGVSLTLHQGEWISIV
GANGSGKSTLAGVLIGFIPLSGGVRDISDELTVRGVLQQPDAQVLGDTIEEEHFALS
PLMDSVEEQLEHRQDALHTVGLQYPPEKAWSQLSGGQKQLLNIAVALAAKPDILILDE
PTAMLDPGARDRIEAIQKITQRGTTVIWITHHLEEATLCDRIIAMERGRCVYNGMPE
SFFYETDLNEKATWENVQLSPCERLGLDPPFTVKTALLLKQKGMMPPEAMPLRPEQLAK
EVARWRSN"

CDS 2935947..2936537

/gene="bioY_1"

/locus_tag="EFAGFIKM_02490"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A2RMJ9"

/codon_start=1

/transl_table=11

/product="Biotin transporter BioY"

/db_xref="COG:COG1268"

/translation="MKLSLRGIVFSALMAAILVLFGYISIPIGFSPVPITLQTLAVML
AGGLLGPLYGFLSVTMVVLLTALGFPLLHGTGGLAVLLGPTGGYVMMWPFSALLIGLL
LARINIKGVTGFILAFVVFELFGSLLVYVSGVPWLAYAYKMDLPEAMIQGFYPYIIGD
LIKAVFAAIIAPVRMVFPQPRLTGNIHSTVIKADS"

CDS complement(2936683..2938152)

/gene="expZ_2"
/locus_tag="EFAGFIKM_02491"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39115"
/codon_start=1
/transl_table=11
/product="Nucleotide-binding protein ExpZ"
/db_xref="COG:COG0488"
/translation="MEKICFELEQVEMTYMDKVILNIERLAVHQLDRIGVVGGNGQGK
STLLKLIAGQIQPIAGKVKRFAEFGYLEQVEPPLPNENLEVDGALLSKLAIPQHDQAW
SGGEQTRLKLAQMFTHYHEVLLLDEPTTHLDQEGITFLLELRYYYGALVLISHDRSV
LDELVTIWEIHQGEVRVYSGNYSYDQAQKRLEREQQNQAHEQFSKEKRRLELAAREK
MKKA EKITQAGSMSKKESKAKTNRMVETKSKGTSQKAVHRAAKAIEQRMQQLHEVKAV
QEDRPMIFRQPKTLELHNRFPIMADRLTLEVEGNVLLEDVSFQVPLKQKIAITGANGS
GKSTLLNHVFRAGDHITMSPKAKLGYFQQMSYRFTTKETVLQFLKNRSQHEESELRSA
LHAMQFSGNDLLKNVGTLSGGEAIRLQLCHLFLGQYNILLDEPTNFLDMHALEALER
FIKAYEGTILYVSHDQRFIENTADQKFQITERQLIQVNI"

CDS complement(2938643..2940532)

/gene="bglF_9"
/locus_tag="EFAGFIKM_02492"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P08722"
/codon_start=1
/transl_table=11
/product="PTS system beta-glucoside-specific EIIBC
component"
/db_xref="COG:COG1263"
/translation="MSQEKLAK EIVELVGGEKNVESLVHCATRLRFVLKDDAKADKAK
LEKTEGIIAVKENGQQFQVVVG NKVPEVYSAIGQISNILDSSDKEKPRKAAKGLGGI
IDISSIFAPLLGVMAGAGILKGLLLIASNIGWLETTETTYTILYAAADSLFYFLPLL
LAVTTARKFQGNMFVAMTIAGALIYPSIVTLKSEGTPTDFFGIPVILMNYSSTVPII
LAVIVMSKLEKFFNKTLHDSVKNFVTPFLLVIMVPLTLLVFGPFGVYVGN GIAAGLV

AAFGSPLLAGAVMGASWQLLVIFGIHWGLIPVFINNVAVYGQDGVKPAATASIFAQT
GAAFGVMLKTKNKKLKTLAGSSTLTALFGITEPAIYGVTLPLKRPFIAGVIGGAVGGA
IIGQAGTLAFASGAPGLLTLPIFYGPGGQGFPGLILGIVVSFVVSALTYIMGFKDPV
EEEIKTESTTSDQQSVRATNASDEIVFSPMEGTIVELSEVPDPAFASGAMGKGIAIEP
TVGRVVAPFDGTVTVAFKKKHALAVVSDTGAEILVHVGVDTVKLDGQHFVSHIKEGDR
VQAGDLLLEFDIAQIKAAGYHTVTPIIVTNSANYEEVIPQATGQVHSQEALLKLSSGN
DQEQK"

CDS complement(2940744..2941670)

/gene="licT_6"

/locus_tag="EFAGFIKM_02493"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39805"

/codon_start=1

/transl_table=11

/product="Transcription antiterminator LicT"

/db_xref="COG:COG3711"

/translation="MSCLFFDASGFFCMPKRRRCITAKRVERDGGIEVKIAKVNNNVI
SIYQADGAELVVMGRGIAFKKKPGDKVDETRIQQVFALKNKQTSDFKMLLREVPME
LIEIVEEIIITYARDHLGRKLNENIYVSLTDHINFAIERYREGVEIKNALIWEIKQLYKP
EFGGLGLRTLEQINTRMNIELPPDEAAYIALHIVNAEMNEEVITTMNITKFIQQIINIA
KYHFKMEFDEDSLSYFRFITHLKFFSQRVLSGTHYDNNYDHFYDMIKEKHPDAAACAE
KIELFVKKEYNHELTNEEKLYLTVHIERVVNR"

CDS complement(2942000..2943442)

/gene="bglH_10"

/locus_tag="EFAGFIKM_02494"

/EC_number="3.2.1.86"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40740"

/codon_start=1

/transl_table=11

/product="Aryl-phospho-beta-D-glucosidase BglH"

/db_xref="COG:COG2723"

/translation="MTNFKFPKDFLWGGAIANQAEGAYLEDGKGLSIVDLLPTGENR
RSIMKGNVPAFTPLATEFYPSHEAIDFYHRYPEDIALFAEMGFKALRVSIWARIFPT
GEDAQNEAGLQFYDNLFDPELLKNGIEPVVTLAHFDVPVHLIEKYGSWRSRELVTLFE
TYATTVFTRYKDKVKYWMTFNEINMLLHLPFLGAGLAFNEGDNIKEIQYQAAHHQLVA
SALAVKACHEIIPGAMIGCMLAAGSFYPYTCNPEDVFQGMKEDRESYFFIDVQSRGEY
PGYAKRFFKDHELNIVMQPGDAEILKNHTVDYIGFSYSSRTTSTDPEVIKNMTSGNV
FGSVANPYLAKSEWGWITDPKGFRITANQLHTRYQKPLFVVENGFANDVVTPEGEVD
DAYRIDYLKRHVAEMGEAIQDGVNIIGYTSWGPIDIVSASSGEMRKRYGYIYVDRNNE
GQGELTRLKKKSFWEYKNVIESNGTNLGEE"

CDS complement(2943683..2944513)

/locus_tag="EFAGFIKM_02495"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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CDS 2944774..2946501

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CDS 2946633..2947532

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/inference="ab initio prediction:Prodigal:002006"

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CDS complement(2947719..2949701)

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CDS complement(2949728..2951203)

/gene="scrB"

/locus_tag="EFAGFIKM_02499"

/EC_number="3.2.1.26"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P13394"

/codon_start=1

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CDS complement(2951351..2952334)

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/locus_tag="EFAGFIKM_02500"

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/inference="similar to AA sequence:UniProtKB:P46828"

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AGYEMGRYVVEQGHRKIVYMGVSEKDRAVGIYRKQGFQRAIAECGGCEVKYYETSFKM
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CDS complement(2952576..2954249)

/gene="rnjA_1"
/locus_tag="EFAGFIKM_02501"
/EC_number="3.1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q45493"
/codon_start=1
/transl_table=11
/product="Ribonuclease J1"
/db_xref="COG:COG0595"

/translation="MNLAHNKLYIAALGGVNEIGKNMYFIQYHQDIIVIDCGSKFPDE
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TGDFKFDMSPVHGPFPDLHRMAEIGKQGVHILLSESTNAERPGFTPSEVVGDHILDA
FIRAKQKVFI STFASNVSRVQQIVNAAFETGRKLTLLGRSMVNVVSVASELGYLQVPD
GLLIEAIDSDQFPPEQVVVLCTGSQGEAMAALSRLASGKHPHVRINAGDTVIIAAGAI
PGNERNLAHVIDNLYVLGARVIYGSSGAAGMHVSGHGSQEELKLMLTLMKPDYLIPIH
GEFRMLYQHRLLAESVGIERDHVFIVNNGDMVQYKDGIASLGPKIASGNSLVDGLIMG
DIGNIVLRDRRQLSSDGMLVIVTTLSKTEKQMVTSPEIISRGFVFKDSEEFMHEIHE
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CDS complement(2954408..2955679)

/gene="rhaA"
/locus_tag="EFAGFIKM_02502"
/EC_number="5.3.1.14"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9KCL9"

/codon_start=1
/transl_table=11
/product="L-rhamnose isomerase"
/db_xref="COG:COG4806"
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EQVELDQIEPKHYENWVKWAKEQGLGLDFNPTCFSHEKSSDGFTLSHPDPEIRKFWID
HCKASRRIGAYFGEQLGQTCVTNVWVPDGFKNPVDRLTPRKRLKESLDEVFGEPLNP
EHNLDAVESKLFGLGSEAYVVGSHFYMGYGLQNDTLICLDAGHFHPTEVISNKLSSL
SLFTSGILLHVSRRPMRWSDSHVIMDDELLEIARELVRHDLLATTHIGLDFFDASINR
VAAWVVGTRNTIKALLRAMLEPVDALKQAELEGDYTLRLALTEEFKSYFPGAIWDYYC
AQQGVPVREKWITDIKTYEQDVLLQRDKSLV"

CDS complement(2955699..2957768)

/gene="hcaB_2"
/locus_tag="EFAGFIKM_02503"
/EC_number="1.3.1.87"
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acid-dihydrodiol dehydrogenase"
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VPYVRPGFTLSKMIAESVFSNPNAELVLMKHLVWGETSEECYAQTIKIINEAEAF
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GQFVSLSANESYNVEYWPLELYKLSLAPAETFSRKVAFITGGAGGIGSETARRLVSE
GAHVVLADLNLEGAQKVAQEINDQYGANRAYALKMDVTDEEAVQSAYADVAVQYGGVD
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CDS complement(2957948..2958928)

/locus_tag="EFAGFIKM_02504"

/EC_number="3.2.1.78"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:G1K3N4"

/codon_start=1

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/product="Mannan endo-1,4-beta-mannosidase"

/translation="MVNLKKCTIFTVIAALMFMVLGSAAPKASAATGFYVSGNKLYDS

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SIHMYEYAGKDAATVKANMENVLNKGLALIIGEGGYHTNGDVDEYAIMRYGQEKGVG

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CDS complement(2959291..2961630)

/locus_tag="EFAGFIKM_02505"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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IDYEGDVAAAHIHHQMLTDHIHYGHSWMLGLKQSRHLLADHALRLSITPTRKGTIESY
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CDS complement(2961682..2965020)

/locus_tag="EFAGFIKM_02506"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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KVTGQYVTALTELAKQNLEKQQPELALELLQKALVYPENLGEGKLEGAGDNPVYFYL

CAYQQLKKNQAAEENFHRASIGLNEPASAMFYNDQPPESIYYQGLAWQKLG NVKEANR

RFNKLIDYAERHMH DHIRMDYFAVSLPDLFLVDDDLNQRNEEHCRYMRALGLLGLGRT

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CDS complement(2965193..2965903)

/gene="treR"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39796"
/codon_start=1
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/product="HTH-type transcriptional regulator TreR"
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CDS complement(2966031..2973533)

/locus_tag="EFAGFIKM_02508"
/inference="ab initio prediction:Prodigal:002006"
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QVQIIPYNTAGSGSPMTVAPFYTLPHVDSLEMKIYPETDHANLEWDFPYVNETFVLL
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/inference="ab initio prediction:Prodigal:002006"
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VHITSDESVTWNQIHEIIAGVLGVKLHAVHVPSEFLAACSDQDLRGGLLGDKANTVVF
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KIRDEK"

CDS complement(2974807..2975232)

/locus_tag="EFAGFIKM_02510"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MKSWFGKTWPWLTGLTVVLLGSFLVYFMGKDVSPGSGSAVTA
QADTPEDLKGYEVIDVDVSNDGFGPDVIEVKAGVPTKINFILTRSVTHVKS VGSQKLG
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CDS complement(2975629..2976582)

/locus_tag="EFAGFIKM_02511"
/inference="ab initio prediction:Prodigal:002006"
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VLHEHVSGLQWFGVIIVLIGVALPELYKLRMRRSRNTPIYS"

CDS complement(2976947..2979166)

/gene="srmB"

/locus_tag="EFAGFIKM_02512"

/EC_number="3.6.4.13"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00967"

/codon_start=1

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/translation="MSDNPFYRLAPFVQEFYKKRWESLRPAQIEACNICFHTPHHML

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VTILEMRRVAARRQERDVFHVHHGSISAMLREETEAALRTGSGPAVAAATVTLELGID

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GSEEIGSITVPPPGYCFSLAGKLWKVEEVDHKHKAVYVKSAGKVDTLWLGAGGDIH

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VGSKSFRTLRLMKHNLSKKLALRSVPMEPYFVVSQKVDERTLLAEIMSECRAED

ASALLAEDEAPYLGKYDEFVAQPLIREAFVDGLDLEGLKAGLQQTLEWDSSSSNRT"

CDS complement(2979163..2980506)

/locus_tag="EFAGFIKM_02513"

/inference="ab initio prediction:Prodigal:002006"

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GLATYRELMTRLSTRTRPDGGALEPILQKWIAGLQQSTMQSQNLRPDDPALPLEVEKQ

IYAVTGEMQNLVHGFDFAKVLASYWNGYKLADDDRKQAALRWLRGEFATKTEAKKELA
VGVIIDDDNWYDYFKLWSEFTARIGYKGLLLFIDEAVNLYKITNSVSRQSNEYKLLTM
FNDTMQGKAEHLGIFVGGTPQFVEDERRGLYSYEALRSRLIDGRYAAKAYANYTGPI
KLAMLSHEEIMILLQKLQRQIHALHFGYSASLTDEQLVDFMQTAVNRLGADELLTTREV
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CDS complement(2980513..2982090)

/locus_tag="EFAGFIKM_02514"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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GILSSEKRFVEEAKQWAEMEGDVSPWVPFMSYWPTYGVMNEAQRKWYLFWRKEVRQGR

YPDTDLSYLHVHIYELINGIGWQNPQDGYDQLKQLWVNYRERLPQLNIYMQEWMVDYV

LVHQMEMSLSEVMGLSGGYLPAEMLDRELQRILQDKVSDISLNMLQRYDYDITLSKF

YRDGGKEVMDQYIPRVMALVDSYLERTQVGLLPECDPNDERTMERTLFRKAVYDEWI

YGRSVSFRYMPIGEHAEFVQMVTRIYRCTENKLRELLGFRGRLRGQTLEPELANLIER

YLDKAYAIEQAESVEQPMIRIDTEKLASLQSEYVRMALTIEDDHPSEVKDEEVNNA

NVTSNPFVDLEARDEITPTEGSMESEPSAEEIAAGAQVESIRLQWDESAEADLEEELWL

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CDS complement(2982506..2983096)

/locus_tag="EFAGFIKM_02515"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTATTIMERLKSETAHYHRQVEQNPYAKAIMNQVTIEEYRXYL

EKFYGFLLKPLEDQAVLLPFWESTELDIEIRGKAGLLEKDLRNLGASEEEISQFPLCEE

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CDS 2983442..2984239

/locus_tag="EFAGFIKM_02516"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDLTVQEVVLHLSDNIELPENTVDQLIMGSLDRKVTGIIAFMP
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RVAGNAEIVCRRAAVLVGFGRNGHV TIPLIQNEQLDLIAGEGFEWETPEYIRDAMQQ
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CDS 2984760..2985185

/locus_tag="EFAGFIKM_02517"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MRGIIFALLGGACITLQGVANTRISTDMGTWQAATITQLTGFI
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CDS 2985231..2985929

/gene="yeiL_1"
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/inference="similar to AA sequence:UniProtKB:P0A9E9"
/codon_start=1
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PVVMLRIHYQWLAELASDYAPLLKFL LKIISHKFYIDSNFSNFMYPVEVRLVSYLL
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RAGLREIAGHNIYE"

CDS 2985944..2986432

/locus_tag="EFAGFIKM_02519"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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CDS complement(2986519..2987235)

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/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P67182"

/codon_start=1

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/product="putative transcriptional regulatory protein"

/translation="MGRKWNNIKEKKASKDANTSRVYAKFGVEIYVAAKKGEPDPEAN

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IDALEDLEDVQQVYHNVEFV"

CDS complement(2987515..2989236)

/gene="cysI"

/locus_tag="EFAGFIKM_02521"

/EC_number="1.8.1.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32213"

/codon_start=1

/transl_table=11

/product="Sulfite reductase [NADPH] hemoprotein

beta-component"

/db_xref="COG:COG0155"

/translation="MVYNNLLNPQRTNSDVEDIKIKSDYLRGSLTETLADRITGAIBE

DDNRLMKHHGSYMQDDRDLRNERHHSKLEPAYQFMLRVRASGGIVTPEQWLMMDRVAH

KYANETIRLTTRQSFQLHGVLKWDLKNTIREVNDSLLSTLAACGDVNRNVMCNPNPQ

SDVHAEVYEWACQVSNHLDPRTRAYHELWLDGEKVIDSQDSDEEVEPIYGKVYLPRKF

KIGIAVPPSNDVDVYSQDLGFIAIVENGKLQGFNVSVGGGMGMSHGDAKTYPQVSKVI

GFCTPEQMIDVAEKTVMIQRDYGDRAVRKHARFKYTLDDRGVEWFVEELTTRLGWKLD

AARPYHFETNGDRYGWVGNNGRWHYTLFIQNGRVKDVDGYPLMTGLREIAKVHTGDF

RLTANQNLIIGNISSQKKKKIEALIQYNLTDGAHYSALRRSSMACVAFPTCGLAMAE

SERYLPSLIDKLEPVLDEAGLRDKEIVIRMTGCPNGCARPMLAEISFIGKAPGKYNNY

LGGSTGHRLNKLYKENIGETEILDTLTPMVNQYAKERNEGEHFGDFVIRAGYVPEVL

DGRQFHA"

CDS complement(2989290..2991125)

/gene="cysJ"

/locus_tag="EFAGFIKM_02522"

/EC_number="1.8.1.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32214"

/codon_start=1

/transl_table=11

/product="Sulfite reductase [NADPH] flavoprotein

alpha-component"

/db_xref="COG:COG0369"

/translation="MELQVTNSPFNQEQVELLNRLIPTLTGQRTWLSGYIAAIQASA

TIAAPANLVQAAPTTGIAPVSAPPVSREVTVLFGSQTGNSSGLSKKLAKKLEEQGLQV

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ALGDTSEFFCQTGKDFDKRLQELGGTALVPRVDCDVFDEAAAEWMNEVLASLNSTS

AAASTVTTEAVTAAVSGGESEYDRTPFKAEVLENLNLNNGRGSRETRHIELSLEGSS

LDYEPGDSLGVFPENHPRLVEELIAAMGWNADERVTVNKNGDQASVHEALLRYFEITA

VTKPVVEQLAKLNPGSGLTALLADDSEFRTVMNSCDLLDLVQDYNLKGIPAGEFVATL

RKIPARLYSIASSSKSFPDEVHLLTVRSVRYEARGRERYGVCSVHLAERIEAGDTLPVY

IQHNPNFKLPENPDTPIMVPGTGVAPFRSFLGEREETGAEGKTWLFYGDQHFATDF
LYQTEWQRWLKDGVLTKMDVAFSRDTEQKVYVQHRMLEHSKELYQWLQEGASLYICGD
EKKMAHDVHAALTTILEQEGGLSSEQASEYLTRLQQEKRYQRDVY"

CDS complement(2991344..2991733)

/gene="ytcD_1"

/locus_tag="EFAGFIKM_02523"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34533"

/codon_start=1

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/product="putative HTH-type transcriptional regulator

YtcD"

/db_xref="COG:COG1733"

/translation="MEQEMKKYESGVQAMLELVGGKWRILILHQLISGKKRTSELRRRA

IPGITQKVLTTQQLRELEKNEIIHRIIHPQIPPKVEYELTEYGLTLQDIIDRICLWGGN

HLDRVYGDKSRVLGDHFSDYIPLSTST"

CDS 2991909..2992469

/gene="azoR"

/locus_tag="EFAGFIKM_02524"

/EC_number="1.7.1.17"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01216"

/codon_start=1

/transl_table=11

/product="FMN-dependent NADH-azoreductase"

/translation="MKVKLVVTHPRQDSLTFVAMNRFIEGMQENSHEIDILDLYHDGF

DPLYGVEDERDWQNPDQKHAPVIRKELDRVLAADAIVFVFIWWYNVPSMLKAYLDKV

WNMGLLNKANSKKALWIALAGGTEASFHKYDYNNMISNYLNNGIAGYARMQESRVEFL

YETISESKEHIESLLEQAYQIGKHYN"

CDS complement(2992661..2997886)

/locus_tag="EFAGFIKM_02525"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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YTGAGQGYPGILPRFQDKNNFYFQMQVPNNKLVFSKRVNGTDTALKTVDYAFKDTW
YTLKMVLSGTTIRGYIAENGSDRLVFDLVDTTYGSGTVGIRNKWQSVHADDVIIAEQP
PGNDIQLSIAEQTASSVSLQWSEIIGASAYRLYRSSTPEGGYSLVTNTGTLGHTDEGL
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DKSTGYRVVRAEAGSDQYEQIYEGKGLTFTDNALEPGNSYSYRVTAAYNAAGESAFTVA
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TFNDSGLMMGTGYFYIIQATVDGIVSPASAPLGVAARTSITPGQLWPDLDGKPIDAH
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NYGKARAGYAISDSPTGPFVYQKSYRMDRAPEGEKDFPSEGMARDMTLFKDDDGTG
YLIYSSEENLTLYISKLNEDYSDVTGWHKEGRTDDKGNPVRDSTYQAEYGVYVRVFP
GGQREAPAMFKYQGKYILTSGASGWAPNENKVTVADNIFGPWSTQTNPFVRTLPSPD
DPSKAFGTQTTSVIPVDPEKGKFIYVGDWNGGNFSNDAAKYVFLPIEFGIGSDIAIK
WYNSWTPDLLNSMGKVDIADPLPEAVALGKVPSLPTTLNVRDGGALVSTPAVWTIDNR
AMTAEDFAKPGPLTLQVTTPEYNNKKQAVRVNVIPENAIYFVNSSGGYETADYSLMGAY
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VPPSKETTVTLEITRTSDDSRALTIPLTVKVPASVPSPGGTDPGSGGNSGGNSGGN
PGNGSGSSSNGGQSGNGNPSAENVVPQPKPEKDRSVLELQGQSDQKGVVQSNVDVSTI
KDAFKVAPSTDAGQRLVELRLKPVLGATAYQLSLPASALIDRGESHVFNIDTELGMLE
LPATLLTKDIVGDGIASIRLVRTELPKTVADQLGTKYGVQLELQLDGGQPWPSDSLIL
RLPFQSSQNAPQDRIVAFAIGANGVATPLPQSYDQNSGQLVFSVTSLTGNYAVVPVE
QIFTDLAEVQWAKKAMEALAVRGVIDAEASGDSTQLHPKEEMTRGQYMQWLMTALGLN
ASSGNTFSDVNENAPYYEAVTAARSLGITSGAGDGSFLPESTITRQEMMTLTVRALAT

AGLVDSEKAGTDNLTRFRDASEIRSYARDSVALLVDLGIAHGYNGEVKPLAEATRAES

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CDS complement(2998312..2999868)

/gene="ybiT_2"

/locus_tag="EFAGFIKM_02526"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A9U3"

/codon_start=1

/transl_table=11

/product="putative ABC transporter ATP-binding protein

YbiT"

/db_xref="COG:COG0488"

/translation="MSILNVEKLSHGFGDRAIFNDVSFRLKGEHIGLIGANGEGKST

FMNIITGKLQPDEGKVEWSKRMVGYLDQHAVLNKGQSIRDVLRGAFQYLFDMEQEMN

DMYGKMGDVTPEELEQLLEDVGTIQDTLTNQDFYMIDAKVDETARGLGLTDIGLDKDV

NDLSGGQRTKVLLAKLLLEKPDILLDEPTNYLDELHIEWLKRYLQEYENAFILISHD

IPFLNSVINLIYHMENQNLTRYVGDIYHFQEVHEMRKQQLESAYKRQQEIADLKDFV

ARNKASVATRNAMMSRQKKLDKMDVIEIAKEKPKPQFNFRDARTPGKLIFETKGLVIG

YNEPLSRPLDLRMERGQKIALVGANGIGKTTLMRSILGEIQALEGTVQRGEHLEIGYF

QQEMKDANYNTCIEEIWQEFPSYTQFEVRAALAKCGLTTKHIESKVAVLSGGEKAKVR

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NCESWTTKV"

CDS 3000066..3000539

/locus_tag="EFAGFIKM_02527"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIEVKQSKLGDGGELNRGVFATVDIAKGTLIHQAPVVPYPNEDH

EHVEKTILEDYVFEYGANHTAILLGYGSLINHSYEPNATYDINFDNHTFDYAYTDIK

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CDS complement(3000426..3000665)

/locus_tag="EFAGFIKM_02528"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MFFVFKLWTVKSLQLLISSFTGVSEFFSHIQQSACELHLGLTLI
TRVRVQGLGFLFFNLIIGLIELQHTLLVIVQEP"

CDS complement(3000770..3001378)

/locus_tag="EFAGFIKM_02529"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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HVGAVVTDITYSDWSLSPVPEWGGRIVTIRASYSNEAVVIRARTDEHPWRTIRVARFAY
PTNKHAGPFLCSPKRAGFEVAFTKWRSTTPDQDLHTDPPITD"

CDS complement(3001436..3002782)

/gene="gor"
/locus_tag="EFAGFIKM_02530"
/EC_number="1.8.1.7"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P06715"
/codon_start=1
/transl_table=11
/product="Glutathione reductase"
/db_xref="COG:COG1249"
/translation="MTQETYDLIAIGTGSAASSVITRCAEAGWRVAVIDEREFGGTCA
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KQAGMDTFHGKASFVDENHIQVGEEVLHGKHILIATGARPAPLEIEGSEHLIYSDDFL
VLEQLPDRLVLVGGGYIAFEFAHIAARAGTEVHILHRSEQPLKSFDAELVESLLQKSK
EIGHVHLNAEVKSIRQEGNAYVVHGTRNGADHQWQCGIVVHGAGRVPNV DGLELEKA

NVSYSKKGITVNEYLQSESNPRVYAAGDVTDTKGLPLTLAGQESRAVSFNLLEGNQH
KPNYKVMPSIVFTVPALGAVGMSTEQAKKGDGYEVQVNDMSKWYTYKRTHEKFAMAKVV
IDKSTGRILGAHVLGSKTEELINLFAMAIQFNLSIDQLNTMNFAYPTAASDLGSLI"

CDS complement(3002833..3004347)

/locus_tag="EFAGFIKM_02531"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSRFTEVFSEKRGQLLSTLLEHIQISFIALFFAVLIAIPLGIYL

TRKPKVAEPIIGVTAVLQTIPTSLALLGLLIPLFGIGTLPAILLVVYALLPVLRNTYT

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AGGLGALILLGIDRNDTALIILGAIPAALLAILFDVLLRQFQRLSFKKTLVTLGSLAI

IAILVITIPFVARGGQKDLVISGKLGAEPEILINMYKLLIEKDTDLTVELKPGLGKTP

FLFNALNSGDIDIYPEFTGTASEFMKETAVSTDRTVEYEQARDGMLSQFNMVLLNPM

DYNNTYTLAVPQSIADQYNLKTISDLKPVEQQMKAGFTLEFSDREDGYLGIQKKYGIE

FPNVATMEPKLRYGALQRGDINLVDAYSTDSELRQYELVLEDDQELFPPYQGAPMLR

QETADQYPQLVEVLNQLAGKITDEEMRQMNYDVNVEGANPEQVAREYLKQAGLL"

CDS complement(3004340..3005314)

/gene="opuCA"

/locus_tag="EFAGFIKM_02532"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34992"

/codon_start=1

/transl_table=11

/product="Glycine betaine/carnitine/choline transport

ATP-binding protein OpuCA"

/db_xref="COG:COG1125"

/translation="MIQFENVSKQYPDGTTALRQVNLNINKGELFVMIGPSGCGKTTM

LKMINRLIERTDGTVRINERPIDEYNIHELWRNIGYVLQQIALFPHMTIAENIAVVPE

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DEPFSAIDPMSREKLQDDILDIQRQMKTIVFVTHDIQEAMKLGDRICIMKDGQVLQV

GTPEELIRQPANDFVREFVGS PNTDTSSQSDFDLESIMLPISPGHVPKSAKTAVPVS

TLTELVDIMAFHGHLLVERN RQIIGEISRADLMKYWSGQLQERGE EHE"

CDS complement(3005537..3006397)

/gene="azoB"

/locus_tag="EFAGFIKM_02533"

/EC_number="1.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8KU07"

/codon_start=1

/transl_table=11

/product="NAD(P)H azoreductase"

/translation="MINDKPLTLIIGANGKTGSRVAAILQKHHYPVRLAGRTKPSHSG

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LGSASIDEEGPFIGKVHQYLKAHAPEWAVLQPSYFMENFTEGPHRETTKQLGKIYSAT

GDGKIGFVSADDIAAVAFHALTDVVPHNTEHIITGPETLSYGQVADVLSRVLGQSIQH

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FIQNHMEVWK"

CDS complement(3006387..3006833)

/gene="yesE"

/locus_tag="EFAGFIKM_02534"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31511"

/codon_start=1

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/product="putative protein YesE"

/db_xref="COG:COG3631"

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FPYAPAGYPQKLEGKAAITNHLHNLGMI EIQQFSEPVILADSTKQQFVAEFTCKGRS

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CDS complement(3006966..3007550)

/gene="comR_5"

/locus_tag="EFAGFIKM_02535"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P75952"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional repressor ComR"
/translation="MGRAKEFDTETVLRKATSVFGAYGYEGTSLSLSELGIARQSL
YDTYGTKHDLFVSALKFYIQKTEAGIRLLNECTSVRQGVTELFNEAVNVLTDTERRN
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FLNYSRLSLTFTAKSGASAEALRDFVQMTLRALD"

CDS 3007718..3008080

/locus_tag="EFAGFIKM_02536"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MYIQITDLAVKRLTESLNDQPGYFKVIYDLEGCGCNGVIAIIIV
DELAALDAQIETNLFPPFYVDPKQQLNLEQHMKLDTEENYPSFKLSSDSGVLSANVRVR
DTRAVTAGSSGGSDACML"

CDS 3008541..3009314

/gene="yodJ"
/locus_tag="EFAGFIKM_02537"
/EC_number="3.4.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34866"
/codon_start=1
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/product="Putative carboxypeptidase YodJ"
/db_xref="COG:COG1876"
/translation="MKSFTRKSIISTILVGSVVAGSAFTTFPITSSLNPVASAASSSF
TQFLHDNAPGRTIKTIKNVATVTNVSSTVVLVNKKRNLPSTYAPQDLVVPNIPFSFSG
SSPKKQMRKVAATAIEKLFAAAKKDGIDIKAVSGYRSYATQKSIFDRNASIKGEAVAN
KTSARPGQSEHQTGLAMDISSASAGYDLQQSFGNTKEGKWLKANAHKYGFIIRYGKDQ

EKLTGYSYEPWHVRYVGVYIAGEITNQKLTLEQYLERAK"

CDS complement(3009449..3009688)

/locus_tag="EFAGFIKM_02538"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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ALYLCHNAILAGVGSWAGTEGLKRLPLVFRKIVGT"

CDS 3009819..3010451

/gene="mhqN"

/locus_tag="EFAGFIKM_02539"

/EC_number="1.-.-."

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P96692"

/codon_start=1

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/product="Putative NAD(P)H nitroreductase MhqN"

/db_xref="COG:COG0778"

/translation="MSELENLVKNRRSAVIFEEGIEISDSELQEMFALNKFAPSAFNL

QHTHYLVIKDEEQKEKVYEASQQYKVKTASAVIVVLGDVNAHHHIRTINEGLNLGAL

TPFQYEQESQSVTEFYESRGRFFQREDAIRNASLSAMQLMLIAQDRGWDTCPMIGFDS

EELQRSLEIPNHYPVVMLITIGKKSEAKQRPRGYRKPINEYVSFNKMHAE"

CDS complement(3010683..3011843)

/locus_tag="EFAGFIKM_02540"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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ISNLDGIEYFRGLQELDCAYNQLTGLDLAQNHKLRLRCRENQLLTDLRSNSELQVL

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QLRRRLDCANNYMLELDVTGCPNLIELRCNHNHIKQLDFRSNMVLESVRCFNNHISKLD
IRHNVQLRELYCSENKLTELDYSANPKLERLQYADNLMFESNHEVPGMGLFQYDVSMS
NYQMSLLIQDKELIVTAQVSTKTEMEALSPYMEETWKRWDMLGEQALKTIAVAHPDED
INALILADAEFQGDQYFRLGYDAGDTPAGRLYIAEFDDEFHMLDTLIYETY"

CDS 3012010..3012456

/gene="sbmC"

/locus_tag="EFAGFIKM_02541"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01896"

/codon_start=1

/transl_table=11

/product="DNA gyrase inhibitor"

/translation="MEMVIENLPSYRIAYVRQVGPYPANAQAMNTLKQWADKKQLLY

ESATLLGIPQDDLTTTPPEKCRYDACIVITESERLEDEFVEIGELSGGDYLICKVRHT

AEAIQQAWNVIIPHLQTNGFQMDNKPVIDDIVGNCLISIIARYVCL"

CDS complement(3012785..3014029)

/locus_tag="EFAGFIKM_02542"

/EC_number="3.4.11.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P24828"

/codon_start=1

/transl_table=11

/product="Aminopeptidase 2"

/translation="MSQFEQTFEKSLEQYAELVVKVGVNIQKGQDLLVTAPIETLEFT

RLIVQKAYAAGANYVQVDFDDDNITRSRFEHGSNDSFDYYPAWKADMMMEKFAEAGGAT

LTIKVPDPELYNGIDSDSVSRATKAAAHARRGYAKYTRNHEISWCLIKAPTKAWANKV

FADIPEEDRINVMWETIFKMNRVDGGDAVQNWREHLDTLNAMSDRLNQKNYKSLHYRA

PGTDLKIELVNNHIWGGGGGENQQGIYTVANMPTEEVFTMPKRSGVNGYVSSTMPLNL

NGQLVDQMRITFKDGQVVAFTAASGEEHLKNLFATDEGARYLGEVALVPHDSPISNLN

RIFYNTGIDENASCHLAVGSAYPFNMKDGTMSNEELLKHECNVSLTHVDFMIGSAEL

DIDGELQDGSIEPVFRKGNWAF"

CDS complement(3014271..3015863)

/gene="acsA_2"
/locus_tag="EFAGFIKM_02543"
/EC_number="6.2.1.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39062"
/codon_start=1
/transl_table=11
/product="Acetyl-coenzyme A synthetase"
/db_xref="COG:COG0365"
/translation="MNFEQWISPESYNLTSEMENHPSDRIALRWLSDQRELEEITYGD
LFKQANRLAGGLRELGLEKGDRLVLMVPRRIIAYVIYIACLKLGIAVIPSSSEMLRAKD
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MQNQPEEMAAVETHRDDTAILAYTSGTTGNPKGVBHSHGWGYAHLRIASSLWLDIQPS
DTVWATAAPGWQKWIWSPFLSVLGRGATGLVYNGSFQPKRYLELMQEHQINVLCCTPT
EYRLMAKADDLGHYDLSHLRSAVSAGEPLNQEVIEIFQRHFDLTIRDGYGQTESTLLI
GSLKDAPVRIGSMGQSITPGLIEIIDEEGQPVPAGEVGDIABHKEMPALFRSYYQDEG
RKEASQRGDYFVTGDRARKDEEGYFWFEGRSDDIISSGYTIGPFVEEALMKHASVK
ECAVVASPDEIRGNIVKAFVVLTDDSLASELMRELQHHVKEITAPYKYPRKIEFVTD
LPKTNSGKIRRIELREQEKRNG"

CDS complement(3016129..3017133)

/gene="gpr_3"
/locus_tag="EFAGFIKM_02544"
/EC_number="1.1.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q46851"
/codon_start=1
/transl_table=11
/product="L-glyceraldehyde 3-phosphate reductase"
/db_xref="COG:COG0667"
/translation="MPYTASEQRYDEMKYVRSGKSGIRLPQIALGLWQNFNGNRTLDV
QEEMILRAFDLGINHFDLANNYGPPPGSAEENFGVIYKKHLRPYRDELLISSKAGYHM
WNGPYGEWGSRKNIASLDQSLGRMGLDYVDIFYHHRPDPDTPLEETMTALDHIVRQG"

KALYVGLSNYNAEQTQEAVSILRRLGTPCLVHQPNYSM LN RWIEDGLQDVLDEQGVGS
IAFCPLGRGQLTNKYVDKIKEERANSTGNLKK EAYTDERIAKFDALQAVAERRGQTIS
QLALNWILRGNRVTSALIGASRVSQIEENVAAFQAPDLTTEELNEIESILDGMGNYPW
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CDS 3017335..3018180

/gene="araC_4"

/locus_tag="EFAGFIKM_02545"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A9E0"

/codon_start=1

/transl_table=11

/product="Arabinose operon regulatory protein"

/translation="MITYMFKNNHFQELQLLHYGTEACTPGHHFGPAMRDYYKIH YIL

NGKGTFEVGGKTYTLHKGQGFLIVPHSVVHYEADQDDPWEYSWVAFQGSN SSSFLQQA

CLSEHHPIFELGNEDDEMRSCLHRMINSRNT HKGWEISMTGLLYQFFSILIDQANSEH

LQPMPDYSKETYVTQVMDFIEMNYANAITVQSIAAHIGLQRSYLC SLFKDQMGSSIQS

YLVHYMRRAAELTDPGLTIGDIARSVGYTDQLLFSKMFKKVMGEAPTYRKHKTAP

SQLSC"

CDS complement(3018249..3018647)

/locus_tag="EFAGFIKM_02546"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A0P8"

/codon_start=1

/transl_table=11

/product="Alkaline shock protein 23"

/db_xref="COG:COG1302"

/translation="MSEIIEKQYNEPEYIAPQSVQMGTIHISNDVLSKIVGMAALSTA

GVSSMSVGLTEGIAKSISGKSLQKGIDVHV KDDQATIQLRINIYGNKMHEVCRELQH

NVQQAVEQLAGVMVDEIKVQVVGISM PETV"

CDS complement(3018676..3019755)

/gene="yhhT_1"

/locus_tag="EFAGFIKM_02547"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AGM0"

/codon_start=1

/transl_table=11

/product="Putative transport protein YhhT"

/db_xref="COG:COG0628"

/translation="MFKVNTFVRFSIALALILVNIYLLSRVSFIFQPLVTMITVITVP

MMLSVFFYYLLRPLVNYMEKKKINRTLSILLIYLVIAILGVFFIIGLWPSLREQLINL

VDNAPSLINSLSEQLRELEQNGAIQALFPEGSTPFSQITEYINKGFNFVTNYVSGFFS

LVSSFAILFTLPILLFYMLLQGEKFGRKLAHIAPKRFQNDREVVIEIDQALSGFIV

GRVLVNLALGVLMYIGFLIIGLPYALLLTAVIIMNFVPPFIGAIVSSVPVIMGLVVS

PSVAIWSLIIILVAQQIQDNLVAPYVFGKKLDIHPLTTIILVLGAGDLGGIILIII

PVYMIVKILLVRIYNMFFKDKWQNA"

CDS complement(3019791..3021248)

/gene="sasA_8"

/locus_tag="EFAGFIKM_02548"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"

/codon_start=1

/transl_table=11

/product="Adaptive-response sensory-kinase SasA"

/translation="MKRPWKAREKRLQTSLTDLFFLNFFLLLLVLIVYLMVSLDVV

DFRISDQVDPDLNVEAHVYVAELENFYSGGGSVSKGKDTEIQRLKDSGGWIEILDA

NRNVIRHVGDKQDAFTQYSEADLYDGLENRSDQEYYSITPLSTEGASAYVLLKIPRD

LVSVRINDNQLITNLKHPLSFYIMIGIGLVLLIFVYSYWARRIKKPLGILSSGLTQ

MIQGNYSTRMSSAEREFVQIGETFNMYADVIENTSAEKRYAEESKQRLIVDLSHDLK

TPITSIQGYAQUALVEGRGEDKDRQQRYLGYIYNKSVQVARMIQNMLELLKVDSPDFRM

HIQRREIGEFVREIMADTYGEIEQKQFVLHVLVPDEVIYARYDPELLSRVIQNLITNA

LSYNPIGTELRLVELIPLDTHVVIEVADTGVGIPQELWSTIFDPFVRGDEARTATGGTG

LGLSIARRNTEKMGGRLILSRRGRETTFVTIQIPN"

CDS complement(3021226..3021933)

/gene="phoP_2"
/locus_tag="EFAGFIKM_02549"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P13792"
/codon_start=1
/transl_table=11
/product="Alkaline phosphatase synthesis transcriptional
regulatory protein PhoP"
/db_xref="COG:COG0745"
/translation="MRYTVLIADDEPEIVELLQIYLEKDYTIKTAVNGAEALQCIRST
QIDLVLIDIMMPVMDGLQLIKQIRATYHMPVLFLSAKSQDHDKILGLGLGADDYIAKP
FNPLEIVARVEALLRRVNQFDATEIPEAKEQNLVLGDLTLDRSQCILFRSGNPVTLTS
TEYKIMELLLDQGRVFTRKKIYEAVWGDYYAHEDSTIMVHISNIREKIERDSRQPEY
LKTIRGLGYKIEAPMES"

CDS complement(3022168..3023613)

/gene="hpaH"
/locus_tag="EFAGFIKM_02550"
/EC_number="1.14.14.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A4IT51"
/codon_start=1
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/product="Anthranilate 3-monooxygenase oxygenase
component"
/db_xref="COG:COG2368"
/translation="MSITMSRGQAYIQRLNDERNVWLDGERIQVTGHQAFQGTLQTIE
GLFNLVDDPETRETVAYWDEQTGSYVHRSFLVPRSLPDVKSRADAFRLWADRTYGVMS
RLSDYARSRLTGWYATRHMTAHDPAFADKISDYFAQAKRKDAFLTIVQRDPQINRSL
PVGEDEDAMLRIVKRNTEGVVIRGAKMVATAAPYADDIIAYPVQRIPDHLPELAHMMVI
VAADSPGLHMMCRESFATKDTDKSHPLSAQYDEMDAVLFFDDVFVPWERVLLHNNPEA
VWQIRCNTASASLAYHQSVIRLHLSKLEFITAVTSSIAKEIGVDSFLNVQEQLGELISQ
MQTIEGLIAAEAQSKPDFTGNWLPEFKYIETARNLGNRYYPRAVEILKTIAAGGLMQ"

IPSGTFEMNEMSSMIGKYLGGVTMQAPQKIRLFQLAWELTGSPLGARHDLYERFYAG

DPVRNRANQYVQYDKERLLGKVEPWLRSLKD"

CDS complement(3023787..3025745)

/gene="yxdM_2"

/locus_tag="EFAGFIKM_02551"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42424"

/codon_start=1

/transl_table=11

/product="ABC transporter permease protein YxdM"

/translation="MNFRQFAINNVRNKRIYLAHFLSSTFSVMIFFTYALLLFHPDL

KAGLKGSSGTVTLLANQGFMAEIIIFISFLFLYSVGSFLKTRKKEFGIFLIIGMT

RKQMNRLLFMENMCIGLASIITGIGLGIIIFGKLILLICGSMLAVENSLRFYFPLKGIA

LTAGAFLLLFVVIAMSSSLLIRKGTLDLVKSEEKPKPEPKASRLALLSVLLIGGGY

AGVFTFWISFSFPLLLASVVVVIAGTYFLTQLSVYIIRALKRNPRLFFRKTNLLFL

SELTYRMKDNAIMFFMVSIISASSFTGIGTMLAIADPGLSSMSNPYAFSYMNSWDTPD

SDRHIRQIEETLIDHQVPYVKGSYAPIGENNNGKIIKLSDYNRLAKALGYEERTLKQI

DESFMTPSNLAIRKEYREQVEQGVSGGKVNLEVDNQHPVQLSTPGTEIVIPFQYEIY

LYVVTDELFNKMRPAYNEEVGMPEGFYSSRTIQFIVKDWMGTRSFAPELIESIQNDRS

DRGYFETSALVVDWLNSKQTNGIILILSGLIGIVFFTFASFTYFRLYADLERDEAQY

RMIGKMGLSRPELRKIVTRQLLLMFFLPILVAVIHSSVAFVALQQLVDFSVFGYSLRI

FLVFASMQILYFALVRWRYLRHMYSKLV"

CDS complement(3025720..3026475)

/gene="yxdL_2"

/locus_tag="EFAGFIKM_02552"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42423"

/codon_start=1

/transl_table=11

/product="ABC transporter ATP-binding protein YxdL"

/db_xref="COG:COG1136"

/translation="MKQISKIYKGIVSYEALSGIDLSIQEGEFVGIMGPSGSGKTTLL

NMISTIDHPTSGELRIAGKNPFELNQDELALFRRKELGFVFQSFNLLNTLTVKENIVL
PLTLDGVSLAEMNTRVEQLASKLGIEGILNKRTYEISGGQAQRRTAIARALIHSPKLIL
ADEPTGNLDSKAARDVMEILETRNQEDQATMLLVTHDAVAASYCSRVVFIKDGKLYNE
IHYGDNRAAFYQKIINVLSLMGGSGHEFSPVRH"

CDS complement(3026804..3027787)

/gene="graS_2"

/locus_tag="EFAGFIKM_02553"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5HI08"

/codon_start=1

/transl_table=11

/product="Sensor histidine kinase GraS"

/db_xref="COG:COG0642"

/translation="MRLFIREHLALTCWVVAILFTVVAVFWYDGYNDWVTAAYAVALG
LFLYIGYLVYRYSHRSFYTRMSRSMDSLKDFVPLNETSPLSLALEKLLDSQYGQYHA
HLHRLEQRQQEYLTFMNQWVHQMKTPLSVIELTVEGQEDDDPRLVSIREEADQMRRGL
ETVLYVARLDTFEQDFSVEPVILKTAGEEAIHELKRFFIRNHVYPEMHIEPSLVVQSD
AKWIRFVLVQLLSNAIKYSAGNGQKIYVRAYEAERSIILEVQDQGIGIPKSDLNRVFQ
PFFTGENGRHFKESTGMGLYIAKEVLTRMNHRLDLESVYGEGETTVRITFNS"

CDS complement(3027784..3028488)

/gene="graR_2"

/locus_tag="EFAGFIKM_02554"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5HI09"

/codon_start=1

/transl_table=11

/product="Response regulator protein GraR"

/db_xref="COG:COG0745"

/translation="MYTIMIIEDDPKIAGLLKSHIERYGDRVLVEDFEMIVQQFEQI
QPHVVLLDINLPSYDGFYWCRQIRTLSTCPILFISARSGKMDQVMALENGADDYITKP
FEHEIVIAKIRSQLRRVYGDYAAARDEERKVELDGLVVYLERLEIQLGDRKVQLTKKET"

ILLETLLRRSPKLVSRILEKLWDDSFVDDNTLSVNVTRVRKRLAELAITDALETVR

GSGYRLNNTWKAASPS"

CDS complement(3028530..3029870)

/gene="nagZ_3"

/locus_tag="EFAGFIKM_02555"

/EC_number="3.2.1.52"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00364"

/codon_start=1

/transl_table=11

/product="Beta-hexosaminidase"

/translation="MYNYRYTSNNKWRKPLHMMCLLLGIVLLLSACGQAQKPSSATDS

NTGSNAGSNSGQSSSSPEQNTAPPQEEVPEEPQEEVDPVQEQLNSLTLEEKIGQMILA

GVQGTTLDDQAKQMITNQKVGGIIFYANNVSTLEGTAKFVKSIKEANQSNPVPIFMSV

DQEGGKVSRRMPETVESIPSSRKVGETKDSALAETMGELLARQVQLAGFNVDFAFVLDV

NSNPSNPVIGDRSFGSSAELVSRMGIAEMKGLRSEGIIPVVKHFPGHGDTSVDSHLDL

PVVNKTEKQLAELEWIPFQAAVKEQVEAVMVAHILFPKLDPDHPASLSDVIIGEHLRG

KFKYDGVVITDDLMSGAIKFNFKLDQAALATVKAGSDILLVAHSYESAKTIFDTLISA

VKSGKITESRIDESVYRILALKQYKLSDDQKASGDLKQLNADIVDWRKQIDAR"

CDS complement(3030269..3031372)

/locus_tag="EFAGFIKM_02556"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P32382"

/codon_start=1

/transl_table=11

/product="NADH oxidase"

/translation="MNVPSALFKPFTSDKLTLSNRIVMAPMTRGFSPEGVPGPEVAEY

YRRRAAGGVGLIITEGTGINHPSSVSGASIPLFHGEDSLQGWANVVKAVHEAGGKIMP

QLWHVGTARRSGDLPNAEADPVSPSGVSMAGEPSREPLTEEEIQGLVQAFAQAAADAQ

RIGFDGIELHGAHGYLIDQFFWEQTNRRTDNYGGDLVRRRTQFAVEVIKACRAVVGPDF

PIVLRFSQWKMGNYEARLVETPEQLEQFLAPLSAAGVDIFHCSTRRFWLPEFEGSELN

LAGWTQKITGKPAISVGSVGLAEFVDRATENQGTGDAHLDDLNEKLENNEFDLIALG
RVLLSDPEWPAKVREDRISEIIPFTTEVLQTLH"

CDS complement(3031706..3033019)

/locus_tag="EFAGFIKM_02557"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQRHTKWTAVILTIVAGMSWMLMGNSKPKNTTSTSQPPATERGL
AKVSNAPISSADVTSKIELLGRPFTKTPYANNVWDMQLYNGKIYLGHNSSNLGVAPN
SGPIPVIIYYDTANAKFKTQSVTNSNPGILPSTKMYVDEEQIDIYRVLNDKLYIPGND
DSEKWELGNFYRLDGEVWTKYRNLPLGVHVDLASYQGKMFAALGTESKPTILISHNE
GETWQKYATINTFGFRAYTMFHLNGKLYASGMMYPANKIWNDKTNILEINEKLEKRDV
VIYGNKMLPGLTYQTGTIPYNKIGKNVNFNNKLLYIAGGVFNDGQLLPKSLNVMTDIN
QARRVNLPDAKALPTDVLRLDGKVYVLTYTRQSANLYINRVYQSTDLTWNEILRFNQ
DTYAKSFEENEGDFYFGLGTDPDVLSTSSGKLLRVNRSDIPVNAN"

CDS complement(3033200..3034249)

/gene="gutB_3"

/locus_tag="EFAGFIKM_02558"

/EC_number="1.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q06004"

/codon_start=1

/transl_table=11

/product="Sorbitol dehydrogenase"

/db_xref="COG:COG1063"

/translation="MKALRWHGVKDLRLNINEPHPEEGVKIKVEWCGICGSDLHEY
TAGPIFIPAQASHPLTGEQAPIVMGHEFSGQVVEVGEGVTRFKAGDRVVVEPIYACGH
CEACKQGRYNLCDQMGLGLAGGGGGFSEYVTAENMVHAIPDSISYEQ GALVEPSAV
ALHAVRQSKLKVGDAAVFGAGPIGLLVIEALKASGASDIYVVELSDERKAKAEELGA
IVIDPMQFNVVEEIHQRTQGGVNVAYEVTGVPRVLQQAVDSTRIGGELMIVSIFEQEA
PIHPNSIVMKERTVNGIIGYRDVFPAVISLMDKGFFPADKLVTKRITLDEVLEHGFEA

LLKEKNQVKILVKAE"

CDS 3034637..3035674

/gene="degA_5"

/locus_tag="EFAGFIKM_02559"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37947"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator DegA"

/db_xref="COG:COG1609"

/translation="MRKEQKLTIKDVAERAGVGIATVSRAINNSEGISSKTRDKVMQA
IEELGFVPNTSAQSLKIRQTHQIALVVPDIRNAIPEISWSVEQTAKQHGYHVVQINT
AGNARTELETIRNVKKLHVDGLIFMPLAYPKTLPGLIDKAPLPISMINYGKKLEPGMK
ADIVLSQPEGKLVMEHLFKIGRTRIAYAGAPKDIEERFRAYEQAVGHVDISLVYFG
EDFSLNTGANAAADYFYGLTHMPDAVYAINDMVAIGLVNRFKELGVRVPEDVAVVGVDN
NQWTTVTSPQISSVSIMGEEVARLATELLKRIREMNTADYEHIQFEPRLIVRESSVA
MIHSSQRGPHS"

CDS complement(3035809..3036777)

/gene="hprA"

/locus_tag="EFAGFIKM_02560"

/EC_number="1.1.1.29"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q59516"

/codon_start=1

/transl_table=11

/product="Glycerate dehydrogenase"

/db_xref="COG:COG1052"

/translation="MNTKLRCVLDDYQNVALTSADWGPLMDRVEIQTFNNYMGSEEK
VIQELQDFDIVVLMRERTPFPEKVISQLPKLKLLITSGMRNASIDLKAAEKNGIIVCG
TEGSSNPPTELTWALILGLSRQLVTENNALRSNRNWQSTVGLDLHGRTLGLLGLGKIG
TRMAEIARAFGMNVMAWSENLTQEKAKEKHGVIWAETKEQLLAQSDIVSIHLVLSDRTR
NLIGQAEFQQMKSSALLINTSRAGIVDQEAMVEALQSGVIAGAGLDVYEQEPLPVNHV

MRTLPNVLATPHLGYVTRGNYEIYYNHTVENIVMFLKGTPIRQLHS"

CDS complement(3036858..3037439)

/gene="comR_6"

/locus_tag="EFAGFIKM_02561"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P75952"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional repressor ComR"

/translation="MVRQREFDTDKALDAAMHTFWDKGFEAASLNDLTAMGIQRPSL

YAAFGDKKELFETALRRYTTQHAAQVRARLQQGSSVREAFRGLFEHIGAEVSVTEPSH

GCFCINTMVELAPHDPKFAVLTREHQMVLGVLFKETIERGQQSGELSTDMNASAVAQS

LVVSMIGLTVLMKSGPDRLFVEQSIQVTLSELLH"

CDS 3037726..3038946

/gene="sotB_3"

/locus_tag="EFAGFIKM_02562"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00517"

/codon_start=1

/transl_table=11

/product="sugar efflux transporter"

/translation="MQTSSPDAQLSNKDRPAMSRLVALLFAVCSGLAVANIYYAQPLL

DSIAQEFSLSPPSIGIVITVTQICYALGLFLLVPLGDLLNRRKLIIQMLLSVLALVL

VGTAQSSSLLFMGMAVVGLLAVITQTLVAFAAHLAAPSERGRIVGLVTSGIVIGILLA

RTVAGTLNDSLGLWRSVYLFASLTLLGIVALFFVLPRQQSTQIKQNYTQLLGSVLQLY

RELRLVRVGVLAAMLIFTAFSILWTSMLPLSSPPLSLSHTVIGAFGLAGAAGALAAA

RAGKLADRGLGQKTTGVALVILLWSWLPIGYVHHSLWFLILGVILLDLAVQAVHVTNQ

SLIYEVPRPEAQSRLLTAAYMIFYSIGSATGSIVSTQVYAWAGWTAVCWLGAGVSAAALV

FWMIDRYMHRNLDR"

CDS complement(3038948..3039106)

/locus_tag="EFAGFIKM_02563"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDNEYFVGWGTALINAGLAQGKNRSGRNWFLISLLFGPLATLF
IVVWNKLD"

CDS complement(3039142..3039597)

/locus_tag="EFAGFIKM_02564"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIEVTTEITIHASIERCFDYARDIDIHTQTVWQHTRERAVAGVT
TGRIGAGDTVTFQATHFGVRQKLKSRIVQFERPFLFVDQMEKGAFKSMRHEHHFSVIG
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CDS complement(3039773..3040858)

/locus_tag="EFAGFIKM_02565"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRIHIMNLQDGDRLTADTFSDAGLHVLGKGTVIKGEDITLLMQH
RVDYVDIESREEEITEAEFFAAAAKHASGITTKPEEPPEELKSQFIQTVHNYQNAFLE
ALTVGKFNATMVDDALQPMVEGLDEQKDVVHLLMMLERDDVNNYTHSIQVGLLSFYLA
NWLGYSQKESYQISRGGYLHDIGKCKVSHRIRNKTEPLTADEQLEMQRHTIYGHEIHK
NSMTDEATALVALQHHEREDGSGYPMQLEKSEIHPYTQIVSVADIYIGMRSGNHGGSN
PNLINNLRDIYGMGFGKLNEKPVQALMQHLLPNFIGKQVLLSNGEKGIVVMNNTSDIF
KPLIKVESEEYRDLKERTLAIDELLI"

CDS complement(3041142..3042977)

/locus_tag="EFAGFIKM_02566"
/EC_number="4.1.1.61"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9Z8L0"

/codon_start=1
/transl_table=11
/product="4-hydroxybenzoate decarboxylase subunit C"
/db_xref="COG:COG0043"
/translation="MKYRNMEDCINDLEEHHGLIRVKEEVDPHLEMAAIHMKVHEAKG
PALLFENVKGSKFQAVSNLFGTVERSKFMFRGTLEGVQRMMAVRDDPMKALKTPFQHV
RTGLAAWQALPKQKSISLPVSAQEIQISDLPLIKHWPMDDGGAFTLPQVYSEDPDKPG
IMNSNLGMYRVQLDGNDFEMNKEIGLHYQIHRGIGIHQAKAVKKGEPLKVSIFIGGPP
AHTLSAVMPLPEGLSEMTFAGLLAGRRFRYSYKDGYSNDADFVITGDIYPGETKPE
GPFGDHLGYYSLTHEFPLMRVHKVYAKPNAIWPFTVVGRRPPQEDTAFGDLIHEITGDA
IKQEIPGVKEVHAVDAAGVHPLLFAIGSERYTPYQAVKQPTTELTIANRILGTGQLSL
AKYLFITAEDQQTLDTHKEVEFLTYILERMMDMQRDIHFHTHTTIDTLDYSGTGLENLGS
KVVFAAYGDKIRELCSEVPESLKNIRGYENPQLIMPGIVSIQTSFTSYADTAQEMQA
FTSLLKEQGGLDSCPMIILCDDSSFLSANLSNFLWATFTRSNPSHDMYGVNSGYDHKH
WGCDQVIIDARTKAHQAPPLIPDASVEKSIRFFVKGASLGSIKI"

CDS complement(3043193..3044536)

/gene="sasA_9"
/locus_tag="EFAGFIKM_02567"
/EC_number="2.7.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01837"
/codon_start=1
/transl_table=11
/product="Adaptive-response sensory-kinase SasA"
/translation="MKMFRKSLRLRIVATFIGIVLVSLILSFMINNGSQEKTPIRFRMV
TFAQDLATLINLIDDPEKVKSSLEIFARYGLNITPVNEQSEVLFSLPEDKVHLLFDGS
TTDAIFLSSKDGIATIGVPGTNEGIGTFLIQSDFSSLFHTLRNTLLTSLLTVLVIGSL
LILFMSGYIVKPIKRLTAAKEMSSGDLVRLKHNNQDEFGELMESFNHMASELQKID
SVRDDFVSNVHEMQSPLTSIRGFTRALQDGVIPLEEQKEHLDIYEETLRLSRLSDN
LLRLASLDSEHHPVHFTTFQVDEQLRRAILLAEPQWAHKDIQIELDLLPCEITVDKDL
FDQVWQNLINNAIKYTGPKGTHVEIETSSSFVKVLIRDSGQGIPEEALPYIFDRFYM
VDKARSSSLRGNGLGLSIVIKILKHQCTIDVESEVGKGTQFIVTIPRSTITPSS"

CDS complement(3044533..3045201)
/gene="hssR_2"
/locus_tag="EFAGFIKM_02568"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A6QJK3"
/codon_start=1
/transl_table=11
/product="Heme response regulator HssR"
/translation="MNTILVVDDDSHIRKLIRIYLEKNQFSVLEAADGQEALDILSHT
KVDLAIVDVMMPRIDGIELTEDIRSYLDIPILMVTAKGESKDKVRGFNAGSDDYLVKP
FDPVELILRVKSLLKRYNKSSSNMIQVSGVTIDLGNLIVVAGGQTIELKKKECELLFS
LASSPGKIFTRTQLIDDIWGDIDYEGDERTVDVHIKRLRERLEPVPELVISTIRGLGYR
LERA"

CDS complement(3045229..3047193)
/gene="btuD_7"
/locus_tag="EFAGFIKM_02569"
/EC_number="7.6.2.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01005"
/codon_start=1
/transl_table=11
/product="Vitamin B12 import ATP-binding protein BtuD"
/translation="MKILEVKNVKKSYTLYGKERVPVLHGLNLSFETGEFVSILGESG
CGKSTLMNIIGGMDSDYEGDVVVRGKNLSAMTEKEMDDYRKNNIGFVFQNFNLIPHLS
VLENTIAMQMTDTNEKDRNQRAVDILTEVGLKDHLNKRPNQLSGGQKQRVSIARALS
NNPDII LADEPTGALDKENG DQILALLDSIAKKGMLVIAVTHSQKVADSGTRIVKVEE
GRISDDIHLKDPSTAVYESGQDSSRSLSLASFKMALKNMKLNGKRNVLVALGGSIGI
LSVLLMLSLGNGITTYMNDEINSSMDPLLVDITKPSEEAKDMQGPEALMAPGEPFTEA
DVETILNFPNVDHVETITTITGQSTMVNEKQSVGLTQLTTLTDAFDPALMTTGVLPAE
NQMLLPLDTANKLSGNDQADSMIGKSVFLYINEMDSNNKPVTLKEVTISGIYEAADP
RSPMQQSPGYISSETLGQMYTDKGISIGPIQVNAYATDMKYVNEINEAAVDAGFAGSQ
MAKVMENITTYVSMASIVLAGIAGISLIVSGIMILVVLYISVVERTKEIGILRAIGAR

KKDIKRIFFSESALLGVFSGIIAVIFAVIISYVLNILLDNAFGAKLINLSGYILFGL

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CDS complement(3047391..3049340)

/locus_tag="EFAGFIKM_02570"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFQPKKKRPRIKTMISGLIALTLSSLILPNVAGAEPVEPSQVQ

FANVSVQAGQTVHVPVALKKSYFGVKAYNMQIDYDTSALEIVRITPKSVNVISTSPNE

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QSDSEHWHFTNVEHNLSGAQLSGGTITITAANSGGDNSGSTPTPNPGNSSGGGGSVSPT

SPVVTVPSTPAVTKGVDIYVNGQKQEQSATATTSTVGNQVTTTVHVDNNKVINQIGS

GLKTL LLPITGTGKGAVVGELNGKLVKTMESNAEVIQTDSGTYTLPANQIQVDQIL

NQFGGTTPLEDITIQAIAIPSTTSKQTTIQAAAEKLENTTVVATPVDFEVKAIWNGQQ

VNVDRFNSYVERSITLPEGVDGSKITGVVLQPDGSLLHVPTKVIKGNVQDSAIINSL

TNSTYALIHYPATFSDVSSHWSRDDVQDLASRLIVQGTGENVFAPDRSITRAEFTAVL

LRGLGLHSPNSTEAASFTDVKTGSWYEDEVQTAVSYGLISGYADESFRPNNEISRAEA

LTIVSRAMKLVGLAQADASETTSLLSTYSDSAKVQSWAAEPVASAIKQELVQGADGKL

MSDADISRAQSAAIVKRLLAKAGLI"

CDS complement(3049390..3050418)

/locus_tag="EFAGFIKM_02571"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKGKQNKRLKPILKKSMLTALGLGIALPIGGTLPQANAGEIGP

EIKISRPVLNDGIHWLNYSSEQNDPSFVSGVPIEVTNRTVTIDLSTHFNSNEFNIIISA

TSGDYSVASVYIEGGNKLVVVPYRSGKINIELKANYTVSDVPETVTDNFELYISKKGD

VNADGKVNSLDAADLLEYLRNMVSRRGFSYVEMNRMDVDRNAEPTLGDMNALLNGYAN

KTLGAKNNDYVLTFFQQVDDAPYVLNGQLKNYMENAIATDYLLMDVDDDHVDYINTPSY

QWYRATDPSEGDMVSIEGETQEQTHTVTFEDEDHYLVLEVTAHSTSDANTKPRRVYIVG

KEKIQRPD"

CDS complement(3050611..3051903)

/gene="mtaD_2"

/locus_tag="EFAGFIKM_02572"

/EC_number="3.5.4.28"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9X034"

/codon_start=1

/transl_table=11

/product="5-methylthioadenosine/S-adenosylhomocysteine
deaminase"

/db_xref="COG:COG0402"

/translation="MSILIQQATILTMKDADAPFMGDIRVEGDRIKQIADHILPQPQD
EIIDGRNKVAMPGLINAHQHTPMSLLRGFSDDLKMDWLERKMLPAEARMNPEDIYWG
AKLSIAEMIRSGTTAFADMYIHMNEIAEAVKQTGMRASLTRGMVFMEDGGRRRLQEAI
DLVQRWSGAAEGRITTMYPHSPYTCPMEPLREVIAMAVTEDIPLHIHLAETKGEVVK
IRERYGMTPTLEYLEEAGMFEQAHVLLAHGVHLNRRDIGRLKGMRGVVAHNPVSNLKLK
CGIAPITEMLAQGINVGIGTDGAGSATTVDMFEEIKAATWLQKLDYGDPTRLPAKDV
L
SMATRGASALLGLQDEVGILEVGKADLILIDLAKPHLQPVHEVESLLAYSVNGADV
D
TTIVNGQILMRGRKLLTIDEEELYREVKVRAKRIVEGI"

CDS complement(3051982..3052275)

/locus_tag="EFAGFIKM_02573"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNCVAVLPYYKVQREVTGLAQEIEMNARSMILYSDKIVTKYREF
NITEVFDMSFRRMGDEGGFFYLHTSTGVYPYMVEIDPKPFIQTFRKMTIQKLK"

CDS complement(3052329..3053447)

/locus_tag="EFAGFIKM_02574"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MQFETSVKPIKDQIWVVGGYGQVGQMICTQLGKMFPGKVWAAGT
RMNRAEEFSRSTSGAVLPLQLDVTRPVEPSMLRPVKLVIMCVDQSDTRFVEACAQAGT
DYIDISAKYDFLAQVEQLHTKMQRSKSTAILS VGLSPGVTNLLVREATMHMDQVEEAD
ITVMLGLGEKHGKAAVEWTVDQMNATYQVMQEGKPAEVQSFGDGKRIDFGAKLGQRKA
YRFNFSDQHVVARTLRIPTVSTRCLDSRWITGSMAISKRAGLFSLLRIPSIRSGTVK
AFGLIPGGEPMYAVKVDVAVGWENG EQIRVEQLLVGAKEADATAAVAAVAERVYKTEL
PHGVFHIEQCLSLQDIQDALHTPLKVTTKITKSHVLLL"

CDS complement(3053431..3054138)

/gene="cmoA"
/locus_tag="EFAGFIKM_02575"
/EC_number="2.1.3.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01589"
/codon_start=1
/transl_table=11
/product="Carboxy-S-adenosyl-L-methionine synthase"
/translation="MNHNLSPMSWETAEVHRYEQSIALKIPGYSHMHDLMERLLSASF
ANNNDIHILVAGAGGGKEIALLGSRHAGWTLTGVDPSQPMLQLAEKRVTEAGIGSRVK
LQPVTVEELPEDIVYDGATSMMLHFLQGMEAKRTFLTSLAARLKPGAPLIIAVNAD
LCSPAHPPTMMQAWKDHMLSVGVLPEEWERFAASLGRES DPISSEEMTQLLTECGFSHI
TRYFGAFWVEGYAIRN"

CDS 3054268..3055374

/locus_tag="EFAGFIKM_02576"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTSRIDRNHRLITSLEKGTWTSRTYREAVLKQIHTVVHYDAYCF
TTVDPLTLLSTGAVTEDGIEAIHDRLFINEYMEEDIHKYAE LIRSGEHTATLHTSNLQ
LEQSPRYINILQPAGFGDELRAVLVSGDACWGYLTLYRKTESAVFTEEERMMIQSWTA

SIASMLRSTSLTLIDEITSESPEEPGILITSDTFQLLSLNASAQYWLSQLRMLEHVGP
DVLPRPVRAVSSHQQRKNRAELVVGQTQIATDLPSKVCIQLPDGRYLILHASLMQQLTG
PDQIAIRLEQAMPQDLLPLLAESHGLSSRERELLYVLRSSYSSKEIAAAMHISVYTVQ
DHLKSIFAKTKVSSRRELIWYFVSRFQLSDEPAI"

CDS complement(3055617..3056630)

/gene="feuC_2"

/locus_tag="EFAGFIKM_02577"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40411"

/codon_start=1

/transl_table=11

/product="Iron-uptake system permease protein FeuC"

/db_xref="COG:COG0609"

/translation="MIKRRYTMKRGIIINVLMVLILVFAIISMNSGKMNLSPLEVLN

VLIGNGTDKQNLIVFDFRLPRIVLSILVGLGMGAAGVVMQSLLRNDMASPGTLGISSG

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VALGSGYGALTFTLTKLDDSQMNFMLYWLASLWGDDWGYISILTPWWLILLGYIFY

KARILNALHLGNQTAQGLGVSVNRQFLGLSIAAVALSSGSVAVGGSFFFVGLIAPHMA

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KAK"

CDS complement(3056627..3057652)

/gene="feuB_2"

/locus_tag="EFAGFIKM_02578"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40410"

/codon_start=1

/transl_table=11

/product="Iron-uptake system permease protein FeuB"

/db_xref="COG:COG0609"

/translation="MKSKPEQKRRGAMNFTMYMVIGLGLTVLMSAASIMFGAADMRLA

TVWEAIFRFDPMLEHQIIQTMRLPRTVADLIVGCSLAVCGAIMQGTTNRNPLADSGLM

GISSGAFAIALCLAFLPGYSYWQMMLFACLGAAIATGMTYFTASLGNCGMTPQRLVL

AGLSISMLFGALSQYLAINYNLGRALTFWTAGSTAGVKWGEELLIISPLFVAGILLALA
LSPSVTLTSLGDDVASGLGIRSLVKILSTIIVLVTGLAVVVVGPVGVFVGLITPHIV
RYMVGVDYRYIIPAAALYGALLTVSADLAGRLINKPFETPIAIIFSIIGVPYFLFLAR
RQRREYE"

CDS complement(3057770..3059737)

/gene="rhaS_23"

/locus_tag="EFAGFIKM_02579"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MQEEEARQGFTPEMIDMMASIWTRSITLIDVRFQNIESQYPLE

QYKMPSSMFIYAYGGEAQIQLNETTFAMERFGLVHGGKGSLLSITPKEETVKTFMVFY

RAESPLFFKKHLQQLLEQVNPVQQFGYTPSNPILLRDWFQRMNGWKRGKEMDQLQA

KSFLYQLIHEVYRDLEGGEIRYLQPDPAKSAKVYLDKHYREPIMFQQIADMFGISGGQ

LTRLFKKREGMNLQEYLIQRRIEAAACHDLKHTEATVKEIATGAGFTDEKNLFRMFKKH

YKMTPSDYRKINALSMQVDGIDNDSHLPYDERELVSLVKSYPDGESEMMFGTLRSKEMI

LAAISMMLLLTACTSGTPANNGGTANTTPAQTQQATQQEGSETKASEAVSQTRTIST

VKGDVEVPNNPQRVVVDYLVGDVVALGVTPLGVARAARGETEPVYANQITDSIKVAME

PEDIMTLEPDLILAWSDESYDDLSKIAPTIVPYGDMTEERIQFISDVLNKQEEAK

DVLNAYTGKIEEAKLAFQNAGLSDVTITVGEFSDKSNYIAGAKHAVGELVYDELQLQA

PSKVQTDIIDADKYWGDVSMELPAYSGDYMIFLGDGNVASDNAVWNAIPAVQHDRV

KVDSSLSWSTDVMTSSALIDYIVSQLLALAK"

CDS complement(3060025..3060912)

/gene="yidC2_1"

/locus_tag="EFAGFIKM_02580"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9KDP2"

/codon_start=1

/transl_table=11

/product="Membrane protein insertase YidC 2"

/db_xref="COG:COG0706"
/translation="MEHKTNKGFTFTSGKGRIYGLIVILFAVMLLAGCSNNVSEITSS
TPGFFNHYIVFPLSYLIQHIATIFSGSYGVAIVITLVIRLALLPLMMRQAKSQQGTR
VIMNAMKPEMDALKKKYEGKNDPADKQKLSQETMELYKKHKFNPLNIGCLPMLIQLPI
LSGIYTAIRLTPELSSHSFLWFKLGAPDYVLAVVVAVIYLIQAKVSQANMAPEQRKQF
AIMGYLSPLMMAFFSLTAPAAMPLYWTVGGSFLVLQTLLFRKMYPVEHPQEPVVVEVS
NKKNNKSSSAKPSRKPAKS"

CDS complement(3061292..3062911)

/locus_tag="EFAGFIKM_02581"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIDKIMASPQRALITLLSAWMLAIHQYLFYGNEIGVSYPIFVI
LFYVFMYLFARDRMRSFKFIDAFVAAVVLLSLTFLLYDNELLYVLNFLVIPGVVILH
MTYLMGRKQKQWWEIGLIGTAIDHMLPQAIRHWGTVAIAVRAGGRGIGKSQKTVVFK
VLIGLVASLPILIVVALLSSADGVFDQYLAGFPEWLNQLAFTPGIPRIIWIVIAGVL
LFGYVWGFVQPMQYEAEKRANAHWKNGAVSTVDKRDNTYIFSPVDP AIEGKATNKITP
EPERTPIQREPFRLDPIIVGTMLIVINCVYVLFVLVQFSYLFGAGEGHLVPDLSYADY
ARSGFAELILVTGINFFILIVALQYTRSSGKTGSIVHQVLLLILVSCSAIMLYSAFMR
LNLYEQAYGYTYIRFLVHAFMIFLALLLIAGLRIRYTSIPLIRWYIVLALTAYVAVN
YVGMDKRIAELNIERYHQTGHIDATYLASLSADAVPLLREFALEEYPDLKREMLERQA
YLDVDSSDRSWPSYNVARHRAEQELSKLRTE"

CDS 3063046..3064836

/gene="sgrR_2"
/locus_tag="EFAGFIKM_02582"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01449"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator SgrR"
/translation="MKLHQQYLLLHRHYGHTEHELTADLAELLNCTHRNTLTIVKK"

MVAHDWIRWVSQRGRGRSSLTLLVPADQIAAEYMMQAMNRRELQEAAEQVSAFSSST
IMQDHLNQWLLGYSGHHTEAGTNNEQIDTLRLPLRQQQLHALDPLYINLLAESFVTSHV
FDGLVQRGEQGEILPCLAHTWDVSADRKTWIFYLRKGITFHDGQLLTAHDIVHTFERL
QSTDRTLYRDVSKQILSIEAVDSLTVCFQLKNPHELFLSFLTTSRAAIVPSPGTNEH
KMKHSSDVHGMQKPVGTGPFKVTAWDDHLCRLEAFSSYFQGRAHMDRVDILQIPWSAS
AKMDDSQDIETPFFHLVHNPSSSAGADWTQISAGVMVHKLLTCNTQKNGPLNDPEVRA
HLQSCLAGMYRDDGHADDSEVVETNFSAVNTKKVQVHSEGFSDISSVSSSPISLHI
ATIPQYRRDAQHLASILEQCGFSCTVRTATMEQFKGNLRLESDLILFSLIRDRDEELR
RYDLYSTLSEHLED SARITIHEILQTIVASPIAADRTCELDRIEQFLVGQNLLFHLSE
KPVETAYLPSVRGLSFNSQGWVNL RHIWFP"

CDS complement(3064898..3066250)

/gene="mrdB_1"

/locus_tag="EFAGFIKM_02583"

/EC_number="2.4.1.129"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_02079"

/codon_start=1

/transl_table=11

/product="Peptidoglycan glycosyltransferase MrdB"

/translation="MTNRHERIQHYLDHMCVQVKAREVHNDLRDELGNHMEEIKLYKK

QEGYTEEEAIAAIEQMGDPAVVGKSMHRLHRHRMHWGIVSGIIVLATISLILMWIFT

TNTTQARYQYLYSYHVKN TVVGLMMMSFFIFFDYRKWKKAAWWIYILFNALLWINPML

SSAYNGIDRYLSLPFGFVLDVTTVSMWILPLAIGAIMLDKLR TSCSIQSVLSYIAMVA

LPAVLLFQISDWVRMLLFGIVSVILFGWITRKWLYMIIAAITGSLSLILLFMDEYR

RLDRFSVVFNLQDDPNGNGFVYNSIMDIVRTAGWWGNGLDTRFDLIKS NYFD FPGVML

IDVFGWSAGILLIGIFWFVSSMVKILPRIRDDYGRMIILSVTTILSLQMIYSLVVIT

GKVPISIAPFFIGYGTHLIFEYAMIGLLLGVYRRKDTISKKNEKIRQKVDADLLTNS

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CDS complement(3066247..3066582)

/locus_tag="EFAGFIKM_02584"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MQVNKQMIKGSTETLILNLLQERPLYGYELIKELHRQSEGVFNL
KEGTLYPILHAMEIEGWVESYWMEVEGRKRKYYSILDKGMEALQSKKAEWNLFRAVD
RVLGEGGLT"

CDS 3066867..3067451

/locus_tag="EFAGFIKM_02585"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGKLIFFLGGAGSGKTTAKALSRKHKAFFDMDILLRPAAEI
MTLQGLDPSDRDSPEYKRLCRDLGYRITMDAALDNVQLGIDTIVGPFKEIGTPDWI
AQELARIGHTLDDTDVRVAYIYLENEALYHKRITARQSPLDEWKLANWDAFTASLVRK
EIAWPLPASSVAYIDNSSDDPAIAYAELERRMYE"

CDS complement(3068042..3069010)

/locus_tag="EFAGFIKM_02586"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MMYTDKQEYSFSTCWNKRHTNGQGMIEEIKSLGFKQVELNYNV
TEEMLQTIEPMIERGEIGVSSVHNTFPHVADPDYGTDSVLLGFDDEPRRRRAIELLLR
SAEYAHRYGAKAVVHPGEVPFEYNIDEALKKIYHDQGPDSPAYQSLWQEMLEKREDG
SAHYLSRIQESLEEVC DLSEQRGYGV SFGIETRSRCYQMPTLHEAGTIIGQMKGAPLG
LWYDIGHGMMMDRMGLYDNVREANALIDHVGVHIIHETVGLSDHWCPYIHSKDMTYFD
SFLDIIDRSPVKVYELKAACTPEEIDESHGIITARIAERHASHQRG"

CDS complement(3069310..3071016)

/locus_tag="EFAGFIKM_02587"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MTQRMVEKMSKEQQYLVNQSMLMDSFYDKEMDLLRSFEEEDSS
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PAGHYAWKSFAPGTAYFLERTFDKVSAQFIHKLQEDGSLLEAADSKQLKRLFHSAVN
QILPPVWISYDPNWREFIACVCVVVTAIEFGELIPETLMKRM DHAMELAVQGSIERRLS
DVIPMNTNIELMHIFMTHYYGHRLNRTEW IQHSDEQAEGLMKEFEQYDGTFAEFNTTT
YYGVDSLVLGMYRKYGLTERLVEIGHRIAHLWNNIALYNNANLENLSGPFSRAYDME
MREHSSIGVFIYLLLGEGYEYLAGINCESGHDPMIALLGVDVPAEAVPFFKAHQEDRL
VQKQFMELCERN DPTS NRNLCTAKAWIGEDRMIGAMSGSVNTNGQMHPATIH WQTERG
ERYYLRLIRREVGE GWNSHLRGVTFDADLTPDSL TIDVELDTAEEIDVYFEIRGPFLR
QQDITPVLWQFPGLTCTVKAEAPEPSVLMYVNHAEIYRYVPGKTANRMR FELTLRED
NG"

CDS complement(3071038..3071910)

/gene="araQ_17"
/locus_tag="EFAGFIKM_02588"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94530"
/codon_start=1
/transl_table=11
/product="L-arabinose transport system permease protein
AraQ"
/db_xref="COG:COG0395"
/translation="MSENTANRIFNTVNVILIVITMVLCLAPFIHIIAISLSSNRAIG
SGEVSFFPKELSFEAYTKVFADGSMIRSLIYTIWLTVLSTVLSMVMTIAAAYPLAKSN
LKGRKWFMLVIVVTMFFSGGIPEYILIKNLHLLDSIWGLILPGLISPFYMIILITFF
RGIPESLEEAAGIDGSSHFGTLMRIILPLSLPVMATLSLFYAVGRWNGFQDALMYITK
PELYPLQLKLYQMIQQNQITELMQNEGIGAVQVLPESLKAASVIFSTLPILLVYPWLQ
RYFISGVMVGAVKG"

CDS complement(3071949..3072851)

/gene="yteP_23"
/locus_tag="EFAGFIKM_02589"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system
permease YteP"

/db_xref="COG:COG4209"

/translation="MKTSIYFRRNWQLYALLLLPMIYFIIFKYGPMYGVQIAFKDFNF
FQGIAGSEWIGLDAFREVFQNNQGFYTALRNTLVNMLDLLVSFPAPLILAILLFELKK
AWFKKLAQTLLYIPHFISWVIIGGIVLQVFGTQSGFINNILMSMGFDPLPFLSDKNYW
LFTYLAVGVWQSAGWGTILYLASLTGINRELYEAAEVDGASRLRRIWHISLPGIKTTI
VTLIIINVGNMISIGFDRPFIIGNVAVREYSDVLSTFVYRVGLQSGQVTLATAVGLFQ
ALVGLVLILGANYTSKKLTDESIM"

CDS complement(3072963..3074564)

/locus_tag="EFAGFIKM_02590"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRLFQRRKAGKASSILAVVTAFTLLLSACSSGSESTSSSGESGS
GEKTTLKVEIFDRGNTPAGYTISDSYLTRFIQEKGDPNNIDVQFVPVPRSEEVQKLN
VLMSGSEVPDIVFTYDSGTFNRYAQQGGLTELDLINQTGPNLKKLLGDETLAYGQY
DGQQFAVPGKRLVLGKYASYVRQDWLDALGLPSPETAEEHLTKAFKEKDPGKVG TG
LIPMGMSIASAQYEPLIWSFIEPLTEEQKYTLTQQLGSNDYPTLLPGFKEALKYMNTL
YNEGLMSKDFGLDKDKKKLWEDVSNKGKVG FYTEDAGEIYISGTYKNLQTNQPGAVMTP
IDAFKNSEGKFAKPAYAPNAMYVMIPKSSKNAEAMKYLDWMASGNNLFDLQFGVENE
NYELVDGVPLIKDDASPEIAGRIYNSGDIAIIVNGKYVGDDKKNEEAYVVQVESKYRD
DMRKSV AISNTDTIQPVRFSKPIDAEARYGNGLKDKFMEFFVKTISKPADFEATYDS
MMKDYMASGGQAILDERTEAYKAMK"

CDS complement(3075152..3077395)

/gene="rhaR_23"

/locus_tag="EFAGFIKM_02591"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaR"
/translation="MKVNLKRNWHTKLMYSYFPIFLTISILIFLSFLIVNELSRNET
QKADMISTRYIVDTLERSLSDIELRLLEDIGANKTYSRFLEAGQGQLSSQFIYDAASG
LGRMLDQQDMIQSIYLYRMSDSQILTPRGMMRLEDFEDRAYIEQALKDRENLGWNLP
DYKERSFDVPSQVISMNKWLPLPWGGEGLLVITIRMYAVERQIDNMTNEKLSVLQVRD
KSDNLIYTAHQMDPSAGEILNRVTADKLGVLVFESGIQSGQLYSWVSLVSYVWIGIGLL
TIVGAVAGLIYITRRNTRPIQLIMNRIQALQPRAEEDEVAPSVKDELALIDRALEHLI
AQTVDYEKQHHEENLLIHRRLVLDLMEGERMDSFRQLRHLQPLEERFMEPKSAVLI
AEMNGDDLSTNQNILKIALMNVVEELVQNESQFGGWAIEWFGNRRILIVVIASDEQEGLD
RELLMDLAKQMHHMWIAENFRLRFTFGIGRTVSGWEEITRSYASADAGLQHRLTLGKDA
IVLSEQLPDRIELQSYKYLQMLADFVREFRLTGDGWRTQLDQMFVAFNEDQITDNDIR
MLLQALIQMLSREFGELSERLQSQAEEILRLRSDIQQVETLEGIQEILQEWLKEVY
RNYVSVNETKSHRAMINELRIYIEEHFDDPDLSLKHLSDRFQISGKYASYLFKEEFEM
KFVDFLVKLRVEKACRLLSASDMAVQDIALQVGYANAISFGRVFKRIMGVTPGDYRKQ
SGKQGDQ"

CDS complement(3077417..3078640)

/gene="nupG"
/locus_tag="EFAGFIKM_02592"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_02049"
/codon_start=1
/transl_table=11
/product="Nucleoside permease NupG"
/translation="MRSRHMKAYTEKIKADSNDAKRVLLQLQGLYLFMGLAGGMFNPY
INPILVAQGFSSKETGFIMAFGTLVSIILQPIWGILVDKFKKTRFVLVISLLVPASLA
YFYNIQVYFILILIYTLCTIFQVTQIPVADSYAVTAARTANTSYGMIRLFGSIGTGVG
GFAAGMYLSQFSIHMLWLPFLLFNILSAILASTLPRQTSISSSSVTFVGLARLLRNR
TFLLFLTGCFLVNQTLTAFNSFFVISFQMAGGSVTMTGTALLASITNVPSMLAAAFI
LRKWGHERTMLLAAGAYMLRWGIQWLWPTPEVMIGVQVLHGLSFGFFYIAAVEYVASV

TGREMQATGQSLFNMVFAGLGGIVGNMLNGYLLDSGGPSL MYLACTISAALGSVILYI
VSRQAKEQRRAYSLE"

CDS complement(3078690..3079742)

/gene="glcK_1"

/locus_tag="EFAGFIKM_02593"

/EC_number="2.7.1.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54495"

/codon_start=1

/transl_table=11

/product="Glucokinase"

/db_xref="COG:COG1940"

/translation="MTESVKNVSNNYQSNQDGTVGGDPSGWIAGIDIGGTKLMLLSS

QQAGNEVHERILPTLASDQPDEFFRWLFAEMETFCREVGCSLDQLKGAGLGFPGVILQ

EEGILRNAPAFQWPELDIRPVIKYYSGNIMLDNDVNLAAMGEYDQGAQGHQHCV MV

TVGTGIGSALILNGQLYSGQTGAAGEIGHFIAGEEGLHTGYVADADSFGVFEQVTS GT

GITEQARRYFAAGKGSSLSLIMSLAGGEAEQIEARHVFKAESGDLAALEILELPMRY

MARGLANITALLNPSIIVIGGGVAASNPSYYLNEVRTRLQRYTVLPTLLAIAELGNKA

GAIGALAAIKSSLTRT"

CDS complement(3079779..3080957)

/gene="nagC_1"

/locus_tag="EFAGFIKM_02594"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AF20"

/codon_start=1

/transl_table=11

/product="N-acetylglucosamine repressor"

/db_xref="COG:COG1940"

/translation="MAGTPQYIRNLNENLIMDALITQGTMSRADISRQTGLSKPTVSL

AVEHLIDRNLVREMGPADNAQGRKATLIRFNETAYYVCGIDIGATRIRIALSDLNGEI

IAYRTYPMVVQGAYERAEATMLELLRSHMNELLDENHLNWDQIQIGFGIPGVVLPDS

GRINRIVDPLAGLEEA FSLESLSGAFFCEVILENDVNLAALGEYRSGAAAGYPLFVFF

SIGTGTGAGIMVHGQLLRGLGGLTGEIAEMLVDDGRRLEEVLSADGLMQLAKDYLDQH
VVADDLHRHLTPEKLFEAARSGEVEALDILQQYSQKIASALRQISVVLAPDLIVLGGG
VGGNGDVLLPLLRQIISEQFPVQPQLICSKLGEQAVVTGAVQVAIQQTMLNLQQEAME
"

CDS complement(3081627..3082466)

/locus_tag="EFAGFIKM_02595"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKRITDILFIMAGAFLLFALAVNLFVIPNDLAEGGVGTGITILY

YLF EWSPGLMNLILNGILLIVGYRFLDKTTT VYTIIAVVFNSLFLHLTESWTIASDEL

WINTIFAGLFAGLGIGLIVRVGGTTAGTVILARLANKYLDWNISYGLLFFDLIVAFSS

YFIIGPQGLMCTIVLLFVGTKTMEFII EGLNPKKAVMISSKQDEIAKQVIEKMDRGV

TVLSGHGYTKNKKEILYIVISKQEV SMLKKIVRAEDEIAFITIHDVRDVFGE GFIEL

SKT"

CDS 3082840..3083898

/gene="des"

/locus_tag="EFAGFIKM_02596"

/EC_number="1.14.19.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34653"

/codon_start=1

/transl_table=11

/product="Fatty acid desaturase"

/db_xref="COG:COG3239"

/translation="MNRSKEMALKKEVTPYEKNDLRLSIRQLINTLLPLFLLWAAAYF

SLSVSYWLTFPIALVASGFVLRTFIIFHDCCHGSFFKSKRANDILGTITGVLT VTPYQ

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YVFLLAYRFNRKGARRKERINTHTTVLIVVLYAFMSWLVGWQAFVMVQAPIFFFSGF

FGIWL FVYQH QFEETYFEHEDEWSYVKA AVEGSSYYKLPKLLQWISGNIGFHHVHHLS

PRVPNYFLEEAHNATPPLQKATTITLRSSLVALRFRLWDEDSKQFISFRQLKKLSRKP

YVQPPIRVTNPAGLTEKP"

CDS 3083998..3085134

/gene="desK"

/locus_tag="EFAGFIKM_02597"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34757"

/codon_start=1

/transl_table=11

/product="Sensor histidine kinase DesK"

/db_xref="COG:COG4585"

/translation="MQNFYKKTGLNLYVWLAFFILPFYFISQYSKLWTMVTGIIILV
FFVCYLLAFITKGWQVYMWIGMLIAISITMTIAYDYAYFSLFLAFFIGNIKNKAGFFT
LYSVNLGASFVTINYGFINQSSLLVSQLPFVFINLMASILLPISTYNKNKTEHLEGQL
ENANKRLDDLKMEERQRIARDLHDTLGQKLSLIGLKTDLARRLLRNNPDQAEIELND
LRQTASTALKEVREMTTMRGTQLVDELFRAEQILKAASIEFVLEGNPKLQDTSQLNE
NVLGMCLKEAVTNVVKHSQATTCTIIIKETLADNVLTIQDNGIGIERTRKQDRRGTI
LGMKERLEFVNGCLDIRSATDLPGTAIHHVPKLVRKPIKEAES"

CDS 3085131..3085730

/gene="desR_1"

/locus_tag="EFAGFIKM_02598"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34723"

/codon_start=1

/transl_table=11

/product="Transcriptional regulatory protein DesR"

/db_xref="COG:COG2197"

/translation="MIRIVIAEDQRMMLGALSSLLNLEEDMEVVGRASNGQEALALVQ
ELAPDICLMDIEMPVKSGLEAAEELKGMCKVILTTFARTGYFERALKGGVRGYLLK
DSPIEELAESIRQVMNGRRIFAPDLVDEAYVEENPLTERENAVLGLMADGKNTKEIAG
HLFITGTVRNYISILNKLNASNRIEAITRSKEKGWFK"

CDS complement(3085918..3086826)

/locus_tag="EFAGFIKM_02599"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKQPLWITIPVTTAVLLALAGCGGPDSNAASSENSSSPTTTVG
EQTETGSGGADFSNENETGKTENTGTTDNEDTSGSKAIDNQVATGQSGVNDVIKQVRK
QLKMKDAALPTSFTLDKGTSLGAAILSNTADAFKVNIFYATTQSVAINDQSLTASDSKI
PVLASYEVKTYKDPNQPEIFPETDLKDIPADMAVDLGHGIGKMSEGAAGSQYLTWQEG
RWTLEIRSVSEDEMNNSGIAKKMVEYLESHTLPVPKDKGYIKVEYPSGGKSVHVMISW
QDGNQIHQLKTDQVPLEALGMVSVK"

CDS complement(3086871..3087611)

/locus_tag="EFAGFIKM_02600"
/EC_number="3.5.1.104"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q81EJ6"
/codon_start=1
/transl_table=11
/product="Peptidoglycan-N-acetylglucosamine deacetylase"
/db_xref="COG:COG0726"
/translation="MLHIRKSIMVTLAILLIPLLLSQSVSAKSAASKDGASKANSKI
IYLTFFDDGPTAHTGQLLDILDQYHAKATFFMLGPQMEKFQKATKRIVADGHGLGLHGV
THVPSKFYKSAYSGLKEMQQANVSLNKVAGVKTSVVRTPYGSKPYLKPTFRNVLLGQG
GFHLWDWNVDSEDWKYQKDHQKVYNSVMKQIHNVQKSGTTPVVLMDQEATLKVLPQV
LKTLLKAEGRFEVLSKKVQPVNFWNDKR"

CDS complement(3088083..3088586)

/gene="ftnA"
/locus_tag="EFAGFIKM_02601"
/EC_number="1.16.3.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7A4R2"
/codon_start=1

/transl_table=11
/product="Bacterial non-heme ferritin"
/translation="MSQTLTESLNEQMNFYSAHVYLAMAAYCSSKSLDGFANFFIV
QAEERFHHGMKIYKFLNDRGQRATLAALPEPKNEYASMLDVFEHGYAHEQQNTKKFYN
LADIALNEREHATMYFLKWFIDEQVEEEALFDNIIQKLRRIEKDSNAFYMLDAEFGKR
SFTAPAE"

CDS complement(3088743..3088862)
/locus_tag="EFAGFIKM_02602"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSEVLGGETRGYGYGGFTSVGAILVLFILLVIISKAFLV"

CDS complement(3088963..3089220)
/locus_tag="EFAGFIKM_02603"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAKAKVAKRPTRDEFEEELGNQLVEAFRERSEVLLTVWGKEDQ
VQGVIVKMDSRTRLVHVEYTEEEFTAKVPFLDIMRVQSPRY"

CDS complement(3089374..3091065)
/locus_tag="EFAGFIKM_02604"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSQSSGPLSHWLKNQSLVRFSSGATELEQVSYSNTVVTWPWIGPR
LEVRKVCNVTEAALGQSLIYRVEIVNTGNLTALVYLLDQLSAETALLPNSVLRDGIPL
PGASPERGLPPAEIAPGATLRYHFQVVILRLPQALKLLNQAQVNYEFLTPEGRTVTGM
EQSNIVEVNLVSSRLEISFQADHIYTFSGDIVMYTVIVSNPGFITATNAQVTISLPQG
IVFIPASVIVDEMFAQVTPDTGIQLGEILPGSSIRIQYRVQVTRGSDANGISSVAVL"

AYISAGQQETVYSNQVTLEVIQPQVSVVKSVPVTATLGDVVQYNITVSNASSYAVDG
TLLDVLPTGMTFVEGSLGWNGVKRPGTNLAKGLNLGTLTARSVLNIQFEAKLPDRDES
MPDDYRYVNHASLMYFRLPDSRSVQRMITSNEAVVELKAPIIQAYVQVPTLVEQGG
TVTFQVRVGNTGNLPARVQLGCILPEGARWLGGATGEIQLSLPEYSTPRVLHVGVIIEP
GTEKNISYVAKLASEKTGTLQGALIARYTYDWNGQKRAGETRSNEYSIIIVEYGEE"

CDS complement(3091062..3097772)

/locus_tag="EFAGFIKM_02605"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIFIPLVVRSTVNATGAITFTGNTLGLSRSETAGVPGTQDSIGG
FITTNTSLQYGTYPGLTTSLYQSNSSAAILTLPA GSTVLYAELIWGGSYINGTVNLSA
AINNPVTFITPAGTSSVTPDPLTYNQFDLGGGAAGYVRSANVTTLVQNGGAGTYITGA
VVGTVITNDSTANHAGWTLGVVIYQNP NLPFRNMSLRAGGVLVQSTSPPVVTTLTGFA
TPLSGVLGGRILFSAQEGDANRTGDQALFGPTSATSVALSGPNNLAANFFASQINGDT
GALNTTGTFGTRNQINGAPGTNIIGGRQGWDITNVDVSARLINNQSSAVLTLTTSGDA
YIVNANAIQVDINAPKITLAKATVAAGAVAGDSILYSVTVTNAGTASAASVVLSDSLP
AGLTFIPGSVTVAGVSRPTLDVTAGIPLGSLTLSSSVVVTYRALIGQDASILQLVNSA
NAAFTFQSVAGGPVITGVIPSNNSTLT VYSPNLSIVKSASTTNATVGDLVTYTLQVNN
GGNVAANVTLRDNIPSGSSYVAGSFRLNGNVIAGANPVTGVNLGSLAAGSANTVTFQV
LVTSLPTPPTLVDQATASYSFNSPDGRTITGNIASNTLTIPVTLPNVTTVK SASVTDV
AVGETFTYTVVTTNSGIQVINNVLT DALPAGITFVPGSATVRGTVVPSANPSSGISI
GTLAAGSSATVTFQVNVQSLPASGSLVNRAVVSYS SGAFTGISNSNSITTPVYQAVVG
INKSASQTNASLGDQIAYTLVV TNSGNITTQVNVTD TIPAGLTFVPNSVTVNGTARPG
TSPLTGITLGSLLPGVTATV VFRATLTTLPTPTLENQGTASYTYQLPSGRNLSGSSS
SNIVRISASAPNISLSKTVNTPDATVG DVLTYTVVATNAGISAVQNLVISDAPSGAEF
VPGSVTINGS AVPSASPVAGIAVGTLN SSSSVTVTYQTRVNSVPSTGLVSNQANAAFT
SGSFNGVSSSITVNTPVFLPVMQV VKSASTTSLTVGDSFNYTIQINNTGNIAATVTLT
DPIPAGAVFSTNSVIINGVPTPGVSPETGISLGEI AVASSATVTFVATVTSLPDARQV
INQAVASFAYTLPSGRTVAGFSSSNTITIPVSLPNVTIVNSDNVEYG VVGDVIRYTSV
IRNNGTVAVNNVVYVNNPLPSNTPFVPGSVIVNGTSFPLSNPTAGIPIGT LAPGAEVTV

TFEVTITMPIPSQINNQSTVSFTSGSFSGSSSSNTTQTPVIQPQISLVKTANTVNAV
GDTVYTVTVSNTGNLEANVTLTDTIPAATTLVANSVVVSGVPQPGATPAAGIPVGIV
AAGATAVVTFAVVVDSLSPQQLSNFATSSFTFTPPDGRTLGSATSNTLTFPVSSPN
VAVVKSTASTAATVGDTVYSILVTNSGIAPVNNIQFSDPIPAGASFVTGSVTVNGVA
QPGANPAGGVPLGTLGPGTSATVTFsirVDAIPPSDQLSNRSTVSFTSGTFSSTTFN
TVVTPVYQPILSAQKTASTQNATVGDTVSYTITVSNQGNYGAIINLTDLNLPAGTILVP
NSVIVNGQPLPAGNPATGIPAGNVAPGATTITFSVVVDLTPSPQQLVNQASVALSYT
LPDGRNITESVLSNVLTITVSAPDVDVVKSTTSTAVSVGDIVTYSIAVTNNGIATVNN
VVFTDAVPTSTVLAPTGVFVDGVLPRGANPSTGVTLGSIAPGVTVTVVFSVQVTALPA
SAVLNNQSTVSFTSGAFSATTFSNTVTTVPVFQPILAAVKTDQTIATVGDTVYISAI
SNTGNYGASVTLTDTIPAGTELVPNSVIINGASAPGADPASGIPLGVVSTTLVTFVS
VIVTLPLSQSITNQASATFSYTLPDGRTLGGTITSNALNIQVSAPNVSVVKTPVIDA
VVGDTVYEMVVTNEGIDPVNNIVITDPINPATTFTGSLVDGAPRALANPALGIAL
GSLAPGASIAVSYAVRVNTLPTPPQVSSQSSVSFTSGVFSGAAYSNTVVTPIYQPIIA
VTKTGSTSNATIGDTITYSFAINNSGNLDAILTLTDNIPNGAVLLPNSVLIDGVPQPG
ANPETGIAVGTIPSGGTIVVTLEVTVDSLPQDQQLVNQAVANYTFSPPDGRLLTGT
VSSNVLVIPVSAPNVTVVKSTSAVDAVVDVITYIVVTNSGIEVVNNVVMVDPVPVG
TVFVPGSVTVEGVPRPTGNPNTGITLGSIAAGASVTVTFRVEVVI"

CDS 3098080..3099144

/locus_tag="EFAGFIKM_02606"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLHAYWVVIIAHFAIQIGCFLFLEYDRTPIDFLMNVLFWPTAVS

SSCILFASWVDRRFSSYSFYTMSIASTVIAWTIIHVNYDIRIILAICLLPIFASVLFF

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LDDLQASMLAKQDLIVRNAIMTKQSKTDGLTNLYNQSSFKDYYEKAFEYANSGMSLHL

ALIDIDDFKSINDTYGHRVGDIILEKVSIIQETITSSDIAARYGGEEFALLMFEQSF

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CDS complement(3099249..3099770)

/locus_tag="EFAGFIKM_02607"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSGKYTSVPYGYEPPAASRKGTLTIFYDSFEHVTDEQLERAAATV
DTRSFQQLVLYPLHESTFKRMSKDSIQAYYKREDRLHDWRREHPTSRRIRVEGLEGKRK
KYTPVDSALRHITAEPAPHFLYLTIEMANLFASFDSFKDWIKELRLIIDGSSEYLHP
MLEQNRHRWEWAE"

CDS complement(3099842..3101482)

/locus_tag="EFAGFIKM_02608"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSFKISTVLTVIFAVLSLLVTLTIGSIFSQKSFVAVETEIGHSL
TGTSQASDKLDRFMSARAGELDLLGQMASLEDEFQPDIEQMLLDQLQDSFPSFSWVG
FMDPKGKVLAAATDGILLGENLSERPVIYQEGIKGKFIGDVHNAVLLAKLLPNPTGEPLQ
FVDISFPLKDSKGMIIQGVLAHLSWEWAKEVEESVLAPLKREKDIIEFFIVSKKEHTV
LLGPKEWVGKPLVLPGLIEEAQLNKSSWSIEKWPDGNEYVTGFAYSQGHLDYPGLGWT
VIRQVKSSAFASVFDLMWFNVWSGLAVTVLFALIGWVVSRLISAPLVRLTRVANRLRA
GEELEIPAIGIKEIEVLSRSLRDMLTSLMNKNSLVVMQNLAHFDQLTRLNRTALE
VYLEESLETESENHTLTFLYLDLDGFKRVNDTLGHQTGDVLLQKVAQRLSALVQVKGI
TVRLGGDEFLIVLQSVGSHPREEMAYAEAIQSLNKPFIIEYERIRIGCSIGGAIEYP
TNSDNPSEIIRMADEALYESKRAGKNRMTFYSELKQDR"

CDS 3101784..3104738

/gene="mrpA"
/locus_tag="EFAGFIKM_02609"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9K2S2"
/codon_start=1
/transl_table=11

/product="Na(+)/H(+) antiporter subunit A"
/db_xref="COG:COG1009"
/translation="MSLLHVAVILPFAAGILLAMLHRFFRKNH LGWPVLLVPALLFVY
FASLIPAVSQRNTVSGNIPWIPSLDIGFNLYLDGLSLMLTLLITGIGVLVVLVSIFYM
DMKEALNRFYLYLLMFMGAMLGVLSDNMIVLYGFWELTSITSFLLIAFHYKRKASTS
GAQKSFLITVFGGFAMLTGFMMMYLITGTFSIRATITGLGQFQESALFLPALILILIG
AFTKSAQFPFHIWLPDAMEAPTPVSAYLHSATMVKAGLYVVARFTPIFGGQGLWFWLV
TGVGLLTLCYGSFLAVKKNDLKAILAYSTISQLGLIMSLLGVGSAALYFGYGESSAMY
TVAITAALLHLFNHATFKAALFMVVGIVDHETGTRDIRKLGGGLASFMPITFTVALIGS
LAMAGIPPFNGFLSKELFFQAMVEVTHLRIFGLGWSVLLPVFAWLASVFTLIYALII
VFKTFLGRSQSEIPA EKLHEAPAGMLIPPVVLGVLVVVVFG LFPNLLAGSLIEPAMAAV
LP SLLNGNERFDVHFSLWHGWTP ELIMTIGVVILGITLYKLLPRWRNIYEHYPQGLTI
NNMYHVVL DNLQHYARKWTEAYMNGSVRNYLVYIFSFTVALLVYAFFRSGENITWNLQ
GNAPYSFYEVVLLVTLIGA AVSIPFAKNRLSAVIMTGAVGYLV TLLFVLFRAPDLALT
QMIVETVSVALFLLCFYHLP ELQRGKSSRSYLTVMIVAIAVGIVMTFVALAASGTAS
LDSISTFFLQEAYDSAGGKNVVNVLLVD FRGFDTLLEIMVLGVASLSIYSMINLNLEA
KDLGARLKFRKKDESKES EPALDDETDNTKKYGNRERSSSSWDTVPLQSN DVLLQTTT
KVVVFII LTFAMHLFFAGHHNP GGGFIGGLVTAAALVLI ALAFSTD TIRKALPVDFRI
LTGIGLGIALLTGAGSFIFGVPFLSQTFGYFELPLLGETELATAM LFDLGVYLAVLGV
TMTIILQIGEDR"

CDS 3104740..3105078

/gene="mrpC"
/locus_tag="EFAGFIKM_02610"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O05260"
/codon_start=1
/transl_table=11
/product="Na(+)/H(+) antiporter subunit C"
/db_xref="COG:COG1006"
/translation="MEILMCIAVGILFAVAVFLILSR SLLRIVLGMSILTHGVHLLLI
TMSRLKTGAPPLLGE MAERYVDPLPQALILTSIVINFG LTAFFVLSYRSYLKKTDD
MEEVRGRPYE"

CDS 3105071..3106549

/gene="mrpD"

/locus_tag="EFAGFIKM_02611"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O05229"

/codon_start=1

/transl_table=11

/product="Na(+)/H(+) antiporter subunit D"

/db_xref="COG:COG0651"

/translation="MNNLVVLPILLPLITGVLALLFFRKTNIQRIISVIGLLFTAAS

TILITRVTTQTGVLTLNMGGWAPPYGIVLVADMVSALLVVAASIIALACLLYAFRSVNK

EREEHHFYPPFFHFLIAGVNGSFLTGDLFNLFVSFELMLISSYALIVLGGTERQLRETI

KYVLINIVSSALFVASIGFLYSITGTLMADLSVKIAEVGQSGVITLIAVFLIVFSI

KAGLFLFFWLSGSYAAPPAVVTALFAGLLTKVGLYAIVRTFTLIFYHDPDFFHALIGW

MAGATMVLGVIGAISYRDVNKILIYNVAGVGAFVAFGMASASRPALLEGLLFYMLHDML

IKTLLFLLGGALIAVAGTSKLDNMGGLIHRYPLLGWMFFISALALAGLPPFSGFPGKL

LLFEGGLQAGLYGLTGIAVLSSLLMLYSVLRIFIQAFWGEPPAGVTRRPYAVNGLLIP

AGILFVFIIVMGVGAEGMFQLTSRAGDILLHPNIYIDAVLKE"

CDS 3106556..3107032

/gene="mrpE"

/locus_tag="EFAGFIKM_02612"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9RGZ1"

/codon_start=1

/transl_table=11

/product="Na(+)/H(+) antiporter subunit E"

/db_xref="COG:COG1863"

/translation="MAFQIVLNLIIFVWMFLNNAWNGVGFLIGYLLGLLIGGMRRF

FPQRFYIVRVWAIKILINLLFKELVRASIEVIRQIIKPKLDIRPGIFTYKTQLSSDWE

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CDS 3107032..3107316

/gene="mrpF"

/locus_tag="EFAGFIKM_02613"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9RGZ0"
/codon_start=1
/transl_table=11
/product="Na(+)/H(+) antiporter subunit F"
/db_xref="COG:COG2212"
/translation="MLSSLLFISLLLSLAILGCLYRVLRGPSMADRITALDTIGINV
IAIVAVLSMMLQTQAYLDIILLIGILAFLLSTVAFARYIERGAVFKNDGDR"

CDS 3107300..3107692

/gene="mrpG"
/locus_tag="EFAGFIKM_02614"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9RGY9"
/codon_start=1
/transl_table=11
/product="Na(+)/H(+) antiporter subunit G"
/db_xref="COG:COG1320"
/translation="MMEIVKVAETAIGLLVLLGALLSALSAFGLIRLPDVYLRAHAA
TKSMTLGVFCVLSATFFYFWYFDNYISARLLLIGILFVFITAPVAGHLNGRAAYRTDVP
LWEQSVQDELEPLLKGKKVNHEAKDMME"

CDS complement(3107818..3108990)

/gene="yxiM"
/locus_tag="EFAGFIKM_02615"
/EC_number="3.1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42304"
/codon_start=1
/transl_table=11
/product="putative esterase YxiM"
/db_xref="COG:COG2755"
/translation="MKWSISVKLLLCFVLFASTMGIGLGSSGGQVAEAATDNYRFDG"

SGAVESGYTGVSAGDAYTPTKGYGFNTPAQMRNVASGSGVKSDAVQFLTYGTKSTNT
FNVNLSNGLYEKVVVLGNTARASVAAEGVYQIINMTGNGATDQFQIPVTDGQLNLLVT
EGKTGTAFTLSALEIRKLSNQTVTNRTIYIGGDSTVCNYYPLGSSVQGGWGQLFPSYV
NNSTFQVRNMASSGQFARGFRDDGQMEAILKYIKPGDYFILQFGINDTNAKNNTTEAQ
FKEIMRDMVRLAKNKGATVILSTPQGRATDFNTANVHQAENRWYNQSTRALAEQEEGV
LVELNKLSSAYFTSIGPAATLALYMTGDSLHPNRQGAAELARIVAADLRRQGLNGF"

CDS complement(3109042..3110061)

/locus_tag="EFAGFIKM_02616"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSDIEAYLQQTNLRGRSAYHADQPLELWRSQLRTRVKERLGGF

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DAPPGVSSCTKIAAHLLMVGKTLAGHRVYETTRVLDYVSTRPEVDSERIGSMGISGGG

LVTAFTAALDERFRATVSGYANTFQGSILDRNHCLDNYPGILREAELPDLIGLIVP

RPLFIEAGSDDQVFPIHAAREAHARLTHIYEQAGASESLDADFFTGGHEISGAKAYDW

LDQVL"

CDS complement(3110253..3112484)

/locus_tag="EFAGFIKM_02617"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WJT9"

/codon_start=1

/transl_table=11

/product="Heme uptake protein MmpL11"

/db_xref="COG:COG2409"

/translation="MGYRRLAVLISRYPRFIILCWVFIIGMSAVWAWNLPDIVQDHGL

KRVHGDAQAVELVLEDEFGSPADPVILVFEKKENTSPLQFRQWIKDRLTQVQVLPVAVT

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VQQDVNHLSFRDLERAEMVGLPIALIVLCFAFRGLYSALIAVMMGISAVITAMGVTSL

LGYHLELSNFIINVIPMVGMALSIDFALIILSRVREEVQRAYEDEGEANVLGRSLDMQ

SEILQRTLRTAGRAVLFS AACVLLG LLG LLWIRLPMFLSVSLGAIIVLLLSLLLNVTL
LPALLSLSADRVFRRKLVHSLPRRSVWHRWSAMVMKRPVSMAIGGTVVL L LCVYPVTR
LELSVPDASSLPEKMESRQAAEQ LQHDLGKKSTSAIEILIGGQQELLTASHWQLAHNK
ARQLLQDSDVLSIVSPWGLLQPNQIDSQSLFQIPPPALTPSIEGEESTRASWLRSTVS
DHSIRLIATVHGEPGSEQVADWLERIRNRDHAPGFNNVKLRYGGEEAAKQYEIMQEVTS
QLPKVLV FVVVTNYLVLLAAFRSMLIPIKAILMNLLSLAASF GILVWVFNEGHLGMEP
SAIAIMIPVFIAGLVFGISMDYGVFMLSRIQEVYRRTGDS D VAVQQGLASTGRLV TSA
AAILLAVTVPFAFAEVAGVRQLGIGITAAVLIDVT LIRLILVPALMKLMGRWNWWLPG
QMK"

CDS complement(3112593..3113747)

/locus_tag="EFAGFIKM_02618"

/EC_number="2.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WPF1"

/codon_start=1

/transl_table=11

/product="Alpha-pyrone synthesis polyketide synthase-like

Pks18"

/db_xref="COG:COG3424"

/translation="MNQLEATTGASIMGIGTAWPAHRIEQKDVSARLAQALEHEPDAR

RWAKRIFNQCGVETRYTCEPNLLEPVDSCRYLPFTNADEVPTTSERMGKYKAAAVPLG

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AAGLKAIQLANSIVTTDQKATVLIVCVELCTLHFQPSAKRDDLYAASFFGDGASACVI

GASGTDNRNECFRLGRGHSTLLPDCAEEMIWEVGNTGFDLYLSPQIPKLLGLHLGPEVE

RLLEGSGFPEIWAIHPGGRGIVDAVQKLYQLTDEQVSYSRNILRDYGNLSSVTILFVL

QAIREDYRQKEEHSSGIALAFGPGLTAELLPFTYIPAPIANRTPVNHGIQ"

CDS complement(3113982..3114602)

/locus_tag="EFAGFIKM_02619"

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/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYTLDPREITGRDNYKLMSGSVVPRPIAFVTTLSDKNGVINAAP
FSFFNVVSSDPPLLSISIARKDGIVKDTARNVLAHQELVVHICDEAIITEVNETAAIL
EPHESELERTKLTIVPSTKVAVPGIQEALIRMECELYQHIPITNDDGKPVSDLLLVR
VQYHFSEQVYNPDKGYILMDHLKPVSRLAGNDYAKLGERFTIIRPE"

CDS complement(3114760..3115737)

/gene="yfiY_2"

/locus_tag="EFAGFIKM_02620"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31567"

/codon_start=1

/transl_table=11

/product="putative siderophore-binding lipoprotein YfiY"

/db_xref="COG:COG0614"

/translation="MIMLLMTVMVMSIWLAAACGAKPAENGAAGENDTTTETETQTEAA
TERTLTDAMGHEVTIPANPERVIASYLEDLVTLGVKPAAQWSINNGNGLQDYLQNDL
NGIPGIASDLPFEMASFSPLIIMGSESTVEGEKYEQYNKIAPTYVLGDEVNKDWRQ
ALLKIGEILNKSDVAQKALDDYDAKAKEIKEKVIAITGGTKSAAALWLFNNKFYVVS
NVSSGEVMYNELGLAEPNVVKEASAKATGNWSEISLEKIAEMDADYLFLVNSDKGAGS
EALQDAVWQSIPAVKTGNVFEFESTSSWLYSGVQANTQILQDIQSSIVK"

CDS 3115992..3116642

/locus_tag="EFAGFIKM_02621"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLNAEYDDRKDVLYMYEYNPYLSYGEDRSFQLPPLFPGGGGGG
TPGGPTFPGIPGGQGTYPPIPGGGPGPIPGGIPGTIPGTAPGVPAQLTQGNLPTLL
SAYPRPVGQPPAEMFLYNLIKSSPGLLPLFLQQQPQSLTQAVQFAQTGAAAPRDNEE
RALPNFCYNRWSLVFTYNDVYLMWPAINLFGFVVGYPFLTPGILSNTQILFALC"

CDS complement(3116780..3118015)

/gene="bcr_2"

/locus_tag="EFAGFIKM_02622"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P28246"

/codon_start=1

/transl_table=11

/product="Bicyclomycin resistance protein"

/translation="MKSTTASLNMNSTSRVRMALILGTLSAFGPLSLDMYLPALPTLA

DEFGSSTSYAQLSLTACMIGLAVGQLLAGPLSDVRGRRTPLIAGLVLYTIASILCLVS

PTMGPFVVLRFIQGVAGAAGIVISRAIVRDVYSGPELTRFFSLLMLINGVAPIAPII

GGQLTYTSWRGVFILLSLIGILTLLAVIFGLGETLPSNRRSSGGLKQTLTFRQIAG

DRQFMGYALTQGFVAAGMFAYISGSPFVLQKIYGVSPQMFSVCFAINGLGILASQIA

GRLAGKVSETRLLIVGLLTAALGGTSLIAILAGGNLISVLIPLFLVSSVGLVNTAS

FALAMANQEKSAGSASALIGVMTFLFGGIVAPLVGLGGEGTAVPMGIVACADLGALV

IYFLMVSRRGRKRHNDQVLS"

CDS complement(3118022..3118768)

/locus_tag="EFAGFIKM_02623"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMNAPHPIDQFKKFKYEITRFMMIYKFALDQMETKIEVLKEEFQ

SLHDYSPIEHTKSRLKSPESIMNKMFRKNHELTFESIKQNIKDIAGVRITCSFISDIY

RIKDMLCNQSDLRVLEVVDYIENPKPNGYQSLHLLVEVPVYMSNGEERACVEIQIRTI

AMDFWASLEHKIFYKYNKDVPEHLTREKSAADSANALDQQMERLHREIQEIKDADNE

RDEEELRRIINNQQFTLPSNLLKLLGSGE"

CDS 3119197..3119886

/locus_tag="EFAGFIKM_02624"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHDTDNIPQWPVLIYCRGGLGSYGGVNTVWLEQFVHKGYIVFA

PSYRGNEGGEGRDEYGGGRDAEDVHAAYRLIQRLPFVDPTRISLMGFSGAINAVHTAT

AYNEGPDRVHKLVLWSGVADVERTYHERTDLRRTLKRVLGGSPRAVPEAYLARSPLSK
ANKLSCPVLIMHGTSQTQVNYSHGTRMYHWLKRGGVNVTFHAYGGQDHHFHEKIHQSA
VNNMFDWLTAP"

CDS 3119973..3120689

/locus_tag="EFAGFIKM_02625"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSQSTLQKYAMLLLCMSAGMVDLIGYLGLGHVLTANMTGNIVLL
GIAIARAQEFVVLRSLLALIGFIAGNAIAAHMVGPVQTKNGWSSRVTAVFTVESILL
LFAIAMISPFSGQLSYLLIVILAVAMGMQTTAARRIGIAGISTTVLTNNLAAVVEDTV
SILKKLRHANIRSLAKALSTDAYLRAGAVVIYLVIAAALLFHRVPMIAVWIPVLII
GGVTLYARLHAWGTSQQSKS"

CDS complement(3120806..3121702)

/gene="cmpR_5"
/locus_tag="EFAGFIKM_02626"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9F1R2"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator CmpR"
/db_xref="COG:COG0583"
/translation="MNLHGLRLFHAIVRYGGVTRAAEELNISQPAVSSQVKKFERELG
IQLFVSEGRRLVLTDAGIQLTGYAERLFMLKQDVENFVQDFREGKKGLIRLTATYLP
NFLPGWIARFKQMHEDEIVVSTNTRMAFDQLLRYEAEIAVYGGSGITHAGVQWDE
LFDDEMWFVHPDHPYAGKEIELHEMMAEPFIMREEGSATRERLVSLCTTNNLAAPRI
ALQFNGLNETISAVKAGYGANFISSLVVNEDVQQGRLARVFVRGVQLRNTVAVCTRAG
EVLSPAAQHLVKLIRQEVALMK"

CDS 3121841..3122545

/locus_tag="EFAGFIKM_02627"
/EC_number="2.1.1.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07431"

/codon_start=1

/transl_table=11

/product="Catechol O-methyltransferase"

/db_xref="COG:COG4122"

/translation="MKNINTTNLQHTWTQVDDYMNDDLIPSDSLEHTLQSNAEAGLP
AHDVTPNQGKLLQLLLQIQGASRVLEIGTLGGYSTIWMARALPEHGRIVSLESESHHA
DLARANLTRAGLMHKVDLRVGPALTLPDVQEEYREPFDMIFIDADKPSNPNYLRWAL
RLTRPGSLIIGDNIVRDGEVIRTNSTDPRVQGVRSFLQLIADYPRLEATALQTVGSKG
YDGFVIARVIDAPEPK"

CDS 3122623..3123933

/locus_tag="EFAGFIKM_02628"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRVLQHINDEIRGWSRNIQLFFLASILYQIGNGMFSVLYNLYIQ
GLGYNDTMNGQIVSIQSLATAIMFVPIGLCGDLFSRKRLITGALFSGIFLIGRSFDY
SATGLIWFAVFSGLFAGVFQVLAIPYLAENVKKSQRLKMFSYSSVLASQVLGSLGG
GVFADLLHTAGLAKVTGLQTVLFVGGAAATLAAFIPLLFTGKAAPQTTIPAPVLQP
NADLKESSTNTPSTDDSIKKKDSRLIGQFIVTQLLIGLGSLWVPLYNLYFTNRFSV
SLSGMSLLIALGQIMTIVSMLIGPTLAAKVGSVRVVIFQVMSLPFLLLTGFTNLLFI
ASLSFLFRQALMNAANPIHSAILVDRISDKRRGIANSMLQTSFMIGWATMGVPVQSYLV
TTYGTYWGYAITFSITGCLYVISSLMYYVMFREPKPSATALAGS"

CDS 3124082..3125197

/locus_tag="EFAGFIKM_02629"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MELMRKLGSHVVFRFFLSLGVSVLGGLLFAVIHTPIPWLLGPMV"

FMLLSQVAKWPLIWPASIRDYGILIVGYSIGLTLTKEALHGILQQLPMMLLMTLLLI
GLCVITAYIASKVTDFFPSLLVGSIPGGLSQMVSLAEEMKSINLTLVTFLQVTRLIM
IVFCVPFLLFSPWIGGTAGGGLDHPFIDVATWGTLFPEILLYVPLCVAGAWIARKLRF
PTAFMLGPMIVMCVVQLSTTMHTPSLPTSLLNVSQLMIGSHVGLMLKPEQLQRKTQTV
TLAVTSSVLLIVGALGLSYLLMNVFSLSAATSLLSMAPGGMDQMSIMAHEVNADLSV
SGYQLFRILFIFFIVSSVLKMILVHMLKEEKAKPYLQ"

CDS complement(3125326..3125529)

/locus_tag="EFAGFIKM_02630"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGLVKRFVLVVNMIGELWMGFYRRNSDYYDHQTSESKSIGYY

AFIIGATVVTVGIVGWMYNRIYS"

CDS complement(3125607..3125870)

/locus_tag="EFAGFIKM_02631"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AFT8"

/note="UPF0153 protein YeiW"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MECRTGCAACCIAISSPIPGMAHGKPAVRCVQLTDDNRCGI

FGQKDRPAVCSGLQAEEMCGSTDQEA FNILTWLEQETAPKVI"

CDS complement(3126026..3126874)

/locus_tag="EFAGFIKM_02632"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTRVAVMVIHGLGMRKEGYADKLIACLHKELDQVMVLPGA AKQM

LDIEPVYWADVFEEREEALFQQLVSSPGLNYQTLRRFVIHYLADAVAYQPVENQGHNY

DAVHRTLNQAMHTLAQRNGPEAPLCVVAHSLGAVIASNFFYDLQYPSSRVPEIVDVNS
ALERGDTLTHFYSFGTTLPLWSLRYHDFSCPIQVPSSHVNHYTGLEGEWVNFYDRDD
ILGYPLRPIDPAYEKAVKEDIEVNSGGLALSWNPLSHGGYFSNRSMNRRIAQGLARTW
TWVNRS"

CDS 3127709..3128026

/locus_tag="EFAGFIKM_02633"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAIKGQKYKTYSEKIKKEAIRLHTVEGWTYRKINEHLGIHDPGR

MKRWMRKHREQGEFGLMDQGRRRKEYLDQERYVQCLKRENELLKKCLVIWKEEANKKD

FRS"

CDS 3127975..3128859

/locus_tag="EFAGFIKM_02634"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISBth8"

/codon_start=1

/transl_table=11

/product="IS3 family transposase ISBth8"

/translation="MLGNLEGGSKQERFQIIEKVAAYGDIQKLCDFGVSRSGFYAYV

KRKRFRDRAKAKKQVLQTYQRYEGKYGYRQLQLFLWQDQGIWMNHKKVLRLMQMLGIQ

SRIRRKRRSNSSYAPAQRVAENRLKRDFSAEKPNQKWVTDITQYRVGERWIYLSAID

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QRKLKKLTPVEYRRQFAA"

CDS 3128955..3129806

/locus_tag="EFAGFIKM_02635"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSQKIAVIVIHGLGKQHEDFATIFSDNLHKTFTTVSGMKNPELC
IEIRPVWWASVFAEREEELKRKLVGAPYNLRYEELREFMIHYLADAVAYQPLRDGGEQ
NYDAVHHTISKQLNRISIEVGPDTPLCVVSHSLGSVIASNYFYDLQNAKEKTKIIDPS
SPLERGETLSLFYTCGTTPLWLSLRYTSFDHPIQVPSKDFLT MHPNIAGEWINFYDKD
DVLGFPLKSIHPEYDKIVKEDRDVNVGTIIDRWTP LCHNGYLHSNKVIRPIAEG LHKI
WQQINGL"

CDS 3130528..3131484

/locus_tag="EFAGFIKM_02636"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:ISfinder:IS658"
/codon_start=1
/transl_table=11
/product="IS30 family transposase IS658"

/db_xref="COG:COG2826"
/translation="MSYRHLSIERSKLEVLHRQGRSSRAIAKELGRHPSTICRELD R
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RDAVSFKTIYRWIYAGRLVRGV LQVLRHKGKRQKPAETR GKFAIGRTISDRPKEVRSR
ETFGHWELDTVVSGRGKSKGCVATLIERKTRLYTAVLMPDRTALSMEIALGVAISQYP
TGFTLTATADRGKEFACYAHLETT HNLHVYFADPYSSWQRGSNENANGLLREFFPKGT
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CDS complement(3131628..3132329)

/locus_tag="EFAGFIKM_02637"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MNLTKIISSELEDKLKELS FDFEDSSNPWIFVRAREGYVKDYIE
IDKSNWESNAIRCTFQTGSES VSSPKLAERKVDEWYVYQNEEELTEVLHKL RKIIEQY
ALPWFAENTQLIPSATPNYLDES WKDSIQEFMKNKIDINNSES VGILDQLVISNLSQ
KDIYFISYCYGEIIISQFGGEWKYDANNGPRVDNIGGNPAFKRLPHDFVNKV IENKNL
SLQRYIEDIAFVLED"

CDS complement(3132558..3133964)

/locus_tag="EFAGFIKM_02638"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKGPFGNTVYYTNDVMNRMTSVGTAKDAPDAQYKYYGNGLFKSS
ESLNDVSTLRTYNGLDLVSLEQVRGQDTLALYNYSYDSNKNITKRVQQGVQDDFTYDQ
LDRIATASGNNEQYTYDKQGNRLTMQSDKEVNSVESEYQYDTSNRLTQVITDVAKVNY
QYNGDNLLVERTENGVAIRYYDDRAQIIAEAEVLNGTPELKANYIRGAKLEAIVYAN
GSKAYVQSNHGDITELRDVDGALLNKYQYDVWGNLELKEEKVHNPFYSGELWDDTT
RLQYLRTRWYDPNTGRFINEDTFEGELDDPLSLNLYAYVHNNPLRYVDPSGRAKFGST
AYGQYAHKALGNIFKLINLFTKNDVAFTEKTVKLANGNSGRVDFALKVGESQYEIYEL
KPISWNNNPQLNKSGRDQLKSYIHGILNGFRGDSTATARAGTTWNPNNVVIPSPFNS
RKEIVFYTYATQPGMIY"

CDS complement(3133961..3134458)

/gene="rhsD"
/locus_tag="EFAGFIKM_02639"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P16919"
/codon_start=1
/transl_table=11
/product="Protein RhsD"
/db_xref="COG:COG3209"
/translation="MEQTDGNGNVKTFNYDVMGQLRQVTSANGEQTQYNYNLVGNIK
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LTGQR"

CDS complement(3134510..3138688)

/locus_tag="EFAGFIKM_02640"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MKQSITKKYISILLIVSVFSGLFGNWIPAITYAEKQNEQEVSTG
QNPSPLESLSLIAEQFDRTEGFIQGYLDQGYTLNEVISALYKARDEQIGFDEALQAVR
PQEVNESASVTSDVYTDSALAEETPLTGVEADQSSIMQRYETFAVEEELTAPPDTDLE
KDNEPKEEEDKQAEGEEKEQVDPDDQSEGEKESEGTEETAPSTETTTDDENAPQTNQD
VGQEPTAPSSSENTSTLEGKPAAESKETPSSQESAEIPSSSMESKSEPKNISEKVS
SVPEKGQVKENNDASITNKKQSESSSPSKQKSKSDVKPLAGQTSVPDPGKHIAEKAPV
YSKKSFNAPYTVGENGESISTMSGGLMLEHVDASLPGRAGMSFSLERQYNSNSAQFY
DPAVGNTYEPVYNYFLTYQAVKKKIITKYHVYKYNKWWQEDYNGDGLKDNDTIV
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TVEGKTITLRSSVTATKACPSPNKSVANYVCTKTWEARYNGSVSIPESDTRVYSQSY
IGSVVKPGQYSQQRYDSWIAGKAPYQYRYAYSVREQPWVEQEVTEGPAETITLYTDGT
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VPATADKRAPLGKGSWKL PFTETENGTSYMN MADGGRYE IAGNTLKG YDWE GITVNP
DTSVTVNGESSTLVLTSSDGLTKQYFSVDGRLLQISDGQKNDVQFFYENNSVYNSKLL
TQVKDAIGNTISISYTSSAVTIVQGNRTVTYNKQTKNGIELLDSVIDPLGRKTTYSYK
LADAKFNLPGFSPERAALNPYALLTSVQHNTGAKTFY EYENGTVKRYIGEDSFNDAYR
VLSRKDQITYENGSTEDFNRQTYSTSDIGASFSQDTTFAVLVSNGLTNTQYN YRKDF
INNDTQAQFYLDGTMVSAEGKTQTTNTYGKTVKGRSYAAPTPVTTVTDNQA KDLT
TTVQLDDYGNITSVTDATGR TTTSTYDDTRHWVTSVTDMVDATNKKYTVLTRDNVGN I
KQIVNRKDSASGELLTQADYTYDAYGNLLTQHISDGKHERNATLEYDGRYQNAFPTRL
STNVTDVDGR TTQINSLSEYDLSTGALIASTDEEQRTTKYRLDAIGRTIEVTQPDGTM
LRADYDDINNTIKVTDELGQQRLNKWNSLGQAIEKGYFSGNSYIVSQRNGYDPYGRVS
WTDDALGNRTRNTYDSWSRTVM TTTGADGTSTSMKYDDV VHTATSTDAEGYVQITTYDK
WGKGIKTEEKTQLD"

CDS complement(3138758..3139603)

/locus_tag="EFAGFIKM_02641"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPKNLKLEILSHTSVIVSWDNIKEVNGDVVGVNIIYQDNVLIGAT
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LMVTKYLKGGKITFTPEQIILADMNNDGIIDESDVKNILSFSVSNSSGNSSLEVPKDLK
LEILNQTSIKLSWKALDELNGGKGFNIYQDNVLVSTTNETSQVVNFLDPQKTYTFLV
RSKNSEGDESEPSNLIKKTPFKQYTYNYDSSGRLNSILTPSGKKIAYTYDANGNLIKK
TITNF"

CDS complement(3139588..3139929)

/locus_tag="EFAGFIKM_02642"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDEGRELLILKSSRRVFLTCIIFLFSFSLLLDEVHSAELAVLKG

DVDGNGAVTANDALMVTKYLKGGKITLTPEQIILADMNNDGIIDNADVVSILSIHVGTV

TEKKRQKCQRI"

CDS complement(3140586..3140732)

/locus_tag="EFAGFIKM_02643"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDAAFRNWDPKRYVLKKVHVGSFLQVVDYAIQHDGLRIILEHG

LNHY"

CDS complement(3140960..3141136)

/locus_tag="EFAGFIKM_02644"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDFSGESIACRRHDTYDVQFEFLTYNFTVTELSECTLEEVEEMF

YSVNQSVINIYREN"

CDS complement(3141422..3141880)

/locus_tag="EFAGFIKM_02645"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKGQDTISKGFALALMSIARKQRRDFAWIPFSSHASDAIIYERG
KIEVPDMIQLATVFLDGGTNFVQPLNKASEVIKQSRFNQADIIFVTDGEAHVNNDFLK
AWSSLKEQKGFSVLSLLLGKESIHGVGGFSDRVVRASSFEDQSIQQAFDI"

CDS complement(3141877..3142482)

/locus_tag="EFAGFIKM_02646"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTDQGYLDFREFTRLDDLAAAIGTTKYNENVLGWVKEQATEALS
AALNQNGSQLSQILAQASDEAIETKENVNFMLGGIQAGSSDSELKKVPLKEQLFLAEK
LSHNKNLKEIAKWTRMKVIASRKQRYKHKDAIDRNGIRQGS DIEQLLPMELGSYASP
PLAKWIFYADMRKDRHFSMTPREKNISVKGPLSCVSINLVV"

CDS complement(3142486..3142653)

/locus_tag="EFAGFIKM_02647"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MPKLHMI EELKRVLIEGYNEAKLERN SYDEGWAQIYSAKQNDLI
LQADMVGVEVK"

CDS complement(3143720..3145738)

/locus_tag="EFAGFIKM_02648"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MAIDKKQVEEIVRAVGGKENIEAATHCVTRLRFALYDESKVDTE
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IQRAIKTSLDIFIPILPAITAGLLLGINNILTGPGIFFDGKSLVDVYPAWKDLASII
NTIASTAFITFLPALIGWAAVKRFGGSPLLGIVLGLILVHPDLLSAYGYADAVNNGTVP
TWNLFGWIEIKIGYQGQVLPVLVSAYLLAKMEIFLNKRVHDSIKLLVAPVTLLITGF
LAFTIIGPVTFAIANAITSGLIYVYDSYAALGGLIYGGLYALLVITGMHHTFLAVDVQ
LIGSQGGTFLWPMLALSANIAQGSAAALAMMLVLREKKMRGLAATSSVSAFLGVTEPAIF
GVNIRYRYPFIFGMIGSAIGGVLLTMNNVQATSIGVGGVPGFLSIFPNKWGVFFIGMA
IVLVVPFVLTVLFGRALKRKEDRSASNETINEPKAATSQSASVTSSTAKTDPNQTR
SAAQVGDEAVNTLEIMAPLTGQAVSLEQVPDPAFAEKQMGEGVAIEPSGNVVVAPFDA
QVAHVIKSKHAVILEHASGLQVLIHVGINTVSLKGEFNMHVEAGEHVKAGQKLLEFD
RKVIEDAGYPLITPIIPDGQDMVERVEVTTGDVTSNQNGVLKVHLKG"

CDS complement(3145767..3147488)

/gene="treA"

/locus_tag="EFAGFIKM_02649"

/EC_number="3.2.1.93"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39795"

/codon_start=1

/transl_table=11

/product="Trehalose-6-phosphate hydrolase"

/db_xref="COG:COG0366"

/translation="MSSNNTTPSSWWKTSTVYQVYPKSFNDTTGSGTGDIHGLTEKLD
YLQHLGIDIVWLQPVYVSPQHDNGYDVADYYRINPDYGTMEDFDELLKGLKARDMKLM
IDIVVNHSSTDHEWFQQSRSSKDNPYRDYYIWKDPAPDGGVPNNWQSKFGGPAWQFDE
QTGQYFLTLFDKTQADLNWENEEVRKAVRDMIKFWAEKGVDGFRMDVINLISKDQRF
DDGGSVSPGDGRKYITDGPVHEYITEMYDEVFGPHNMVTVGEMSSTLEHCCIYQSNP
ASREFSMTFNFHHLKVDYPNGQKWELMPYDFEAMKQLFSEWQTGMQAGGGWNALFLNN
HDQPRALSRFADDGDYRAESAKMLATTIHGMQGTPYVYQGEEIGMPNPVWNDVSEFRD
IESTNMYRLLQEERGKSAEEAFQIVKERSRDNSRTPMQWNGSKNAGFTTGPWLKVDE
RYPsiHVEQQLADPDsiYYHYRKLIALRKQVNVLTdGLYERLDDAHPDVfAYARTNGS
ETLIVVSNFskRDVtFSLPEAVWNDHIASKSAELLIGNTEAAPALTQEISLSPYASYM

WLVPQQD"

CDS complement(3147865..3149220)

/gene="dctA"

/locus_tag="EFAGFIKM_02650"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A830"

/codon_start=1

/transl_table=11

/product="Aerobic C4-dicarboxylate transport protein"

/db_xref="COG:COG1301"

/translation="MSFMKSLFFQIIVAVIIGIGVGILWPDLGSLQLPLGTGFIKLIK

MIIAPLIFMVIVTGIKIGDLKSVGRIGLKAIVWFEIATTVALVLGLGTANLLRPGAG

MNVDPSTIDASGIEAKTNGSELPHTVDFIMNIIPTSVVDAFAQNALLQVLLVACLFGV

ALAATESKAKENVLTLIENLLGIVFRIIGYIMKLAPIGAFGAMAYTVGAYGASTLSSF

GLLILACYGAALLFLVMLALAAWWITGLNFLQFVKYTRSEVMLAIGTGSSEVVMPRMM

DKLTKAGCDRAVVGLVVPTGYSFNLDGASIYLSLATVFVAQAVGIELTLMQQITILLV

LMLSSKGMAGVPGSAFLALSATAVAVNAFPVAVALLLGADRMDTMRVFTNLMGNVCV

AAFVVAKWEGLLDQKRMRAVLSGEISAAELEREEQAALSLLKLNMQEKQGKAVVSP

S"

CDS complement(3149459..3150151)

/locus_tag="EFAGFIKM_02651"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P99149"

/note="UPF0173 metal-dependent hydrolase SA1529"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLNITFHGHSSVQLGTEEKSLIIDPFLRGNELAVTKPEDIKTDV

VLLTHAHMDHILDAEPIAKANNAKVVAIVELATYMSWKGLDTLGMNMGTVDLDFQAQ

KMIQAFHTSGIVLEEEQRIMYAGLPAGYIINIGGKTILHAGDTSLFGDMKMIGDRHDI

DVAFLPIGGHFTMGPEDALQAAEFWNAKLTIPVHYDTFPVIRQDAEHFVQQLAAKGLE

GRVLAPGESITL"

CDS complement(3150250..3151962)
/gene="mall_3"
/locus_tag="EFAGFIKM_02652"
/EC_number="3.2.1.10"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P29094"
/codon_start=1
/transl_table=11
/product="Oligo-1,6-glucosidase"
/db_xref="COG:COG0366"
/translation="MNNVESEVGDIVWWKESVYQIYPSSFKDSGDGYGDLQGIYEK
LDYLENLGVDVIWLCPIYDSPGHDNGYDIRDYYGILRKYGTMEDFDRLLAEAHKRGLK
IMMDLVLNHTSDEHAWFAESRSSKMNPKRDIYIWRSGKNGQVPNNWESYFGGSVWKHD
PETNEYYLHLYSEQQPDNLWNNAQMAEEMYEMVHWWLEKGVDFRFDVAHAIAKAEG
PSAHNPDNLPVVPAYQLFSNLEQVHSILKKLNNMILKPYGPMTVGETSGLGPEQALAY
VGTDRDELNMVFQFEHMFIDAKSSGIGKWNKYEWKLTDLKEIMSRWQTVLHGRGWNAN
YMGNHDPQRPVSRFGDDGKYRVSAQMLATWMLTLEGTPYIYQGEEIGMTNVAFPNIE
RYRDIETKNYFNHYIGQGKSKHEVMQAIWLKSRDNARTPMQWDETEHAGFTQGQPWIIQ
VNDNYPEINVADAESDPQSILHYRKLIALRKQHKVLIYGAYELLLPDDPDYAYTRT
LEDEQMLVILNFRGHEPEMHWPEGWTSEHAKLVISNVSRRYSTDEGAIQLQPYEARVY
RKQR"

CDS complement(3152085..3152543)
/locus_tag="EFAGFIKM_02653"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNEKSWLHSHKWMLTIVACMAALYILIMANLLFVSGRTPGMYQY
NLVPFETIRPLLMEERYNTDTWVKNLFGNIVLFIPLGIWIPWLFRRCRTFLTFTSTV
VWLLLGVEVTQLITRVGSFDDVDDIILNTIGAWIGYAGFKLVLYSQKKTRN"

CDS complement(3152799..3155231)
/gene="glgP"

/locus_tag="EFAGFIKM_02654"
/EC_number="2.4.1.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39123"
/codon_start=1
/transl_table=11
/product="Glycogen phosphorylase"
/db_xref="COG:COG0058"
/translation="MFDNKETFKSIFTRNLVSKLGKPIEEATQEDVYHVLGSMIREYA
GQDWAASNQGFQKQKQVYYFSLEFLIGRLLGNNLLNVNELELVRDSLAEFGSLEE
IEEQEADAGLGNGLGRLAACFLDSLASLRYAGHGCGRYKYGLFEQKIINGNQVELP
DNWLDKGNEWEVRRPDKKVEVQFWGRVEAHEQDGEYQFVTKDAESVVAIPYDVPVIGY
GQTHVNTLRLWSAEPKRETS LDTPSNYYGYLDYSRSVESISEFLYPDDSQYEGKLLRL
KQQYFMCSAGVQSALRTFNKLELPYDRLPKVAFHINDTHPTLVIPELMRILIDVKGY
GWDEAWDITTRTVSYTNHTTLSEALEKWPVSMISRLLPRIYMIIEEINKRFCGMLLDR
YPGDQDRIGHLAIVANDQVRMAHLAIVGSHSVNGVAALHTEILKEREMAPFYELYP
FNNKTNGITHRRWLMHANPKLSDLITDTIGNEWITEPGKLDQLAGFADNTSFQEQRFS
IKRDNKERLAAYILDHTGTAVNPDSIFDVQVKRLHGYKRQLLNILHVMHLYNRLKND
SFDMVPRTFIGAKAAPSYFAKKIILINNVA DTVNRDAAVNDR LKVFFLENYSVSL
AEKIIPAADVSEQISTAGKEASGTGNMKFMMNGALTIGTMDGANVEMAEQVGEENMFI
YGLRADEVLEYRSGSYRPNEIVQHDERIREVVEQLVHPGAF CYRDGEFWDIYDSLLA
HGDEYFVLRDFAAYADAHA AIDQAYRDIPGWTRKAILNTAHSGIFSSDRTISEYATDI
WGIHPVSGNWKG"

CDS complement(3155701..3156804)

/gene="glgD"
/locus_tag="EFAGFIKM_02655"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39124"
/codon_start=1
/transl_table=11
/product="Glycogen biosynthesis protein GlgD"
/db_xref="COG:COG0448"

/translation="MKPLIGVINLDHELEELKELTYFRCGAAVPYAGRYRLIDFVLSN
MMNAGIESIGVFRRKYSRLMDHLGDGKPWDLDRKHGGMFILPPDWNDPTDTSQGDLO
HFHNNLDDFFHRGAGQYVHAGSRHVTKADLQDVYRYHISKGADVTLVCKKVDQLLPEH
DACVKVEHDGDGNVVDIHQSANHPNIYTEIFIMEKELFLRQVQRCIDHGESHFFRDVI
QKNPDGLNIAAYDGYHAVINSIDSYRNSMDLLNTGQYEQLFKEDPIQTKIKYEAP
AKYLDTADVKHSLLANGCIVGGEVEDSILFRGVQVAKGAKIKGSIIMQKCYIGEGTVL
ENVILDKDVKLTGGQTLIGDPSNPYILAKSTII"

CDS complement(3156831..3158003)

/gene="glgC_2"

/locus_tag="EFAGFIKM_02656"

/EC_number="2.7.7.27"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39122"

/codon_start=1

/transl_table=11

/product="Glucose-1-phosphate adenylyltransferase"

/db_xref="COG:COG0448"

/translation="MMAKKEVVAMLLAGGQGKRLKGLTKSLAKPAVYFGGTYRIIDFP
LSNCSNSGIDTVGVLTQYEPLVLHSYIGIGSDWDLDRKNGGVYVLPHEREDGSNWYR
GTADAIFRNLNFIEQFDPEHVLILSGDHIYKMDYEKMLQYHKEKDADCTISVIDVSLE
EASRFGVLNTNDYSIYEFEEKPPEPKSTLASMGYLFKWDVLKRFLIQDEQQASTSY
DFGKDIIPLLENEKSLYAYPFEGYWKDVGTIRSLWESNMDLLDEDTPFNLNDPDWRI
FTRNPNQPAQYISPSGKVRNCIISEGTVVHGEVNHSLFYGIEVGENSAVIDSVIMPR
VKIGQNVRIYRAIAEGLVIPDGTQISPAPEDESDILLVDQEELERQLRQGITSKA"

CDS 3158631..3159719

/gene="ddl_1"

/locus_tag="EFAGFIKM_02657"

/EC_number="6.3.2.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00047"

/codon_start=1

/transl_table=11

/product="D-alanine--D-alanine ligase"
/translation="MELINKYLDEITQQKEKVTVVLVTNVNDNQTNEFEDYHNNSLISE
YLSESELEVLNQGFENFGFRTIIHFDETEFIQKVATSKHPILNRDHIGIVLSMAQKGK
KIGRKSLPAFCDLYNLKYTSSDPYTVSLCRNKYHSGILLKQHGILVPESWLYTKKGW
LFEQKPPQGCRVIIKLNNESASIGIDQNNIINYESNDLMIEQLCIEYGQEIIVQAFI
EGYEVEHPFVVDKEITPLIPMGIQLNDSRNLSDQILTYEIRGKDQYSFYNYSTENQVI
NAKLIETTAAAAEVLGITGFGRVDYRINQKNEFFVTDIATNPHIVKHSSFHQSFIELG
YTYNEMLATFVAITIAKYDLGFRPELNI"

CDS complement(3159690..3162176)

/locus_tag="EFAGFIKM_02658"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTHSLLHHQQEIKQHILGGIRDNRKLFLIEGLSGTGKSYLTHSI
ISELSLIDFEIFLMEGDSQCITRDYYPFERCISSKKSGLKNRNNSKTLKKTVSKASK
GIPFVGDLAEHISEEFLNHNDNKFDKDNSYLTDSERSIIRIRYLTKKRIVFIIENFQ
FWDEKSVSLIYQILKERENNLSILEELVIIIINWTSQALNNEKFKNEILKEFHFDYY
LNVIEKVGYSALVSMGLLKEINNDLINGLYSITGGHLHLTKEIIQFFNHSSIESTEL
ISLGNTEKIMTLIEDRLKNLGARGEVISEVLKYASILGISFTFFELEKITKKNQAELO
QIITEANKLYFVEENNKKVNFVHEIIRNLFESKLEDKKTYFQAYAECLKVIKPNDYIA
RARALLKASYVDQAALQYILAYVKKLRNSETINHDFSQEILMSVSELRAAEYVDIMQQ
AYSDYLNKDFDKVIEELGWIEDSYPIILLRAERDYLLAMCLTKKIDSDSRNKSVSILDK
YKDINSLDGESELWSRILSLQMISYIHINDKTSIAKNENLLMHYLGDRASYDMAEDK
INILRRKSSAVHSIIFAQRSTMKSVKYFGPLENGGVPLNPIQYYFSLNNHIANLTVLG
KFEESFEDATQLRKFIANHKGIPFPRPEIPLNNYILSGIASENISFEKGLEIYNEMFN
KIKSSADSILLKINQAVLYAATNQLDHARDILDTLKKKLIRQKNIELYYQFYVDSNLM
VVEYLLGNQSEALELWNTISYMPSIGDQNYYEKRHELIKELFDSNIQLSGLEWFTVID
KMYPEFVERSKEKSFGNGFLMSDIQFWSES"

CDS complement(3162219..3163157)

/gene="xerC_2"
/locus_tag="EFAGFIKM_02659"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A8P6"
/codon_start=1
/transl_table=11
/product="Tyrosine recombinase XerC"
/db_xref="COG:COG4973"
/translation="MRLSTSNLNTYIKQYETYLSVERNLSLKSİKAYLSDLNRLVEWL
DTKHIHDVTRENLRMYLEQLNSEHTLKDSTIKRKYICFAFFNYLVQNGDIIESPIIG
FGKKFKTARRIPKTLNVNEVEKLLNAPQEHEMKQLHTSFRRRINLRNDAIIEELLYVIGI
RIGELVNIDMEHIDLEEKTVLIFGKGRKERLLYISSSEVIHKIKTWLHAREHFDPQSD
ALFLNKYGDRLSIYSIEDIYSKYRDLKSVSKKSTPHYLRRHSFATHLLNNGADLRVQE
ILGHTNVSTTQIYTEVSVERKKDVLSTFRNPRNNFKV"

CDS complement(3163315..3164466)

/gene="adhB"
/locus_tag="EFAGFIKM_02660"
/EC_number="1.1.1.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0DJA2"
/codon_start=1
/transl_table=11
/product="Alcohol dehydrogenase 2"
/translation="MATHAYYVPPVNLNMGRCGLQEAGQMIEQMĞIRKALVVSDRQLIT
SGVAEQVLSILRKSGLDYVVYDEVQPNPTCQNVHDGLQVFQNHGCDAIISIGGGSPQD
AAKGIGIVATNGGHIREYEGFHQSKHKSVPLVAVNTTAGTSSEVTINYVITDEERKVK
MVMVDRNSLVSLSVNDPELMLSKPASLTAATGMDALTHAVEAMVTPGGFTVTSATAAA
AVELIFEYLPRAVRDGSDLEAREHMTYACFLGGIAFNNAGLGYPHAMAHQLGGVYDLP
HGVCNAMLLPYVEELNAKHVPKFRHIAKAIGMDVKGRSDEECSDYVIEAIRQLSKEV
GIPEKLSELGVKDPDVELLADNAMKDASAPGNPYQPSKDEVMELEFRKII"

CDS complement(3164714..3166408)

/locus_tag="EFAGFIKM_02661"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKFSEYTYTRPNLEHIKTSFRELLSGFEAAATVEEQSGFMDQIN
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ELEQKWGSQLFQLADLSLKTFSPETIIIEELQKENKLSTEYNQLIASAKIPFEGEERTLP
QLHPFELSTDRSMRERASEARYTFMAEHESEFDRIYDELVKVRTQIAKKLGYPSYVEL
GYDRMNRTDYNAEMVANFRAQVRDYIVPVATKLRERQRNRIDVDTLYYDQGGFSFKTG
NPTPKGADWDIINGKKMYAELSPETDAFFQMMTENELMDLVSKKGKQGGGYCTFLND
YKVPFIFSNFNGTSGDIDVLTHEAGHAFQVYESRDFAVPEYNWPTYESAEIHSMSMEF
FTWPWMQLFFKEDTDKYKFDHLSSGLLFIPYGVAVDEFQHFVYANPDATPTERKQAWR
NIEKTYLPHINYKDWAYLEQGGFWHKQGHIFSSPFYYIDYTLAQICAFQFWKRSNEDM
KSAWADYLTCKAGGSLSTGLVELAGLNSPFEDGCVSSVIGDIEAWLDGVNDKAL"

CDS complement(3166670..3166762)

/locus_tag="EFAGFIKM_02662"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTYIIIMAIIMVGMVGMGVFYQIMDKDQS"

CDS 3167012..3167767

/locus_tag="EFAGFIKM_02663"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTRIPLRQLFTVLALMLSVLTACADGEAHLTVNMDGSTDL
LNLNVKNSALGKIGQDNLMPLIADALNRNMFQAEVSEQGDQKQLTATSHYEKSNKTSF
DTSKLPQGIKVEQSTSPGFFTSKMHITAEADLMESMPDGEIKNQMNKVPSFLKNLLK
DVNFDFKLSLPIKAANSNADQVEDGGKTLIWHVSPLQMNKLDLTVQVPNIRNIIIAV
IGLLLIAALLIWWFFVRRRRRARQRHSARSHREKN"

CDS 3167885..3168097

/gene="khtT_2"

/locus_tag="EFAGFIKM_02664"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07535"
/codon_start=1
/transl_table=11
/product="K(+)/H(+) antiporter subunit KhtT"
/db_xref="COG:COG0490"
/translation="MNIRECPLPGIGVKYQFDTKGGHQLVIIVHEDGRRELFVDPQD
NEELTLIADLEDECVTL SGLIGGWS"

CDS complement(3168181..3170928)

/gene="rscC_8"
/locus_tag="EFAGFIKM_02665"
/EC_number="2.7.13.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00979"
/codon_start=1
/transl_table=11
/product="Sensor histidine kinase RcsC"
/translation="MSKSITESRSLFEQLYTHAPIGIAVASHVNGRWLQLNPAFCEML
AYSEDELIDTSVIHMIYEEDLHMEEFRSKFWEMTHETSPMYETEVRLKRKDGSLWAT
IRACIVRDETNGEPLYLLVQAADITKQKDAEEILIVQRKQLEESSRISRLAESSLDL
IAIHDADSSRTFKYVSNACKSMLGYELEEVIGKPGTFVIYPEDVPLVEAYVEEQRKGL
APKRLNYRLLHKDGSTVWADTITHYVYDDSGELMEMVAVTRDITASQQQQLSMQEYRS
LFDCNPLGVASLDLEGNLLKANMGQEQLTGHTKEELLSRPF DHLIDPVDLEKTRYHFE
ETVKGNAQSYEIGLIHKNGQRIETNVINVPILLEDKVVG VYGITSDITESKRYVEEIE
NLSYERALILNGMSEGVIGLDLEGNLNFANPAAAEIMNFCPSELNGKPLEQMMIQMQS
EGIPYPSKDT PILQAVREGRGLPRTESVFWRPDGSSFLAEFQLKPIMDQGRTRGAVLV
FRDMTSVKDIIRAKEAAEHADRAKSEFLAIMSHELRTPLNGIMGMAHLLMETELDDEQ
KGFAEIMIDSGESLLYILNEILDFSKIEAGKMDLERAPVDIKAMLGGVIELFALKASE
KNIELYCEVSDHIPERIRGDETRIRQILINLVGNAVKFTEQGRIMVSVGADFSDEHGE
DNLMLTFKVRDTGIGIPIEKQHQLFQSFSQLDPAINRKFGGTGLGLAISKKLVELMGG
AIGVQSEIGEGAEFQFTLVVERWLEESNDPIEITTNDELQLDRASLAHDIKILIAEDQ

AVNSHLLLEMLRKFGGVCDIVENGAQAVDSLNVQYDLVFMIDIQMPVMDGIEATCHIR
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CDS 3171139..3171963

/gene="tgl"
/locus_tag="EFAGFIKM_02666"
/EC_number="2.3.2.13"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P40746"
/codon_start=1
/transl_table=11
/product="Protein-glutamine gamma-glutamyltransferase"
/translation="MIIVANQPVELNRSEWSDFEWYWLQQLQNRPTRYVYQSMHDLRF
EWDLRGSLVDAAEGLDRSGVSFASFEKSRCPAYWNRNAEGGFELRSNVTPADGIRDI
WRNGHLYAFECATATVIVLYGGVLGSIREDAFNSLFRNLLLFDWHYDSLRLTEKNGS
ETALPGDVLYFKNPDVSPETPEWQGENTFMLRENLYYGHGIGIASGEEIIRTLNQFRV
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CDS complement(3172145..3172636)

/gene="infC_1"
/locus_tag="EFAGFIKM_02667"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P03000"
/codon_start=1
/transl_table=11
/product="Translation initiation factor IF-3"
/translation="MIKNEKIKAAEVQLTGLNGEDLGVMSTQEALLAKQHKVDLVCL
SLMTSPPPCKLIGAGAAKAEAAQAKKKASKSPDKRKVKEIRLNLAMEDHHRDTKQSQA
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CDS complement(3172757..3173689)

/gene="ppaC"
/locus_tag="EFAGFIKM_02668"

/EC_number="3.6.1.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37487"
/codon_start=1
/transl_table=11
/product="Manganese-dependent inorganic pyrophosphatase"
/db_xref="COG:COG1227"
/translation="MEKALIFGHKNPDTDTICSAIAYADLTKLQGQDVEAVRLGEVNG
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FETSGPLYFRAEPVGCTATILNKMYKENGIEVSAPIAGMLSAIISDSLLFKSPTCTE
QDVAAARELAAIAGVDADSYGLDMLKAGADLSQKTIAELISLDAKEFVMGQSKVEIAQ
VNAVDVNDVLVKQPELEAAIDAISSKGLDLFVFFVTDILNNDVALAYGTSTKAVEK
AYNVTLSDSRAILKGVVSRKSQIVPVLTEAFNTL"

CDS complement(3174134..3174886)

/gene="pphA"
/locus_tag="EFAGFIKM_02669"
/EC_number="3.1.3.16"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P55798"
/codon_start=1
/transl_table=11
/product="Serine/threonine-protein phosphatase 1"
/db_xref="COG:COG0639"
/translation="MRRCVISDIHGCYDEFNALLKLADYNPQQDELILLGDYVDRGPS
SKQVIEQIMQLQQQHIMVIKGNHDAMMVKALTQDVEQYDQHWIRNGGLQTMASYLDL
ELTYDEQQIDWEAYAEAKKWIRTHYEHHLRFLEQLPLVYEIPGYIFVHAGINPDIEDW
RSQSERDFIWIRESFYSRPTTIRETVVFGHTPVKHLHDETGIWFDPSGDKIGIDGGCA
YGAQLNLLIESEDGSLQTFFVRQGQSAEEPEI"

CDS complement(3174986..3175993)

/locus_tag="EFAGFIKM_02670"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLSVLEHGHINEGRSVQDTLQETVKLAQHADQLGYSRFWMSEH
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LGIGRAPGGMPIASRALNEGKSSNVQFFPQQIADLGGYFHEQLPEDHRFASLVAGPSV
PTVPEVWLLGSSSEGARIAAAQGTSYAFAQFFGTPGGEEAMKHYRRHFKPSILNDKPH
SMIAVSAFCAETEEEEAAELARSNELFFLRLGRGLEQSSFPSLETVNNYPFTAMEMEQI
RQRRSFSIVGTPDQVKDKITAMAERHEADEVIIASAVHSFEARLRSFGLIAEAFGLKQ
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CDS complement(3176229..3178166)

/gene="ltaS2_1"

/locus_tag="EFAGFIKM_02671"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34952"

/codon_start=1

/transl_table=11

/product="Lipoteichoic acid synthase 2"

/db_xref="COG:COG1368"

/translation="MYNSKNERTSSRTLFAVLFILMLLKLSLLRYFFFQGLSGIGLLT
DALGALTIVCLLDLIVPKGWKRAVYGGFNILFSLVLFAATLYNVHFSSVPTYTVLSEL
GQVAQVRGSIGPLVRPEHFLFFADIVLALPIWLMRRRAGGRNYSSYRDSGLTFGRIR
RRYWGKLGVALTA AFCIVLSGSFIVKGETIDNELVRAENLGFLNYQVSSAILTSKENE
AIANGNINETIAKINELVSQYPYQDTPSDGTAVKAKYFGQAKGSNLIVLQLESFQNF
INASLDGQELTPVLNDLAKESYYFSHFFQQIGQGNTSDAEFMSNTSIYPTGVVPM
SAGYSDRELPSLPKLLGKEGYESETYHVNDVTFWNRNKMYPALGFTRYFDKPSFEND
RFND FGPSDEELYRVGVEKMTAHQAANQPFYAQFITASSHSPFTVPADRARITIPATIT
NKL LHDY LQAINYTDYAIGQLINELKANGLWDNTTLVLYGDHFG LPADEEITQQIQANL
GV PYDGKVS RFNIPFMIHTPKQTKGQVIEQPGGQLDMLPTIMNLMGVSLQDEKFTAF
GHD LLNMDHNAFGIRYYLPTGSFVNNDIMFIPGAGFDDGTAYSLKTYEPVTDLEPYR
SDYE HVLSLMKLSDEYVKLLPKRAP"

CDS complement(3178282..3180657)

/locus_tag="EFAGFIKM_02672"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTKRVILLEEGTAEMKGLMVSKGADLAELIHAGWSVPAGFVVT
ECCREFCTRLGHLSGEGEEEEIINAIRHLEQQTGKFFGHSENPLLLAVRTDQDRASATA
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DQDEVELELTITEFKYLIEAKGRNPFQDVQIQFKEAVRAVYHSQRIKASRSQDEIMR
KSYIISSEQSAPVLIQTMIHGKCGESSGAGTIYTCNPLTGEKGITGQYVPTGNASQTD
HGLERLRNDEPELYTSLLEIGSQLETHKGEVQEITFVIKSGALYVVQTQPARLSSIAT
LRSTVDFVHEGLITKEDALLRIQPAHITEVQKLYTNPSSISEASNGHLP IQIPVTND
ECPAYNNSGSLLSADLQLLNWADEVKELKVLANADRPQDALTSRLLGAEGIGLCRTE
NMLLSPARLPFVQKMILADSESERRRGLERLLPMQQSDFEQIFEAMDGYPTIRLLDS
PLHELLPDLGVLEKRREWLRAEEWQEQKDHQIELEELERVIRRVSELHEHNPTLGQQA
CRLSTVFPEIVDMQLEAIFRAAVKGIRQGWVVRPEIMIPQIGHVHELQVMRDLVDHVA
DQVLGEEKRHCHYRVGAMIEAPRAALTATHIARQADFFSFGTDELTEMFTGYSRHEAE
KRLLLLQRDTSRPVTNNPFHVLDIEGVGQLIEMAVVQGRIRKPHLKTGICGENVIDL
ESITFCHRIGLDYVSCLEPIPYARIAAAQAAIKGQREGADTQNTDISTIA"

CDS complement(3180919..3182013)

/locus_tag="EFAGFIKM_02673"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKTTFFKKVGLFLGAFIFTIGFASNSGVHAAVDYSGGLMDKMVM
TLSDTESKGSKFTYALTDNNEATSIIIEKWNTPTSTAVDHAVGIFNGTVTANAIRVKAD
FDVSIGLFDSTGKAILPTYWYTVKANQADGRLIYLPTYKGIKVNLFNYSNTRTVSV
SEFQLYNMTPPANPLDLAASADESSIGLTWNEVTTATSYTIKRSTTANGPYTTLATGV
TKANYTDLDVTPGTTYVVVTGVNPVGESVNSNEASAIIESNGQVDPEAEQPTTPEPE
EPTTPEQPEEPSTNRAIFVVTMTTGLEKEFDLSMKEVND FIDWYEAKQAGSGKASYAI
NKHDNNKGPFKSRKDYILFDRVLTFEVSEY"

CDS complement(3182203..3182520)

/locus_tag="EFAGFIKM_02674"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRKKIWALLLVAVIGMIPAKATSTTTVAESHEISGEDLPESLR
YDSNHPDIIYVKDCGVFEKVDSSLVDYGEEEEIVFDDIQVTNKTNVIVAYDATYIKKG
EWE"

CDS complement(3182837..3183067)

/locus_tag="EFAGFIKM_02675"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIKDKIPLWFWCTSVVVVIMLVYNLFQVDSRINMLALGILNIAN
AIRMWKKYRNSAIIFLIIGVLCVLFYKLLQ"

CDS complement(3183292..3184956)

/gene="rhaS_24"
/locus_tag="EFAGFIKM_02676"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaS"
/translation="MCHTIIQLIPKPWLCSLQHMEYVDHHKSHIDKRLLYRMSTSHSI
FVVTSGKGSIVCSDRESHLEKGMIMFVPAGTSVKIEGSPWTENELQYYKLDLMVAELK
EETSNGLSRRNTEEKQELFQSPDSSTLLPLMQLSFSPWSSCLEALEQILRQQVTGDWL
EQWEVQLRFQEWFRALIRQSAPKTEVPDDRARLQSSIRYIGDHYDQTITVDELAADIG
LTRASYTRQFKRITGKLPLEYVNAVRLERSKQLLQLTDDRIHEIAQNVGFSSEYYFGR
RFKQYSGISPGLYRRHHRQEVRFAPYLEDFVLALGVKPVLCSSHHSWGRQHLYGLDD
VPEFDVSQQDAQFNVGNIPDFIMLNKGYDRWNLNRFEQVAPTFYVDHLGEDWRSILKS
TADVLGKVNVRVQDVIGEYEDNAMEAKGRLARSLRGQTVAFRLISALDITLYGDRQGYV"

GPVIYQDLGLTPHSRVQQWTRHERRIFIGLDQLSQLNADHLLITFDTGNSAKPGEERE

LLDRDEWKRLPAVKSGNVYEVD FMSWMNYGVISHGKKIEDILRFMA"

CDS complement(3185062..3186060)

/gene="yfiY_3"

/locus_tag="EFAGFIKM_02677"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31567"

/codon_start=1

/transl_table=11

/product="putative siderophore-binding lipoprotein YfiY"

/db_xref="COG:COG0614"

/translation="MVGFIKGFKGWTITLLLMGLVISGCSTNTATNAEQTPATESAAS

GENTTETETAPATRVVQDEF GDVTIPVQPQRIAGIYVEDY LKALDITPVVQWYHPLWG

VQDYLELDVPQFDTTGSIEALLEHDPDLIIVDGGVDMKEYEMYSKVAPTYRLPESVLQ

DSNLILKTIADVVGKPDKGEEVAAAFGAKIADAKAKLQESVGDETVAVVRLNVNDDTL

ALFGVKNRFTGFIYSELGLTPHPLVSKMEEYQEILSEEAI PQLDADHLIIFPSNGEWS

SPENKEALKVLD SKLWKSLPAVKNNQVYIMERSHWQSGAITANS MKIDDLLEKMTP"

CDS complement(3186239..3186613)

/locus_tag="EFAGFIKM_02678"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKTDVEKLLADLNEGRILTQQT FEGLDVEVYLDERDASAFAD E

WMQAFERWAQDTAVAE EEEVLRACREQA FKQTLALTGEPELAGYVSDDMGLIGAALLQG

TANDSFVDQLLESYRQGR LPLR"

CDS complement(3186636..3187298)

/gene="polC_1"

/locus_tag="EFAGFIKM_02679"

/EC_number="2.7.7.7"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P75080"

/codon_start=1
/transl_table=11
/product="DNA polymerase III PolC-type"
/translation="MKITLLPDYFIENLSVSSLQDRMYCIFDLEGTGINPVVESVTQ
FGAMYYQRGQRCNTTFSSLTRANKPIPEAVAKLTGISNEDMVEAPSFVEAFQEFQKFI
GDNVLVTQAGYEYDLPILKRHCDEYSLPMLTNPVLDTKAMFTYIHPEITEVVSTDFLI
RYYDLNTDGIHRHNALADCGVIAGIFESILSEYEELQLDHFTADPNRMMKRFVPEMY
LT"

CDS complement(3187360..3187935)

/locus_tag="EFAGFIKM_02680"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSEASTFLYFVRHAESRYVDGQERERGLTEQGHQDAETVASLLH
GEQIQLFYSSPYRRAVDTIHILADRSGGIVVTEEDLRERQLSSSDVKHANFREAKQRL
YRDPTYAYPGGESGEQARSRAVAVIEKILDKHVGHKVVIGTHGDVMTLILQHYDSSYG
YDFWESTTMPDIFKLQFDGTRKLVQVTRLWE"

CDS complement(3187935..3190157)

/locus_tag="EFAGFIKM_02681"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLHSLKAIQSYKSGNTPEAQQQWLQLLAAAEKPHINLERIHSIA
ELEGTNPVLDYTERTLHVLEKLQVSFWVREILEEVLWSETAKAGSLEQRRVWQKQGV
NLFVHNVGSAQLYDLYAGAEHLNDIDDKTKETSIYQLGSPSGALSNNADISEHDALNT
HTPRQEIIRTLATHGLIGQYIRGEIPFAENASLHALIVKGWLTDELHTILMALNVC
IIAGVDPALWNQVQAEVQRIVGWIIVGPDHEDWSVKERLSRLRSSSIRQGEAMDTAYA
KLQTELDVEQALAPLAHRTLWYVESAMQDFSLQEMVKVFLTLRSESMHPTSMESRSE
IVRHISFEPLMNTMYDYRGVKKLNIYKKRMIEKYLEQYSWEQIVSGEQIVYPHLTHR
IERHADLPDTLFTFEFSPAEEKLIAFCIEAKSPLEYKAVLLLFDLFLRRDAYDRF"

HNEETYLSDMNSSGDYKKVLLEYIVGKRILDIGPGGGILLDLIEQEKPEVEPIGIDIS
ANVIEALERKKQREGHRWQVMKGDALQLEQYVQPGTVDTVIFSSILHELYSYIELDGR
RFNSDTVVAALRSSFRVLSPGGRILIRDGIMSEPEAQKRRIRFLEADGLRWLERYAED
FQGRAIQYERISDNEVEMPINDAMEFLYTYTWGEEAYVHEIQEQGIFTPTAYENCIR
EALGEQAEIITFEHFLQEGYTEALGERMIFMEENGEPAPLPDSTCLIVIEKKKGLADG
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CDS complement(3190352..3190678)
/locus_tag="EFAGFIKM_02682"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAGDPAGDMAQSWVILMSGTLPEDTEPAIRMGFETVRESLVEYY
IHHYMQLSGITREAIESWMLPVAAARLDEDLPAQERAAQVCSGTNSSVIKVELHIIYT
DTTMTE"

CDS complement(3190803..3190895)
/locus_tag="EFAGFIKM_02683"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MERIGQGRTAEIYAYSNEHIMKLYRMDFPL"

CDS complement(3190898..3191491)
/locus_tag="EFAGFIKM_02684"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTESSSFNPIMLTIPESFHTERLSIRAPQWGDGA AVNEAVRESA
EQLRLWLPFAEKIPSLEESEVTVRKARLQYLERTDMMLHLRDRHTDDFVGSSGLHRID
WNARCFEIGYWIRTSRAGEGLMTEAVRGIEQFAITHLEANRLEIRCDARNVRSKVAE
RAGYTLEGILRKMRDSTGTLVDCMVFSKVRGSEFGG"

CDS complement(3191500..3191946)
/locus_tag="EFAGFIKM_02685"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIEARLNELGIILPQASAPAAKYANAVIVNGIMYVSGKGPDTSE
RGKLGSDFTTEQGYDFARNAGLEVLAVVRDVLGSLDRVKRVVKVQGFINASASYQEH
KVLNGFSDLMMEVFGDQGVHARSVFGAVSVRDNLPLIIDSIFQVEE"

CDS complement(3191943..3192845)
/gene="rhaS_25"
/locus_tag="EFAGFIKM_02686"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P09377"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaS"
/translation="MTEPFSADFHDPTDLLHIEYDRRIGYFSMTDDHLHDHYELYLL
SGERIYFIKDRTYRVKAGDLVFVDRNTVHKTLESGMPDHERMVLYLKPELFAAIAISP
ELVEALKEPFCWEIPIVRFPSQVTEVLERMVSEMVDEMLRPQGSNLLLRHRAIELLL
HAYRNQHLGRLSSDDREPVLHPKTQAVVRYLNENYQKPLTLPEVAGMFRISPHYLSRL
FKQTTGFTFSDYLNLLRVKEAQRLRESEESITDIAGWLAGFSNFSHFGKMFKRTVQVS
PRVYRQEYKESGSRVTIKEGENIR"

CDS 3192973..3194262
/gene="yteT_2"
/locus_tag="EFAGFIKM_02687"
/EC_number="1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34371"
/codon_start=1
/transl_table=11
/product="Putative oxidoreductase YteT"

/db_xref="COG:COG0673"

/translation="MSNKKRYVLVGTGGRAEFFYGALTRDYRDTSELVGFC DINQVRM

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HFEWLLNTRHGADYFRRWHRDKRNSGGLLVHKSTHHFDLVNFWIGSQPDTVFAFGDLM

YYGRENAEERGVTQFYNRATGNPIAKDDPFALHLDSDAHMKSMYLD AESEDGYQRDQS

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HRAANHVDGARSILT GIAANRAIATGLPVNVNNLVRF"

CDS 3194379..3196196

/gene="sasA_10"

/locus_tag="EFAGFIKM_02688"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"

/codon_start=1

/transl_table=11

/product="Adaptive-response sensory-kinase SasA"

/translation="MFFSLKNRLIAFIWLVFLAFGTL SYLLFKESRTVIRSYIESSA

LEKMEEYGSYVDMVQM QIYDVASLVFNSDMGKNWDNAIGDSNLSEGEKMLANLAMSRF

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QHERVRDHGNPVV SLLMPIGTFHHATAQSVMK VNVSESYFLEPLRRIHLAESSTIFLL

GEQGNPILSQQVDTLGAVATAEIDRFRNSPLKSGVAYLTN QEGQRDIFVFKKLGR TGW

MLAGLAPEKEMYLSLHKLQSTIMVVTIALILV SLLAAAWLSHGVTKPLTRLVLAMRQV

QRGAFDQAD SLLPPDKNVKSEISYVIFTFRY MISQLRQHIQNEFELKLLRQQA EYKAL

LIQINPHFMFNTLELVSSLAIQRRTDDTVQVIEDLGKMMRFSINTNDDR VPLTEELDY

VQRYISILQTRFGHKLDISVTLEGT LNSVVIKFI LQPLIENAVKYSFQHQT TAQVQI

RINRMYDRLHISVSDNGPGIPAEIIHKLQHPVAPPSLESILHNEGWHIG LGNVIARCR

LHYGALFTVHME NDESGGACIELTLPVQEEYDVQRINRR"

CDS 3196171..3197727

/gene="rssB_6"

/locus_tag="EFAGFIKM_02689"

/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00958"
/codon_start=1
/transl_table=11
/product="Regulator of RpoS"
/translation="MYNVLIADDEIEVREGLKLVWDWYGMGFVITGEASNGIEADELL
KSEHFDLLITDMNMPVMDGVRLLDVCRSYNPSIQIVIITGYEDFQYARAGVRSQVMDY
LLKPVARDELKATLGKIKADLDDQRKVRGDSELMQWRFSQYYREMKERFLDLVKGNR
LPPSSMPERLRLFHLESWQDQKVCFITASISQSDKQAIKDRLEQMHLPFEMVCYEI
AQSESDNVQVFHDSAHAHAGIMHFMVQDGMQHEFIQQLAGHTASVFSMELKIGVGLSDSG
LEHWKEGYIHSLAWSAERAGNTPNPRAGTDYSPLLPEETTRTLHRCLIRGELDSFR
SIIRKELHEAFQLSPSRMTRSILQISLLMDCPMAPEWILWLKTPDQAERLLMQWAQDF
LGRQLPSEDGDGTVIDLAKRYIEENYMQVLTLLAERFNYYPTYFSELFKEGAGTSF
IQYVTGVRMKHALQLKETQLTVWDITELTGFSPPSYFSSKFKRMFNMSPSDYRLLHS
EKIDSHDPKK"

CDS 3197844..3198758

/gene="lacF_4"
/locus_tag="EFAGFIKM_02690"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P29823"
/codon_start=1
/transl_table=11
/product="Lactose transport system permease protein LacF"
/translation="MKKQTKPLYGQHNTTAYLFLLPWLIGLFCLTLGPMVASLYLSMT
KFNLLSSPTWTGLSNYVHIFTEDDTFRRSLGLTFYVFLSVPLRLAFALLVAMALNKG
IRALGIYRTVYYIPSLGGSVAIAIWWRLFEENGVLNQFLSWFGISGPSWIAHPDYV
VYTIITLSVWQFGSAMVIFLAGLKQIPADLYEASDVGAGKIRQFFGITLPMLSPVIF
FNLIMSMINSFQAFTPAYVIGDGRGGPLDATMFYTLYLKGFSSFFDMGYASALAWIM
LVIIIGVFTAIVFVTSRFFWVFYGDNQEGR"

CDS 3198758..3199603

/gene="dasC_6"
/locus_tag="EFAGFIKM_02691"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9K489"

/codon_start=1

/transl_table=11

/product="Diacetylchitobiose uptake system permease
protein DasC"

/db_xref="COG:COG0395"

/translation="MHMPIKRQLVQAGRHAAILFGLLMLYPVLWLILSSFKNHLIF
TSGSLFPTSFTLEHYINGWKGLQGISFGRFFGNSVLISVMSVLGNVISCSLAAFAFSR
LKFRFKGLWFSMMLVTIMLPYHVTLPQYILYNELQWINTYFPLILPKWLAQDSFFIL
LMVQFIRGIPRELD SATIDGCGQSQIFFRIVVPLLVPALITTAIFTFLWSWDDFFSQ
MIYLSKIDLFTVQLGIRSLFDPGQSDWGALLAMSTLSLLPVTIIFLLFQRYFLEGIA
TTGLK"

CDS 3199642..3200967

/gene="yesO_1"

/locus_tag="EFAGFIKM_02692"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31518"

/codon_start=1

/transl_table=11

/product="Putative ABC transporter substrate-binding
protein YesO"

/db_xref="COG:COG1653"

/translation="MFKRFMIGMITSLLLFTACSGTDHTGTNDASNGNDNGTTEGGQ
VELRIMWWGDQKRADITNEALKIFQAKHPDIKIVGEFAPSSGYFDKLNTQLASGTAPD
IFFLGGNVVDYAKKDVLLNLDPYVGNELNLDGMDETMIEYGRLDGKLQHISAGANARG
IIVNKALFEKAGLPLPASDWDWADYAAISKELSDKLGEFGTYNFTVDGMDIYLKQR
GKQLYDMKNGTLGFAKEDILEWFQYWEKTSASGGVVTPELQVSNPHDDTSKSLITGK
AAMTLLPSNQLAAFQSLTEDPLVLLPVPRGPKGTGVVFESSQGLSGYANTKHPKEVAT
LMDFWIHDPEAAKILGNDRGVPVTEANRNLLQEGAGPVVEIVYNYTNLVSEATKTEPF
DVSYNPPGFAEFSKLAQTTNQEIGFGRKSVEQAVSDFYNGTVRIFESNQ"

CDS 3200991..3202637

/locus_tag="EFAGFIKM_02693"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTEEILNRLRNISIMDQVQVPKPEDQQLQEWHASGIRFVASGG
RVEATYYAAVEKLLACILPMGDNDPILQEGGIYLG CWLESTGTINAELLSRLLPSVSE
TTYLAFAKQQRDDGLLPYKLTANGPSFRQIQLVTP LARSVWNHYQLQGKHSSFLNTMY
KAMVRYDEWIAHNRNTRGTGCVEAFSTFDTG HDLSPRFWHVPDTPYMNDASAYHPDSP
ILPFLAPDLTANIYCQRMYSRIAEE LGESGTDWKAKAESSLES LFRYCYDEQDMFFY
DRDRNDELVRVQSDVLLRVMACEVG DRELF DNLLRWYLLNTSKFFAKYPFTSISMDDP
RFDPFSSYNSWGGASNFLSLIRAPHAF EYHHRYVELTWVMQPILSALS KDKRFGQVLS
PWTGKQGFTETYSILCLLDYVERLCG IMPVGSNQLWFTGLLPIDMDHGEIVSGNTA
YSRKVNGVG YELVNTPD RMTVYLQGKVHLDG PSGIRLVTDHSGHLEGVIGMSVRTVEG
ELYYKGECIPIRIKGNEMQRYADGNLRTERDIGI IYPTYR"

CDS complement(3202711..3203055)

/locus_tag="EFAGFIKM_02694"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIVEMYKDLIKDERGNY LQVIEGNE LTVNAFVEAAFTPELI
YNEEFRTKHKEMEGGFVGKIAMDLLR HDVVMGMKQIDRKLLNLS DVEQQFTVNYIDTI
EFYRHPAWN RKV"

CDS 3203179..3203601

/locus_tag="EFAGFIKM_02695"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSWQHLHTGKTLQQRLA ELQGH LAELNTPLSGLEPGRIRRVYPR
QFIKVNRQLFIPLSLNSIRVFDIPRTRRGVRVGIRTTF PSRNAFNNIRLVGVGLDYLE

LQGKGRVPSRILFPLSSVESIYRPTTGRKNLKRPCRK"

CDS complement(3203801..3206974)

/locus_tag="EFAGFIKM_02696"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81BF4"

/codon_start=1

/transl_table=11

/product="Bifunctional cytochrome P450/NADPH--P450
reductase"

/db_xref="COG:COG0369"

/translation="MPPISVPQPKTFGPLGNLPQLNFEEPVQSLVKLAEEYGPIFRME
YPGRSELYISGHELVAEVTDESKFDKRVWAPLAKVRAFAGDGLFTSWTEEPNWKKAHN
VLLPSFSQAMQGYHNKMIDLAVQLVQKWSRLNPDETVNVPDDMTRLTLDTIGLCGFN
YRFNSFYREEPHPFITSMVRALDESMSSLQRLRLQDKLMITKKKQFEQDIRSMFSLVD
HIIAERKEKPKQEGADDLLSHMLSGKDPETGETLDDENIRYQIITFLIAGHETTSGLLS
FAVYYLMKNPDTLAKAQAEVDQILKDPVPTYNQVRNLKYVRMVLNEALRLWPTAPAFS
LYAKEDTVLAGQYPLQKGDSVSVLIPKLHRDREAWGDDVEEFRPERFEDPSKVPHDAY
KPFNGNGQRACIGQQFALQEATLVLGMVLKHFDFIDHSDYQLKVKETLTKPDNFTIRV
RARGGQPVMAVPGVAVEEPKPAKRTEPDAANAHHTPMLVLYGSNLGTAEGIAREIAD
TARYQGFRSEVATLDDRVGKLPKEGAVIIVSASYNQPPSNAKMFVEWIEHADANEFK
GVRFAVLGCGDHNWASTYQRIPRLIDEQLSSRGAERLSPLGESDASGDFEKQVGDWTE
QLWPDARTMGLKLNSSNSERSSLSVQFVSGLAVTPLADTYDAHVAEVLENRELHDA
GSRSTRHLEIKLPEGITYKEGDHLGILPQNPPELVERVLRRYGFTGTEHLVLDASGR
SAAHLPLHQPVNLYDLLSHSVELQEAATRAQLREMAAYTVCPPHKKELEALLDESVYM
DEVNRKRISMLDYLVKYEACELPFERFLELLPSLKARYYSISSSPRVQPDQASITVSV
VRAPAWSGQGEYKGIASNYLANLKSGDEIVMFTRTPESGFQLPEDAQVPVIMVGPGTG
VAPFRGFLQARHVLKEQGQEVGEAHLVFGCRNPEHDYLYKNELEAAQGGGIVKLHTAF
SRVDGEEKCYVQHLMRDDAHHLIPLFEEGAHLVYICGDGSKMAPDVEAALQQAYADIHG
KSAKEAEDWFNQLQQEGRYAKDVWTGI"

CDS complement(3207274..3207828)

/gene="gpx1_1"

/locus_tag="EFAGFIKM_02697"

/EC_number="1.11.1.22"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P74250"
/codon_start=1
/transl_table=11
/product="Hydroperoxy fatty acid reductase gpx1"
/translation="MSIFS YQVPFIDRHESDFS AFKGKVLIVNTASRCSYSRQFSEL
QQMYEKYGDQGLEILAFPCNQFNEKEPGSSAEVAEYCRSQFQISFPILEKVEVVGQSM
HPLFRYLITESPFQGYDLDTKEGEWMDTFVKEKHPELYQGDGIKW NFTKFLIDRSGNV
HGRYETTVAPLEMESVIQNLLKNS"

CDS complement(3208044..3208769)

/gene="lutC"
/locus_tag="EFAGFIKM_02698"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32259"
/codon_start=1
/transl_table=11
/product="Lactate utilization protein C"
/db_xref="COG:COG1556"
/translation="MVTEHQQWLAQLEKKSMEKQEQFMNDIASKLRRPRQRHAPTQPF
RGAPDFWTELEWDEEKRIQAFTDNFVSGAHIA RVQNMEEV SQFIANKSHEL SARYII
RQNEQALQDLGLEEQLPDVQISVWNSQADENWRARAAEADIGVVMADYATAYTGSVTV
LSSPEKGRSVSLLPTVLIIPVDRLYTRLGETLDRFDEAGRENLPAGIHFISGPSRS
SDIENDLTIGVHGPGIVYGLIMG"

CDS complement(3208759..3210279)

/gene="lutB"
/locus_tag="EFAGFIKM_02699"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07021"
/codon_start=1
/transl_table=11
/product="Lactate utilization protein B"

/db_xref="COG:COG1139"

/translation="MSQPGVMDTTVKERAGLALNDDFLRKAVKFTTERLRNGKKSASE
EHGNWDEWRERGRQIRLHTIAYLDYYLNEFVNNARANGVHIHFADTSVEAAAIALDIA
AHKQASTVVKSKSMVSEEVHLNHVLESAGIEAIETDLGEYIIQLAGEAPSHIVIPAIH
KNRYQIAELLSKEAGEILEPDTTVLAGFVRKKLREKFLEADIGMTGCNFAIAETGSMV
LFENEGNARMVSTVPKTQITLMGMERIIPSWTDLEVMTLLPRSATGQKLTMYMSGIT
GPRRTADGDGPDEMHIIVDNGRSLQLGDPEFQELLNCIRCGACLNACPVYRHIGGHA
YGGTYSGPIGAVLTPALNGNIDEWNDIAGASSLCGACYEACPVKIPLHDMVLVYLRRLK
VEDGHGKNKMESMGMKGFAAVVSNSKRFSAAIRLGQIGQKAIVRNNGISLKLGPLKGWN
NYRVAPSLAKKSFRQQWNKLDQELDQEQPTMDSSVRSRMEQIIREREEGEGAKHGH"

CDS complement(3210276..3211004)

/gene="lutA"

/locus_tag="EFAGFIKM_02700"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07020"

/codon_start=1

/transl_table=11

/product="Lactate utilization protein A"

/db_xref="COG:COG0247"

/translation="MKVSLFITCLSDAIYPRVGEAMVRLLAAHGVRLDFPPVQTCCGQ
PSYNSGYWDETRVAAKTILEAFDDSDFVVCPSGSCTYMIHHYPELFADEPVWLEKAKR
LEAKAYEFTQFLVQVLGITDLGAHFPHKVITYHPSCHGSRLLGVKDEPMALLSQVKGLE
LVPLPFAEDCCGFGGTFAIKMSDISGAMVTEKVDHIKETQAEVLVGLDMACLMNIAGN
LRYRNEPVRVMHLAELLYEGVRTG"

CDS complement(3211118..3211879)

/gene="ydfF_1"

/locus_tag="EFAGFIKM_02701"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77721"

/codon_start=1

/transl_table=11

/product="putative HTH-type transcriptional regulator"

YdjF"

/db_xref="COG:COG1349"

/translation="MLAAERYDRIVEMVNVKGS MRVSELSERCRVTEETIRRDLDRL
E QAGRLRRSHGGAVSVKEDQPEIPYRIRETTAAEEKKRIAQAALTMINPGDRILLDAST
TAGYMAANMPDFPLTVLTNSIQIATELSSRDKEVISTGGQLASRSLSFVGPLAERSL
ETYHVDKMFMSCKGVHLEGGGISESNELQAKLKQKMVGISDQVILLADASKFGVRAFA
RVSGLNAVHTIVTNQPLEAEQTDRLSGYDIGIITV"

CDS complement(3211881..3213374)

/gene="rhaB_2"

/locus_tag="EFAGFIKM_02702"

/EC_number="2.7.1.5"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q1R415"

/codon_start=1

/transl_table=11

/product="Rhamnulokinase"

/translation="MSVLAYDLGAGSGRALLGHLNDRGIETSEIHRFKNEPVKVG
ERM HWDILRLHHELMQGLILVKQQGEKPESLGIDSWGVDFGLLGSNGELLGNPYHYRDTQF
NGMMDQVRQELSSQRIFERTGIQFLGFNTLYQLATLQRSGSPLLHEAERFLMIPDLLR
YFLTGEAVNEFTNATTTQLYNPSAGQWDSSELLTHIRISEKLFGEAVLPGTRVGQLRSS
ICNDLGLSAIPVITVAEHD TGSAVVAVPATER SFAYLSCGTWSLMGTEIDHPAISSQS
LALNFTNEGGAGGTFRLLKNIMGLWILQESMREWDRQGQGISYDALLAQAEQAPPFAS
LFDPDDEL FMPAGDMTTRIRQYCRDTGQVVPEDQGA IARAILESLALKYRRVLEWTEQ
LSVQTFNGLH MVGGGIQNRLLCQWTANSIGKPVWAGPAEGSAIGNMAVQWMASGAFKD
IWEARKAIRDSFPVTVYEPQDRSIWEDAYGRFLRV TASSNSQAGSEV"

CDS complement(3213610..3214125)

/locus_tag="EFAGFIKM_02703"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MALTSVSSSMGRLSVDGFGVFDDMNGVPGFEGNQGGFFSGFNEF"

ATMNAFASIFIGGIFLIIAGVIVFVIISGVRTWSSNNAALLTLHSTVVVKRTEVSGG
SGDSRATTRYYVTFEFDNGERTELIVGGNHYGMMVENDRGMLTYQGTRFKHFERDVQP
QMGVSKGQFYT"

CDS complement(3214237..3216039)

/gene="pepF1_2"

/locus_tag="EFAGFIKM_02704"

/EC_number="3.4.24.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54124"

/codon_start=1

/transl_table=11

/product="Oligoendopeptidase F, plasmid"

/translation="MEKIRTRAEVNPETTWDLKDLFVTDVEWEQELRSLPLAAAIET

FKGRLGKGAEQLLACLDAREALQERIGKTASYARLKQSEDSINPVNIENSAKAGDILS

NLSSSLSFVNSEIVDLPDGTVERYIQELPGLEPYARSLERLIREKEHRLTPETEKVLA

SLGEVLDSPIRYILRGKLADMTFDDALDGEDNNRPLSWSFYENNYEMSSDTKLRRSAY

AAFSSTLNDYKNTFAEGYATEVKKQVLSRLRGYDDVTDMLLSPQQVSKEMYNNILDI

IQQELAPHMRRLAALKKRELGLDKLMFCDLKAPLDPEFSPVITYDEACILIREALDVL

GPEYGEIVERAFSDRWVDYADNAGKSTGAFCSIFGSHSYILISWANNMRGAFTLAHE

VGHAGHFMLAGRYQRLTNTRPSLYFIEAPSTMNEMLLADHLLKRSDNPRMRRWVILQL

LNTYYHNFVTHLLEGELQRRVYARATKDEPITAKTSLKGDILSEFWGPDVIDEGA

KLTWMRQPHYHMGLYPYTAAAGLTASTAAQQIREEGQPAVERWLDALKAGGSLTPQE

LMKLAGVDMMSGPEPIRSAVAYVGSVLDELERLYS"

CDS complement(3216491..3216850)

/gene="hxlR"

/locus_tag="EFAGFIKM_02705"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42406"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator HxlR"

/db_xref="COG:COG1733"

/translation="MAAEVKERINLKEINCEKELTLAVIGGKWKLIILWHLGLEGTR
FSELKRLIPHITQKMLTNQLRELEEDKLIERKVYAEVPPRVEYTLTDHGQSLMPVLHA
MYNWGKNYGENVIWKES"

CDS complement(3217116..3217679)

/gene="hxlB"

/locus_tag="EFAGFIKM_02706"

/EC_number="5.3.1.27"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42404"

/codon_start=1

/transl_table=11

/product="3-hexulose-6-phosphate isomerase"

/db_xref="COG:COG0794"

/translation="MSKTQYAADILKEERTLSQIDDAEMQAMAEHILAAEQIFVAGA
GRSGLMGKAFAMRLMQMGLRVYVVGGETVTPGISSKDFLLCSGSGETGSLVAMAQKAS
QAGAPVGLITIKPESTIGKLATTVVRLPASAKEDTATSGAAVTIQPMGSLFEQGLLIG
MDALILTMMEMKGMTGADMFRHANLE"

CDS complement(3217684..3218319)

/gene="hxlA"

/locus_tag="EFAGFIKM_02707"

/EC_number="4.1.2.43"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42405"

/codon_start=1

/transl_table=11

/product="3-hexulose-6-phosphate synthase"

/db_xref="COG:COG0269"

/translation="MMKLQLALDLVNIPEGIALVKEVEQYIDIVEIGTPIVINEGLHA
VKAMKEAFPNLQVLADLKIMDAGGYEIMKAAEAGADLITVLGATNDSTIKGAVAEAKK
QNKQVLVDMINVPNLEQRAREIDALGVDYICVHTGYDLQAEGQSPFEDLQTIKAAVKN
AKTAVAGGIKLETLPVIKAQPDLVIVGGGITGQADKA AVAAEMQRLVKQG"

CDS complement(3218693..3219775)

/gene="pgl_1"
/locus_tag="EFAGFIKM_02708"
/EC_number="3.1.1.31"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34499"
/codon_start=1
/transl_table=11
/product="6-phosphogluconolactonase"
/db_xref="COG:COG2706"
/translation="MSESKRLLVLAGSYAEAENEGIYAYELNEDTGSLSKLDGIAGVK
NPTFVNVD AEGNKLYAIGETASAEGNKMSEAVALSIDPSTGKLTLLNRNDSISAPPCH
IQRDPGSKYLILSSYHGGVLGLQALTDNGEVGALLDEKKHEGQGAHPERQDKPHVHSA
FFSPDGKYYMMVQDLGADNIAIYSIDADKNELVLHSETKTHPGAGPRHLAFHPNGEFAY
VINEVDSSITSFKYDAAAGTLTELSTVSTLPDGYDGKENTTAEITVSNDGRYVYGSNR
GHDSLWVFAVDADKGHLSLVEHVSAEGEHPRHFALTPNGKLLIAANRDTNNLVFTFTVD
QESGRLKYTGHS TGVS KPVCKPVYL"

CDS 3219990..3220919

/locus_tag="EFAGFIKM_02709"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLHSFLLTYHVFLPISLPVIGGILLKRFKNWDTRSLSTFSLYI
LSPALIFNTLLHAEITWTDVTSTFWFSIINLIALWALAELLSRVFRLGASEKAGLTLV
STFTNCVNYGLPLVLLAFGQLGLDKASVYVIGQMIIVNTVGIFFAARSEFTVKDAILS
VFRMPYSIAAGIAIALRASNLSPALDGGISMLAAGYSPVVLAILGAQMLRPGKATV
PWLPNVRRAFWTGLVVRLLAAAPILSWLILTVLQVEGTLFSVLLILASMP TAVNAVILA
EQFNASPQFVSRCILWTTAASMLMLPIMIVMAS"

CDS complement(3220897..3221487)

/locus_tag="EFAGFIKM_02710"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNTQKRKTNRWVRLTRAMKLNFLKLLRAPGGAHKVSTGFAIGFG

LELIVISTASLIYLVFYPIVRLSGGSVPAAIVGNVIGKLTFLPIILMPLAKQIGSWIL

PAHSMGQGPPVHESAFMELFRGNWSAVSELLLGGLDILAGMSVFGVILGVISYFVVKFF

YVRALNRRYERRLEKRRQADIASVSPVLRKPSQS"

CDS complement(3221546..3222004)

/locus_tag="EFAGFIKM_02711"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKHPFHLKAVWNGGRNSEGTIDAGGLKTVISIPQEMGGPGTGTN

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LSADASEADLTKAERLAHKAESSCMISRAVAGNVQMETQPVIVTTGANAV"

CDS complement(3222025..3222792)

/gene="ydjF_2"

/locus_tag="EFAGFIKM_02712"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77721"

/codon_start=1

/transl_table=11

/product="putative HTH-type transcriptional regulator

YdjF"

/db_xref="COG:COG1349"

/translation="MLVAERYEKIVEWVDTQGSMRVTELSERCGVTEETIRRDLDKLE

QAGRLRRSHGGAVSVKYKDELQSEIPYPERAVAHAEKRRRIASEAVKMOVESGDRIALD

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RSLDAYHVDKVFLSCKGVHLTKGISESNELQALVKQKMIHIADEVILLADSSKFNIQA

FTRVAEMSSVGKVITDQGVDEEHVSALIEQNITCIRV"

CDS complement(3222930..3224060)

/locus_tag="EFAGFIKM_02713"

/EC_number="1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0DN73"
/codon_start=1
/transl_table=11
/product="putative oxidoreductase"
/translation="MNPKNQMFEQVSLPTGITLKNRIVLAPMTHMSSNADGTISDAE
LAYYARRTGGAGMSITAVGHVTETGIGFPAQFGVYDDRIFGLKKLADTIKQQGSVAV
LQIFHAGRLTPEQAVPSGQVVAPSASERPGSPEPRELTDAEITSIIKDFGEATTRA
IEAGFDGVEIHGANGYLIQQFFSPHSNRREDRWGGSVEKRLTFPLAVVDEIQKVAEH
TKLPFIIGYRFSPEEPETPGLTMEDTYLLVDALKDKNLDYLHVSVNEFWSKPRRGEAD
TRSRMEFILDRVNGKLPVIGVGSIHADQAAEALQGVPLLAIGRELIIEPAWVEKIE
SGREEDIETILTKSDQERLVIPDGLWNAIIHTPGWFPM AEDK"

CDS complement(3224248..3224925)

/locus_tag="EFAGFIKM_02714"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MCNRFSLAADLDEV RDHFKIQRVMYYYYKNRYNISPTQHTPIILH
QDGERVLDEFRWGFIPFWGRDAVNANLMTVHENPSYYKL VETKRCVIPCNGLYYWRQE
GKKSYAVRVVMPDRGLFGIAGLYE VWRDTRKEPLRTCTMLMTGANMVTREFGSKMPAI
LSEEEINTWLDPANTRVTQLLP LLKSYNSTEMNLYPVTPMVANDEHDCYECVEEMDQK
LAYVRSF"

CDS 3225153..3225674

/locus_tag="EFAGFIKM_02715"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKRKFLMSIMLFSAIAMFGSTIYAATFLTYGY PSTTIPIRTYNY
ASAWQTPMDASLTNWN NAGAKVKFTKTSNSPNTITAGNFNNTAYGVNYASVSGSQVVS

FRIELNASTITPDATNLSNFIQSVFVHELGHSIWLGDNPTTSSPSIMSYTRNRNSMTQ
PQTFDINNVRISKY"

CDS 3225718..3226389

/locus_tag="EFAGFIKM_02716"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKNRVLTLLSSIFILSAVGCSSVTPTASPSDAPMTIIASEDY

PSYGSIGDLSERANTIVKGSVVETRVEALNDIVQVTDAAENELNPASDPGGEPASFD

KIYTIHTIQVAESYKGGYTAGEKLEVKQLGGQLGNTEIINDDNLKLIPTKDYVLFLET

YEDTPASLLNSVQSLYVIKPAAKSNQPGQQQSESEVIVSANPENDLTLQLEDLQEIQN

EQKSE"

CDS complement(3226521..3228431)

/gene="rhaS_26"

/locus_tag="EFAGFIKM_02717"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

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MLNQARNPFEEAWATVPDHTLELRELVRNIHECWSGQERVGKIQVKVYFFQLVQLVLLQ

RSRMFNEVQQPSLTDQVLRVYKAHYRESISDLLAQSLSYSPQYLSRKFKETGCTPT

EYVIRLRMGARSLLASTEASLQEIAAYVGYMDPFYFNRIKFKEIGITPGQYRLKQQE

NSKSVSKSTLNATNESIVTGGDERYPLIDDDNHQYKGDDEINMFNHFKAISMLALV

LTLACGTAQQGAETSEVAAEPEQPAVVETQMVNTTFGEVEIPAHPERVAAIDYLGTV

LALGVKPIGGGQFLMNSPYLEGHMDGLETIGDSVEQLMELEPDLITLNPDKAAYEKY

SKIAPTVSIAITFPTLKDEVNYFGKVLGKEAEAEKWLADFDEEIAKIKQEVQSVPA

DVTFVSMQEYDRQVFIFGNQSGRGGRNIYELLGLQAPKNIPSELMQGAYHEFSIELLS

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AEWIIGLNTPSK"

CDS complement(3228668..3229750)

/gene="msrAB"

/locus_tag="EFAGFIKM_02718"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P45213"

/codon_start=1

/transl_table=11

/product="Peptide methionine sulfoxide reductase

MsrA/MsrB"

/db_xref="COG:COG0225"

/translation="MKRTLGLCLLVIALVVSACGNRVESHSSSISTQPVKASSVSEE

NLSNLYLAGGCFWGV EAYMARIPGVQDVTSGYANGEGKNPTYEDVIRGDQGFAETVHV

KYDPQQVSLQKLLESYFRVIDPTSLNKQGNDRGVQYRTGIYYTLPEDAKIIEQAVAVE

QEKYDQPIVTEVMPLQNYYLAE EYHQDYLEKNPNGYCHIDMTVLDDLEIGIDPAQYPR

PTDEQLKERLTNEQYAVTVNNDTEHAFSNEYWDNEEPGLYVDIATGEPLFTSRDKYDS

GCGWPSFTKPIVPEVVTYTTDTSFGMDRTEVRSRAGDIHLGHVFDDGPEDRGGKRYCI

NSASIRFIPLDKMEEERYGYLLSFIE"

CDS complement(3229767..3230348)

/gene="resA_3"

/locus_tag="EFAGFIKM_02719"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01319"

/codon_start=1

/transl_table=11

/product="Thiol-disulfide oxidoreductase ResA"

/translation="MKMARKWMVSVIVFAGTLLILSACGSQQTESKQMGSTSTPASTS

DMSSSTMMNKGETAPEFSLRDLKGNTVGLSDVQGKKVYVKYWASWCSICLAGLEDLNN

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PSSFYIGSDGILTKSQLGHASNEQIMESLQEIL"

CDS complement(3230367..3231083)

/gene="dsbD"

/locus_tag="EFAGFIKM_02720"
/EC_number="1.8.1.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9JYM0"
/codon_start=1
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/product="Thiol:disulfide interchange protein DsbD"
/db_xref="COG:COG4232"

/translation="MTSDLVFLFGVFGAGLLSFFAPCILPLIPVYVSYLSGSMVNGTN
QQQPDSNSVRLRSTLVLRTFLFVLGSLVFVLLGFGSGIVGNLISSPEFIAICGAIVV
LFGIYQTGLIRLSWLERERKLSNDQAKRGGYVGAFLLGLTFSFGWTPCIGPVLAAILG
IAAGEGSPLYGGFLMFLYTLGLAIPFLILSVFSEYVMKRIRRLYRYMGVIKITSGCIL
IVMGLLLMTDRLNSLVTWFQ"

CDS complement(3231127..3232167)

/gene="sasA_11"
/locus_tag="EFAGFIKM_02721"
/EC_number="2.7.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01837"
/codon_start=1
/transl_table=11

/product="Adaptive-response sensory-kinase SasA"
/translation="MKLRTYLVLSLTGIGVLLICLFISYSKMLLTIEQLYWLSAITA
GVGLLSFILQYLLTKPLEKSIARITQQTIRIAEGDFHTEVPLIGTQEFKLLAQQFNEM
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NTIRLETKRLGGLIQDLFELSSLEAQGEVFDPPCHVDELLSTLESFSFHLEAECTLD
VEIDLDPDKLPAAVMMPAQMKRVLSNLLQNAIQYSPIEGKIILAAEEKGPFIRILVTDE
GEGIEAEETSRIFERFYRIDKSRKSNNGGAGLGLAIAQSIVELHGGEIGVQSTKGEES
CFWFTLPIYVSR"

CDS complement(3232164..3232868)

/gene="walR_3"
/locus_tag="EFAGFIKM_02722"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37478"

/codon_start=1

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/product="Transcriptional regulatory protein WalR"

/db_xref="COG:COG0745"

/translation="MNECVLVADDDTNITDVCRRYLEREGYLVVTAKDGLEAIELWHS
QTPSLIVLDLMMPHKNGWEVCNEIRQTEDVPIVMLTARGEEDRLMGLTMGADDYLT
PFSPRELVLRVKAILRRMRTAQASPVTTSEYTINYEGLTIDFTKREHVHISGQAIELTV
TEFEMLYLLASHPGQVFSRNQMLSKIWDFSIEGDTTTVTVHVRRLREKIEQNPSDPKY
IKTVWGIGYKFAGGSS"

CDS complement(3232946..3233425)

/locus_tag="EFAGFIKM_02723"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMKTNKSKKAMVAAVLMMSMASFGLASAADMKTIKKDGMELVQL
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ETMMPAGKTIKLWIGSKKIMVDGMQVNLKSMPVIHEGNSYAAESVIKQYMMPVKGMK"

CDS complement(3233592..3236141)

/gene="lacZ_3"

/locus_tag="EFAGFIKM_02724"

/EC_number="3.2.1.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01687"

/codon_start=1

/transl_table=11

/product="Beta-galactosidase"

/translation="MSTIQSHVFQNWTFKACEDQEWMSAQVPGCVHTDLLKLGKIPDP
FYGTNEKEVQWIDKIDWEYQTEFDVADALFSQEHLELVFDGLDITYADVYVNEVHVLSA
DNMFRVWKADVKSVLKGNNGNLRIRFRSPIQEDLPKLEKLGYPASNDQSDVGGGLGD"

KRVSIFARKAPYHYGWDWGPRFVTSGIWREARLEGWTQVRINDVYIQQNEVSATSASL
TAVVEVETSQAVDTIIRIGADGQRWERSVSLQPGTQTVEIPISIDEPKLWWSRGLGDP
HMYTFLTEVLQGERAVAESTVKTGLRSIRLVRDKDEAGASFYFELNGVAVFAKGANHI
PNDSFITEITHERYRHEIVSAAQSNMMLRVWGGGIYEQDVFYELCDEYGILWWQDFM
FACSMYPGDEAFLNSVRHEAIDNVKRLRNHPSIALWCGNNEIDSAWAHYVENGGWGWK
KEFTAEQRESIWADYEAIFHDLLPEVVEAYAPGVDPWPSSPLVSLTGDDETQHAHPSTA
EGDIHYWGVWHNVEPFENYNVHVGRFMSEYGFQSFPEYKSVRTYAEEDLALESEVML
AHQKNGAGNRLIKQYMDMYMHESKDFPSFLYMSQVLQAEAMKTAIEAHRRRKPFMGT
LYWQMNDWCWPVASWAGMDYLGRWKALQYYAKRSFSDVLVSDGDKEDTTDIYIISDQL
QPVKGQLQIRLLGFDGTVHRDETHDVTLEPNTGDRVLSLRNAEWLEGHDTANTLLRLD
LKQEGAANVVQEHYFVPSKDLALQPANINVSGGADENGVLVLESDVLAKQVWLSSDV
EGVFSDNFFDLIPGIPVKVQFTSREGLQSNNDVISNPGPIEVRSMIDFIRLT"

CDS complement(3236389..3237429)

/gene="exuR_2"

/locus_tag="EFAGFIKM_02725"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9JMQ1"

/codon_start=1

/transl_table=11

/product="putative HTH-type transcriptional repressor

ExuR"

/db_xref="COG:COG1609"

/translation="MSRMTKRVTMQQIADAAGVSKFAVSRALTGKPGVSEHTREMIVR

TAGQLGYFRTEPKRYPGETQISAEMKPEAERQGTILILFPNIRSQNRSSLYWGPVFDG

ISERLNEKGMDILTLEPSSDRMFVNLNPEAISGVITVGTISTSVLLEIYRLRIPLVM

VDHEDPAIYADSVFTDNMKCMKELVLMVLVGKGYRRFQFAGQLPDAASFRRWLGYRMV

LEEKQLEGEQQDGLLGPEYDQIRRSIAEMELEDIPEVIVCANDHTAVIVIQALQSRGI

QVPERCAVTGFDNTQTDEPILASVHINKENLGTRAVDQLLWRIKHLDEPYERKLIYSE

LIIRDEYNASIQ"

CDS complement(3237610..3238557)

/locus_tag="EFAGFIKM_02726"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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/product="hypothetical protein"
/translation="MNGVQVNQGQATRRADIQMLLATVIWGSSYLFMKSGLESMQELN
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GFLISLAVIFVPILTTIQHRRMPDKRLTSLVAVTGLGLLTLQHELSLHTGDILCIL
AALVYAIYIMIAGKFTPKHDPLTLGTVQLGVAAMWGIAATFMMETPRMPDTAESWAAI
LGLGVLCISGLGYILQTLAQRHASPTRTSLIFSLEPLFAAAFAFTFQGESLTLQGYAGA
TLMLVGVLLITEIKLPQPIFWRRKRPVLQSELGDQGAPGV"

CDS 3238722..3239597

/gene="gltC_3"
/locus_tag="EFAGFIKM_02727"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P20668"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator GltC"
/translation="MSLVKYEILNTVVEYGSLTKAAEALNITQSAVSHAIASLETECG
FSLHRSRSGVRVTAEGERILGYTREILRWTELMNQEISLIRGAEIGTVRIGTFASVS
TQWLPGILKQFRLRHPGIEIKLWEGDYAEIEGWLAGGAIDLGLSLGDSSPFETIPLQ
KDRMMCILPLDHPLASEESVSFDVLLEQPFILPKWGGDNEIERLIRQHAAKLNVVYEV
AEDQAIMAMVRNGLGISLLPEMVLQNHTHALALVPLSGDPYRTIGMACPSLGNLSPAT
RRFIEEVQQWLGQVM"

CDS complement(3239640..3239837)

/locus_tag="EFAGFIKM_02728"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNSNQDLKQVNERLDQIEQKLDNLGGSHQNKRSPPGVRFLIGFGI
TIGIISVLILTLGVIQFVSNG"

CDS complement(3239868..3240350)

/locus_tag="EFAGFIKM_02729"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSNLEQAVRWRQEGKVQEAIELLQEITVQEPENANVWYQLAWAH
DSLGLEREAVPYEKALSLGLSGEDRAGAILGLGSTYRTLQYEQAKVWFEGMKMEFP
AYREFEVFYAMVLYNLGEHAEAMQRLLVQLADTSSDKRINDYNRAIRYYADQLDRVWE
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CDS complement(3240777..3241634)

/gene="ctaB1"
/locus_tag="EFAGFIKM_02730"
/EC_number="2.5.1.141"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31652"
/codon_start=1
/transl_table=11
/product="Protoheme IX farnesyltransferase 1"
/db_xref="COG:COG0109"
/translation="MLKDMIALTKPGLRLNVFAVAVGFVVASKWDINWLSLLMVVIG
STLVIASACVINNYWDRELDQKMERTKKRMDYINHLKPGVVLGYGIILGVVGLAVLYL
LVNPLSGWMALLGWFAYIVIYTMWLKRSSTWSTSLGGIAGAMPPVIGYTSVTNEIDAG
AWLLFALLFLWQPPHFWSLGIRRVEEYRAAGFPLLPVVKGVKRTKFQMIPYVFLLLPA
VFLYYYDYVGLVFLIVSLVGGLIWFVHTLSGLKTQDDEKWAKVNFLISVNYLMIVFI
VMVANTVWS"

CDS complement(3241791..3242357)

/locus_tag="EFAGFIKM_02731"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKNATKQWKLGMIGAVVALLGMIVLTTYLLTPANAQGSTDAQQP"

SAKEAQVANSEMFTAYVEGMHIEDGKLFMTVDKIGWYQGEEADAIFAQRNPEAGIDGA
PDGYIVNDSKEQEVEVSANAEVLMQLYDRDGTMQGADIQWNEPVTLSKFESLYENT
RILDLSVFPYHLTVQDGKVTKIVQQYIP"

CDS complement(3243014..3243367)

/locus_tag="EFAGFIKM_02732"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNEENHVIHKDGQVSTDKVDNAIEKIAPEEREQILQNFDFAKEY

LGKRIAMGESIGLSEEQMAKIAEKVADYLAAREEPRNREEKLLQELWNVGKEDERHML

AHMLVRLAQSSTPNH"

CDS 3243614..3243829

/locus_tag="EFAGFIKM_02733"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRDKTKHEKTNDELEPGVNTVIHPDKNNPGPTDMIEGVVGDIVD

NIRKDFSHDSKDEKSSSKSTDSSDKQA"

CDS complement(3243945..3244862)

/gene="trxB_2"

/locus_tag="EFAGFIKM_02734"

/EC_number="1.8.1.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q05741"

/codon_start=1

/transl_table=11

/product="Thioredoxin reductase"

/db_xref="COG:COG0492"

/translation="MREVDCIIVGGGLAGLQAAIQLGRYSAHQVLVIDAGEGRSTLCR

TYHNILGFDPDGVSGEELRERGRMQAEQTVGSFEKDRIIKAARKGEHIQLFGTSGSEYR

SKTVLLATGLTDRVPDIPGLTPTLGRTVYVCPDCDGYEIQNQRTVLLGSGEPGANMAM
ILIQRTNDLLYINHEQAPISAEELHRSMKEAGVRYLEAAVQEVQQIEDGHITGVLTEDG
QIFESERGFIAGGNNRVHYELAEQLGAVIADNKHVEADPRSLQAATNVWIAGDLGLHA
EQATVAMGEGSIAAIWIHKALQQMTKDSR"

CDS complement(3245250..3246881)
/locus_tag="EFAGFIKM_02735"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNNRLKDITNQRIWKMALCGLLTGSGVAGYGSTVQAATVQQQFQ
DTRTSYAKDAITHLVDKGIAAGTSETTFEPKAVTRAEFATFAVRLLGLKPVKNNINP
YQDISMNAWYYGNVAAMTNLFILEGKGQGTGFQPNASITREEAAALLVRMLKQQPVETS
LLSSTYFDAADISDWARPYVQTVYQLGLMRGSGGVFRPHDQVTREEAAVMLDAILQKK
TWSEQLQRGDELGVQLGWQYNSTTTEFKKQVEQSEVNTLVPRWFFLNSSMKVTDHADP
ALISWASATDRQLWPLLGNRSDSAITHQMLSSSANRATVISQVAAYVKTYKLDGINVD
FENVDPADREGLTAFVTSLTATLHALGAVVSDVSPDLGTDWTDADFYAKLGAVSDYM
VLMGYEEHWNGDPKAGSVASLPWVEKALDTMLSEVVRAKTILALPLYTRDWSSVNPAT
SSWDITLADQGMRAHATGSVRRWDASLVQYIIGYNSNGKPRYIWAEDSRSLSAKVLMS
EQRQIAGLAYWYMGGETADVWNAISNASRFESYNF"

CDS complement(3246976..3247575)
/locus_tag="EFAGFIKM_02736"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTTFFDALKNRRSYGISKESTISDAKIQEIVVEEAVKYTPTSFN
SQTSRAVVLLGEQHDKLWNHTEDILREVVGNEEAFKSTA EKMTGFRSGYGTVLFFEDN
NAIAQLQQNFAAYADNFPIWANQSNGMLQLVIWTALEQEGLGASLQHYNPLIDEKVKQ
EWNIPENWRLIAQMPFGKPTAAPGEKEFQPIEERVKVHK"

CDS complement(3247724..3247978)
/locus_tag="EFAGFIKM_02737"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKQRTPDQNNNDTQQEQSHDNPEQYKTEHESLLDRHEEEQTVDP
IPMEDLNMEAQEEKNKDQTKSNSSTEEKYRADYRKKTGEG"

CDS complement(3248115..3248972)

/gene="rhaR_24"
/locus_tag="EFAGFIKM_02738"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01533"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaR"
/translation="MPSMMQFSASLEYSYRSTSIFNPGKSDGFHSHPHYEIYYFHDGE
STYIIGDRVYNLEPGDLVLMHGLTLHRPHPKPGSAYERSTLHFDPSAIRSSLHPDRMA
EVLRPFEELRNCRVNLKGDNRSEFEALLHDLHRLSQSQSNFRQERMNVRLCDLLYFVA
EICQGVDVQEQLPSSERERHVQHIIRYVDTHYMKDIGLDDLALHLHLSKPYLAGMFKEM
TGLTIFKYLYDRRINQAKLLFQFQPEITVTEASRLSGFKRLSHFSRMFKQSVGCSPDL
YRTQLHRQS"

CDS complement(3249044..3249592)

/gene="gpx1_2"
/locus_tag="EFAGFIKM_02739"
/EC_number="1.11.1.22"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P74250"
/codon_start=1
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/product="Hydroperoxy fatty acid reductase gpx1"
/translation="MPTIYDFTVTRTSGERFPLYQYEGKPV LIVNTASKCKYTHQFDD
MQKLYDQYKDQGLQIIGFPCNQFAEQEPGSSSEAESFCQINYGVKFPMFSKLDVNGEA
AHPLYDFLKRSGPFAGFDETDIQA KLLKLMVAEKAPEWLHGDAIKWNFTKFLIDAEGR

VVRRFEPIDSIDEIQESIKQLL"

CDS complement(3249780..3250676)

/gene="araQ_18"

/locus_tag="EFAGFIKM_02740"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MEKQIAANAKPTAPHSPKVKVRMESLTQIRKIILTLLMSGFALL

MIMPFIWIMISTSFKSPADVFTYPIQWIPSSLNWEHHIKVWSGADTFATYYLNSLKISL

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THWALILPGMFTIFGVFMLRQFFLSVPSEISEAAFIDGAGHLRIFFRLILPLAKPALA

TLAIIDFSWHWNDYENALVFLIDKDLYTVPLGLQNFLENNDYNGMMAAATAGIIPM

IIVFLVGQHYIIQGVAGSAVKG"

CDS complement(3250694..3251575)

/gene="ngcF_2"

/locus_tag="EFAGFIKM_02741"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O50500"

/codon_start=1

/transl_table=11

/product="Diacetylchitobiose uptake system permease

protein NgcF"

/db_xref="COG:COG1175"

/translation="MHKSWMKRQSRLGYLFIGPNMIGVLLFFIIPAVYSFYLMFTDYK

FMSPETNFVGLDNIRRMNLDDLFGVALRNTFVFLAVPVSMGLAFIVAVALNKSVMYQ

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IDIIWIWFMGLGYNMIIYLAALQEIPEELVEAARIDGARPWQTIRQVIWPLVSPTTFLL

LITGLIMTIKNFGIIQAITQGGPGNSTTVLSLFIYQNAFRYYEMGYAAAIWALFAII

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CDS complement(3251784..3253097)

/locus_tag="EFAGFIKM_02742"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRIKKGLTGLIVGALMLGLLAGCVGKNETNGGDNGGGAAGGKVK

LTMWGAVPPENGPPQEVVDTWNAEHPDIQVEYVRFVNDGDLKLDLSTGQNVLDLYV

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NMKALDQAGLSVPAAWTWDEAREYALKLKTAGFKYGLVQHTASYVDPLDSVLVKNQYV

KADGTSNLDDPLVTKWLETNLGMMKEDATTPPLGEQLTSKMPVENMFLGGESAMINIG

EWLIRTSNNMTEFPRDWKIAFAPVPRLAQEDMVKSGGLGDFIANSKSKNKEAAWEF

LKQYADGGMMPMAAGGRLPSSNAVDQQTALDHLGDIADSYDKESLEFVLYGDETPTF

VRSIAQEVVDLRAQEYKFFLGNQTAETVQNMVKRHNDWLKQNNQ"

CDS complement(3253262..3254113)

/locus_tag="EFAGFIKM_02743"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5HJF7"

/codon_start=1

/transl_table=11

/product="putative response regulatory protein"

/db_xref="COG:COG4753"

/translation="MWKVLLVEDEVFVRESVREIISWEELGFTVIGESGNGTEALAMI

IQDTPDLVLTDIVMPGMDGLELLKQTRQAGLTKFVMLTCMGEFEYVRRAMEYGASNY

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APPSDLDLPFTPVREPIVKHPEISKIIQYIGQHYDQDITVKSMSRYVMMGENYVSALF

KKKTGHTLIHYLHGVRMEKAAEYLRETDLPVQEIGYRVGFGSDNYFIKIFKRWTGCTP

SQYRHRHS"

CDS complement(3254298..3256118)

/locus_tag="EFAGFIKM_02744"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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/translation="MTKPDWKTFLPHKLRYLFGAFVVLILLPFSVLNVVNYGQIESL
VEQKISEQSHEQLVQMYGSLEDQMSIAFKTLIFLEQDSAVRNVLTSPDNRSPLENKSL
VEEKFKMINNSFFLYNPSVYFTLLDFHDNVYTSYLPKKALAYGPYREQFRKHLGEMTF
IKGNTDSNSFPSEELLYRWDARDTNHVLRELSSSPYLLSLYAYMKDSGGKRYGMARIS
IDYSYWFQSMKDSQSNQEYFLITGNGETIARSSEKAVLSPDVTREIALHPAEAYLTD
NDSDTLINVYIESLDWYMVNRIPLAVLFTEISGLKQRYFLTFFGFTAFAVLMAFMIS
ATFTRPLSHLQNQMKEVVRKNLKVRIPEGRSRGEVLELTRTFNTMLDDANQMIARLKA
EERQKEAVHFHMLLAQMNPHFLLNTLNTMKWSAIRSGNEEISEMCVSLGKLLEVSLNS
QVELVYLKDEIELVQAYLHIQRIRYRDSFEVTCEFDKLEYALVPKLSLQPLVENAIH
HGVGPLEQLGQIRIGIYRQDTGKLMLEVADNGIGMEESRRQQMTRTRPGIGLSNLKER
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CDS complement(3256317..3258650)

/locus_tag="EFAGFIKM_02745"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MRKMIFLKALKFVLMITLLVPLYWAAPSVHAAEGENTLILSHDF
EDGTVQSWSGRGEVETLHASAVAARTGDYGLEVSGRAMTWHGPALDVTELLEVGGQTYV
FTGWVKLPAGASSTNLNMSLQRTLPTDTHYENLTFGTASAGGWTKLTAQFKMLEPANQ
LSVYFEVPDRATASFYVDDFRLEKLPDLGPVIEEDIPSLQDAFAGKFRIGTAFTNNE
LLTEPDKQLLTKHFDSLTPGNVLKWDSTEPQEGMYNFSGSDAAVAFAAANGQEIRGHT
LVWHTQTPDWVFDANGNLVSKTVLYERMQQHIETVMERYQGQIYAWDVVNEVIDTSE
PDGLRRSLWYQIAGEEYIEKAFAHAADPDAKLFINNYNTHPAKSQALYNLITRLQ
AKGVPIDGVGHQTHISLFYPSLSEIESSIVKFKALGLETHITELDVSVYSNDSQSYDI
FPEELKTQQAALYKSLFQIFLRHTDTVKNVTLWGKDDANTWLRTPVARNNWPLLFDE
RLQSKPAYWSVLETVQVEAVPAAPQNLTATAVSDNSINLSWSASASATSYTVNRSLTA
AGPYTSVAAVSGTSYKDMAVSAGTYYYYVNAVNSVGKSVNSVQASAKAQGGGPPEPA
GHILTAYRAGDTNLLDNQMKPQFVIHNGTSTVSLNELTIRYWYTVDGEKQQSFFCDY

AQLGGSQISGSIVKLPAPVPGADHYLELKFGTGAGVIPVGGTSGEIHTRLHKADWSNY
SEGDDYSFNPLQTSFADWTKVTLYRNSELVWGVEPIS"

CDS complement(3259013..3259780)

/gene="rhaR_25"

/locus_tag="EFAGFIKM_02746"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MELLNHIYWKQKGEFALTEDIYTTWVAFAVEEGIFHYEIGGQIG

EASFGDLVLCPPAVPFRRTVITPLTFHYLQFSSSLEEEEFLLPPAGKSLINDTKRLAS

TYAYLRQDSEENKGEVARWKTHFMMDLWQLYQVERRQNRLKERRFTEDARMAEAAALL

EERAEIEISLQELAQRALSPVQLTRRFREAFQETPSGYLKRVRLLKKAQNLLADSSLT

LNQIAERCGYENGFYLSRVFSKTLGISPSEYRRRHRV"

CDS 3259927..3262176

/locus_tag="EFAGFIKM_02747"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKQEHVQYDITVIGGGLAGVCAAIAAARMGQQVALVQNRPVLG

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SNISLYLNTDVHEVEATGDGDERMITSVTGWMMGSEKIRFESQIYLDCTGDGLVGFL

AGAKFALGREARSEYGEEWAPEVADQITLGSTLLFYTKDAGAPVRYIPPSFAKDITQT

SIPRRVIRSGDSGCHYWWIEWGGEHDTVHDNELIRDELWSVIYGIWDYIKNSGKFDA

DHMTLEWIGSLPGKREYRRFTGDYVLTQNDIISQREFPDVAFAFGGWSIDLHPPQGMYA

EASGSKMHADGVYHVPFRSLYSANVRNMLMAGRDISASHVAFGTTRVMATCAVIGEA

AGTGAALCAAMGVSPRELHARHLAVLQQTLLRQDASIIGVRSHDELDLARRAKATASS

TLTGIVLEQPGETYPLGTDVALLLPVYPVLSGLELLLDASSDTALTVELWDTGRKENY

VPHLLQVTATVNVTTGTAQWVKLPLEWRPEEPQNAFIIIRSNAVSLYHSTEAHSGVL

IFFKTEENHVSKNLEDHATDQPVVLWSMQGLARQPFCCRTLSETSAYSSDNTINGYHR

PYGGPQQWMSQPMQSGKPEWVQLTWEETLAELHLTFNDDVNEDLVNLHHHHTTFRV
MPELVRDYHVEVLTPAGEWTQVASVQENHKRKVVHSLDVPVSAQALRIIIDATNGSNY
AELIEIRAY"

CDS complement(3262237..3263307)

/gene="yesR_1"

/locus_tag="EFAGFIKM_02748"

/EC_number="3.2.1.172"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31521"

/codon_start=1

/transl_table=11

/product="Unsaturated rhamnogalacturonyl hydrolase YesR"

/db_xref="COG:COG4225"

/translation="MLNQMVQLQERISKVSQAMESMKNTSINEQFPIGLIDIHLWEWPQ

GVGLYGLLQLHEATKDPKVLEFLESWYNARLMEGLPEKNVNTCAPLLTLISLCELTGN

KEYEHVCEEWSSWIMDGLLRGTGDGAFQHMITGDANDGQILIDTLFMTVLFLAKAGVYF

KKPDMVEEAKRQFLVHIKYLYNKKTGLFYHGWDFNENHNYGAVHWGRGNAWYTAGVMD

FLNIPIEDGLKAYLLDTATAQVRALSKLQGEDGMWHTVLDDPTSYKETSATAAIGYG

ILKGIRYGYLDESYHQNGLRALAVLKQIDDHGVVQQVSYGTPVGQDAQFYKDIPSP

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CDS complement(3263343..3265898)

/locus_tag="EFAGFIKM_02749"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSDTRSGMDTLNYKPMKLGHNQVINHWMISGIYTKPVAFVPTT

MEGDINDWLIDGFAIHENPCRKEFVEHRRTPQVNRFFDQWSEFPSPGDDFVGEENGMP

WALYSPWNNPRVEQSGFWFVPTHLRSYAATRLISPTAHTASLRIKTYGSLTLWVNGEM

VTDFAPLMRNKEQEIVIKAEVLVAGINEIYACWEDLAERDTMYAFAVEYLGDEELVISL

PIAPHLAESVKSAAEEALEQAYFPSDLFRGEQIKLKLPISLPDIVREVDIQYGNFFDGT

ENKTIHIAEKETDLVLAHTNQLGHHYVYFTLAISVSNVVLTKKFGCQSYDTSYDEAAQ

QAADIEARKSLALRCIAEKGSPNIHKAIAMLKTGGNLQEAENILLEGVEGIEQRKDCS
DFYLVGLFRLWRDERNSGLFSESFWDVRKASILGYRYWIDEPGDDVMWFFSENHALLF
HTNELLAGQLFGDEMFSNSGESGEVHRQKAEQRLALWFERFLDEGLAEWNSSAYIPID
AVGLLHIYEFAHNEQLRQQAKKAMDLLFYYITVQMHQGVLTTFGRSYEKELGGYAA
GTTSMCWIAYGVGNNVNNYSISNVALSLSDYSPPAAYQEHLGLDNQQLVFANQQGKGG
YAKLYHCRTREYSLSSIIRFRPGKPGYQEHVQHLSLSPEALIWNHPAEIYKHGDGRP
CFWAGNGILPDVVQHEGIALMMFDIPADNNSDWTHAYFPTHFFTEWVRHENWHFARLD
KGYAAIYAANGTSMESGVTRELERISPLRANAWIIRAGSEQQFGSFDALINQVCSAN
PQFDNQALTTLTDPVYGPIQWGMNKPFLIKEEEIHEGYGVKGQSKLLDMER"

CDS complement(3265904..3266728)

/gene="araQ_19"

/locus_tag="EFAGFIKM_02750"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MVMKPMVKIFIYSLLSVAAVWLLPVLWVVISALKTNSDLYSFP

PKLWPQPITFEHFKEAFSGDFGLYFMNSTIVTSSTLLLLLINSMAGFALAKYRFRG

SAIILIAFVSTLMIPIEVIMIPFKVLSALGLYNSLLAIIPPAATPTGVFLMRQYLL

SVPDELLEAARMGDGAGEWKIYWSIILPIAKPILAVLAIFSFMWRWDDFWPLIAISDP

SKYTIQLALSNFIGEYNVDWGSLLAMSVITMLPVLIVFMVFQRYFVSGMITSGMKG"

CDS complement(3266728..3267633)

/gene="melD_8"

/locus_tag="EFAGFIKM_02751"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34706"

/codon_start=1

/transl_table=11

/product="Melibiose/raffinose/stachyose import permease

protein MelD"

/db_xref="COG:COG1175"

/translation="MSEQQRLNRNTLAKQNRKLIAPYLFILPNLLIFGTFIVFPSLL
GLYYSFHVYDGLNPMKFNGLDNYIKIIGDREFWSTIGRTGIYAAFVVPLIYAAALGIA
LLLAREIRMRGFFRAVFYWPTMISYIIVGLTWKWIFGDSFGILNHLLTVVGVEPVGFL
TSSFWANTAVIIATVWSRAGFFMVIFIAGLQAIPTDYYEAAARLDGATGMKVFRYITLP
LLKPTSLLVVMLTLIDAFKAFPLMFALTGGGPGKDDTYIVQYIYEIGFNRQELGLASA
MSVILFILIGGFSAALQFRLSKGGAT"

CDS complement(3267726..3268997)

/gene="araN_2"

/locus_tag="EFAGFIKM_02752"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94528"

/codon_start=1

/transl_table=11

/product="putative arabinose-binding protein"

/db_xref="COG:COG1653"

/translation="MTRRTTFKLITSMVLVMLFIVLTACGNSGTNANPKQTTLDFLWF
SDGKEGEVIKEIHKDYEQTNTKVKINLIEVGFKDIQTKLKTMLSGGKPPALSRVTDG
SFANQAVDLTPYVDNADQFEDQFIDSLKPYYVINDKLVAAPMDVTANGLIYNKTLFDK
AGVKVPTSPDQVWTWDEYTAALKEVMDKGGARYGMVWDVTPHRWSTLLYQNGGSILTE
DGTAAAINNEAGIRSMEQFKQLHQEGIMPESVWLGGENPNNLFRSGTVATHWAGNWM
SNYKDITDFEWGVTYMPKGTQRSSVPGGKFLMAFKGSGYEQAEEFIEYLTSKEVNSK
YNQESLFMSPRKDSSVLNYEFGKEMFEIFADELKNSSPLAANDWSRQTIISKISTDLK
NNIVEVLSDKATPQEALDRTAKLINEAIGSQ"

CDS complement(3269020..3269901)

/gene="melR_2"

/locus_tag="EFAGFIKM_02753"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ACH8"

/codon_start=1

/transl_table=11

/product="Melibiose operon regulatory protein"
/translation="MLTIHTPTNIALQENEVYVRSEADNFQDEWPVHTHNGYEIHFI
QGDATFLIGDRIYKPLPGDMFIFRGGVPHRINPSREMVYKRSFVNFTLLLLDMLAVS
QLENLMSIFRHPNGLLVHWPPEERKYITAIFKGIKEEMGAGNTGYKTMVKLSLTQLLL
RIYRKTTSQSANPILCSSQKQTSVSRVLHYLNQNYTENVSLDELSKTLHLNKYYICH
SFKETTYGTISNYVIRKRVAEAKKLLLSTDAPILSISETLGFNTPVYFSRAFKQYVGV
SPQLFRKSELLNEAKIH"

CDS complement(3270139..3270933)

/locus_tag="EFAGFIKM_02754"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAQQEEVLSGGNVNQVVRIGETVRRHVKPNLYVVELLLHLEKVG
YDHAPRFLGIDEQGRETLSYLEGIVPGNDYPDLEEYMWSDSLIEVAKLLRSYHDATV
GFTTTSVSTNRYPGITEDEVVCHNDFAPYNNVYKDGRPQGIIDFDMAGPGPRMWDIAY
VLYTSVPLANFSPEMDGKGVMPYVSQAHGTVRKERIALFMATYGLSVPADLKDWVISR
IRFMCKTLTDRAADGDVAFMKMVEEGHLAHEYKEVIFLENHWDEWV"

CDS complement(3270951..3271226)

/locus_tag="EFAGFIKM_02755"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNNINKILGVVLMLGSVFISTMERISIRVSDAIVEAGYASGGTN
VPQFAQMNEHPTGLLVYFMFFVGFILLVAGFPGSYKKNRNHGYNKEV"

CDS complement(3271329..3271868)

/locus_tag="EFAGFIKM_02756"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MLKKRDLQECHSLYSLMMDPAVFPYVRYACQSYEGYLFLTKQLM
AEEEEQKTVISRTILNETGQPIGTIDLYHIEHQTGFLATWIGSPFFGNGYSQKAKSAFF
VELFLEHGIETVFMKIRKQNIRSRKAVQKLPYVKLANDMYPDVYQRINLNEQMYDLYY
VERSAFFQNSMDLHQVVAT"

CDS complement(3272073..3273260)

/gene="celA"

/locus_tag="EFAGFIKM_02757"

/EC_number="3.2.1.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O08342"

/codon_start=1

/transl_table=11

/product="Endoglucanase A"

/translation="MFKKWKRFVSSSLALVLVAAVAFTGWSPKASAADASQVVAEMGA
GWN LGN QLEAAVNGTPNETAWGNPTVTPELIKVKAAAGFKSIRIPVSYLNNIGSAPNY
TINAAWLNRIQQVVDYAYNEGLYVIINI HGDGFNSVQGGWLLVNGGNQTAIKEYKKV
WQQIATKFSNYNDRLIFESMNEVFDGNYGNPNSAYYANLNAYNQIFVDTVRQTGGNNN
ARWLLIPGWNTNIDYTVGNYGFLPTDNYRSSAIPSSQKRIMISAHYYSPWDFAGEEN
GNITQWGATSTNPAKKSTWGQEDYLESQFKSMYDKFVTQGYPVVIGEFGSIDKTSYDS
SNNVYRAAYAKAVTAKAKKYMVPVYWDNGHNGQHGFALFNRSNKTVTQQNIINAIMQ
GMQ"

CDS complement(3273468..3273884)

/locus_tag="EFAGFIKM_02758"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLSEFIELEEESDESRYCYTLPNTVQIFKHCIQDEDLNDVRISV
STNTPLVSIVDKIEDYIKWFSTCETVFREYYENELREKVHQNWFNEIEVYRADITFNS
IADYGATISCGDHILRDHIMIIDFDREQIQAIHLNG"

CDS complement(3273911..3274939)

/gene="rutD_5"

/locus_tag="EFAGFIKM_02759"
/EC_number="3.5.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00832"
/codon_start=1
/transl_table=11
/product="Putative aminoacrylate hydrolase RutD"
/translation="MRKKIDKTLKYSIFSILMVIVALIFPTWTPKIKGENSISMLEQ
VEINGTGHEVMIRGVDRTNPILIFVHGGPGCSEIPYVRKYQKELEQHFTVVHYDQRGS
GKSYHFFEDYSNLTTDVLVDDLLALRDYVSKELGQETVILIGHSFGTYIGMKA-AAKEP
TQFHAYIGIGQMANTLQSELESLEYTYEQAKQAGNAEDVKKLELIRSSIEQGKELTPR
ILLQKYGGAARLINENRDYISGFLNPEYNGLDMIRFYSGMFSSQDILLKEAFDQNLPL
DIVDHLIPTYFVTGKYDYMTTANAARDYFDVLDAPIKDFIVFNESAHYPQFEEKEKF
VKWLNELF"

CDS complement(3275104..3275649)

/locus_tag="EFAGFIKM_02760"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MATTMITYRTLTLDDVNQLQEIDHSEHIDLIYEMRENRLVELEQ
NNECSNWDEMLLKEIQNRYVYELEQGGMAYGAFADDQLIGFVLAHQYRGKERNQLQV
DLMYVSRGYRRQGIGKRILNELGEEAKKRGAYLYISSTETKSAVSFYKSQGSQIASE
IDQELYDKEPNDIHMIKELGT"

CDS complement(3275678..3275947)

/locus_tag="EFAGFIKM_02761"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNKNKGLIMSLLLLLLLLILLWDSFRTSIFEAVTVQKISENEMTV
INFNNLERTIAVPMDSKLIENKEYTILYDKRVFDKYRLRSIKP"

CDS complement(3275998..3276465)

/locus_tag="EFAGFIKM_02762"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSHWFDLDEFDP ELIKFAVMIAKYNNKFIIK NKRKRGGWEIPGG
NKEIGETILHTASRELYEETGAVRFELTPYGVYEWNGSFGMVSYAEVKLLENLPESEI
DEIKLVDVLP EGMNFGDMFYHFSDRWDGLENHKLK KYTIEINHLNELPEIKIS"

CDS complement(3276621..3277079)

/gene="bltD_2"

/locus_tag="EFAGFIKM_02763"

/EC_number="2.3.1.57"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39909"

/codon_start=1

/transl_table=11

/product="Spermine/spermidine acetyltransferase"

/db_xref="COG:COG0454"

/translation="MNIKIQPV TRENWEEALKISLYEHQVSLVPSVIEGIAYAYIKPW
DEAFDPYVLEIDGKVFGFFYLSYTPDSTDNYWIGGFQIDQSYQGKGMGKN AIRAILDY
ITKQHPLCKVISV TVERDNEIAQNLYKSMSFISENRTNSDDEVIYRLEIK"

CDS complement(3277076..3277645)

/locus_tag="EFAGFIKM_02764"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRIRIIGSCGSGKSTLAKELSDKYGIPSYELDNLIWDRSAENLR
YPEHVRDES VQSIVSSEAWIIEGVQCKDWTIKSIQEADLIFVLAPNVFIRDYRIIKRF
VLSRMGLQPWNYKQSFKNLCKMIVKWNHQYNIEEVICSINENHKTATITKNKKQVIQL
IEHHLKVVVSENEKNLRGNQRLSKEEIQW"

CDS complement(3277686..3278246)

/locus_tag="EFAGFIKM_02765"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISSpgl1"

/codon_start=1

/transl_table=11

/product="IS1595 family transposase ISSpgl1"

/translation="MTPFPELETKRLLLREIKHSDSQDIFHIFSSDEVTRFYDLESFT
 NTKQAEELIQRWKERFENGQVIRWGIALKSDNRIIGTCGFHGWMMQHHKAVLGYELAP
 EFWRQGYMTEVTQKIVEYGFKNLELNRIEAFVEPENVGSRKLEKIGFSEEGILKEHY
 YWKNRFVDNVIYAFLKKEYKSKTDVS"

CDS complement(3278249..3278746)

/locus_tag="EFAGFIKM_02766"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="METERIKFRKYTKNDFDLLFEMTCEPNMMKFIRHGGPWTKETM
 QSLEKFINWNKDDKGLFLAFNKEDNKLIGTSGLPQIIEGNDELEVGYWVVEQYWGMG
 YGYEQAKAWKEYGMDHLKQKRLISLIQHGNVGSMAQKNGMKHEKDVDIIGKNVAVY
 SIEVK"

CDS complement(3279143..3279610)

/locus_tag="EFAGFIKM_02767"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNRGIRFEIPNAYGRFLGEILKPMEVSNFDWFIGEEESYFVVDD
 TLGDDLFPDMIMGMNGEELQKLIDNNEYLLIFANLKAFPKGTQITDVITYEDYMLSDC
 QMVLVIDSTYVTYCKDLEKVEELYNHINRQGFESLAYLTDENDARTKLSVW"

CDS complement(3279744..3280286)

/gene="speG"

/locus_tag="EFAGFIKM_02768"
/EC_number="2.3.1.57"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9KL03"

/codon_start=1
/transl_table=11

/product="Spermidine N(1)-acetyltransferase"
/translation="MSRIYGERIMLREYQDSDLDIKQWVNDPEITGTLSDNFLYPHS
SYETEVFFRTMVEGKSSNKSFIIGLKDSLIDYIGQIDLYKIDYKNRFACLAIVIGRKEF
LGKGYGSEAIRLLQKFVFEELNLRLELEVYNEYIAYKCYLKCGFKEEGRYRKKIYK
KGKYWDSVCMSILKTEYEQS"

CDS complement(3280415..3280945)

/locus_tag="EFAGFIKM_02769"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MSRNLYIISGPPGVGKSTTSKLLVQTLERSAYISGDAVSHFPVK
GRGKPWLDKDTNDLTWKNISLVKNLLDYKYDVVLDYVALPEDIDGLMTELADYHVRI
IYVVLMDRQTIIRDRRLRAEEYQMKERSIILLDEFENHPDLRVDNKLYTNHFTEEQL
PEIVSGIINNEKYRLK"

CDS complement(3280958..3281452)

/gene="bar"
/locus_tag="EFAGFIKM_02770"
/EC_number="2.3.1.183"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P21861"
/codon_start=1
/transl_table=11
/product="Phosphinothricin N-acetyltransferase"
/db_xref="COG:COG1247"
/translation="MTTVTFEEVTEQHLPEIREIYNYVMNTTISFHTTELDLDQIKS"

SVMNKDTRYKTYVILETDQMMGYVLITQYKSKQAYDICGEVTIYLPDILGKGLGKQA
LRFIEKIAKEQGFHTLIATICMENTRSKSLFERNGYEQCALFKEIGYKFDRKLDIGSF
QKIL"

CDS complement(3281583..3282116)

/gene="tmrB"

/locus_tag="EFAGFIKM_02771"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P12921"

/codon_start=1

/transl_table=11

/product="Tunicamycin resistance protein"

/translation="MIIMINGAFGSGKTSAAEALQPLIANSMIYDPEEIGYMLRKLLP

ENCREERERTDDFQDIYLVKILTVKTAKEVKQKYNKHLIIPMTIYKEENFNIIYISGLK

EIDQDIHHFCLTVTEETIYHRLAKRGDEYGGWQYQQAPKCVEAFKDEKFQTRIITDHL

ETSEIIEILIRKVLSIK"

CDS complement(3282306..3283370)

/locus_tag="EFAGFIKM_02772"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFKVKLAKAVISLALFGTLFSIQGVDPDARAADASCPNGYVGLTF

DDGPSGNTTNMLNALKQAGLRATMFNVGQNAQNNKSLVSAQVAAGMWIGNHSYTHPNM

TTLNSSQMSSEITRTQQTISITGSSPKLFRPPYGATNATLKSIVVSQNGLKEVLWNVD

SQDWNGASAAQIVAAVNTMKSGDVILMHDQYQTTLQAIPQIAQNLKNRGLCSGMISST

TGRAVAPDNSTTNPPSNGTKVEAENMTKGGQYTGNISSPFNGVVLYANNDLVKYTQNF

ATSTHNFSLRGASNNANMARVDLKIGGQTKGTFFYFGGSAPAVYTLNNISHGTGNQVIE

LVVTADDGTWDIYIDYLEIH"

CDS complement(3283590..3284642)

/gene="ytfQ_1"

/locus_tag="EFAGFIKM_02773"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39325"

/codon_start=1

/transl_table=11

/product="ABC transporter periplasmic-binding protein

YtfQ"

/translation="MRRHVNWLCLFILLLLVGCTTPESESVPPPISSNNFETLPSVEE

WMESAVARDTSTKPIVLGFSQLGRESAWRLANSTSIRNAAAESGISLVIKNAEQSQT

QFEAVRSFIRQKVDVIAIAPVVEGWDGILQEARDAGIPVIIVDRSVDVKDTSLFVTT

IGSDFYEEGVKAGKYIQDRMRNHPLIRIAELQGTSGSTPSIQRGEGFRSIFETRADI

IFSQSAPADFTEDNGKQVMKEFLQVPEDKRPQVLFANDEMAFGAIQAIEEVGLKPGE

DIIIVSVDGSRKALEILASGKINAVVECNPLLGPQLMQATKEIAGRTLPKRMVPPED

IFTQESAKREMYNRRF"

CDS complement(3284751..3285725)

/gene="yjfF"

/locus_tag="EFAGFIKM_02774"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37772"

/codon_start=1

/transl_table=11

/product="Inner membrane ABC transporter permease protein

YjfF"

/translation="MFLNRKYL PVFVTFGLLAVMFAIGSFRYTGFFSTQVLLNLLIDN

AFLIITAIGMTFVIVSGGIDLSVGSVIALTTIISASLVEKQGWSPAIVIPMVLVMGAL

FGTVMGAIHIFYKIQPFIVTLAGMFLARGLCYVISLDTITNPFYTQVAQAKISLPG

GSFVSINVIILVIVLLAIFLAHYTRFGRNVYAIGGSEQSALLMGLPVARTKILVYTF

SGLCSALAGVVFTFYMLSGYGLHAMGLELDTIAAVVIGGTLTGGVGYVAGTFIGVLI

QGAIQTIISFEGTLSSWWTKIVIGLMLFVFILFQRLSRRVSSKSLH"

CDS complement(3285715..3286758)

/gene="ytfT"

/locus_tag="EFAGFIKM_02775"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39328"

/codon_start=1
/transl_table=11
/product="Inner membrane ABC transporter permease protein
YtfT"
/translation="MAGKMRKHHLFWPLCMLGLLLIFNLLYSPDFFSLVMREGNLYGS
LIDILNFGAPLILVSIGMTLVIATGGIDLSVGSIVAISGAVACMSISRGVDQSSFGLM
LGALGLSIGLSLILGIWNGALVSVARIQPIATLILMVAGRGIAQLITSGQIITVSNA
NYAYIGAGSLAALPFSIFIVLTVLLVASLLTRKTALGLFIESVGSNANASQLAGIRSK
TVILTVYVFCGLCAGIAGLILSSNVSSADGNNAGLWYELDAILAVVIGGTSLNNGGRFY
LMGTVVGALIIQTLTTTIYMIGVPPEVTLVVKAFVVLAVCLIQSDSFRNSMVIRWKKR
KFPAEQGVNRHVS"

CDS complement(3286763..3288274)

/gene="fruK"
/locus_tag="EFAGFIKM_02776"
/EC_number="7.5.2.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q8G847"

/codon_start=1
/transl_table=11
/product="Fructose import ATP-binding protein FruK"
/db_xref="COG:COG1129"
/translation="MAEQAPILQMTGITKQFPGVKALSSVSFRLFPGEIHALMGENGA
GKSTLIKVLTVYSIDEGTVTMDKRHLISISGPLEAQKAGISTVYQEVNLCPNLTVAEN
IFIGREPMRFGKINWKQMNKDAENILRDLHLSDVKAPLQTVSVAMQQLIAIARALS
ISAKVLILDEPTSSLDKNEVQQLFRIMHKLKSEGLAILFVTHFLDQVYEMSDRLTVLR
NGELEGEYIAAELPRMELVLKMIGKELEVLEELPKEADAAQAESGELLITAKALGRKG
AIEPFDLDIRKGEVVGLAGLLGSGRTEIARLFFGADRSDVGKLLVVDTGSTVKSPRHA
IDQNI AFCSEN RKTEGIIDDLTIRENIILALQATRGWSKPISRKKQDEIAEKYINLLN
IHPKNPEHLIKNLSGGNQQKVLLARWLLMNPDLLILDEPTRGIDIGAKTEIQKLVLSL
SKQGMVLFISSELEEIVRVSHRIAVIRDRKKVQELSGDQIHQQQIMKAMAGG"

CDS complement(3288360..3289382)

/gene="ytfQ_2"

/locus_tag="EFAGFIKM_02777"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39325"

/codon_start=1

/transl_table=11

/product="ABC transporter periplasmic-binding protein

YtfQ"

/translation="MRTKKKWGLAITLAMVMLVSTACSSSTNGGAGSDNETSTSGNGST
PASAKTITLGSQVGAESGWRSANTKSIQDSAKEYDLKFSDAQKQENQIKALRSF
IQQKVTVIAFSPVVEGWDTVLKEAKDAGIPVILTDRAVDSPDKTLYKTFIGSDFVEE
GRKAGQWLSDQYKDTQDEINIVELQGTTGSAPANDRQEGFMELIASNSKLKVIASQSG
DFTRAKGKEVMQAFLKAHKKIDVLYAHNDDMALGAIQAIEAAGLKPQVDITIISVDAV
KDGMQAAADGKINFIVECNPLLGPQLMEAVQSVVDGKDIEPRIVTDETTFTSEQAKEA
LPTREY"

CDS 3289626..3291437

/locus_tag="EFAGFIKM_02778"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLIQWIASSLRLKLLSMFIILSSVPLIVGLISYHKSYTVVSN
HNKASTQLVADQLARNIDILFEDTERLLELGKNPQVLQYLYSQSESYPEAKAILQTYN
LYRETYKYDKVLNISFVNFYGGKISERKGVFKLERNPLRNPYFKYLIQYPDAILRIPH
SAAYAENRLDGFAYPKQNALSITTVKERITHEVIGFIVIDLNDLFIDDFLTNTPIK
DSGFFYISDQYGNTLFRPDVTPASITMMDQIRSVPLHLQHDSFILSAGSKPQFVVYST
SKQTGWKMIGVAPYQEIIAEANSIRQLIIITVLLSAFFAISLYFFLNNRILPIRILM
NKMRKAANGYLEAKVTPHGSDEIADLGKSFNVMLDKLKMLIEKSIRENEQVKIAELRT
LQAQINPHFLYNTLESILWMAEAEKKENVIKLVQALSKFFRLSLNKGFDWVSIQTELE
HARSYLVIIQMQRYHDILTYEISVDRELQDYPILKMTLQPLIENALYHGIKNKRGQGLI
SIHGYVEDNSIILTVQDNGIGMSADRLAQLREELEKPADSRSPQDDEQEGGFGLLNH
HRIRLYFGPAYGVEMESTYMEGSTFMIRIPKSKEVNH"

CDS 3291434..3293032

/gene="rhaR_26"
/locus_tag="EFAGFIKM_02779"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01533"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaR"
/translation="MKKVMIVDDEIGIRENIRSCIDWEKEGFHYCGDAPDGELALPLI
HEWAPDILITDIKMPFMNGLELTSIVRTQQPDIKIIIMSGHDEFSYAQEAIRLGVTEY
CLKPISAAELIQMLHKVSKQMDEEHQRMTNRTITKEKLLADLCGGLIGTTDAIESAKQ
LSLPLSARYYTIVIIDVRLTDDSPDPESLMKKLLPILEETRDPHVELLPYIRSRTLV
LLLKYHSDDSISIYLEQLRGRVRMELEHTFKCNIILGIGSQQERLQGIHVSYLEAEED
KYITRLTLQNRASLREINLDEQTTFLGRNSFLEFLKIGSPNQLDHFVQEFAAPLQSF
DWKSSSYGFYLLNDLTLESFRLANQLFRMSDHSDENITSLQQTIRKITSWEDCTQYMC
SLLNLLWQRRACSGKYSDVIDQVKAYLSREYNNEQVSLKMISAHVRISPSHLSKIFS
QETGQTITEYLTQIRIGKAKELLKTTNNKTFEIAVKVGYNDSHYFSNIFKKTGTGFTPR
EYRTQGTEESQARPADMRKEQMYE"

CDS 3293025..3293990

/locus_tag="EFAGFIKM_02780"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNKARFALLLTILVFPMIISGSAHIRPQQMATAFPATSPVEK
SAASKTFGIYPMTYPTYEMITKDATEYAGKQNITLIVNAPDEANTEQQIRIMENMIK
QHVDGIAISPVDAALTPVIDAAQAAGIPVITFESDVPSSHRIAYVGADNYLTGQQFA
MTTTRLLHNQGMILVENGLEEMQGLQQRLNGFIDYIRSETDIEILEVRYHQGNEDQAM
SDMENMIQAHPHFNAIIGLDFVSVSASTLIWKAKGLNRHLIAFGDSPTSENGLLNGQL
SAVISQNEGVWGTKMMETLLLASDGVVPVKEFIDTGII EINHEGSN"

CDS complement(3294124..3294648)

/locus_tag="EFAGFIKM_02781"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISBce8"

/codon_start=1

/transl_table=11

/product="IS4 family transposase ISBce8"

/db_xref="COG:COG3385"

/translation="MITFQYFEPEDFDQLIEWSGDEAFLLQWAGPQFQYPLSREQLSD
YLHGANDKNTSNKFIYKVMDESTQEIVGHIALGGIDRYNRSGRIGKVLLGKPYQGKGY
GKQMINEALRIGFEEEEKLHRISLGVDFDNVSAIRCYEKAGFVQEGLIRDARRYEDTFW
NLIEMSILENEWKK"

CDS complement(3294687..3295010)

/locus_tag="EFAGFIKM_02782"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKHVHIIFSLFIMLGIVITISKMIEEVIPKLGAAAFQSAAAG
SYTPSDYQVNFALNYWIAAICILGGVICLISTMNVVRNYIREMNIRNRAFDETHNYDD
TRELK"

CDS complement(3295211..3295357)

/locus_tag="EFAGFIKM_02783"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIHLKRVSDNWYACTQLDVTEEQRKSFPRQLYIGLLRLWKRSV
EEVD"

CDS complement(3295542..3296480)

/locus_tag="EFAGFIKM_02784"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNIVQSFQELVVRGDHQGMIELLKNFEQSRKLSVHERGWVYWNI
SDGYALLREPEPLYANHREFFEWGRKNLAPEQLHWIVSDSTQALSLSLGNFYDHWMDW
YQYACDHAPKLDTNRGVRFESHRLGGSLWVLERYSEMDSVLENMNQLIQEDETWSNI
LFARITYNKQRLAYLHHAGEVAGVEVLINETMDWIDEINDGAIPISRKDEVVGSWEDI
NVSRSQRDINIALNNLACILTDIEREYESVKLFVQIQERGYHMNAYGFSKWIYSIWK
TRGTEAVKDALATNASYEIADVVKHTPELSEIKGLV"

CDS complement(3296515..3297342)

/gene="COQ5_3"

/locus_tag="EFAGFIKM_02785"

/EC_number="2.1.1.163"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01813"

/codon_start=1

/transl_table=11

/product="2-methoxy-6-polyprenyl-1,4-benzoquinol
methylase, mitochondrial"

/translation="MSDPRSTYSIQTAVLSLQEELERLKMQAVMGWSKEFRNLEWYGL
KNGMRVLEVGSGBPITYEQLLNSLPDSELSLEIDRSLQAQAKERLKNIPSKRLQFVE
SSIQMDLPDDSFDFVVARLIFLHLNNPDEAAKEIYRVLKPGGRLAIDVDDGVFGAV
NPDVPALHTVLMKISNYVAQHGGNRLIGRSLPRLLSESGYIDVDIDSVLQHSDLLGIE
GFKHQFNLRVHFHAEKGVISSEFAQLQQASEAINHSPEAYAMMNFITACGTKPLT"

CDS complement(3297408..3297815)

/locus_tag="EFAGFIKM_02786"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTIHTIELTQEIPVDGGYPAGDGHARQGDGEVSCQAIECPMEV
VDITINVINDMILTNPRAHTPSGWITFGFHEDLNEATVQALDGMLNLMGELYGLDRVE
AIALGSAVIDLRITQIVNGVKGVHAVLPHDAFK"

CDS complement(3297906..3298286)

/locus_tag="EFAGFIKM_02787"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQGLIHDISKFFPQEFIPYAIHFYSKQKDEDTHLRWKNAWLHHQ
NHNKHHWEYCIVNRNTKEALPMPTKYLIEMVCDWRSFSRKWGRKVKDSNLVERMINSQ
DIILHPVTREELEQLFIRKDEKFI"

CDS complement(3298400..3298909)

/locus_tag="EFAGFIKM_02788"

/EC_number="2.7.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WL55"

/codon_start=1

/transl_table=11

/product="Putative O-phosphotransferase"

/db_xref="COG:COG3896"

/translation="MEKGKIIFLNGVTSSGKTSIVEAMQSYDDPFFYVVANDLFENTI
GDKHLQTDYWKYLSEATVMMYHTAKVFSDHGKHVLIDGILVERPELALHYEQVKQIFE
GFPLDIVELYCPLDICRQRNIERGDRREEQSDEQHQIMASDIQYSFVDTSVHTPEEC
AEKIIAALF"

CDS complement(3298963..3299445)

/locus_tag="EFAGFIKM_02789"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSYKAILIDQLNACYHDKSWFIPLHDILTDLNAAEAAYVKNEGE
HSIWAIVNHLIFWNEKWLERIYVEQVDGQNSVNNEDTFDIDLSNLNDVEWGKTLHRLK
TVFGDWNRALEDSEEHLTREIPSYFNAPWWGVISNLCIHNAYHIGQIMLLKKSMKHT
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CDS complement(3299477..3300133)

/locus_tag="EFAGFIKM_02790"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDIKNKSGDVLGKIQIESLRNDNAIDRIVIDLKPGDGKAIYTAD
VIENQFTQQTNAAIPWEDGLEQLQKHYSWPQPKFPIDSDIDAIHVFYGFNLTPEI
DEMIEESNRSGRNVVIRDLKPNKKVVGISITYKEYGGYKLNIFGTTKSRIALPDHDGT
KVKQAAVRGVQAFYIFNNETSQLVWIEEDVHGKALQYEIIGRNMSDELVMKIAKSMNG
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CDS complement(3300176..3300730)
/locus_tag="EFAGFIKM_02791"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLIVDENVPDCSVEIRTVDIGGLTKPQLIQKLDQYSISLNKYG
EQLLNDERFIVSSTKQSLQTVELTIRQLGFSNGATTFELFRRANDLGLECCPVELGPY
LRMQHLDQPEICSTNISEGNKAPSGSITIASAALTENHEFPKGFYLRRLNDKLWLRGY
LADHLHVWSPNDRFIFCRAQLSIV"

CDS complement(3300853..3301248)
/locus_tag="EFAGFIKM_02792"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGKGRILGIAYNVIPVKDLEVSAAWFVKHFGFNIRHQREGYLSL
FRGDRPILDLIQSDNETRATFEVHQKKRWVITFFTDDIGSLHDYLTSENVKVGAVSDE
GQYGKFFVLEDLDGNLFDVWEHRDCELNF"

CDS complement(3301282..3301809)
/gene="yfiT_1"
/locus_tag="EFAGFIKM_02793"
/EC_number="3.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31562"

/codon_start=1

/transl_table=11

/product="Putative metal-dependent hydrolase YfiT"

/translation="MDEKIRFPIGHFEP SLKFSNEDRIHIIGQIPGITKTLREITQQL

NDDQLRTPYRDGGWTFQTIVHHLADNDMNAYIRFKRALTEDEPMAS SYREDLWASLHD

YRNTPIEDSILLMDILHKRFLTLLSGLHPDQFRRKL RTEVLGTMSLDIAIQR FVWHGQ

HHIAQIKSCITSQGW"

CDS complement(3302109..3302510)

/gene="ndx1_2"

/locus_tag="EFAGFIKM_02794"

/EC_number="3.6.1.61"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q75UV1"

/codon_start=1

/transl_table=11

/product="Diadenosine hexaphosphate hydrolase"

/db_xref="COG:COG0494"

/translation="MKFIVSASVIVLNEHNEILLMKGRRGWEMPQGCVEEGETIRQAA

VREVKEETGIDIELIKFCGLYQ NITRGVCNNIFTGKPIGGALTTSDESEEVGYFTLEE

AQQMITWGNFYNR IHNALDEKSH PFLIEFSE"

CDS complement(3302564..3302992)

/locus_tag="EFAGFIKM_02795"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKIIRNSEELEGTGYIEVLPRKYLGCWNENSIYFDEEVFGYIE

KTIENIFSGYDHYAFNEIHRKTWEVILEDLRTFANLLDEKVTIELINEHVYFFFGNSK

DEFQQDFLNSVQKLRELIIEFV VVIKEQLTTQDYVSVLGI"

CDS complement(3303302..3303826)

/locus_tag="EFAGFIKM_02796"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSRPLRIHIIGSTGSGKTYLGQVLSEKLNIFYEYLDVTMWSSKV
EFSGKNSPDVRDKLLHKIIDNSWIVEGVYKWLSDSFSRADVIYYLDTNVLRHFRF
IMRFVKQGIGVERSIYKQTLRGLIEMLVWNHKNSTNRKEICSFLSPYKDKVILKTN
RKMISLLNEGSEIP"

CDS complement(3304032..3304235)

/locus_tag="EFAGFIKM_02797"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MISYKPFQKLLIDREIKKQDLLKMTGISSATMAKLNTNEYVSLE
VIDKLCTALGCQPGDLLEHIEDQ"

CDS complement(3304844..3305245)

/locus_tag="EFAGFIKM_02798"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTIMFKEIKDIDTQAIQELFHSVDWKSGDFPEDLRQAINNSHTV
ITAWDDNKLVLINALSDGVMTVYFHYMLVHKEYQSLGIGKRMMEQMLSRYSNIKTKV
LISYDSAEKFYGLFGFKSEEGTKAMFISDMV"

CDS complement(3305432..3305653)

/locus_tag="EFAGFIKM_02799"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MNIIKCNIRELMAEHRIDDITELMAKSGLSRNSINKLYRETNIE

TTKLETFLFKLCDTFNCKLSDLIKYPGEK"

CDS complement(3306134..3306790)

/locus_tag="EFAGFIKM_02800"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKGKILLLVFITIVFSSCQNSSQSTTLNSETKSKMNSELPPDV

STGDGTESKEITEGLSDTANNKKILPMSIGNLDLKGEFYDEMLRNRIDHDYEVEFNEF

QNSKEIITTLWGAFESKYTEIWDNELNQIYKMLLSKLDRESKEALIESQKEWLQHHL

RETKFVEKTFIDNGYLGSKGSVSLTTVIRERIRERTMQLFEYRYLLDGEVEFLYQSTK

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CDS complement(3306983..3307240)

/locus_tag="EFAGFIKM_02801"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDQGMSYFSQFNDPRMITSISLAEIARSKKIEDFGAPLDLRLV

LLIARTHKFQGNNRNAKEYAQWGLNNGKATGLIKDFEGIS"

CDS complement(3307206..3307415)

/locus_tag="EFAGFIKM_02802"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEMGVYLDFLPNSIGESKSSNEITTYDCEFRKRLNKKANWLKRF

FTMERERWFQYGVIFGSRNELFFSI"

CDS complement(3307787..3308329)

/locus_tag="EFAGFIKM_02803"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSKKTIIIEYNNEWPEMFSDLKSIIEQRLGDLVLRIEHVGSTA
APGLAAKPILDIDVVIDSMDLLPDVIQGLES LGYYHEGNLGVENREAFARKDANVPYS
IVKIQKPEHHLYVCNKERKELLRHISFRDALISNPEFVVEYANLKKELAIKYGENRQS
YTDGKTEFVNKVLNEYGKNL"

CDS complement(3308558..3309019)

/locus_tag="EFAGFIKM_02804"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIRTVSLCVIRRGDELLLEEFFDEAVGITYYRPIGGTVEYGESS
KITVIREVKEEIDADISEPILIGVIENIFNYRDQIGHENDFIYEAELMNRSYDLEEI
DGIEGSKPYKAVWKPLHYFKGNLTVKLVPDGLLELLQDGT DGRYIKHLSKP"

CDS complement(3309252..3310046)

/locus_tag="EFAGFIKM_02805"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:ISfinder:IS655"
/codon_start=1
/transl_table=11
/product="IS3 family transposase IS655"
/translation="MCNVLEIAKSTFYHEAKEKPNEDELTEAIVEIFHKNRKVYGTRK
IKAKLQERGLIVSRRRIGRIMQEQLVSTYTVAQFKPHKTACNEEKT VNELGREFDQT
EAKRFVVS DLT YVKVGH RWHYICV LMDLFNREIIGH SAGPHKDAALVS RAFSTVEGDL
SQIQWFHTDRGSEFKNHAMDQLLGTFGIGRSLSKKGCPYD NAVA EATYKVMKTEFIYQ
MEFRNLRHLELELYDVNWFNRHRIHGS LGYLTPVQYRQEALKKVV"

CDS complement(3310088..3310372)

/locus_tag="EFAGFIKM_02806"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:ISfinder:ISEfa8"

/codon_start=1
/transl_table=11
/product="IS3 family transposase ISEfa8"
/translation="MPKQQRRTFTTEFKQMVFQFENGKSRAAIVEEYDLTASALDRW
IKQSQATGSFKEKDNRSPEENELMAMRKELERLRMENDILKQAALIMGRK"

CDS complement(3310555..3311004)

/locus_tag="EFAGFIKM_02807"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MELYNTKNELDRIDFHDCIVESIYLEENKITFNIESVNVLVGHM
LNPYDVAKNTDQCTLEFINVERYESGYFEREKDTRIDIELIHNNDFEILKFDILAEEG
MNLTKLFGMASNFNNEFSEIIIRAETNIKWKNKYVSNWFWVNWPKTK"

CDS complement(3311208..3311432)

/locus_tag="EFAGFIKM_02808"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQQAKSIDPFLRSFKPLERQECTNVFRKASEKGSSSATMAKLNT
NEYVSLDVIDKLCTALGYQPGDLLEHIADQ"

CDS complement(3311506..3312216)

/gene="hdl IVa"
/locus_tag="EFAGFIKM_02809"
/EC_number="3.8.1.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q51645"
/codon_start=1
/transl_table=11
/product="(S)-2-haloacid dehalogenase 4A"
/translation="MMMSIKAIFLDFYGTLVHEDDDIIPLICKEIQENSVEECEVSDI"

GRYWWNIFSSMFKNSYGETFKSQRELGILSLSETISKYRSNCDVNEIIQKQFDHWSEP
KIFSDTIPFLETQGYEVYILSNIDTADVKAAYHGIKVNEITSEDVKSYKPRPEL
FIEALERHNLSPKEVLHIGDSLMSDVGGAGILGIATVWLNRLNLIKTDIAEPNFICRD
LKEVRDIISGIEEGSIVV"

CDS complement(3312369..3312761)
/locus_tag="EFAGFIKM_02810"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQQIDLTKTLEELENDYWDEPNFASSLVIQVHQLRKKPLCELNN
EELRLLIGQQMNLDLFLRLIALEKLIQNPFGSGDLYIGDLFCSVLKVEKEYWNEHQELK
NELNEVIRIYEEVRRTLDEQIIKYRSSL"

CDS complement(3312964..3313311)
/locus_tag="EFAGFIKM_02811"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKFGNNSQENREIKISKDSKTFLELREIVNRDPVNLVEGGAPD
DEHDRLTTEILMLLSQESMDEIRDLLINCEIWYGYDPNDIKEEYKERFNSKIDRTHKE
ILNWHTKNKNQEN"

CDS complement(3313641..3314246)
/locus_tag="EFAGFIKM_02812"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
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PLYHNDFKLLNGKLLEYDFTDEMRNAINNKAGEVIDLDEVKSRDVIEFVPHVIGDME
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CDS complement(3314515..3314940)
/locus_tag="EFAGFIKM_02813"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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IMAAAYRELFEETGISNKDIILHHLMDFKYYIQECYVEVYFGKLNHYHLDVYGDENELYW
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CDS complement(3315194..3315670)
/locus_tag="EFAGFIKM_02814"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MKFEIIQANKECKEVLANLMQFYIYDFSEFIKCDVEENGLYGAY
PLEDYWIEKNHRFPYLIKQNDKHVGFVLRLIETAERDYYSIAEFFILKKYRREGIGK
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CDS complement(3315906..3316952)
/locus_tag="EFAGFIKM_02815"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
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EYYEYIKKTVTIEDYYKAFPEVKEYEQYLSIIYSTSKEEQVTHWSNLLYEFIIGNETE
GTRSLKQMYRHKYDVEEIIKLGVIASREVVTLEVFSGYTPSIDGQIIQSDSHTRWM
FLSILIDINNANEETINRLKQILIRKYEVDNEVQECINIARTLHTLDSVRFPEEMHDE
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CDS complement(3317118..3318188)

/locus_tag="EFAGFIKM_02816"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
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ELLDTRVEDILYVINHLDLLFSQSLLEGFSYRSIGIVGHSLGGAAAFEVAKRDNRIRA
GVMFDASFHLLDLEKNEKIDTPFLIMRQEKCTYDELLTELSEGIINPFISGFEEKLYKQ
LNGYKAAVKVQGAHHMTFSDVPIHFKDIEAINKHEIISDYSTAFLSEFIQGKSYSLQN
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CDS complement(3318382..3319041)

/locus_tag="EFAGFIKM_02817"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTLIATAYAHECIVMGDTLLQRTEYQTNKIIGYGSIQKLFFI
RKTGTGISVRGRASWGEKTIKQILQNFTHTVESSMRQCDVADALQLYIKSNFPQLETS
YHIAGYQDTEPFYDLDFDSGLNLVRENVDRKGFLRYSVLARIDDEVRNQVLPLPDF
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CDS complement(3319370..3320467)

/locus_tag="EFAGFIKM_02818"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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QGAIGKVQVMGTGPHRLNAGGRPDWFFKHEQYGGILCDIGSHQIEQFLTASCTDAE
VGFSRVHNFNHPQFPELEDFGEASLIGDNGASGYFRVDWFTPDGLGTWGDGRTVILGT
DGYIELRKYIDVAREPEGDQVYLVNHEGEYRYNVKGKVGYPFFGQLIRDCLDRTETAM
TQEHAFKAAELCLIAQHKAMSERVVWSSGAK"

CDS complement(3320531..3321703)

/gene="iolG_6"

/locus_tag="EFAGFIKM_02819"

/EC_number="1.1.1.369"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01671"

/codon_start=1

/transl_table=11

/product="Inositol 2-dehydrogenase/D-chiro-inositol
3-dehydrogenase"

/translation="MSIVRVAVIGIGNMGAAHARTLVAGEVPGAELVAVCDVRREMES

WVSSHLPATVTYWQDAEQMMASGTIDAVIIATPHYDHPEQAIQAFQHGLHVMIEKPAG

VYTKQVRKMNEAAAASGKVFSMMYNQRTNPLYIKLRDLIASGELGEVRRTNWIITNWY

RSQSYDSSGGWRATWAGEGGGVLINQDPHQLDLWQWTIGMMPVRMRAFCSFGKYRNIE

VEDDVTAYVEYENGATGVFVTTTGEAPGTNRFEVNGDWGKIVIEDGKLTFWRLRESEP

EFNQRFTGGFGQPECWKCEIPITGVETGHPGLIRNWVDAIRTGVPLIAPGEDGIHGLT

LSNAMLLSTWTDNWVDLPIDEDLFYEHLQERIAGSTTKKDKAFSGSQPADLNQTFK"

CDS complement(3321700..3322614)

/gene="iolE_1"

/locus_tag="EFAGFIKM_02820"

/EC_number="4.2.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01672"

/codon_start=1

/transl_table=11

/product="Inosose dehydratase"

/translation="MKLSVFTVATPDLNAEELASAAAATGIDGIEWRFRGIPEDAMSE

EPSYWRNNRCSVDPSRWEEQVPVFREAALGQGRKSIALVPYLNCDLSDATKQAFQAAA

GLGASMMRVGVPGYDRKTSYPELYRKAVDYLSEVQDLAKQYNIKAIVETHHQTIAPTA
SLAYRLVQSLDPQHVGVLVDPGNMVHEGYENHRMGLELLGPYLAHVHVKNAGWFEAEG
KDSQKANVTEKSRGVALNTVWKCHWTPLTEGMVDWVQMVRDLRAVGYDGYGIEDFSG
ALESKAMLQHFADVFAEIERRVDEEEQS"

CDS complement(3322959..3323456)
/locus_tag="EFAGFIKM_02821"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKIVVISDTHCSRKSRKLPTRLLDVLPSADLILHAGDWSWSDSVY
PLLSEYAPVEGVAGNTDPSEIAEKLGYSRIVEVEGLRLGLVHGHLSKSGTEQNAIHTF
AGQHVDIAVIYGHSHIPVMHTVDNTLVFNPGSPTDRRFQKQYSFGIMTIDQGRIQAEHV
FFDRD"

CDS complement(3323700..3324134)
/gene="ywnA_2"
/locus_tag="EFAGFIKM_02822"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P71036"
/codon_start=1
/transl_table=11
/product="Putative HTH-type transcriptional regulator
YwnA"
/db_xref="COG:COG1959"
/translation="MSTHFSVSVHCLLLSLSAPERITSAHIAGSVNTNPVVVRRILG
GLKKAGLVNSSPGTRGFYLAKPSSEITLAMIYQAAKDEGPLFPIHGNCNPDCEVGLHI
DSLLTNLYQVAEAKVEQFFASITLEDLERSCTQMMAVPSQTE"

CDS complement(3324177..3324554)
/gene="gpsB"
/locus_tag="EFAGFIKM_02823"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_02011"

/codon_start=1
/transl_table=11
/product="Cell cycle protein GpsB"
/translation="MDEHMKRRLDKQRQLFKQLGVQLDALSIHEKQFNYKLRGYDPDE
VDAYLDLVIKDYERFYANIADLMDKWQEQQLTIRDLKSSAKPVEDPTKIDRKQLDDIV
KQLEYSVRQLKIRARPEKDLFSE"

CDS 3324753..3325319

/gene="dksA_2"
/locus_tag="EFAGFIKM_02824"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00926"
/codon_start=1
/transl_table=11
/product="RNA polymerase-binding transcription factor
DksA"
/translation="MSTLTQDQHQILKNALLEQRENLQRHFESSMEDGAPVESLKDST
GELSSYDNHPADAGTETFERSRDLAIDDTLTDEFNQVNDALERMEQGTGTCVTCGED
IPFERLEAIPYTAYCIDDTPNREISNDRPVEEEVMTMPPSGAGEGRQKRAGKFDNADA
WEAVEEYGTNSPATAAKRDVKGYDENM"

CDS complement(3325509..3326201)

/locus_tag="EFAGFIKM_02825"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAHKVLSTIEEIKIYSDPYRIQIMNMFNKQGRPSTVKEIADQMG
EVPKAVHYHVKKLEKIGLLTIVSTREINGIIAKYYEPFTGEIHLRHEDEDKENSPLKQ
VFRSETLKLLNEMFEQSRQRFMHQAENEDRMFLSDITLYATREEVEQLYKNIKLCEP
YTTKENRQGEQEVFLFSALSKPIVKIPASKTNAKEKKKATSDKDKATTKKSRSVSKR
QESASSGSESEE"

CDS complement(3326335..3327624)

/locus_tag="EFAGFIKM_02826"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSDNTAVGKQGMGELIRIRPYMQFMLSQVVSFRGDSIDSIAYSW
MVYILTGSKVLMGTLLAVNFLPNILLGLFAGALVDRMSPKKVIVITNTGRGLLVGITA
LLFGLGQLEVWHLFVITILISLLECFTTPAEVSSVPRLLPPSMLLSGNAMSSSATRVA
ELAGLAVAGALIAITIGIAWTILIDAGLFALSALMSRVGYPEVLTSANNEDKTSYEMN
SHPSDKSSIFSEMAEAFHFLRKHALLLIVSILFAFVNFCLMPFNVLRTPYVIETLHAG
AGGLSLLSGLMVGGMLLSGVWLTQRGANYRKSVLVISGIVMLGLSYAMTALPAYMTSF
QLPVAAAFCLLMGMIPLATTPLATYLMVTPSEMLGRVYALQSMVLVSVAPLGSLAS
GALADWMTMPVLFIVFGIMLAMSAGMLLFSKSFERSAL"

CDS complement(3327886..3328161)
/locus_tag="EFAGFIKM_02827"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P11540"
/codon_start=1
/transl_table=11
/product="Barstar"
/db_xref="COG:COG2732"
/translation="MNTVILDGEDFASSVELHQQLKVKLKLPDFYGGNLDALWDCLTG
TIELPLELKWTNYQISEERLGNEAGRVRDLMLEVQAEQAGFQLLVEK"

CDS complement(3328176..3328616)
/locus_tag="EFAGFIKM_02828"
/EC_number="3.1.27.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P00649"
/codon_start=1
/transl_table=11
/product="Ribonuclease"
/translation="MKKLISTALLALLTFVFLTGSQFTPVAQQKASAATCTIINTFT
GVANYLSANGTLPCNFITKSQATGLGWVASKGNLAVVAPGKSIGGDTFGNREGLLPSA"

SGRTWREADINYTSGFRNSDRIVYSNDGLIYKTTDHYASFTRLK"

CDS complement(3328885..3329892)

/locus_tag="EFAGFIKM_02829"

/EC_number="1.1.1.384"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:B3TMR8"

/codon_start=1

/transl_table=11

/product="dTDP-3,4-didehydro-2,6-dideoxy-alpha-D-glucose
3-reductase"

/translation="MNRQLQWGVLTSTIAKNAVIPAQQSERGEVLAIASRSKEAE
TLAEELGIARSYGSYEELIADPDIEAVYIPLPNMHKEWTIKAAQAGKHVLCEKPAAL
NADESTEMIEVCHQQGVLF AEAIMYRYHPKHRRVQEIIASGEIGIVRAIHGNFTCNTA
DDKENVRFKREMGGS LFDLGVPISAARMYLGQEPEAVTVHALFSDEHDGVDMMASG
LVEFPNSVALTFCGMWASGRAEMEILGTEGRIELPKVFGWENS DIPPQIIVHTDSVS
REERVSVSNSYVLQVETFATAVLEGEALPFSPENTIQNMRVIDACLESARTRQRVQLI
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CDS complement(3329895..3330269)

/gene="rtp"

/locus_tag="EFAGFIKM_02830"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0CI76"

/codon_start=1

/transl_table=11

/product="Replication termination protein"

/translation="MAFMIAQRAFIKLYLITMVEQHRGYGYEMLEAMKQEFKDYGYVP
PQSEVYRALHELVQQGVFYRTKKLKGNDPKVDFQEIVLYHFTDDGAEKAELYKKQVKT
DLDRCLGMLHKA EEDNYGTKGR"

CDS complement(3330783..3331931)

/locus_tag="EFAGFIKM_02831"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MPRKERITEIESLRGIAFGAVVLQHSIAHYSLPETRLEDGVLL
AILLMLSFAVPLFIFITGMVLFYNTGDKLHYGQFMRKRVNDVIVPYLIWSLIYFTLA
PRGWTGFGWNDIPDLGLKLLTGKTTSHFWYIIMLIQFYLLFPLFLHAIRYVYNRYEAK
GRLIALLISGVVYLVLADQLRNIAKFMERLNIPVLTDFTTYADRNFLYFFIYFVLGA
VAGLSVQHWNEWIHRLRWIYWTVFIVLGLRFTYLLMLEFQKPEGIKITFYTVSLIRPD
MALFLIASIMVMYQLAGKLHNLRASTRLLGWIGGVSYGGYLMHMLRLRYSYIPDELFFYV
AMGWNPVVRMIITWLLALTLSCVVTWLISRVSWSGKWIVGAVPKSVRNK"

CDS 3332006..3332398

/locus_tag="EFAGFIKM_02832"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIHISSTDKDVTITDSKYVQQHLANERTFLAWVRTGIAMAGIGF
LAAGFGFNSSAYDQLAHIAAITGITSIGGISIIVYSAAAYHRKRTQINEQTFQAST
GLIRFLTMMLLVIGLALAVLLYVLLFPA"

CDS complement(3332576..3333181)

/locus_tag="EFAGFIKM_02833"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQKKIVGVFNTEREASQAIEGLKAQGFTSDEISVVTQDRDELKA
IREETGTKAPEGVAAGAATGGVLGGVAGLLAGIGALAIPGIGPILAAGPIAAAFTGAA
VGAGAGGLVGGLVGLGIPEEDAKQYEEYVQNGKILLVDSTDRSDVYDVFSGNSQLN
RDRAEAAHRGDVPAERPDLMEERRLEAQTKATRLGNNTFL"

CDS complement(3334047..3336566)

/gene="hrpB"
/locus_tag="EFAGFIKM_02834"
/EC_number="3.6.4.13"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37024"

/codon_start=1

/transl_table=11

/product="ATP-dependent RNA helicase HrpB"

/db_xref="COG:COG1643"

/translation="MHIELPIQEVIELRQLFRYQDTGVLIAEPGAGKTTVPLALLE

EPWVAGRKIIMLEPRRLAARSAASRLAATLGEKAGQTVGYRVMDTRVSQATRIEVVT

EGVLTRMLQQDQGLEDTAMIIFDEFHERHLHGDGLALTLESRAMLRPDLKLLVMSAT

LDPVPVCVLLGEGTKSIHCPGRTFPVETRYVPRPAAMPLEQFTAQTVNRALAEQEGDV

LVFLPGAREIHRTERELSNGLPGHVKVHSLYGSMPEQQDEAIRPAAEGSRKVVLST

SIAESSLTLAGVKIVVDAGLSRASAFSPRTGMSRLVTLPVSKASADQRRGRAGRIAPG

VCYRLWSEEVHGGLPEAARPEITSADLAPLALAVWGVQSPAELQWLDTPPDAAAYGQ

AQALLRQLGGLDDAGRITPFGRRMNTLGVHPRLASMLLRAAELGLASYASMLAALLQE

PAGLRSSGSAGAGTDLRPRVEALLTADSSGMPQAAAADGAAVRRMLQESRQLRSAL

GPAADPVRPDEEDSCGLLLSFAYPDRIGQRREDGRYLLSSGRGVRLAATESLSRAAYLV

AAEADDQGADARILLAAPLQEQTLQAGQHLLHDEVQVAWDSNTRSVRAHKRLRIGAL

VIKESSIAQPPEDQVLEALLTGIRMEGLDCLPWTKTSRQLADRLRFLHLHLPEWPDLI

EDELTEELAEHLTPYLTGMRSAADLKRLSMQDVLLGGLSWTQRQQLDDEAPTHIQVPS

GSRIPVDYSRPEDPALAVRLQEMFGQQETPRIAGGRVPLTIHLLSPAQRPVQVTRDLA

NFWRETYFDVKKDLKGRYPKHYWPDNPLEAVATNRAKPRGK"

CDS complement(3336711..3337517)

/gene="lvr_2"

/locus_tag="EFAGFIKM_02835"

/EC_number="1.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9LBG2"

/codon_start=1

/transl_table=11

/product="Levodione reductase"

/translation="MTQHNGKSRFQGKVAITGAGSGIGKATAVKLAKEGAHVAFDL

VNDRISETAEINALHPGAARAFDVIDSDPARVEKAVLETVELFGGLDIVFANAGING

VSAPIEEIQVEDWQQIITNLNGTFFTIKYALPHVKKRGGGSIITSSINGNQRFSSF
GMSAYSTSKAGQVAFKMAALELAKFKIRVNVICPGAIATNIDQSTVKTDLDLQIIIP
MEFPEGQQPLADGPGQPEHVADLVSFASSES RHITGAEIVIDGAESLLS"

CDS complement(3337701..3338543)

/locus_tag="EFAGFIKM_02836"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRAMRLATLSAGDKGGHAEQRHGNFRYVSVQTGEQPLTRYQGTF

KCRYGYGRAAETVHQGDTGQDFAAVRMKGNVCNVLCDGVGMSYLGDFAAARFLGNALL

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VCGRIELTGGGRKSRVWLAWQGDSRIRLWRNGQEQSELFQTHCKTNERWSTLEGPVGG

KPHICEMKGSAGDSLRLQLYTDGLNDLDAIQAYVPDEHIQVLLDATHTGGLEDDAFI

ELEW"

CDS complement(3338554..3339306)

/locus_tag="EFAGFIKM_02837"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNYTIQASQRTPALIIYLIDISASMNMVLENRRRIDVVYDALSL

AIRQMVFRSTKGNRLTPRYRIAILAYSDDVYDLLNGIKGIDEIAAVGSLPDLTPRRFS

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LVENIFISDHLLEGPIAEPRRWKGISSETNLQDEHGEKLRNMSSVLPESYREMLVEAD

YLLAPGALMMLPGTCAELVSIGFQMSAATPVR"

CDS complement(3339340..3341415)

/locus_tag="EFAGFIKM_02838"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSFQPNPGDEVVINDIAYTIGQHPAAPGLAYAQAGRQGIVYQLL
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KHPDLLYAVLMPWVQGQTFWFDVISDQRQLTAEESLKLARALAGTGSAMEQRGLAHCDM
SAPNVMIPFFSEVENLGKMSAVELVDVEQMYGSKMDRPDALLAGSPGYAAHRTVHSGL
WSSYADRFAGAVIIAEMLSWSDPVIVEKAWGESYFDQHEMQTVSERYAMRESLEKRW
GSKLSDLFIRAWESHDLSSCPTFGEWYVALAAIDVDQANAAAAVTAEAAAANSSEADV
NLKKSSEPVPSEPVNTQDGNRSQTPHSPDQEAVVNRLFLQARALEDKPAAALEVYRS
LYHFIPHNSAMQMEVEAAIKELDARLNPKEDETDKVPVPFYRSKKFMISSAVLIVLLA
GGVPTVKILADQAEVKQKEQQEATRLADIKAAEEAEAKAAALKQQEEQEKQKAADAA
KLDAEEKKKLAEAKQKEAEAKKKEEERKALQAKYDKQAKYEAFLVKQEQQKKEAAKKA
EQEKYDKQAKYEAYLVWKKENDAKLAKQEADRKAAAEVKRQQEIAQKAALKKKRAQNV
VTLIAHYNKTYNAQKGRKIENAESYARDFKNLYNTDAAYFKGVGKVAARMSAINKFLS
NNSYTLPNL"

CDS complement(3341574..3341849)

/locus_tag="EFAGFIKM_02839"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAGRILVTPEQLDQVSNQFKQSGEQSQQIVSTLTQSITSMEGQW

EGMTKQRFFQEFEASKQMQSFVQTLNSISAELTAIANKFRTADQAR"

CDS complement(3342036..3342584)

/locus_tag="EFAGFIKM_02840"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRIRVEPDVLRALSKQIQYAAEQIQKMTVLDQAIHSLEWEVES

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NMLNLVQNNRTGEIMPAHSATVAVVSDPLSAMAAYRVQDAAPPDGPATLVQAMQPE

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CDS complement(3342591..3343421)

/locus_tag="EFAGFIKM_02841"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLTVHDSKQKVVTLQTKELFFLAGILGSDRLLGVEDPFRGYMAE
DIAMEWERVKTSLLDKGYLIRDQDTDELIMTPTVFSRVAIAGLSDRACWIRYTINGKS
YESYIHCTDERVVEVSRVDDVPDSFRLSDLGSVREADVLIERMKWSGHSPAEPALM
CSKKKFYDVMNELENSGVQTVAAELEQETSDPEGSLALARCLVGKESDGELRLLVWNE
DGWKSQSAAFAASAVSNWLFRMSTAASDDWLVAALTREQFHEMLLDWLKQPAGEEER
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CDS complement(3343438..3347442)

/gene="essC_2"
/locus_tag="EFAGFIKM_02842"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q2G184"
/codon_start=1
/transl_table=11
/product="Type VII secretion system protein EssC"
/db_xref="COG:COG1674"
/translation="MNVLYQRSPRMTPVLKEERLEILRPPTEPSKPTFSMISIIVPIM
MTMVSIGFYVYINMTGKMNNSSYMMFQMMTMVMMMLTSYTIPFFVYLSNKKSYRKKEE
RKIMYLAQLDKHREELKEAQAEQVKSLEYIHGDPGVCLQVVKNRNSSLWERSPEDDDF
LQVRIGTGEIPRIKLQVPRIDGYEKDELIEAAHELAAEFQTPDASITLPLFQSKVM
GLVGDRREEVLTSLRVIISQLTVRHSPDELKLAIFYEEKDSKEWDWLRWMPHIWDEDQG
QRYMADRHSGAHQLADSLFSVLNRRRSNKEDRYKKSQVTPCYVILSDTQLIEEEPLL
PLLLSAHEIDVCTIILANRKESLPMHCQLIMDASKGKGVYIKKTEDADVIQQTYKPD
VISKEMTEALSRYMSPIRLKRSSASDIPQVLPLFDMLSTSRVEDLDVVSRWGQTRYPD
TLPVPMGVRAGGKKIAINLHDKIERQGHGPHGLIAGTTGSGKSEVIQSIVASLAAEFH
PHDLAFMLIDYKGGGMSNTFVDLPHVVGTITNLDGNLIERANISLRAELVRRQKILND
AGNLQHIDEYYKILRSRHEQPLPHLVIIIIDEFAQLKRDQPEFMDELISIAAIGRTLGV
HLILATQKPAGVVDDKIWSNSRFRICLRVQSEGDSRDMIKIPNAAWITKPRGRGYFQVG

SDEVFEEMQFAWSGAPYNQQEDSTTVLPVMEVRLNGKREPLLTGERRAVLKGEDVPKQ
LQVFIDYVAQSAADAGIRRLPGPWLPLPETLEWEGQLQEWQEEENRDLLLDGGASGLK
PLVGLLDDLPNQRQQPLALPVDQGHLLVYGMPLGLGKTTFVQTLLMSLARSHRTEPWHG
YIIDMGRMMKDFaalPQIGGVMMaEEEDRIKRLFRYILKLSAQRKDIISEAGVKTISA
YRRTAHAAVPQVVVVIDGYLSFRNAYPEENELLEILREGGSLGITFVLTANRVTDVF
EKFRSNIPNAVSEFELSDPSDYYYAVGRPSKAPSQLPPGRGLVKGQVPPLMFQAALPSS
GADEGKRSSALRRTIAEIRQGTGEEAPQIAPLPEEIQLKDLLIRTGSYGQAWDTSSV
TVPVGLLTDDLEPFELNLREGPHFMTSPMEGGKTTFLTWMLSLAYHASPEDVQIYT
VDMRYGSGGLGEISSLPHVRGHVSREEQLAPVIQQLYDEV LKRGEISGGPELV LVIDD
ADTL SKQLNDFNVKDQLGAIVRQGRDRDVHVILSGVPADFPTFGSDWVTDVKASQSGM
LFGTLDPNDSLFFRIPYSESGSSGGLKVLPPGQGYVVKRKYSRVKGAVPCDDSWKMT
DWWSEIRDRWHVVV"

CDS complement(3347497..3347817)

/locus_tag="EFAGFIKM_02843"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MILTVYSGREEGEWFDIDVPDECTIEHLKTL LGVRIFGQAPGDG

IQYILEAKFPEGLWFS PQNAQQLMETGLRQGSCVRVQRAFFTSEEAPVYGRSLFQQ

DSNE"

CDS 3348239..3348478

/locus_tag="EFAGFIKM_02844"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRTLITFQNK SIPVYFNQENKQPMQKTLRLSSALEHKISNGKR

AIQKCLHSLISIEIVNGEAILHSRSENDSLALSLY"

CDS complement(3348601..3348753)

/locus_tag="EFAGFIKM_02845"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSIDRFILRKLNTCQEEHTRANLVRLFVIRIRKAEIAEEHDAVY
VLSKLH"

CDS complement(3348998..3350473)

/gene="pchA"
/locus_tag="EFAGFIKM_02846"
/EC_number="1.2.1.96"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q59702"
/codon_start=1

/transl_table=11
/product="4-hydroxybenzaldehyde dehydrogenase (NADP(+))"
/translation="MTLMDTEHTTWTKQYINGSWVNGSGEKTMENINPYSGEVIATWR
SSNKKDIDKAYESAQKNSIEWAKSLPAAKEEVLRKVSSLMAERKEEIIQLLITESGST
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LHLCLRSVAPAIALGNVVIKPASDTPITAGWLIADLFEQAGLPEGVLNVVAGSGSEI
GDYFVAHPVPKVISFTGSTEVGGIGKLAGHEHLKETALELGGNNAMVVLEDADIESAA
EAAVFGKFLHQGQICMALNRIIVHADIYDQFVESFVAKTKNVQAGDPADANTLVGPLI
REKEVERLQELVNKTKAEGARLLLGGTSKGSVLSPTVLADVKPEQDIVQQELFGPVAV
IMKAHDEQEAVRLANDTPYGLSGSVFTKDLNRGYQVAQRIESGMVHVNDQSVNDEAHV
MFGGEKASGIGRFGGDWAIEKFTRTRWISIQHQYREYPGVK"

CDS complement(3350644..3351183)

/locus_tag="EFAGFIKM_02847"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLIRQAREGDAQGIAHVHTESWKTTRYGIVPDDFLDHLTIESRL
SQWEKTIRSGEKDQILVVAEQDDGNIVGFACGGKEREKLPYDGELYAIYLLKEVQQT
GIGQQ LATHVVHHLQTHNMKRLIIWALERN SACRFYEKMGGTPVQTQSLRIGGQDLME

VGYGWEDLSLFGEKSLPDC"

CDS complement(3351346..3351684)

/gene="ykuD"

/locus_tag="EFAGFIKM_02848"

/EC_number="2.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34816"

/codon_start=1

/transl_table=11

/product="Putative L,D-transpeptidase YkuD"

/db_xref="COG:COG1376"

/translation="MPDYRIIVDLSDHMLYLLDGNQVIKGYPVATGKMLTQTPNGEFT

IINKQSNPGGPFGLWMGLSAPHYGIHGTNEPWSIGKSVSHGCIRMYNSDVLDLSSKV

SVGTRVTIRP"

CDS complement(3351741..3352886)

/gene="rsgA_2"

/locus_tag="EFAGFIKM_02849"

/EC_number="3.6.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01820"

/codon_start=1

/transl_table=11

/product="Small ribosomal subunit biogenesis GTPase RsgA"

/translation="MFTRLERSKQLILGGIFILDNHIEKYGWSAKWQELWQETGMEEQ

EKKPARIADHGHQLRLITEEGECWGRISGRMRHDSLETSLVPAVGDWVAITGQAGEE

AIHNLVPRRSRVSQAAGPVTKEQLIAANVDTLIVAALNHDFNLRLRLERYVMMAWN

GGVRPVIILSKSDLCNNVEEQIRSVEGIASGVEVLASAVEGQGKSLRLERYLQPGLTV

ALTGSSSGSGKSTLVNWMGEDVQLTQSVREGDSRGRHTTTTHREMFVLPQGAVLIDTPG

MRELNLWDEGNDGLSHAFGEIEELAATCRFLDCSHTREAGCAVKEAIQNGSLDEKRLN

NYLKMQKELQYQQRKEEVASRRRTASSKPANSRKPKHRSRSVKEWEEA"

CDS complement(3353299..3353892)

/locus_tag="EFAGFIKM_02850"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQLEKIVAYHKALADPTRLRMLLLLAQGELHGQALAERLNLSQP
TVTHHASKLREAALIKERREKNTVYFTLNPSFIRENAQASVDFIFNREEVEDMSDVNE
TLKASVMRNFFSKDGRLRQIPAQYKKKLIVLGHLEQLEFGRKYTEKEINTFIKQYHE
DFATIRREFIMHQFMYREEEIYELNPKEMWTRWDQVK"

CDS 3354071..3355069

/locus_tag="EFAGFIKM_02851"

/EC_number="1.18.1.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8KCB2"

/codon_start=1

/transl_table=11

/product="Ferredoxin--NADP reductase"

/db_xref="COG:COG0492"

/translation="MEDVIIIIGGGPCGLSAAIECERLGLSAVIVEKYNIVQSIYLYPT
HMQFFSTAPLLEIGNVPFSTPNDKPFRYEALAYRRVAEHFGLRVHNYEEAREIKRKD
DGTFEVHTLNRRGEAIVHVGSNVVVATGYFDHPNYLGIPGEDKDKVTHYFREAHPYTR
TRVAIIGGSNSAVDAAMELVRVGAHIDMVYRGSGLSQHIKPWVRPLFESMVTKGHITL
HLESRVNEILDDSIIRLIHTDGSTRELDNDFVLAMTGFRPDRQLTSGVEMSDDMDKP
LYDAQTMESSVPGVYVGGVIASGRNANEFIESGRWHGRYIAEHIVSKQRGQTEGK"

CDS 3355066..3355518

/locus_tag="EFAGFIKM_02852"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKTMDMTSLLLLVFAALGISSNTPVTVMVFLLLLRVNLNQA
FPWLEKYGLTLGIIILTIGVMAPLASGKMSLQTIGESFLHWKSLLAIGVGLLVAYLGG
RGATLMGTQPTVVAGLLIGTVLGVALFKGVPVGPLIAAGILSLLLGKS"

CDS 3355935..3356447

/locus_tag="EFAGFIKM_02853"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSRQFITEAVMVAIYGQLLAPPAPVEYIVPYTTILELYEFQTSP
DPMMDNPADDQHVKSKINEMISYFEEPLNKKKIERALLVPWAKSPSILFGDQVSIALL
NAIDTAQYGEYFDPIETELLTSQRLSIPILTDQVELIARIIESESPVQVFDIDDFDF
AMDDEPLDQV"

CDS complement(3356547..3356996)

/locus_tag="EFAGFIKM_02854"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNLPPRDLAQYIAKRSHIVVKA AVRAENEQGELLLIQHAEHGHW
RLPAGEMRPGEAIEDAAHRELWEETGWTADTMTLEGLYSGPDLRYLHSSGDEEYVIA
LFRTVIIQDDLVESRVNSDAGLKFFALESPLPLNQISRILLARDIAE"

CDS complement(3357073..3357369)

/locus_tag="EFAGFIKM_02855"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTIHVSDQAARWYKEELNLNEGDSIRFFARYSSGGGLHPGFSL
GIAVEKPRHPADQTEVSGIQFFMEDHDYWYLGKQHLHVDIVDEGQDIEYRYTEV"

CDS 3357855..3359600

/gene="yhel_2"

/locus_tag="EFAGFIKM_02856"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07550"

/codon_start=1

/transl_table=11

/product="putative multidrug resistance ABC transporter

ATP-binding/permease protein YheI"

/db_xref="COG:COG1132"

/translation="MFSVLKNLAWFFRLERKRYLTGVILLILVGIAELLPPRLLGNAI

DEIVRGSITGTSLTRYILLILGTVIIIYLVTVVWMHKLFGGANLVERLLRSRFMDHLL

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LTLAAILPLPFIAIAMMIYGKAVHQRYTLAQDAFGDMNDQVLESIAGIRVVRAYVQER

LDEKRFADVTEDEVYRKNLAVARMDALFEPTIRLFVGLSYVIALAYGIYLVFHNEITLG

DLVSFNMYLGMMIWPMFAIGELINLMQRGSASLDRVNETLSVVPVAVQDVEQPAHVNTNP

EEIAMQDVTFRYPSSTVDNLSHISFSLRRGQTLGVVGRTGSGKSTLLKQLLHEYPAGS

GTLSISGHPIQDIKDDLHWSWIGYVPQEQLVFSKSVRQNIQFGKPGASDEFIMEAIRT

AAFDGDLGTLSDGLDTLVGEKGISLGGQKQRVSLARAFIANPDILILDDALSAVDAR

TEAKIIENIRNKRSGKTTLISTHRLSAIEHADRIIVLEHGKITEEGTHQELLAMNGWY

REQYERQQVESNLST"

CDS 3359613..3361703

/gene="yheH_1"

/locus_tag="EFAGFIKM_02857"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07549"

/codon_start=1

/transl_table=11

/product="putative multidrug resistance ABC transporter

ATP-binding/permease protein YheH"

/db_xref="COG:COG1132"

/translation="MKSNTGKRLLDYALKAKGTFFIAALIMLTIGVAAELAGPFIKSM

IDNHLLAIEQPFYETTASDEAAVYNGKNYKREGLFEPDENKGSEVRVLQAGRSFYFVN

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IFLVISVIMEFGKTFWLQSSANKVIQRLRNDVYAHIQRLPVHFFDNLPAKVVSVRTN

DTEAVKDLFVAVLSNFFSGIITITGVYVALFLLDVRLGLISLFVVPMLITWIVLYRKF
ATRYNTIIRSRLSEINAIINESIQGMSIIRVFRHQKQTKQEFEDLNDDYMKHQNKMLN
LNAFTSHNLVNVLRNIAFAVVLWYFGSSVLDGTSIISLGVLYAFVDVLGRLFPITGM
VNQLANLDSSLVSAGRVFELMDEKGEAVTDGSMTRYKGNVVFDDVSFAYKKDYVLNNI
SFKASQGQTVALVGHTGSGKSSIINLLFRFYDPQKGKITIDGQNVKDLPKQWIREHMG
IVLQDPYLFTGTIASNVSLGDEKISRERIEQALRDVGAERILAHLPQGFDEPVIEKGS
TLSAGQRQLISFARALAFDPAILILDEATANIDTETEALIQNALEVLKKGRITFIIAH
RLSTIRSADQILVLRGRIVEQGAHDELMELKGRYYKMYQLQQGAQAAASATSENPSG
EIIPTSTSFAGGNA"

CDS complement(3361886..3362512)

/locus_tag="EFAGFIKM_02858"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTSKRITERWILMTVLAVVLVGILWTVVTAVRISAYTDEDSSRI

SDAAILGAAVAGDNPSVPVFRERIEHGIELYRQGTVRNLLFTGGSSGDGEHTEAVVGQ

KYAI AHGVDPADIRIETKSRITEENLVNSIPIGEQAGYQTYTIVSDPLHMKRAMKLAA

GLGMDAVPSPTRTTAYRTWRSKFPFLARETVMYMGYTIKGWIDNPQQP"

CDS complement(3362509..3363054)

/locus_tag="EFAGFIKM_02859"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQNTDIQNGDMLDSEHSRELFAYYGLAVYYGQALEQQLVNLILL

MKMSQGKAVSEEDLEDLYERKMSSSLGQLIHEVRHHFTFSEEETRQLNELWQQRNRIV

HHYFKERIHETFSPEGRSRMIKELEDFKDRAQELEIRLQYTGAWIAELGLDAESAAA

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CDS complement(3363154..3363864)

/locus_tag="EFAGFIKM_02860"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIYLTRYLLRHHIRSQKYFAPVIFYIITMLLIYSYKPNPIADSY
SVTAMLLFLAAAWLGVMVMNTEPAKQYQLLV LHAGSRRKVVTSQLICAWIMQFMLTAI
TVLYPVFAGMFERQPTGEEWMMTWLGHGLSLLGLGISVFFQKSYIPLLSRSMPALII
VLLLSFIQGSLSERLPESLEWLGRILPPAFYLVGEMMLFDESKVDSFVSVMLWTVLYA
LGLLIHVVWLSGRRDLRS"

CDS complement(3363861..3364916)

/gene="btuD_8"
/locus_tag="EFAGFIKM_02861"
/EC_number="7.6.2.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01005"
/codon_start=1
/transl_table=11
/product="Vitamin B12 import ATP-binding protein BtuD"
/translation="MTWSTRGLFKKSDQATLDPSGRGILLQQVSKRLGNAQVLDEINL
EVKQGECALVGRNGSGKSTLLRMLAGILLPDTGSIQRTMKGSDGYAVDSLPRLPFTS
GEYLWDMGRIRGIRPEILRERIRELSELLYLDTAIDQKLPLLSKGTLQKVNLIQALLP
GPGGLLLLDEPLSGLDIPAQEAVVSLLGQWKDEGTSIVTACHEPLLIERLADQVIVLK
KGRVLRYSREDILQAGEPVVRIQSLTEAEEDLANDLSIVQQPGVLSLVRNTSSGISN
VWLWDWKVVQQSTDDVLRILASGGSVSVQQEESQLHMESLLEGQHPAVHASLRGVT
ESVDLSSSMDDAGGEAK"

CDS complement(3364924..3366654)

/gene="argS_1"
/locus_tag="EFAGFIKM_02862"
/EC_number="6.1.1.19"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q54869"
/codon_start=1
/transl_table=11

/product="Arginine--tRNA ligase"
/db_xref="COG:COG0018"
/translation="MLMKQAAADIAPLTGLNEQEVLRLLLEVPPQAEMGDAAFPCFALA
KSLKKAPAVIATEFATGLQASGIEATPAGPYVNIRFNREKLAPNLLKELGNAGFGKLQ
LGQGSRVIDMSSPNIAKPFGIGHLRSTVIGAALYRLYNEAGYTSVSVNHLGDWGTQF
GKQIAAYKRWGNDEALQTDPIRTSLELYVRFHDEAENDPSLEIEARDWFRKLEQGDDE
AQRLWAFFVEVSMKEFNRMAYERLNVKFDHTLGESFYNDKMGAVVEELKAKGLLEESDG
ALVVRLEDENMPPCLIIKKDGTIYPTRDLATAVYRHEVMKADRLLYVVGGEQKLHFR
QVFAVLSRMGHEWSAKCEHIPFGLMRFEGRKMSTRRGKVIFLQEVLDEAVARALQIIQ
EKNPNLENPQKVAEAVGVGAIVFGDLRNSRLNDVDFSLEDAVSFEGETGPYVQYTHAR
IQSVLAKAEEAIRVENENPMPKPNLAEGENNTVTTPSLIGDTSWALLKLLGDYPEYLE
KAIHRNEPSVIAKYTIDVAQAFNRFYHAERIAADAPSDVRSFRIALAERTAERLAHTLY
LLGVQAPERM"

CDS complement(3367190..3367525)

/gene="yhjQ"
/locus_tag="EFAGFIKM_02863"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07571"
/codon_start=1
/transl_table=11
/product="putative cysteine-rich protein YhjQ"
/db_xref="COG:COG1145"
/translation="MTQQQYQQCIDACLECMNACNVCISSSLKEYDLAMLRCIRLNR
ECAEICSFAAQAMTRGSDFIAEICELCVKACEACAAECGKHHDHCQTCAEACRRCAE
ACRLMAAVA"

CDS complement(3367599..3368717)

/gene="yciC_2"
/locus_tag="EFAGFIKM_02864"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94400"
/codon_start=1
/transl_table=11

/product="Putative metal chaperone YciC"

/db_xref="COG:COG0523"

/translation="MNETILKEQSIPVYILSGFLGSGKTLLVQLIEHWQQGLRPAV
VMNELGEVNLDGQIVDSTVPMTEMLGGCICCTVRGDLGLQLADLIQEESPdVIIIIEAT
GAANPMEILDAVTETSLYMRLELKSLITVVDAAHLSGLYQEQKGQTFKLMQEQIRCAS
VLLLNKTRVSAQELKDLEQLLAKWNGFAPVIPTVKCEVEMDLLLRSGVDVHVRDSAS
EAGKPAHQEHHVHTEACGTHGCNHGHEHTDHTVQGDATNTDASHSYSHDHGHEHSAPH
ASHEHVMVYTHYFShpVNSEAFEQFVSALPRDVYRAKGILSFSDTASRFWFQYAYRES
DYMKITPQGDVPNVAVFIGEHFDQTVIRDQLLELEAIK"

CDS 3368889..3369407

/gene="moaB"

/locus_tag="EFAGFIKM_02865"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q816R0"

/codon_start=1

/transl_table=11

/product="Molybdenum cofactor biosynthesis protein B"

/db_xref="COG:COG0521"

/translation="MTNSVEQHRQEAPTTVSCMIVTVSDTRTKDTSQQLMHQLLDE
AGYQIVEYIITPDENIRSIHQDAAVRDDIEAVLLSGGTGIAPRDTTYEAVSSLLDK
ELPGFGEIFRFLSYTEDIGSAAILSRAVAGTIGRTAVFSMPGSKGAVKLAMEKLILPE
LRHVMREIYKPV"

CDS complement(3369479..3370033)

/locus_tag="EFAGFIKM_02866"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MWFGRKGRSLAGRTMKSVLVSGVLITSIWVSLVACSASSIEQERK
VYTREATDEGNMRAQNQGHGLNGELVSEISKSFESKGIQLMNNMSADDGHGGISMYL
LNGSGRHIVKVHIFSDKAARAASKQMYSEDRDEAVLENALGRTTIRSKGYVSLVYTA
SGGEKDKYEQDVMQVFQRVLGQLR"

CDS complement(3370108..3371127)

/gene="yhfP"

/locus_tag="EFAGFIKM_02867"

/EC_number="1.6.5.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07615"

/codon_start=1

/transl_table=11

/product="Putative quinone oxidoreductase YhfP"

/db_xref="COG:COG0604"

/translation="MKNHFNAYVVRKEEQGGVKASIEQLKKEDLPNGDVTVQVQYSSV
 NYKDGLATLEKGGVVREYPMVPGIDLAGTVEESVSGRFAPGDRVISTGFEPGVSHYGG
 YSEYARLRSEWLVLPPGLSEKEAMAIGTAGFTAALSVDALLQAGVTPEMGKVLVTGA
 TGGVGSMATAVAILAKLGFVTAATGKKEQEEPLLRNLGASEVITREEADTPAKGAMGKQ
 LWAGVVDPTGGPALAERLKQIQYGGAVAVSGLTGGTAFESTVLPFILRGIQLMGIDSV
 YCPMERRERLWKLGGGEWKPERALELGIREISLGQLPLTLETILQGGAVGRTVVNTIS
 DLPSA"

CDS complement(3371238..3371888)

/locus_tag="EFAGFIKM_02868"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRWILGLVWIAFIAYALLLAPGQSPGSDPIFKELITMQSKEPWL
 LTVFSWLGIFPAVYACMLLRRTSAKERGRVPAWPFVILSFG LGAFALLPYAWSSSANR
 ASGYASLHFGRQRESGIGRVA AHKLTHVLLLLTLGTAFYAVMQGHPDVYMEAFKQSA
 FVHIMTIDFVLLTLLSMIAIYRDTEVSRRSAAWAAAGIPIVGPLIYLLTLRRDRV"

CDS complement(3372286..3373740)

/gene="pncB2"

/locus_tag="EFAGFIKM_02869"

/EC_number="6.3.4.21"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WJI7"

/codon_start=1

/transl_table=11

/product="Nicotinate phosphoribosyltransferase pncB2"

/db_xref="COG:COG1488"

/translation="MQTTSLALHTDKYQINMMYAHWWNGTHKRKAVFEAYFRKLPPFGN
GYAVFAGLERIVNYISQLRFTMDDIKFLSKQEENYDPVFLEELLQFSFQGTIHSMEKEG
AIVFPDEPLIRVEGSIMETQLVETAILNFMNYQTLIATKASRIKQVAQQDTLLEFGTR
RAQEADAAIWGARASYVAGFDATSNMLAGERFGIPTAGTHAHSWVQSFMSQEAFDVY
AKVLPDQVTLLVDTFDTLNSGVPHAIAKTAKKLESQGKKMNAIRLDSGDLAYLSIQARQ
MLDEAGLDYVKIVASNDLDENTIFNLKAQGARIDTWGVGTQLITASDQPSLGGVYKLV
EREVDGAMLPTIKISANPEKVSTPGKKEVFRIIDPKHGKAIADYICYPEEEQPLQGGP
LKLFNPLHPYLKKTVTRYEAVNMLEPIFVNGRKVYELPNLDEIRAYHREQMNLFWPEY
QRKLNPEIYRVNISPAAWNMKQKLIAEHVKSTEE"

CDS complement(3373938..3374495)

/gene="rutB"

/locus_tag="EFAGFIKM_02870"

/EC_number="3.5.1.110"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00830"

/codon_start=1

/transl_table=11

/product="Peroxyureidoacrylate/ureidoacrylate
amidohydrolase RutB"

/translation="MKALIVIDFTKDFVTGSLPVGQPAVEIEETIAAVTEAYCKNKHE
VIMAVDLHEENDPYHPETVLFPPHNIRNTEGRQLYGRLAQVMEERKTDIQWMDKTRY
AFCGTDLELRLRARGITDIALIGVCTDICILHTAVDAYNKGFHITVYEDAVASFPAG
HEWALGHFRSSLGASVVKASETVLA"

CDS complement(3374563..3375366)

/locus_tag="EFAGFIKM_02871"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MSENYEHFNAESDEQAARAYSSQKYRTPDGV PADIVMFTLTKRE
RKT VTKLPIRELKVMLIKRKGWPFAGRWALPGGFCQENESIYGA AKRELMEETGVDG
GHLEYLNVYSQPGRDPRGWIISHAFFALVEEWMLDQRQAADDAEDVGLFTIQEALQEL
ELAFDHRTIIEDAYRRIQQQMLETTIARQFLPRDFTLSELYQVIQSVVPDFEEPNFIR
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CDS complement(3375445..3375849)

/locus_tag="EFAGFIKM_02872"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSILDKMVEDGDGRFWGFLGCRYIKGDGKEVQIALTAGEHHTNS
MGIIHGGVLTSLMDQAMGMVATAAMEVDGCVTTNLNVHFLAPMKQGELTVTATVLHQA
GRSVTTQSEVRDASGTLGCMATATFRIARPRT"

CDS complement(3376059..3376508)

/gene="ymcA"
/locus_tag="EFAGFIKM_02873"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31779"
/codon_start=1
/transl_table=11
/product="putative protein YmcA"
/db_xref="COG:COG4550"
/translation="MAQEEVQYNHYGMPTYDTRNLVIRDDIMGKAKELADMLGTSEEV
RQFQQAETKIRDHERIQQLIATIKKKQKEIVAFESFKNVEMVSKIEQEI EDLQSELDS
IPLVTEFQQSQSDINYLQLVISVIRDTVSEKVNVEAGTDSPTSCG"

CDS complement(3376772..3378328)

/gene="miaB"
/locus_tag="EFAGFIKM_02874"
/EC_number="2.8.4.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31778"

/codon_start=1

/transl_table=11

/product="tRNA-2-methylthio-N(6)-dimethylallyladosine
synthase"

/db_xref="COG:COG0621"

/translation="MAKDSKKDYSQYFDFSDAKVISQDEFSSKKIRIRGREINIKSEPN
HRQEKQRGKEDVQVLYENAVPDELKNIGKGKHYIVYTYGCQMNEHDSETIKGLLESMG
YQATENRKEADIILLNTCAIRENAEDKVFGEGLGHLKTLKLERPGLLLGVCGCMSQEEG
VVNRIMQKHGFVDMIFGTHNVHRLPHLIQEALFSKEMVVEVWSKEGDIIENLPKKREG
MRGWVNIMYGCDKFCTYCIVPFTRGKERSRRPEDVIAEVRDLARQGFEITLLGQNVN
AYGKDFTDLNYSFGDLMDAIRQIDIPRVRFITSHPRDFDDHLIEVLAKGGNLVEHIHL
PVQSGSSEVLKRMSRKYNREHYLKLADKIKKAIPDVVLTTDIIVGFPGETEEQFEDTL
SLVREVG YDFAYTFIYSPREGTPAAVMEDNVPMEVKKERLRLNETINEYSHRSNEKQ
RGKIVEVLVEGESKRNSEVLAGRTRSNKLVHFEGPKELIGTFVQVEITDPMTFYIRGN
LLPEPVAANQ"

CDS complement(3378641..3379213)

/gene="pduL"

/locus_tag="EFAGFIKM_02875"

/EC_number="2.3.1.222"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9XDN5"

/codon_start=1

/transl_table=11

/product="Phosphate propanoyltransferase"

/db_xref="COG:COG4869"

/translation="MSKTPVGVVSARHIHVSQEHVEILFGKGYELTEFKPLSQPGQYA
ANETVAVIGSKGQFDKVRILGPVRPETQLEISMTDSFAIGVKAPVRESGSIEGTPGIT
IKGPAGEVTIDKGVIVAARHIHFHTSDAAKWGIEDKQMLKVRLGGDRGLVLENVLARV
SDSFALDMHIDTDEANAAGARNGDTAEIID"

CDS complement(3379407..3380408)

/locus_tag="EFAGFIKM_02876"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSMSDWRVADFHCDAISKILMQPALS FENAPQLDANLQRLKEGN
VGLQAF AIYLPEVLGRGKFEHVMGQLEIYRRRVERS QERPGGTQTLLWREQVAQVGQT
EGPWGLITLEGVDGLEGNLFYLELCYQMGVRIIGLTWNYANWAADGVMEKRGAGLTEK
GKELVRQCNEIGMLLDVSHLTEKGFWEADLSKRPFIA SHSNSYSVCPHVRNLKDDQI
QAIAREGRIGLTFVPWFVKQEGEIKIEDLLPHIEQFCSLGGQHHLMMGSDFDGISTY
IQRLEHSGHYPKLTEILLKHYDEHLVRGWLWGNAMSYLGEHLPESNPKMQMKGN SMK"

CDS complement(3380494..3380754)

/gene="spoVS"
/locus_tag="EFAGFIKM_02877"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P45693"
/codon_start=1
/transl_table=11
/product="Stage V sporulation protein S"
/db_xref="COG:COG2359"
/translation="MDVLKVS AKSNPNSVAGALAGVLRER GNAELQAIGAGALNQAIK
AVAIARGFVAPSGVDLICIPAFTDIVIDGEDRTAIKLIVEPR"

CDS complement(3380872..3381666)

/gene="ymdB"
/locus_tag="EFAGFIKM_02878"
/EC_number="3.1.4.16"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31775"
/codon_start=1
/transl_table=11
/product="2',3'-cyclic-nucleotide 2'-phosphodiesterase"
/db_xref="COG:COG1692"

/translation="MKVLFIGDIVGNVGRKALKENLPYLKSKYKPHVVIVNGENAAAG
RGITGAIANEFFNWGVHGITLGNHTWDNKKDIFDFIDDEPRMIRPANFPPGTPGRGYTV
VKGEGKELAIVNLQGRFTLPALDCPFRVADEIVDELQRQDHKCILVDMHAEATSEKIAM
GWHLDGRASLVVGTHTHVQSNDDRILPGGTAYLTDAGMVGPRDGILGMEREAVLRKFY
TQLPVRFWDDGKWHFHGVFVEIDEATGAATRIEKIRLTEDEWRME"

CDS complement(3381821..3383362)

/gene="rny"
/locus_tag="EFAGFIKM_02879"
/EC_number="3.1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31774"
/codon_start=1
/transl_table=11
/product="Ribonuclease Y"
/db_xref="COG:COG1418"

/translation="MEIAITIALVAAALFIGFGVGYFIRKSLAEAKISSAEQAAVQIV
ENAKKEAEALKKETVLEAKDEIHRIRAEAEKDTRERRNEIQRQERRLLQKEESLDKKL
ESLERKEEQVANKEKRIDETQQQIEMIYKNQVTELERISNLTMEDARSIILSNVEQEV
RHETAQMIKDIEQQAKEEADKKSREIITLAIQRCAADHVAETTVSVVTLPNNEEMKGRI
IGREGRNIRALETLTGIDLIIDDTPEAVILSGFDPIRREIARTALEKLVADGRIHPAR
IEEMVEKSRKEVDERIREYGEQATFEVGVHGLHPDLIKILGRLKFRTSYGQNVLKHSM
EVAYLAGLMAGELGEDVTLARRAGLLHDIGKALDHEVEGSHVEIGVELAKKYKEHPV
INSIASHHGDCEATSVIAMLVGAADALSAARPGARRETLETYIKRLEKLEEISESFEG
VEKSYAIQAGREVRVMVQPEKIDDAEAFRLARDITKMIENELDYPGHIKVTVIRETRA
VEYAK"

CDS complement(3383673..3384410)

/gene="recX"
/locus_tag="EFAGFIKM_02880"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P66003"
/codon_start=1
/transl_table=11

/product="Regulatory protein RecX"
/translation="MDQHDEDLYEAEQDGLSQFPDNEELIITRVERTKSRQARYRIT
FGIHSITVLEDVMIKYRMTQGNTFMKKDLEDIILADERQRTYAQSLRFLEHKPRTRHE
LSQKLRLQKEFAAPLIEEALDRLERENLVDDDLFAKEWTRQRMGKRGKGLWIRQELRQ
KGIANDLIVEALEGISTDAEFETALSAGRKKWNQVKGDVKEKKNKTLFPFLMRRGFSMD
MVERRVFNCLIEEDEAGDPEDDEALLWD"

CDS complement(3384693..3385757)

/gene="recA"
/locus_tag="EFAGFIKM_02881"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P16971"
/codon_start=1
/transl_table=11
/product="Protein RecA"
/db_xref="COG:COG0468"

/translation="MSDRRAALDMALRQIEKQFGKGSIMKLGESTHMNVEIIPSGSLA
LDIALGTGGLPKGRIVEIYGPESSGKTTVALHAIAEVQRAGGQAAFIDAEHALDPQYA
SKLGVNIDELLSQPDTGEQGLEIAEALVRSGAVDIVVIDSVAALVPKAEIEGEMGDS
HVGLQARLMSQALRKLSGAISKSKTIAIFINQLREKVGVMFGNPETTPGGRALKFYST
VRLDVRRIESIKSGNDMIGNRTRIKVVKNKVAPPFKQAEVDIMYGEGISREGSIIDIG
TELDIVNKSGAWYSYEGERLGQGRENKQFMKEHKDIADIIQKIRVASNLVTAVPAP
TSEEQQKEAAEEQELFEINE"

CDS complement(3386001..3387257)

/gene="cinA"
/locus_tag="EFAGFIKM_02882"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q8DRX2"
/codon_start=1
/transl_table=11
/product="Putative competence-damage inducible protein"
/db_xref="COG:COG1058"
/translation="MKAEIIAVGTELLLGQIVNTNARYLSRELAAMGIDVYFQTVVGD"

NLNRLSEAIRIAQSRADVILFSGGIGPTQDDLTKDALAAVLNRKLHTDRMAMDKIESF
FRDRNVDMTENRRRQAIVIDGGTPLANETGLAAGNAISDNDKYYVMPGPPKELIPMF
EQEVKPWLFQHVLTEEMPIYSRMLKFAGIGESALEDRLMDLIDAQTDPTIAPYASEGE
VTVRVSTKAASEGEAKLKLDAMEVQIRERLTEHLYANEDVPIEYTIVTMMSDMGTLTS
AAESCTGGLVMQSLTSVPGSASMLKGGIVCYSNEIKEKLLNVPHDYLEGEDAPGAVSP
EVAKVLAEQIRMIGDADFGLAVTGVAGPGYSERKPPGLVFIALAERKGKETEIHRLIN
GNRETVRIRSAKAILYRLWQKLVAMD"

CDS complement(3387365..3387952)

/gene="pgsA_1"

/locus_tag="EFAGFIKM_02883"

/EC_number="2.7.8.5"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P63756"

/codon_start=1

/transl_table=11

/product="CDP-diacylglycerol--glycerol-3-phosphate
3-phosphatidyltransferase"

/translation="MNLPNRITLARICLIPFLMVFLLVDFPFYPEPLQLGSLSLPYNQ

LIAAVIFIIAASDGDGYLARKNNMVTNLGKLLDPLADKLLVTAVLISLVEMGKLDS

WIAVVIISREFAVTGLRQIALLDGSVVAASAWGKLKTVVQIVAILLLLNNFPFSYTG

IHVDIIAVWAAALITIWSGIDYFIKNKNLLHLTKA"

CDS complement(3388272..3388802)

/locus_tag="EFAGFIKM_02884"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0QRM0"

/note="UPF0234 protein MSMEG_1165/MSMEI_1134"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLQNIRLTERVTGLSSENSFDIVSKMDLQELTNAVQTQTEKEIGA

RYDFKGSKSSLKLDKDALDIVSDDETKLKAVIDVLQSKMAKRGLPLKNIDYAKVEPAS

SGTVRQRLNFKQGIDQDIKKINILIRDSKMKVKSQIQGDQLRVTGKSKNDLQAVMQL

LNGANLPLDLQYTNFK"

CDS complement(3388920..3389084)

/locus_tag="EFAGFIKM_02885"

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/inference="ab initio prediction:Prodigal:002006"
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/codon_start=1
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/transl_table=11
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/product="hypothetical protein"
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/translation="MTVSWIVTGLGIIVSLLGYYLTPSAWGYGILGFGLAHVLLGVLD

MFRQPNRSRY"

CDS complement(3389158..3390207)

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/gene="rodZ"
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/locus_tag="EFAGFIKM_02886"

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/inference="ab initio prediction:Prodigal:002006"
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/inference="protein motif:HAMAP:MF_02017"
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/codon_start=1
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/transl_table=11
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/product="Cytoskeleton protein RodZ"

/translation="MSELGQQLREARLQKGMSLDDVQEMTKIRKRYLEAIEAGDYKVL

PGSFYVRAFIKTYAETVGLNPDELLEGHKKDVPEEETEATMEPVVIQKRSSRPVERSNR

WMSVALMWTFVLIVLLYVYVVYNNGDESENPGLDOVKITDSOOQPEDKPDOPADNG

QASNPPATDSGTDSTGEGDAGGNGGGTDTEGQTDGQTDGQTDGQTDETEKEPTDNSPS

NVSV AEDGKSGNITNFKVNGSAGQPVTVTIKATGHSWLEVYKGENSSGEKLEYGNTAE

GDSYTFELDSTGMYIKSGYAAATTIEVGGQVVTGDKATNRIRLKLGEDSSGTTSTGV

ENGSTDGTGGTTGSE"

CDS complement(3390274..3391041)

/locus_tag="EFAGFIKM_02887"

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/inference="ab initio prediction:Prodigal:002006"
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/codon_start=1

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/transl_table=11
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/product="hypothetical protein"
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/translation="MESKQWMEYKIHKNRPGLLGDIASMLGMLEVNILTINGVEGKT
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RGMLLESDDDEKIRLLGEMLGKVNSITVSALRQPKLVDILAVRHGRYIDRDSDDRKTF

RFTRDELGLLVDFLGEVFKREGNQVIGLRGMPRVVGKTESIIAGSVCAMKRWTFVSSTL
LRQTIRSQMSEDELNPNNVFIIDGIVSTIRSSERHYNLLQDIMSPSTKVIEHPDIFV
QESEYDFNDFDIIILRNPNNEEIIYDTFTASYTDEL"

CDS complement(3391239..3391502)

/gene="yflH"

/locus_tag="EFAGFIKM_02888"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34306"

/codon_start=1

/transl_table=11

/product="putative protein YflH"

/translation="MSTEKTVLSSFDTWKKFLGDRVLQAEKMGMSEETINKLAYEIGD

FLDEKVDPANHSNRALKELWDVGDADERRTIACLMVKLAKQNA"

CDS complement(3391666..3392436)

/gene="fabG_6"

/locus_tag="EFAGFIKM_02889"

/EC_number="1.1.1.100"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O67610"

/codon_start=1

/transl_table=11

/product="3-oxoacyl-[acyl-carrier-protein] reductase FabG"

/translation="MERGTGQLKAIGEMTVLVTGASGGIGAAIAERFARVGMNVVIHY

MRSHEAANEAAARRCMEQSGKIMTVSADLRSREQIERMREKLESHNLMPDILVNNAGI

SHYGMLADVTEEIWDEVMAINLKGTFMCTQEMMPHMISQRYGRIINVSSIWGLSGASC

EVLYSTTKGGVNAFTKALAKELAPSGVTVNAVAPGAVQTSMLNHLDQSELKMLEEEIP

AGRLAQPDIESSLVYFLALPESGYINGQIISPNGGWLT"

CDS complement(3392438..3393718)

/locus_tag="EFAGFIKM_02890"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MESIRYEHQLQETLYEVM DNGLHVYILPKPGFQKTYATFATKYG
SVDNHFQVEGQEEVKVPDGHAFLEHKMFEEPTGDIFATFASHGASANAFTSFDQTVY
LFSATEHVNENIQLTVDFVQNPYFTDQNVKEKEGIGQEIDMYADNP DWRVYFGLIEA
MYQKHPVHIDIAGTVESIRTITKEMLYECYNTFYHPSNMLLFVVG GVDPPQEVIDMVRS
NQEQKDYKPPQGSIQRFEPPEPEQVGEARREAKLAVSLPKCLFGFKETDVGLTGEQLLR
RDMTTQLMMDLLFGSSTRLFQKLYDEDLISDSFGHEYNSSPQYAFSAIGGDTKDPDQL
LARIRREEVDAIVEKGFDDSTDFERARKKKIGGYLRMLNSPENIAHEFTRQQFRGGDFFN
MLPLYESITLEDVNLRLREHIRWDHLAISLVVSP"

CDS complement(3393722..3395002)

/locus_tag="EFAGFIKM_02891"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNTSGFERGNKREFRIHVLPTKRFKTF AISLYAGVPLREDTVTK
VALTPFVLRRGTESYPETTQFREQLEHLYGAGFGFDVYKRGDYQIVQFRMDTINDSFV
GGDEQLLDRSFAFLGEVLTRPAQENGHFRTSYVQAERETVRKKLESIVNDKMRYAAER
SIEEMCKNEPYRLHPLGERRDLPGIEPDTLTASYQEWLQQASMDLYVVGDTTLEEVEN
LVQRHFNVDR TSSSDYQTQAAVRGDKAVETVVERLNV SQGKLN MGLRTSITYGDPQYA
AALMYNGILGGYPH SKLFVNVREKESLAYYASSRYDGHKGIATIQSGIEIPNYEKAVT
IIKQQLEEMKSGTITDLEMSQTKAMIRNLLKEMQDSAFEMIAYDFNRQLSGKERTAE
LLAQVEHISKEDVREAAEQFRLDTIYFLRDEKEE"

CDS complement(3395129..3395959)

/gene="sleB"
/locus_tag="EFAGFIKM_02892"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A3V0"
/codon_start=1
/transl_table=11
/product="Spore cortex-lytic enzyme"
/db_xref="COG:COG3409"

/translation="MRKMNIWLFTAILLMSALGIRYLLPENAATESSNQSTPQVEEKA
LPTFSSNAVKYGSYGQDVYELQGRLKYLGFYNGKIDSNFGNSTLKS VKWFQSEFGMKA
DGVVGAETKLKLYNASTKWSPTETPLHKKKTSGGSDSSNNTADKEQDNMG SANALGLS
ENELKIMANAVYGEARGE PFEGQVAVAAVIMNRVKSPSPNTPSGVIFQPGAFTAVAD
GQIYLEPNAQAKKAVEQALNGWDPSSGGCLYYFNPKTATSKWIWTRPQVKTIGQHIFCM
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CDS complement(3396155..3398893)

/locus_tag="EFAGFIKM_02893"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MARRKKRKKKGAGFSGVLKYEIYGIVLITLAVIALSGEATVGRS
LSKMFGMLGKFYFAIPLVGIYYGLMVMIH RKWPSGWTRKTGLVLLVFAL TLMSTVS
AMHQKLIPVGALEPGAVITQVHNDMQTELLTPATPGERDSMLNKDISGGYLGAGQFVL
FLWLFGSLGARLIMVMFVISFMLITNLSYVDLIRIFRTKIWDAGSSMYKKLESRPSA
RSASASDARKRGNTRKVVPVPVEDDEDEYEDELEEQHLPKRNSPIFFQLFEKWGAKRE
QATSGREMDEVDSAETE QIVYRAEQDHNLEAWQDATEDVTNKSASSRVPVQAKPNSAP
IIRDFFEHVRAEEASIEDDLDDAYPFPDNLADPNVQQGEHTIKITDELVETEWSASD
AGTNGMNAVDEIQSGEEVSNDAMQGTDTPTPEGQDTQPVKPPPPPKPYKLPSFRLLA
KPNNGGKAGDQKDYMQTARKLEATLESFGVRAKVLEVVRGPAVTRYEIQPDIGVKVSR
IVSLTDDIALALAAKDIRMEAPIPGKSAIGIEVPNGEVS VVTMREVMETATFQDAESK
VTIAFGRDISGQTIIGNLARMPHLLVAGATGSGKSVCINGIITSILYKAKPDEVKFLM
VDPKMVELNVYNGIPHLLAPVVTDPKRASLALKKIVVEMEKRYELFSKSGTRNVEGYN
NLMKDNPAAVLPYIVVIVDELADLMMVAAGDVEDAIARLAQMARAAGIHLIATQRPS
VDVITGVIKANIPSRIA FGVSSQVDSRTILDMGGAEKLLGRGDMLFMPMGASKPVRVQ
GAFMSDEEVENIVNYVRGQGEAQYDESLVPEVDDSIQAEDEVQDDLYEKAVQIILEAK
QASVSLLQRRMRVGYTRAARLIDSMEARGVIGPYEGSKPREVLVSLEQYQQNKISS"

CDS complement(3398984..3399214)

/locus_tag="EFAGFIKM_02894"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MTLYTVMPPPEQLWSGMWKEGEDTKEIKMNGLLMQVRPVNDNEAV
IVRLDCPLEAYLN PANMPGSTIPISGNWGSA"

CDS complement(3399211..3400011)

/gene="tepA"
/locus_tag="EFAGFIKM_02895"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q99171"
/codon_start=1
/transl_table=11
/product="Translocation-enhancing protein TepA"
/db_xref="COG:COG0740"
/translation="MFLEKGIIEMNERMNGKQASRSNQPEVEAPEIPIQEDKAISPT
ETIQQFGQTQSPAGESNIFCMTIIGQVEGHLILPPQNKTTKYEHIIPQLVAAEQNQRI
EGILIILNTVGGDVEAGLAIAEMIASLSKPTVTVVIGGGHSIGVPIAVASTYSLIAGS
ATMTIHPIRMNGLVIGVPQTFEYMEKMQERVVRFVTSHSNISEEMFKELMFKTGELNR
DIGTAVGSADAVKHGLMDAVGGIGQAIAQLNQLIGDKRQTLQAGGYTQ"

CDS complement(3400206..3401885)

/gene="rnjA_2"
/locus_tag="EFAGFIKM_02896"
/EC_number="3.1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q45493"
/codon_start=1
/transl_table=11
/product="Ribonuclease J1"
/db_xref="COG:COG0595"
/translation="MSKKNNDKLMIFALGGVGEIGKNMYVIQYANDIVVVDAGLKFP
EEDMLGIDIVIPDISYLTENRDKVRGIILTHGHEDHIGGLPYVLKHLNVPVYGTRLTL
GLVENKLKEANLLGDTKRILIDADSEIQLGSVLKASFFATNHSIPDSVGVCVETPEGA
VVHTGDFKFDHTPVNGQYADLQRMAQIGTNGVLALLSDSTNAEKP GFTPSEKNVGIVL

EDIFRKASQRVVVATFASNVHRIQQVINAAEVTGRKVAVIGRSMVNVVGIASELGYLE
IPDGMIIPEEEVGKMAADRVVILCTGSQGEPMSALTRMARSTHRKVDILPGDTVIIAA
TPVPGNEKYVGRITIDELFRLGANVHYSGANSGVHVSGHGSQEELKLMLNLMKPKFFLP
IHGEFRMQRRHAVLAESVGVEPENIFITDIGEVIEIQGGAARRAGKVTAGNVLIDGLG
VGDVGNIVLRDRKLLSQDGILVVVVTLISKQDGKIVSGPDIISRGFVYVRESEGLLDEA
NRIVSSTLQKLMSENVNEWASLKTNVKDALGRFLYEQTRRRPMILPIIMEV"

CDS complement(3402362..3403240)

/gene="dapA"

/locus_tag="EFAGFIKM_02897"

/EC_number="4.3.3.7"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q04796"

/codon_start=1

/transl_table=11

/product="4-hydroxy-tetrahydrodipicolinate synthase"

/db_xref="COG:COG0329"

/translation="MDFGRLITAMVTPFNEQGEIHWEETARLIDYLVLDQKSETLVVS
GTTGESPTLSDEKVLFEFAVKHAAGRCKIIAGTGSNNTAHSIHLTQEAERAGVDGI
LLVVPYYNKPSQEGLFKHFIAIAGSTKLPIMLYNVPGRTVTSLSAETTLRLAQIPNIV
ATKECASMEQVTLIAASAPENFRVYSGDDASGLPAIAVGAHGIVSVASHVVGAEKKM
IDAFYGGAPLQAAQIHQQLFPVFKGLFECQPQLPNPVAVKYALTLRGLDVGSVRLPLI
PPTEEEQVYIKGLLNL"

CDS complement(3403288..3404508)

/gene="lysC_2"

/locus_tag="EFAGFIKM_02898"

/EC_number="2.7.2.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q59229"

/codon_start=1

/transl_table=11

/product="Aspartokinase"

/translation="MRIMVQKFGGTSLSTVQAREHVL RHVKRELEAGLSLVIVVSAMG

RRGEPYATDTLLDWAAQNGNALSAREKDLLCCGEIISATTLSSLLEHEGIPTTVLTG
AQAGFVTDDNFGNARILDVRPVRVLEQLQLGRVVVVTGFQGGQTENGDFTTLGRGGSDT
SATALGAALRAEMVDIYTDVNGILTADPRIVEDARPLTVVSYAEICNMAHHGAKVIHP
RAVEIAMQSQIPVRVRSTFADTEGTLVTHPEGFQDVQTGIVDRYVTGIAYVSNVTQIT
VDVPGGGADRLQLKVKFMAENSISVDFINVTSGVVYTVFSDSEKAIQVLQEIGLK
PQSLSGCAKVSVIGGGINGVPGIMARIVESLTLADIQILQSADSNTTIWVLVKKEDMV
QALRALHASFELHL"

CDS complement(3404887..3405483)

/gene="dpaB"

/locus_tag="EFAGFIKM_02899"

/EC_number="1.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q04810"

/codon_start=1

/transl_table=11

/product="Dipicolinate synthase subunit B"

/db_xref="COG:COG0452"

/translation="MNWQGKTVGYAITGSHCTFEEVMPVISRFVAEGANVIPIISNSV

LTTDTRFGTAQNWQKQLKDITGNDIISTIVEAEPLGPSKLLDVLVIAPCTGNTTSKLA

NAMTDSPLVMAAKAQMRNQRPLVLAISTNDGLGLNAANIAKLLVAKYLYFVPFGQDDP

VKKPNSLVAKMELIPEACWSALEGKQLQPMIVERSSQA"

CDS complement(3405480..3406379)

/gene="dpaA"

/locus_tag="EFAGFIKM_02900"

/EC_number="1.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q04809"

/codon_start=1

/transl_table=11

/product="Dipicolinate synthase subunit A"

/translation="MLTGVRIIVLGGDARQLEVIQKCAELDATVSVVGFDKIERISIPG

IEHQELEDEVFASADVLLPVVGCDEQGVSTSFSDTPIYLKKEHIAALPEHCIVFTG

MAKPFLRELCLENGLRLVEVLDRDDIALYNSIPTAEGAIAIAIRETDFTIHGSECIVL
GIGRTGFTMAKTLQQLGANVRVGIRREEDAARATIMGWRPFMTTDLAAQTGEVDLLFN
TIPTMIITAQILSRMPQKAVIIDLASAPGGCDFRYADKRGIKALLAPGLPGIVAPKTA
GGIADALIRLLLEEQNAREVKS"

CDS complement(3406536..3406979)

/gene="dut"

/locus_tag="EFAGFIKM_02901"

/EC_number="3.6.1.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2YRG4"

/codon_start=1

/transl_table=11

/product="Deoxyuridine 5'-triphosphate

nucleotidohydrolase"

/translation="MHYVQIQKLPGNEDIKLPQKMSELASGFDVVAALQEDVVLQPGQ

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EPFTIVRGERIAQIVFQTVPAVELTEVNELSETVRGEGGFGHTGK"

CDS complement(3406942..3408225)

/locus_tag="EFAGFIKM_02902"

/EC_number="3.4.24.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WHT5"

/codon_start=1

/transl_table=11

/product="putative zinc protease"

/db_xref="COG:COG0612"

/translation="MKKIQLGNGLRVVMEQIPTCRSVSFGIWVKTGSRNEQPASNGVS

HFIEHMLFKGTDYDAKIAIEQFDAIGGNVNAFTSKEYTCYYAKVLDEHLPIAVDVLS

DMFFRSKMDDGELIKEKNVILEEISMYEDTPDDMVHDLMALAAYGEHPLAYPILGTEE

RLKAMDSSHLRAYMKEHYTIENTVISIAGNIDDSVIDLMEKHFGAFDVNGVSEAVTMP

AFQSGQLFHKKKTEQNHICISFPGCKIGDPLQFAMVVLNNAIGGGMSSRLFQEIREKR

GLAYSVYSYHSSHADSGLFITYAGTAPKQTKVLDLTKEVLRDLAVNGLSEDELKRGK

EQLKGSILSLESTGSRMNRLGKNELMLGRHHTLDEMITKIEQVTMDDINAVLDMFA
EPFALAMVGASDKTIAGLRDDFVALRSNTETAGQ"

CDS complement(3408325..3409320)

/locus_tag="EFAGFIKM_02903"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGNQSKKLAAGVAVILIGQVGSVRTYITEIRDGPQTQNAF

DMFKEATGEDALLSAIRDKAAETKIAPVNARVDRVWKAIPGYNGMEIDVEATYRKALS

GTLNTKIAYVYRQIEPEIQLKDLGAHPYRGNNANKPMVSFMINVAWGNEYIKPMLDTL

DAEKVKATFFLDGSWLSKNVELAKEIQKRGHMSNHAYSHPNMSRLSAERAKLEISK

QDLLHKTGLENRWFAPPSGDFNQKTVDIASSMGLQTVLWTVDTVDRKPSPDVAVAK

IAKNTEAGTLILMHPTAASSGALKGMIQSIRAKGLVLGTVSETLSSERVNTSAVE"

CDS complement(3409496..3411598)

/gene="pnp_1"

/locus_tag="EFAGFIKM_02904"

/EC_number="2.7.7.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P50849"

/codon_start=1

/transl_table=11

/product="Polyribonucleotide nucleotidyltransferase"

/db_xref="COG:COG1185"

/translation="MEQRVEMQLGGRKLTLETGRLAKQANAAVKVTYGDTVVLCTVTA

SSEPKDLDDFFPLTVNYYEERLYAVGKIPGGFIKREGRPSEKAILSSRLTDRPIRPLFPE

GFRNDVQVLNIVMSVDQDCEPQIAAMIGTSAALSISDVPFSGPIGGVKVGRIDGEFII

NPTIAQLEVSDELVVAGTKNAIMMVEAEANEVPEEVMLEAIMFGHDEIQNIIAVIEQ

LVQVAGQEKMAVKLRVNAEVNSSVREFASARLVEAVKIAEKHARQDAIDVVNDETVA

HFEEKYIESPELFKDVKEVLHDIVKEEVRRLITHDKVRPDGRGLAEIRPIECDTSLLP

RAHGTGLFTRGQTQALSVCVLGALGDVQILDGISLEETKRFMHYHNFPPFSVGEARPL

RAPGRREIGHGALGERALSKVIPSETDFPYTIRLVSEVLESNGSSSQASICASTLMM

DAGVPIKAPVAGVAMGLIKDGDHVSILSDIQGMEDHLGDMDFKVAGTPEGVTAIQMDI
KIAGINRQILSDALTQAKEGRMHILGKMNEILKTPREQLSQYAPKITTMHINPDKIRD
VIGAGGKIINKIIEETGVKIDIEQDGRVFIASSNQEMNDKAKAIIIEGIVREVLVGEIY
VGKVKRVEKFGAFVEVLPNKEGLVHISQLSTERVAKVEDVVAIGDSITVKVTEIDPQG
RINLSRKAVLTAEAPAQS"

CDS complement(3411858..3412127)

/gene="rpsO"

/locus_tag="EFAGFIKM_02905"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P21473"

/codon_start=1

/transl_table=11

/product="30S ribosomal protein S15"

/db_xref="COG:COG0184"

/translation="MALTQERKQQLIDEHKTHESDTGSPEVQVAILTENITSLTDHLR
THKKDHHSRRGLLKMMVGQRRKLLAYVKNKDVKRYALIEKGLRR"

CDS complement(3412105..3412239)

/locus_tag="EFAGFIKM_02906"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIYCTTSLIEATLTLLAWLLALTGGDEANGDYIEGGEQDGIDSRT
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CDS complement(3412287..3413225)

/gene="ribF"

/locus_tag="EFAGFIKM_02907"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AG40"

/codon_start=1

/transl_table=11

/product="Bifunctional riboflavin kinase/FMN

adenylyltransferase"

/db_xref="COG:COG0196"

/translation="MKTVMLTYPQTLHSTELSTLPQVLAIGQFDGLHLGHASVILSAV
RIARETGMQAAVMTFHPHPKEVMRKGDYEGYLTPLRDKEDILAGMGVDVLYVVEFNED
FSRLTPQQFVHDLIPLQTRTAVVGFDLFRFGHKGAGDEQLLRTLGEGEMMVETVPPFL
LNGEKVSSSLIRGLLKRGEDEASQWLGRPYSIRGTVIHGEKRGRTIGFPTANLELTD
HYVTPSKGVYAVRVQYGEQELHGVMNLGVKPTFHESGMKPTFEVHLLDFDGHLYDQEL
KVELVHYIRAERKFDSIEALISQIREDALTAGRLLS"

CDS complement(3413296..3414219)

/gene="truB"

/locus_tag="EFAGFIKM_02908"

/EC_number="5.4.99.25"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P65855"

/codon_start=1

/transl_table=11

/product="tRNA pseudouridine synthase B"

/translation="MVKPFEGVLPVYKPAGFTSHDVVAKMRRILKMKRIGHTGTLDPO
VTGVLPLCLGRATRVEYMQELPKEYLATLRLGLSTDTEDMTGEVIERAETTVEVTQE
QVQQVLEQFLGTISQVPPMYSKVDGKRLYELAREGKTVERKSREVTIYELELTGIE
TQGETTDISFRALCSKGTIIRTLCDIGRQLGYPSTMVQLERTISAGISADRCLRIEE
VEQLMADGTLAEALIPVDEAIAIPAHKVGEEQAKGALQGQKLSARLLEPPVEQPGLL
RLYAQDGTFLGIFERDELKPTVRAVKVFLPE"

CDS complement(3414213..3415190)

/gene="nrnA"

/locus_tag="EFAGFIKM_02909"

/EC_number="3.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5SM25"

/codon_start=1

/transl_table=11

/product="Bifunctional oligoribonuclease and PAP

phosphatase NrnA"

/db_xref="COG:COG0618"

/translation="MHTYEQALQAGKQFLLEHDDYLVVSHVQPDGDAVSSTVTVGWLL
SCLGKTFTMINEGEIPGRMQFLWEAGNIVNMTEQPPQRKYKAVICVDCADFARVGLTR
HYFEEDAVILNIDHHPTNDGYGTVNIKSDAAATAEILFDLNLFQVTWDKDVATAVY
TGLLTDGGFRYANTSPNVMTTASRLLEHGVDGPYLAQTLLEQVTLQPVRILNQALSS
LQMTDDGKIAWVVITPDDMVACGAANEDLEGVVNYPRNIQGVGVGIFFKVINENAVKV
SLRSAGKIDVAALAQTFGGGGHVLAAGCRLEGRLLDDIIAKVLKQVNSQW"

CDS complement(3415210..3415569)

/gene="rbfA"

/locus_tag="EFAGFIKM_02910"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P65967"

/codon_start=1

/transl_table=11

/product="Ribosome-binding factor A"

/translation="MAKIRTGRVGEQIKKEISLLIQSELKDPRIGFITVTGVEVTGDL
SQAKVYLSVFGEQEQKDNTLKALAKANGFLRSELGKRIRFRHVPPELIFKIDESIAYGS
RIEKLLEDIGSDKNESQ"

CDS complement(3415595..3418180)

/gene="infB"

/locus_tag="EFAGFIKM_02911"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00100_B"

/codon_start=1

/transl_table=11

/product="Translation initiation factor IF-2"

/translation="MSKQENKDKLRVYEYAKSLNMSSKEIITLKKLEIPVNNHMSVM
ENGSVGKVEQFFKDIKSTAASKQGNDAPVATSAVRSDKPVDSPAGGVNTPISSNP
SGSPVQTKIQEKQVGMNNRPNNSNNNGTQRPSTGQDSRNRTNSSQGSSQGGQSTNRPR
PAQGGQSSTASRPQGTGQRPNNSSGGGQVRTSGPNSGGNTGTAGNRSGGQGGQSGGQQR
RSGPGGTTGSNNNSGNRSNSGGGGRRYDDNRGGNFRGNRGGKNNRNRNQYQYQREKI

DNTPKKIIVRGDMTVGETAKLLHKDASEVIKKLIAMGVMATINQELDIETILLLSGEF
GVEVEVKIVLEDDRFETLEENDDAADLQARPPVVTIMGHVDHGKTTLLDAIRSTNVSD
GEAGGITQHIGAYQVEINNKKITFLDTPGHEAFTAMRARGAQVDTMTIIVVAADDGVM
PQTIEAINHAKAAGLPIIVAVNKIDKPGADPDVKVQELTSYELVPEEWGGDTIFVNVS
AKQRMGLEGLLEMILLVAEVNEYKANPDKRARGTVIEAELDKGRGPVARILVQHGTLK
VGDAFVAGNCFGRVRAMVNDKGRKLKEAGPSTPVEITGLTEVPGAGDPFMVFEDERKA
RSIADKRAITQRESDLGTHTRVTLDDLQFHIKDGEIKDLNVIKGDVQGSVEALKGSL
AKIEVEGV RVKIIHSGAGAITESDIILAAASNAIVIGFNVRPDNQAKSTADQE QVDIR
LHRVIYSVIEEIEQAMKGMLDPIYKEKVIGHAEVRSTFSISKVGTIAGCMVTSGKITR
SAEARLIRDGIVLYEGKLDSLKRYKDDAKEVAQGYECGITLDDKYNDLKEGDVIEAFIM
ETVQR"

CDS complement(3418173..3418502)

/gene="rplGA"

/locus_tag="EFAGFIKM_02912"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P32729"

/codon_start=1

/transl_table=11

/product="putative ribosomal protein YlxQ"

/db_xref="COG:COG1358"

/translation="MTNIKTL SYLGLSMRAGKLV TGEEIVLKAIRSSEAKMVIVAGDA

SANTQKKFRDKCGTYKVPLLIGFDRDSLGS SIGKDTRVVLAVTDRGFAKMISKQVGIM

SEVEYIE"

CDS complement(3418495..3418800)

/locus_tag="EFAGFIKM_02913"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKPKKVPLRKCVACQEMMPKKQLIRIVKTPEDVLIDLTGKKSG

RGAYLCGKESCFKLALKNRALDRALKGKVSPEIYEQLAADFIAVEDEFIAAQEREHD"

CDS complement(3418826..3419923)

/gene="nusA"
/locus_tag="EFAGFIKM_02914"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P32727"
/codon_start=1
/transl_table=11
/product="Transcription termination/antitermination
protein NusA"
/db_xref="COG:COG0195"
/translation="MSTDFIEAMNELEREKGISKDVLFEAIEAALISSYKRNFNTAQN
VRVDMNRNTGVIRVYARKLIVEEVLDSTRTEISLPAAREINPHFQLEDIAEIEVTPRDF
GRIAAQTAKQVVTQRIREAERGLIYNAFVDKEEDIVTGVVQRQDLRNIYIDLGKIEAA
LPLTELMPNEKFVHGDRIKAYITKVENTTKGPQIILSRTHPGLLKRLFELEVPEIFDG
VVEIRSVAREAGFRSKIHAVHSRNEEVDPVGSCVGPGRMRVQTIVGELRGEKIDIVRFS
DQVDEYVANALSPSKVLEVHVFEEEKMARVIVPDYQLSLAIGIKGQNARLAAKLTGWK
IDIKSESQAEQEFGREKDSSEMHHQDSVSVD"

CDS complement(3420047..3420508)

/gene="rimP"
/locus_tag="EFAGFIKM_02915"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q97S61"
/codon_start=1
/transl_table=11
/product="Ribosome maturation factor RimP"
/db_xref="COG:COG0779"
/translation="MSTTNIKSTVEEMIQPYLNEQGFELVDIEYVKEGSNWFLRVYVD
KEGGIDIDDCVLISEKLSAKLDENDPIPTIYFLEVSSPGAERPLKKPEDVTKAVGKNV
FVTTYEPVNGLKEFEGKLLSFDDEELVIEAGKKQHAISYDKVASARLAILF"

CDS complement(3420765..3425084)

/gene="polC_2"
/locus_tag="EFAGFIKM_02916"
/EC_number="2.7.7.7"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P13267"

/codon_start=1

/transl_table=11

/product="DNA polymerase III PolC-type"

/db_xref="COG:COG2176"

/translation="MSGFEEKRKRFEELMKQAELPAGLLEPYFLDGWIEQVETNRSNR
EWNILIAKDMLVPAPIYRTFCLHIQEKMNHIAKISFGFKYTDQVQNGDIVSEYWNFL
EWTREIPSVNGWMNRRTTFECEEDLLQLTMSDATSMELARKKQIDQAITKFYDKYFHL
PLRIKMQVGEVGSNKEAMEQFQAQKRVEELEVIEKMMSEVDTEIPVDEEQGDLRLQMG
YDIKEPAVPMQEIQDEEEKVTLQGSVFGLDRKELRNGNTLFTFYLTDFDSMQMKMFA
KTKEDVKILSLLANGKWWKVRGRVEYDRFMQIPELAMIPSDLIEVKAPPSRKDNAPEK
RVEFHLHSTMSTMDAVTSIDKYVKMAAEWGHKAIIVSDHGGVQVYPEASKAAKNGIK
MIYGLEANVVNDSVAVVMAPQPLDLQTATYIVFDIETTGLSVTQNKIIEIAAVKMQDG
KEIDRFATFVNPHERIPYNIQQLTNINDDMVKDAPELEPVIRDFVQFAGDGVLVAHNA
RFDMGFIQASLKQIGLPELPNPVLDLTELARLLFPKNKNHRLNTMADKYKVGLESHHR
AIDDTIALAGILIGLLNDAAQMKGRLRLDRLNDYVGVDLSNTRPFHCGIYALNDVGKK
NLYKLVSLSTEHFKRVPKIPKSKLINLREGLVIIISGCEKGEFFEAFLNKSLEEAEEI
AEFYDILEIQPLTMYMHLVDKGLVATPEEIKTAIRKVIDIGAKFNKPVIATGNVHYLE
PRDKLYRDITIHGITGFSPDKDQRKPDAHFRTTEEMLEEFQFLGQDKAYEVVVTNTVE
LSDRFEEIKLFPDKLFTPILEGADEEIRNTCYDTAKSIYGEELPEVIVARLEKELIPI
IKYGFSANYLISERLVKKSNDGYLVGSRGSSVATFLGISEVNPLPAHYICVNS
ECKHSEWFLDGSVRSGFDLPEKECPDCGGTLKGEGQDIPFETFLGFKGDKVPDIDLNF
SGDYQPHAHNYTKVLFSEKSVFRAGTIGTVAEKTAFGFAKKYEEHHQKKWRGAELNRL
ASGCTGVKRSTGQHPGGIVVVPDYIEVEDVTPVQFPADDVNAEWKTTHFDYHAFEENL
LKLDILGHDDPTMMRMLQDLTGVDPTTIPMNDPKVMSMFNSTEALGVTPEQIRSPVAT
FGVPEMGTKFVRQMLVESQPTSFADLLQISGLSHGTGVWLGNQDLIKNGTCNIKTVI
GCRDDIMLFLIYKTGMDASLAFKITESVRKGRGLPQEWIDEMKNCKVPQWYIDSLKI
QYMFPKAHAAAYVISAVRTAFFKLYHPIEYYATYFTVRADEIDIELMCQGYDAIRKI
MEIEQLGFQAPPKEKNMLPVLEMGLEMAARGFSLKSIDLYRSEATKFIVDGKTLIPPF
SALAGIGDNAARNIAAARDHGEFLSVEDFQQKSKASKTIVELLSNMGCFRGLPESNQL
SLF"

CDS complement(3425428..3426882)
/gene="proS_1"
/locus_tag="EFAGFIKM_02917"
/EC_number="6.1.1.15"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9L4Q8"
/codon_start=1
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/product="Proline--tRNA ligase"
/db_xref="COG:COG0442"
/translation="MSKENDKQFVTEITPQGEDFSRWYIDVIKKADLMDYAPVRGCIV
FKPDGFEIWEHIKDELDRRFRETGHRNAYFPMFIPESFFQKEKEHVEGFNPPELPWVTE
AGGEKLEERLAIRPTSETIIGHMYSKWIQSYRDLPLINQWANVVRWEKRTLPLRTS
EFLWQEGHTAHETEEEEAREETMKMLEIYREVVEEYLAIPVIVGQKTKSEKFAVAVDY
SIEAMMKDGRAVQAGTSHYMGTNFAKAFEIQYLSRNNVLELAYTTSWGVSRLIGALI
MVHGDDRGLVLPPKVAPTQVVMIPGPPKTRDAVVGRADELFTLKKAGVRVKMDDRS
DVRPGWKFNEMRGVPIRLEIGPRDMENGVCVLVSRITGEKKVVEQANLVEEIQAML
TQIQVDMLERARTFMSDNFYSDTLDEMKELMENKRGFTLAGWCGSEACEDKVREVTG
ATSRNIPFQPAEEKHTCLACGEQAEHTVVFARAY"

CDS complement(3426945..3428216)
/gene="rasP"
/locus_tag="EFAGFIKM_02918"
/EC_number="3.4.24.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31754"
/codon_start=1
/transl_table=11
/product="Regulator of sigma-W protease RasP"
/db_xref="COG:COG0750"
/translation="METIQVVFLLVLMFFVIVTVHEWGHYYFAKRAGILVREFAIGFG
PKLFSYKRNETQFTLRLLPFGGYARMAGEDPELVEIQEGQTIAVRSADDQVKMIYLDQ
LDNRKNVIRGEVISIDMERALKLQLDVGGEIQEYRIHPQAMLVSRGKQTQIAPKDRQF"

GSKTVGQRALAIFAGPLMNFILAFVLFAVYAQMAGVPVENPKNLQIGEVLEGGAADQA
NLQKGDIIETINGTAIGTDSQKMVSMIADSKDKPMEWTLRRGSDTFNITITPRAVEGQ
EGGKVGVPTLPTRSVGFVETFKVSGVAMVDTTKIIFEGFKHLINQFNMDDIGGPVRT
FEVTGQIAKQGIEQLTRWAAILSLYLGIFNLLPIPALDGSRLVFLGIEALRGRPVDPN
REGMVHFIGFAMLFVLMLAVTYNDILRLING"

CDS complement(3428330..3429469)

/gene="dxr"

/locus_tag="EFAGFIKM_02919"

/EC_number="1.1.1.267"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9RCT1"

/codon_start=1

/transl_table=11

/product="1-deoxy-D-xylulose 5-phosphate reductoisomerase"

/db_xref="COG:COG0743"

/translation="MKKIAILGSTGSIGTQTLDVVDMHPELFQVEGLAAGGNTDLLIE
QTKRYRPKKVSVGSKELAEKIAPHLPAGTQLFYGNEGLVEVAAGTDAHTVVTAVVGSV
GLESTLAAIDAGKQIGLANKETLVTAGHIVTTTRAAAKGVSLLPVDSEHSAIFQCLNGE
NRERLAGITLTASGGSFRDLTREQLKNVTIEDALKHPNWSMGSKITIDSATMVNKGLE
VIEAHWLFGLQYDQINVLLHPESVIHSYVEFDDTSIIAQLGNPDMRVPIQYALTYPDR
LPSPAQRSLAQAGKLHFRDMDMERFPCLRMAYECGKMGGTATTAFNAANEVAVARFL
RKEISFLKIEDIIASVLEAHHNVDEPDLQEIARCDQESRKLAAASL"

CDS complement(3429540..3430334)

/locus_tag="EFAGFIKM_02920"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKQRLTTGIIAGVLFLGFCMLGGPWYHGLVLLMALIGYYEFVKM
TGVMPSGVALIGYAGVFAIVFPWEMLWEARPLSLFQVIWIVMLVLMTASVVTKNKVP
VNTVAMLFLGVLYIGIGFYIAESRHLHHGLFWTFLLSSIWASDAGAYFVGKLIGKN
KLWPSISPNTIEGALGGIVIAIVTSVIFALVSDGLLSWQRAIVIGIACAVVGQMGDL"

IQSAYKRVYNIKDSGSLLPGHGGILDRCDSWIVVFPFVHILMLLPY"

CDS complement(3430351..3431118)

/gene="uppS"

/locus_tag="EFAGFIKM_02921"

/EC_number="2.5.1.31"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O82827"

/codon_start=1

/transl_table=11

/product="Ditrans, polycis-undecaprenyl-diphosphate

synthase ((2E,6E)-farnesyl-diphosphate specific)"

/translation="MIKRVRSWWNGADKQETLTISEDNIPQHVAIIMDGNGRWAKRLG

LPRIAGHQNGMKAVKRATIAADELGIKYLTMAYAFSTENWTRPKEEVDFLMRLPQEFLA

IELDELIEKNVRIRMMGQEEHLPSTINALREAIRLTEHNTGLVLNFAMNYGSRREMT

DCVKQIALQVKSSELGSAEDITPELIDRHMLTVDMPPDLLIRTSSELRLSNFMLWQLA

YSELWFTDIYWPEFGKKHLLLEAVAQYRRTRRYGGLK"

CDS complement(3431208..3431762)

/gene="frr"

/locus_tag="EFAGFIKM_02922"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P81101"

/codon_start=1

/transl_table=11

/product="Ribosome-recycling factor"

/db_xref="COG:COG0233"

/translation="MPQAVKQHAERMEKAIQALRRDLATLRAGRATPALLDRIQVEY

YGAMTPLNQLANISTPDSRTLMIQPWDKSSMGDIERAIMKSDLGLTPANDGSMIRLSI

PALTEERRAELVKLTKKFGEEGKVAIRNIRRDANDDIKKMEKSDISEDESRRHQDDIQ

KSTDKFIAEVDKVLAAKEKEIMEV"

CDS complement(3431762..3432490)

/gene="pyrH"

/locus_tag="EFAGFIKM_02923"

/EC_number="2.7.4.22"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q831V1"

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/transl_table=11

/product="Uridylate kinase"

/db_xref="COG:COG0528"

/translation="MEQPVFKRVVLKVSGESLSGQNGYGIDADTISSIAQQVKEVVAL
GVQVAIVCGGGNIWRGIAGSENGIDRATADYMGMLATVMNSLALQDALEQIEVPTRVQ
TSIAMQQIAEPYIRRRRAIRHLEKGRVVIFAAGTGNPFFSTDTTAALRAAEIEAEVILM
AKNKVDGVYSADPFKDSTAVKFDQLTYMDILNKDLGVMDSTASSLCKDNNIPLIVFAI
TEQGNIKRVVLGERIGTIVKGSVD"

CDS complement(3432723..3433373)

/gene="tsf"

/locus_tag="EFAGFIKM_02924"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P74070"

/codon_start=1

/transl_table=11

/product="Elongation factor Ts"

/translation="MAVNASAVKELRERTGAGMLDCKKALEEANGDVTKAAELLREKG
LSAAASKAGRAATEGVVESYIHAGGRIGVLVEVNCETDFVGKTDQFKDFVKDVAMQIA
AANPKFVTREEVPADELEKEKEILKAQALNEGKPEKIEKMVEGRIGKYEEYCLLEQ
TFVKDPDKTISQLLNEKISQIGENISIRRFVRYELGEGLEKKVDNFVEEVMSQVNK"

CDS complement(3433489..3434187)

/gene="rpsB"

/locus_tag="EFAGFIKM_02925"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P21464"

/codon_start=1

/transl_table=11

/product="30S ribosomal protein S2"

/db_xref="COG:COG0052"

/translation="MAVISMKQLLEAGVHFGHQTRRWNPKMMDRYIFTERNGIYIIDLQ
KTVKKVEEAYNFVKGIAGENGKILFVGTKKQAQDSVKEEAERAGQFYINQRWLGGTLT
NFQTIQKRIDRLKQLEAWEEDGTFAVLPKKEVILLRKEKDRLEKFLGGIKNMKGLPSA
LFIIDPRKERIAVAEARKLGIPIVGIVDTNCDPDEIDYVIPGNDDAIRAVKLLTGKMA
DAVIEANQGEETSA"

CDS complement(3434484..3435110)

/gene="mltG_2"

/locus_tag="EFAGFIKM_02926"

/EC_number="4.2.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_02065"

/codon_start=1

/transl_table=11

/product="Endolytic murein transglycosylase"

/translation="MDKRSLWIGLGSGMIIGAVLLQLATVGQNALSDSNLDPEQTANM
TKEQLETAAKSLDMKVGISEEELYTEAEWVEKKKQESSELQGETATPPETVTSTETPA
EPEKPQEPTASEGEGQKEITEPKTTEPVTSPNPKGATVSFKVRSGNSLAIVAANLKTA
GIVDDAQAFIKAGKAERINTKIQVGTYALEKGESFKSIIAKITKEPSN"

CDS complement(3435114..3435698)

/locus_tag="EFAGFIKM_02927"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSPWIIIVILGACAIAYACIMPRKNKAQEPGHQLVQEMESTLEH
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HSGNVSQSSEGLQAQALVKSVAEAAQQALEDQQTSEVESLPGRESIKDRYAELFN
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CDS complement(3435764..3436078)

/locus_tag="EFAGFIKM_02928"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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/product="hypothetical protein"
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SL"

CDS complement(3436131..3437570)
/locus_tag="EFAGFIKM_02929"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MESLKGGRIVTQRTALEQCLNIVLSDDKCTAYLEFSKEEEGFA
CTIDELEQFVANKGIKQGVSRERALLFVSNPETYLKDKYKIAKGVAPIQGTGFIKVL
VGMDDTNERRPLESEDGTVDYKEVTRLNNVRSGQIIAERIAPSDGIPGRAVTGEEIPY
RPGKEARFKVGKNVWINPDGSAMYAALDGLVTKTDGNKLNVPVYEVNGDVDYNNNGNI
DFVGTVVIRGNVLTGFKVKAAGDIRVVGVEGAELEAGGSIEITGGIIGYNKGLVQAG
HNVKCTFIQEGNVDAGEDVLVSQSIMHSNIRAGHGVICAGTKGLIVGGSIQAGQNVSA
RVVGNSMSTVTSIEVGVLPKLRNELNDLRKEVREQMDSLDTKKALTLLDQLAAAGQL
TPDKMSMRIKLNATQKSALRISEETKMRIFEIEKALEDTSNARVDILKMIYGGSKIVI
GRYTKFIKDPVSRISFYHHDGDITMVPYV"

CDS complement(3437603..3438391)
/gene="sigD"
/locus_tag="EFAGFIKM_02930"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P10726"
/codon_start=1
/transl_table=11
/product="RNA polymerase sigma-D factor"
/db_xref="COG:COG1191"
/translation="MNERKASHLNHSDLWEKWKEHGDLEAKKTLEKYLHIVNYVSGR
LAVGLPKNVPKDDLESNGVMGLIDALEKFDYERGLQFETYASWRVRGAILDGLRQGDW"

VPRSVREKAKRIEDAYQQLEQSYLRSVSDEEMSEYLDVSTKDFQHMLQEVAVMSLCSL
EDPIREEESETRLSLMVDEKAKNP DYKVNEFY LKEALVQGLDKLTVKERTVVSLLYE
DLSLSEIAEVMSLSPSRISQLHSKAILRLRGTLDKQKDLLMRKD"

CDS complement(3438407..3438850)

/locus_tag="EFAGFIKM_02931"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIGNYRINLGAGIVGFILTFVAYSSNVLM TSLIRGLIGFVAWF

VLAYGLRWGLG LLLNPQIEGNGYGYDSPA QDQ RGSQVDIKIEDDGQELNDLLKSGQN

ASSGDDLPPSETKAPTGFAPLDPPKLVRTKDPEELAQAVRH LTKD"

CDS complement(3438855..3439352)

/gene="cheD"

/locus_tag="EFAGFIKM_02932"

/EC_number="3.5.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40404"

/codon_start=1

/transl_table=11

/product="Chemoreceptor glutamine deamidase CheD"

/db_xref="COG:COG1871"

/translation="MIEDKSVVKVGMADLNIAHLPGVIRTTGLGSCVGLTMYD PHLKL

AGMAHVMLPTSEIAREGKLNTAKYADTALPELLEKMIKLGASHSRIVSKMAGGSQMFA

FAGAGDTMRIGPRNADSCREW LQKLNIPLLAEDTG GNYGRTIEMDCETGLLTIRSVQM

GVKEL"

CDS complement(3439345..3439971)

/gene="cheC"

/locus_tag="EFAGFIKM_02933"

/EC_number="3.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40403"

/codon_start=1
/transl_table=11
/product="CheY-P phosphatase CheC"
/db_xref="COG:COG1776"
/translation="MEMFNRFEVFQMDVLKEVGNIGAGNAATLSQLLNRPIDMGVPT
VQMLPFEEVAEKVGGDERIVVTVFLRVEGEAPGNLFFMMTPEAAKMLLNRLAGFDLKE
GLAFTDMEQSALSEIGNILAGSYLSSLADFTKLSMYPTVPGLAIDMAGAILSYGLLQF
GEMGDSALLIDTSFFEGEDQVEGQFFLIPDPPSFAKIFESLGVPLSHD"

CDS complement(3439976..3440437)

/gene="cheW_2"
/locus_tag="EFAGFIKM_02934"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39802"

/codon_start=1
/transl_table=11
/product="Chemotaxis protein CheW"
/db_xref="COG:COG0835"
/translation="MEEELKVIVFKLGSEEGVIEVDKVQTIERMMPITRVPKTLSFVK
GVINLRGVVIPVIDLRGRFSLPETEYTDQTRIVIVGVDDMQVGFIVDSANDVIDIKSS
AIDSPPEVVGKARYLRGVAKLEDSRLLIMLNLNEVLNKSEIVQLESVEG"

CDS complement(3440479..3442551)

/gene="cheA_2"
/locus_tag="EFAGFIKM_02935"
/EC_number="2.7.13.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P29072"
/codon_start=1
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/product="Chemotaxis protein CheA"
/db_xref="COG:COG0643"
/translation="MDMNQYLMSFIDESNDHLQSLNENMLQLEGNPEDLGIVQVIFRS
AHTLKGMAATMGFEDLASLTHKMENVLDLVRNEKLKMQDYIFDTMFKSLDALETMVQD"

ITEGGQGKADVSSIVASLQAIENGEMTNGNGPATETNKPANASISSAVELDEFQYSVL
DQSIAEGHRVFYVDVLVSEHSQKGVRAVMVFDMLERSGEVVKAYPSVQDIEQEKFER
SFSLYYITTKEAHELEEGIMSISEIESAKLIQLDQETLQQMANQVAATVEAPPAPTAV
AEVASPDKNSVPKEETTTAPAKTAAPKQAAAPSRTIRVDIERLDVLMNLFSELLIDRS
RLEQLASETGNNDLSDTVAHLSRVSTDQLQNIVLKLRMPVDTVFNRFPRMIRDLAKTL
DKKIDLVTGAETELDRTVIDEIGDPLVHLLRNAVDHGVESISERVAAGKPEMGTVNL
RAFHSGNHVFIEIEDDGKGIYRDKLLKTAIKRGVVTEEQGAKMSDDEVNQLLFAPGF
TADIISDISGRGVGLDVVKSITSLGGNVTIHSTPGKGTNFSVQLPLTLSIIAAMLVR
LGSEKYAVPLSSIVETAIVQREQVRNIHGNKMITFRESLIPYLSLSEVFSVPDFNDAD
EQETEIVIRKGDRLAAVAVEEFIGQSEIVLKSMGTYLPAIEGISGATILGDGQVALI
LDPNAFIK"

CDS complement(3442584..3444026)

/gene="cheB_9"

/locus_tag="EFAGFIKM_02936"

/EC_number="3.5.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00099"

/codon_start=1

/transl_table=11

/product="Protein-glutamate
methylesterase/protein-glutamine glutaminase"

/translation="MAAYQVLVVDDSAFMRKIVTDLIQADPEFKVTATASNGREAIQK
SLELKPDIITMDVEMPEMNGLDALKSIMKESFVPVIMLSGINEEQGMKETIMALEAGAF
DFIRKPSISHDQDIAQVGKALVERMRAAMNEIKRKADRELSMKNRDMRLRGAVAPPTQP
VQKELPARDRAEPVKKTIEPVETIQRSLRERTEAFQAKAKKPIEPLSPSKPGRVENKP
EPLPKAERNVGTAKAEKAVRSANPVQTPKEVRLPNAARVAADQIAATSASAKAKDVIKP
NPVPKGGGGLEGPFNKLVAIGCSTGGPRALKTLLEQLPADLPAPVIIVQHMPNPNFTRS
LAQRLNTFSPLHVVEAEEGMVLKKGTYIAPGGFHVKNKTADGKFIVKLTEDQPVNG
HRPSVDTMFESLLPFTSLQRHLVLLTGMGSDGARMMKRLYEAGVTSTFAENEETCVVY
GMPRSAVELQCVRHLLPLQEIASKLVQAVK"

CDS complement(3444059..3444946)

/gene="ylxH"

/locus_tag="EFAGFIKM_02937"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P40742"
/codon_start=1
/transl_table=11
/product="Flagellum site-determining protein YlxH"
/db_xref="COG:COG0455"
/translation="MKDQAAALRSMVSAPLELEGIERDIRSSKIITVASGKGGVGKSN
FTLNFALALQALGQKVLVFDADIGMANIDVLMGTSSSYNLYHLLYRQKSIREIIQLGA
SGLPYIAGGSGMKELFSLSDRDLEFFASQVEDIAQEMNYVIFDTGAGLSRENMKFIGA
ADECLIITTPEPTSITDAYALVKVMHGGQENATPFRMIVNRVEDEREAERVAEKIAGVA
RRFLQTDIPLLGYISEDAQVVKAVKRQMPYSLAYPNAKASKDIEKLALRYLAVPATPG
YGTLTGIRGFMNKWLKRTT"

CDS complement(3444943..3446295)

/gene="ftsY_1"
/locus_tag="EFAGFIKM_02938"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00920"
/codon_start=1
/transl_table=11
/product="Signal recognition particle receptor FtsY"
/translation="MRVKQYVVETMPEAMLQIRKDLGSDAVILSTKEIKVGGVMGMFR
KKRIEVVAAVDKREENKQTTKPVQNQFTPVPRSFVPEAYRQTARSFVAASDESVTNTA
DQSVQDQSAAAPSVFESRNIGSNIDSGSGSSSTDHKPRPQGADFSGSTTGPKPTGSDL
QQDKLMTLQDLKQMVTRLKQGTADPVPEELHTIRERLTEQDVWPEVWESWFDSIQ
AKWSEDGLKEQDVEQIVKLEVMHFLEQRIEEGILPTTRIVYVAGPTGVGKTTTIAKLA
AEQMFKKQRKVGFI TSDTYRISAVEQLR TYASILNVPLEV VQSPGDTQRAISRLENC D
LIFMDTAGRNYRNELLVSELQ SLLAPVENSETFLVMSMTSKSADMVQITEHFSKYGLD
KVIFTKMDETGSCGPLFNLLHRFPLKLAYVANGQNPDDLKPDADSLSKQLLGEWSQ
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CDS complement(3446292..3448325)

/gene="flhA"

/locus_tag="EFAGFIKM_02939"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P35620"
/codon_start=1
/transl_table=11
/product="Flagellar biosynthesis protein FlhA"
/db_xref="COG:COG1298"
/translation="MKIKDIAVLAGIIGIVLMMILPIPTWLLDLLLVVNISIALMILL
VAMNSKEALQFSIFPALLLITLFRALNISTTKLILGEGDAGAVVATFGSWIAGGQI
AIGFIVFLILVVVQFIVITKGSERVAEVAARFTLDAMPGKQMSIDADLNAGLINEQQA
RERRSKIEREADFYGAMDGASKFVKGDIAIASIIILLINLIGGFIIGMTVHGMAFADAM
STYSVLTIGDGLVSQIPALLISTAAGLIVTRASSEGNLADDITGQLFTYPILYIVAF
VIAMLGFFTPIHVITTLPLAGVLAYAAWRMQNNLNKQVAEEQLEEEQQIEEVRSPES
VINLLQVDPIEFEGYGLIPLADNQQGGDLLDRIIMIRRQCALELGLVVPVIRIRDNI
QLRPNEYVIKIKGNVVGGELELLNHYLAMSPGYDEESVTGIETTEPAFGLPALWIDEV
TKDRAELAGYTVVDPPSVVATHLTELIKHAHELLGRQETKALVDNLRENYSALVDEL
IPSLLSIGDVQKVLAKLLREKISIRDMVTIFETLADYGYTKDPDLTEYVRQSLSRQ
ITQQFSQKGETLRVITVGPGLEKKIAESVQQSDQGSYLALDPVSTQSVYQKLSEQVNR
LIQSGQQPVVLTSTIRMYLRQVIERTMQDIPVLSYSELEPNVEIQSIGVVNL"

CDS complement(3448351..3449433)

/gene="flhB"
/locus_tag="EFAGFIKM_02940"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P40727"
/codon_start=1
/transl_table=11
/product="Flagellar biosynthetic protein FlhB"
/db_xref="COG:COG1377"
/translation="MKLQLDLQLFSGEKTEKATPKKRQDTRKKGQVVKSAELSGASIL
LIVFLIMMVFSNFYKERIVRLFTDIFINRLSMDITGENVMALMMRYGIEVLLLIAPVL
LGALLVALIVNYMQVGFLDIGELKPKLEKLDPIKGFKNIFSLRSLVEFAKSILKMSI
IGYLVYSTIKGYQSDIASLSHFSLDAILHFAASITSLGIKIAVALMILAIFDYMYYQK

YDHEKKIRMSKQDIKDEYKKMEGDPLIKGKIRERQRRMAMQRRMMQEVNADVIITNPT
HFAVALKYEGSEMEAPQIIAKGQDYVALRIKEIAKENG VITMENKPLARALFQRAEIG
DAIPADLFQAVAEVLAYVYKLGRTK"

CDS complement(3449457..3450245)

/gene="fliR"

/locus_tag="EFAGFIKM_02941"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54702"

/codon_start=1

/transl_table=11

/product="Flagellar biosynthetic protein FliR"

/db_xref="COG:COG1684"

/translation="METLLQSFPVALLMFCRITSFFVTAPVFSARNVPASVKIGISAF

VTLSVYLIYGIDQTVPTDLSYVLLIIREILIGLLLGFVAYLLMTAVQTAGTFIDLQIG

FGMANVYDPMTGASAPLTGNLKYAFAMLLFTMNGHHYLLDAIVYSYRWVPLSNVFFL

RLADGSIAEFLIQTLGQSFMALFQMSAPIVVALFLTDVGLGFLAKTAPQFNVFAVGLP

LKLLVGLAILLLLVPFSFVFSQLFEAIFRSMEKLLGTIGQRPG"

CDS complement(3450256..3450525)

/gene="fliQ"

/locus_tag="EFAGFIKM_02942"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A1L6"

/codon_start=1

/transl_table=11

/product="Flagellar biosynthetic protein FliQ"

/db_xref="COG:COG1987"

/translation="MTSEFIIGLAGKAVYTSLLASAPMLILALVVGLAISIFQATTQI

QEQTLAFVPKIVAVLLSVLLFGPWILNILVDFTFNILDNLYRYIG"

CDS complement(3450551..3451306)

/gene="fliP"

/locus_tag="EFAGFIKM_02943"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54700"

/codon_start=1

/transl_table=11

/product="Flagellar biosynthetic protein FlIP"

/db_xref="COG:COG1338"

/translation="MKKKIWLACCLLGLISLASVTVAFSEPIPNIQIGNGDGGTPS

TSSLSIILLITVLSIAPAMLVLMSTFTRIVIVLGFIRTS LGTQQMPPNQVLVGLALFL

TLFIMSPTLSSINQVALQPYLQGE LQT EALEKAADPMKKFMFSHTREKDLLLFMKYN

QTEQPKTYQDIPITVMVPAYVISELKTAFQMGFMIFIPFLVIDIVVASTLMAMGMMML

PPVMISLPFKILLFVLVDGWYLVVKSLLLSFNT"

CDS complement(3451303..3451842)

/locus_tag="EFAGFIKM_02944"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMAQGDIPGGAGVGSNYYLQLVWVIVVLAVILALIVYLIRFLNK

RNQQMFRHGTIRT LGGVLGQNKSLQIMEIGGC VYLLGVGED IQLIDKVSDLEEAQRI

IDSFERDAAAQQGNLSPLIAKLTKRFRKEEPPREMELEDTSFHEMFESKLRQMPNRK

EKMEKLLDKDNTTDRSRDS"

CDS complement(3451851..3452216)

/gene="cheY_2"

/locus_tag="EFAGFIKM_02945"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P24072"

/codon_start=1

/transl_table=11

/product="Chemotaxis protein CheY"

/db_xref="COG:COG0784"

/translation="MANRILVVDDAAFM RMMIRDILSKNGYEVVG EAQDGSQAIEKFK

ELRPDLITMDITPEMDGIAALKEIKKIDANAKVIMCSAMGQQAMVIDAIQAGAKDFI

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CDS complement(3452245..3453519)
/locus_tag="EFAGFIKM_02946"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTSKDYLSQEEIDALLRQSESINSSEPAEKTVDNFLTELEQDAL
GEIGNITFGSAATALSTLLGLKVDITTPKVSIIISRTQFEEAFKPHVAVHVNYVDGFE
GINSLVIKKRDAQVIADLMLGGEGNPVDEELNEIHISAVQEAMNQMMGSSATSMSTIF
NRFVNISPPGIDILNLESGEGVSNLPADETLIQVSFRLIGDLIDSNLMQLLPVHFAK
SMVDMLIGGAQESTASAPVASTPEPAPAAVPATPPPVTEQPPVQHQQAPQAPQQAQD
YNGYGQAPMGMPQGMPPQQPYGMPPQQPYGAPQHYGGMPNRRNVNVQPVQFANLQNGAY
GQVDENNLNLLMDIPLKVTVELGRTQKQIKDILELSQGSIVELDKLAGEPVDILVNNK
LIAKGEVVVIDENFGVRVIDIVSQWDRIQKLQ"

CDS complement(3453509..3454507)
/gene="fliM"
/locus_tag="EFAGFIKM_02947"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P23453"
/codon_start=1
/transl_table=11
/product="Flagellar motor switch protein FliM"
/db_xref="COG:COG1868"
/translation="MVDVLSQNEIDALLAALSSGEMDAEELKKEDTQKKIRSYDFKRA
VRFSKDHIRSLTRIHENFARFLTTFSAQLRTFVQINVVQVEQLPYDEFIRSIPKMTI
LNIFEAEPLQGRMVMEVHPNVGYAMLDRLGSGTGAPTAKIASMTEIETIMERIFSRA
FESLQEAWKTVLDITPRMEALETNPQFMQIVSPNETIALISLSTKIGDTTGMINLCIP
HVVLEPIMSRLSTHQWVFSEKKTRAPEEYDALKERVNKAKLPIVAELGESRISIAEFL
GLSVGDVITLNKPVDEGLSIKVGDKLYMGSPGTIKDRVAVQIDKIVTEGVVEEFDE"

CDS complement(3454548..3455009)
/locus_tag="EFAGFIKM_02948"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKMMPWLATMLLAITLIVVVVFVFMQQQNGNKDDHTAAASEA
KKMTADEIVEVSSELGEIKTNLADTDHVIVVSFSFKLADV KAKEDFEKIKEIVVKPII
IQT LADTKSDELATAKGRILFNEKLTGLINEALPESNLSSTSFS SIVIATM"

CDS complement(3455009..3455230)

/gene="swrD"
/locus_tag="EFAGFIKM_02949"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:C0H412"

/codon_start=1
/transl_table=11
/product="Swarming motility protein SwrD"
/db_xref="COG:COG1582"
/translation="MISVTRLNGSPMWLNALMVEIVEETPD TYITLV TGKRLIVLEKA
ADVISKIKDYNREIGVQAATIKVQQTEES"

CDS complement(3455299..3456114)

/gene="flgG_1"
/locus_tag="EFAGFIKM_02950"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A1J3"

/codon_start=1
/transl_table=11
/product="Flagellar basal-body rod protein FlgG"
/db_xref="COG:COG4786"
/translation="MLKSMYSGVSGMRGFQTKLDVIGNNI ANVNTVGFKGS RVMFKDI
MSQTTSGVTAPGDATGGVNAKQIGLGVS VGSIDTLHLAGSPMTTNNPTDMRINGDGFF
LVRLSEDQEV PYLTRAGDFHVD AARNLLTSDGLFVLDN GGGNITIPDDVVSFTIGQDG
TINQTMADGTVEAGAQLGIGKVVNPEGLEKIGGNLYRMTANANPDGELEILTANDAEN
GTGSIITGQLEMSNVDLTGEFT EMIVAQRGFQANSRIITTSDEILQEVVNLKR"

CDS complement(3456196..3456579)

/locus_tag="EFAGFIKM_02951"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSDRITVGQLYAGPITPNMLQRPKTGEASAIPEKPFQVLEDNL
LKLSNHAAKRLEQRGIELKTEQMEQIGSALDKAAAKGAKESLILMQDMAFIVNVKNRT
VVTAMDSESMKDNVFTQIDSAVIIS"

CDS complement(3456576..3457133)

/locus_tag="EFAGFIKM_02952"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MANENVSMNNTWPNYSAANKATTSAATKELGKDQFLKILITQLQ
NQDPMQPMEDKEFIAQMAQFSSVEQLVNISTQLKTLNQSLGAVSGMIGMEVSWLSSNK
DDNGTLRQGIVDSIIVRDSVQYAKVGNDEIKLDEIIQVNYPKQAEESQTPVQNVQDET
PETNESQEVESAEETGDTEDSGKTI"

CDS complement(3457153..3458541)

/locus_tag="EFAGFIKM_02953"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSIVYQMASTASAKATGAGQTTGAQSKGSAAGASGEFLQTLAQS
LSGGNTEGDSSSATGSLTANPLVFSFATSEEGEAASITDILNSLFTDLDSLDEALEND
PALLAGLQTLIQQMYTQLSNPSGTNEEGSDESSNGAESVKTVPAIELSQHPAAVRFVL
QDMLTQLVAGMNDPESNVAKNAPEFKHLLQSLQSQLQEAGVDTTSNKGWTELKSILDT
LTAVKDQTAQVAPSTSLQTSKQDSVVPQVLAAVANSQTQVKAEATTSASNAGGEVE
HSTIITAGELSLRSSGTTAGKPAEPVMQTSQFAKEMTQFVFNKLDIVQQKGFSEATIS
LRPEHLGKLDVQITLQNGQLVARFMTEHTMAKDMLEQQMTQLRSSLQAQGIQVERLEV
TQNSSIGSQMYQDGGRQPGSNSQQQRRSREREEQSDDAIATAGIQEELRNWRSEQVEG

NELQRDTFSAEA"

CDS complement(3458581..3459522)

/locus_tag="EFAGFIKM_02954"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAVKDDSDMEKESGGGWEEKFLMISIPVFTVLLGVLLTLFNVD
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LKAAQEATTTEAKKATDLQKKLDDAEKAAETATAATPETESDYQKQIKDLAKMYADMS
PSKAAPILQNMNEEMVLLLNAMQSSARTKVLEKMDPKTAADVMTMMKDAKPSGDLAL
DALQSRLQKETAATSTASTTTSKNLQKLSQTFASMSASSGAKLLLETYKLSPKTL
TILNSVDDATRSQLLNMSSSEDSVETAKILNRLMGNK"

CDS complement(3459566..3460018)

/locus_tag="EFAGFIKM_02955"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKFRYHFQKVVDLKSNEKTQAEWMLSTAIGKLQTEEEHLIQLLN
DRSNLIGIIQSATENTASVNSLQEMQRYVHHLDECISRKNSDVKHAQVNVQRNQTFNL
GKMVDEKVLGARDKAKNKFQQEMLLREQNDLDEMATVRFAAKAGRAN"

CDS complement(3460030..3461349)

/gene="yycN"

/locus_tag="EFAGFIKM_02956"

/EC_number="7.1.2.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40290"

/codon_start=1

/transl_table=11

/product="putative ATP synthase YycN"

/translation="MKVLSSQRYMEHLRQFDPVRINGKVTQVIGLMVESEGPDAISGD"

VCYIYPGKSAKPLQAEVVGFRDNKVLLMPLGELQSIGPGCDVVGTKPLGVQVGSELL
GKVL DGLGQPLDGSLLPSRMPMYSTSNTPVNPMDRPRVLETMGVGVRAIDGLLTVGKG
QRVGIFAGSGVGKSTLMGMIARNTAADVNVIALVGERGREVRDFIERDLGPEGLERSV
VIVATSDQPALIRIKGAVIATTIAEYFRDRGMNVMLMDSVTRYAMAQREVGLAVGEP
PAMRGYTPSVFASLPKLLERAGTGPTGSITAFYTVLVDGDDMNEPIADAVRGILDGHI
VLNRSIANKGHFPAIDVLASISRVMKDIAPEEQLEAVNNMKRLMAVYKESEDLINIGA
YQRGSNAAIDESIDQIDSIWNFTKQKVDEKVTLSEVQERLILEFARR"

CDS complement(3461336..3462199)

/locus_tag="EFAGFIKM_02957"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSNLIKSFQYVPVDDRKKLENHHHYGDAAESETELYVDSAEGSE
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QDEHLTEALRSQGFQQGFEEGKVQAELDLQVQIEKMMNEAQEVLKEAYVAKDQIIQEA
EPFLVELACGIAEKVIDKQLTIEPDHTLELIRQSLSRKREQGLITLCVAPDQFTFVQA
AREELSLSIDSQAELQILPDSTVKDKGCVIRSSFSGSVDARIDTQLAEIKKELVRIALE
DEERKNQHEGS"

CDS complement(3462192..3463208)

/gene="fliG"

/locus_tag="EFAGFIKM_02958"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9WY63"

/codon_start=1

/transl_table=11

/product="Flagellar motor switch protein FliG"

/db_xref="COG:COG1536"

/translation="MAKASSQGLTGKQKAAILLITLGPEVSAQIFKHLRDEEIEQLTL
EIANVRKVDSSSEKDMIMAEFHQICLAQEYISQGGINYAREILEKALGSSKALEVINRL
TATLQVRPFDFAKADPNQILNFIQNESPQTIALVLSYLQFEQAAAILSSLPQEKQAD
VARRVAVMDSTSPEVISQVERVLEQKLSSTVTQDYNAGGIESIVQILNGVDRGTERT

ILDSLEIQDPELAEEIKKRMFVFEDIVNVDDRSIQRIIRDIDNADLQLALKVASEEVR
DAVFRNMSKRMSETFKEEMEFMGPVRLRDVEEAQTRIVGTIRRLEEAGEIIIRAGGGD
DIIV"

CDS complement(3463220..3464803)
/locus_tag="EFAGFIKM_02959"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNERIAQYRDKASLYWNSFSKKQKVLFISTFLILAAVVLTMQ
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GIIQNGSLGYKSFEESSSPIGMDKEFDVKYNNAINGEVEQLLQRMQGIQDAKVLVNM
PKDNIFAGLEEQDKASASVALQFKPGYHPNQAAVDGYFNLVKTAPNLPVENITITNT
DEAELIPTARGGSGGLSSEVQENMALQKKFENDVRNNVKQFLSQIVGEDKVNVLVASK
LNFDKETRKENLVTPVDVDNMKGIEISVQEIQKSYTGASNPTGGVAGTGQEEVPGYPS
SDATGNSTSEESSSTINYDVNRIAKDIISSPYTKDLTINVAVEPPNGETELQGPVQD
AIENILVNIVRASLADSGTVISDADLTKKVSVMSQGFQSASADNTGFQLSSTMMWGGG
ALIAALIAAVVILLVRRRRRKQNEVEEEEIPLPIATEFPSITLDSVTNESQVRKQLESL
AKKKPDEFVNLLRTWLADE"

CDS complement(3464941..3465252)
/gene="fliE"
/locus_tag="EFAGFIKM_02960"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00724"
/codon_start=1
/transl_table=11
/product="Flagellar hook-basal body complex protein FliE"
/translation="MIQNNMFSTQGIQPLQMKSATSKPSTPAETIQSFGTYLQNALG
SVAAQEAQSHEMSNOFLVGKANVDQVMIASEQALLSLQLTTQVRNKVVEAYQEV MRTQ
L"

CDS complement(3465311..3465760)
/gene="flgC"

/locus_tag="EFAGFIKM_02961"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A1I7"
/codon_start=1
/transl_table=11
/product="Flagellar basal-body rod protein FlgC"
/db_xref="COG:COG1558"
/translation="MNISNSFSISSSALTAQRLRMDVISSNIANAETTRASVSNGEAV
PYKRKMMVLEPNKTSFGTMLQNQMRGSGSGDGVRVTEIREDQSPLKPVYDPSHPDANA
EGYVFMPNVDIAKEMVDMISASRSYEANVTALNSTKAMISKALEIGR"

CDS complement(3465767..3466174)

/gene="flgB_1"
/locus_tag="EFAGFIKM_02962"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P24500"
/codon_start=1
/transl_table=11
/product="Flagellar basal body rod protein FlgB"
/db_xref="COG:COG1815"
/translation="MNLLNDISFKRLQGALDASNIRQRTIADNIANADTPYFKRSDVS
FEEMLQGQMNGDMPVLKGKVTDAHFVIGPSSSVPTPVVNMDQSTSMNNNENNVDIDR
EMSLLAENQLRYNAYIQVNEQIKIMRVGVEGR"

CDS complement(3467156..3468556)

/gene="clpY"
/locus_tag="EFAGFIKM_02963"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39778"
/codon_start=1
/transl_table=11
/product="ATP-dependent protease ATPase subunit ClpY"
/db_xref="COG:COG1220"
/translation="MNTQALTPRQIVAELDKYIVGQKKAKKSVAAVALRNRYRRSLLPE"

HTQDDIVPKNILMIGPTGVGKTEIARRLAKLVGAPFVKVEATKFTEVGYVGRDVESMV
RDLIETSLRMVVKLERTEKVKDKAEAAANERIVHILAPSQSKSKSQRNPFEMIFGNNGN
NVQEEDPEPDTGVAERRRKIKFDLLSGKLEDDIIEIDVEDTAPNMMDMFAGQGNDQM
GMNMQEMFGSLLPRRTKKRKLAIKEARKVLIQEEAGKLIDMDDVTQESIRRAEQTGII
FIDEIDKVASQGRGSGPDVSREGVQRDILPIVEGSTVMTKYGPVKTDYILFMAAGAFH
VAKPSDLIPELQGRFPIRVELSSLTLEEFVSILTEPQNALTKQYVDLLRTENIEIEFS
DEAIREIAKLAESVNQNTENIGARRLHTILEKLLEDLSFEAPELTLERMVITPEYVRE
KLNDIALDRDLSQYIL"

CDS complement(3468673..3469215)

/gene="hslV"

/locus_tag="EFAGFIKM_02964"

/EC_number="3.4.25.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81WK5"

/codon_start=1

/transl_table=11

/product="ATP-dependent protease subunit HslV"

/db_xref="COG:COG5405"

/translation="MDMSFHATTICAVRHNGKAAIAGDGQVTMGQSVVMKNTAKKVRR
LYRGQVVAGFAGSVADAITLFEKFEGKLEHHGNLQRAAVELAKDWRQDRILRKLEAL
LIVMDKSGMILLISGGGEIIEPDDDVIAIGSGGNFALSAARALKRHAVNLEAKDIARES
LQIASELCVYTNNNIIVEEL"

CDS complement(3469242..3470579)

/gene="trmFO"

/locus_tag="EFAGFIKM_02965"

/EC_number="2.1.1.74"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39815"

/codon_start=1

/transl_table=11

/product="Methylenetetrahydrofolate--tRNA-(uracil-5)-
methyltransferase TrmFO"

/db_xref="COG:COG1206"
/translation="MTNEQQVTVIGAGLAGTEAAWQIASRGVRVKLYEMRPVVKTPAH
HTDKFAELVCSNSLRANGLTNAVGV LKEEMRMLNSLVLSAADKHAVPAGGALAVDRDG
FSGEITSTLYQHPLIEVVNEELTSLPEDGIVVVATGPLTSPALSEQIKALMGEEYFYF
YDAAAPIIEKDSIDMNKVYLASRYDKGEAAYLNCPMTEEEFDVFYEALITAEVAQLKE
FEKEIYFEGCMPIEVMMKRGKQTALFGPMKPVGLVNPHTGELPHAVVQLRQDNAAGTL
YNLVGFQTHLKWGEQKRVFSLIPGLENAEFVRYGVMHRNTFINSPKLLLPTYQFKERP
NLFFAGQMTGVEGYVESAAAGLIAGMNAAKAALGQELVVLPAETTLGSMAYITTADF
KHFQPMNANFGLLPKLETIRNKKEKNEALAQRALDGITSFAAAEGLTVPERV"

CDS complement(3470637..3472736)

/gene="topA"
/locus_tag="EFAGFIKM_02966"
/EC_number="5.6.2.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7A5Y5"
/codon_start=1
/transl_table=11
/product="DNA topoisomerase 1"

/translation="MADALVIVESPSKAKTIGKYLGSKFIVKASMGHIRDLPKSQIGV
EVENDFNPKYITIRGKGSILKELKDARKKVKKVYLAADPDREGEAIAWHLAHALELDD
TADCRVVFNEITKQAVKDAFKTPRKINMDLVNAQQARRILDRLVGYKISPLLWKKVKK
GLSAGRVQSVAVKIILDRENEIDDFEPEEYWSITAKLTADGNPF EAKFHKLN GAKTEL
GSEAEVQAILKQIEGADFTIKEVKEKERSRNPSAPFTTSSLQQEAARKLNFRASKTMS
VAQQLYEGVDLKGEGTVGLITYMRTDSTRIAASAEQEEAKEYIVGKYGEFPAPETPRNY
SKKAANAQDAHEAIRPTSILRDPDSIKSFM SRDQFRLYKLVWERFVASQMSSAILDTL
SVDIAAGDTIFRAAGSKVRFQGF MKVYVEGNDGTTDEDRLLPPLKSGDVLEKQEIEP
KQHFTQPPPRYTEARLVKTLEELGIGRPSTYAPTLETIQKRGYVAIEEKKFMPTELGE
LVIEQMEEFFPEILNVEFTANMEGDL DHVEEGSEDWVKVLA EFYESFEKRLEFAEEEM
KEIEIEDEV SDEICEKCGKPLVYKLGRFGKFLACSGFPDCRNTKPIIKDIGVTC PKCK
EGHVVERRSKKGRIFYGCDKYPECDFVSWDRPSAKPCPSCGSLMIEKRNKKGARLQCT
SCDHQEPVDEPDDESAD"

CDS complement(3472853..3473983)

/locus_tag="EFAGFIKM_02967"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEERWILFGLHEMEGIGKKTISKLILGQHELPDLLNYGESDWVA
AGLRKDQAARLASQFTIDWIESKREHVYNQGIEVITYLDQNYPILMKETVQPPWVMYA
RGDVSLHNSSIAMVGTMRMPTVYGRKVGEKLAEQLCNAGLTIVSGLARGIDSVCHEAV
LRAKGKTIAVFGTGIDNIYPPESTLAERITETGLLLSEYPPGTRARQGLFPERNRH
AGLTGLTLVVEADIRSGSLITADAALEAGRDVFAVPGPITSPKSRGAHNLRQGAQLV
TCAADVLEEYRLGLPNAEQLPYNRGRSTETSDPSGRGIFAEVKLSPDEQRVIYLLLEQG
EQSLDQLVELLGWDFGHLHSLVLLSLIKKQISQLPGTKYARV"

CDS complement(3474228..3475157)

/gene="sucD"
/locus_tag="EFAGFIKM_02968"
/EC_number="6.2.1.5"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P80865"
/codon_start=1
/transl_table=11
/product="Succinate--CoA ligase [ADP-forming] subunit
alpha"
/db_xref="COG:COG0074"
/translation="MSILIDKNTKVITQGIGTGSTGMFHTKGALDYGTQMVGGVTPGKG
GTNVDITLEDGTVASLPVFNTVQEAKEATGATASVIYVPPAFAADSIMEAVDAELDLV
ICITEGIPVLDMIKVDRFMEGKNTVLIGPNC PGVITPGECKIGIMPGYIHMAGHVGWV
SRSGTLTYEAVHQLTTRGIGQSSAVGIGGDPVKGSEFIDILKRFNEDPQTHAVIMIGE
IGGTAEEDAADWVRENMTKPVVGFIGGVTAPPGKRMGHAGAIISGGKGTAKEKIAKLE
SCGIKVAPTPAEMGSTLVSVLEERGILNLCCTH"

CDS complement(3475221..3476381)

/gene="sucC"
/locus_tag="EFAGFIKM_02969"

/EC_number="6.2.1.5"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P80886"
/codon_start=1
/transl_table=11
/product="Succinate--CoA ligase [ADP-forming] subunit
beta"
/db_xref="COG:COG0045"
/translation="MNIHEYQGKEVLKQYGVTVPNGKVAYTVDEAVAAAEALGSPVTV
VKAQIHAGGRGKAGGVKVAKSTDEVAYASEILGKVLVTHQTGPEGKEVKRLLEECC
DIRKEYYGVVVDRAVGRVMMASEEGGTEIEEVAEATPEKIFKEIIDPAIGLQVFQA
RKLAYSIPNELVNKAVKFMALYAFVEKDCSIAEINPLVVTGDGNVIALDAKLN
DSNALFRHKDILELRDLDEEDEKEIEASKYDLSYIALDGNIGCMVNGAGLAMATMDII
KYYGGDPANFLDVGGGATTEKVTEAFKIILSDAKVAGIFVNIFGGIMRCDVIANGWE
AAKQLGLTKPLVVRLEGTNVELGKRILGESGLNIVPADSMADGAQKIVALVK"

CDS complement(3476625..3477080)

/gene="ohrR"
/locus_tag="EFAGFIKM_02970"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34777"
/codon_start=1
/transl_table=11
/product="Organic hydroperoxide resistance transcriptional
regulator"
/translation="MQTDSLKLDNQLCFAIYACSREITKMYQPYLEVLGVTYSQYLV
MVLWEREECTVKEIGEALYLDSTLTPLLRKLSAGLINRERSAQDERKVLITLTD
RELNRKALSIPESIQGDACLNSTEFETLLGQFKGLLEKVHETNTNAKK"

CDS 3477559..3479169

/gene="comM"
/locus_tag="EFAGFIKM_02971"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P45049"

/codon_start=1
/transl_table=11
/product="Competence protein ComM"
/db_xref="COG:COG0606"
/translation="MYGKLHSACLYGIDGVLEIVETDLSNGLPQTSIIGLPDSAIREA
VERVRAAIKNCGYQYPLQRITINLAPADLRKEGSSFDLAIAIGLLMTSGQLVLPPQER
TLVVGELALDGSIRSVPGILSMVDLAKRQGFTSVLLPLDNVEEASLIRGIQVFGIRHL
QDIAPENLDQSGSSVGVPNKANTGPVVLKNYAHLAAPITDKTHKMADRKPRQTPLFAD
DYSVDLGQHHVKRALMIAAAGMHNILLVGPPGTGKTMLIKRLPSILPPLSEDEALEVT
KVLSAAGKLKEAPQGLIADRPFRSPHHTISTGLIGGGGIPKPGEVSLAHRGILFLDE
LPEFQRQVLEVL RQPLEDRVTISRARAFTFPAQFMLACSMNPCPCGYLSAHSEEQR
CICSPARVAAYRAKISGPLLDRLDLQVEVPPPGEWKSAASPSSEEMQAKVIHAHQIQ
ATRYAKSSVRWNSQLSGTLLRRTIHL PQEAEQLLEQTLQTLNLSMRAHDRIIKMAQTI
ADLDHEGEIVTAHVAEAIQYRQLDLNLF"

CDS complement(3479342..3479893)

/gene="ydjA_2"
/locus_tag="EFAGFIKM_02972"
/EC_number="1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0ACY1"
/codon_start=1

/transl_table=11
/product="Putative NAD(P)H nitroreductase YdjA"
/db_xref="COG:COG0778"
/translation="MSKATKTINEVRNAIQNRRTVKKFKKEAVPTQQIIELLDTAVWA
PNHKLREPWRFLFLTGNRKKLAEDAEMGEDNKFSPNIMQVPSVMLVVLEEDPRQN
IWDEDFAAVSALVQNFM LAAWSEDIGTFWVTKPFLYAPKFRKPLGIEAGEKIVGMIYM
GYPDVIPSAKERTPAKDKLTLFE"

CDS complement(3480179..3481357)

/locus_tag="EFAGFIKM_02973"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MQTSIKWIIRLSTLSLCFILFGIMYSGVSYADPSTQASVSGKVT
DLEGFPIQDATIKYSLRYQGEETESVKTDGNGSYSILESVDYTEISFIIIEAGYVT
DRHRNTYYLSEGEQILVNFELYEPSTIVGSVTDQTKPILDALVKVTGALDRPVKTDQ
QGRYAVTGLDYDYNPNIAIWVDSADYMLYEQDRLNVQAGKTLIEDVVLTEAAHVGRKV
VDEAGNPVSGAKVNAGGSATTTTDAQGNYFIKRVPTGTRTITGEAAGYLKSTQNVTLV
QGDHNTFNIVLKKDADITPPVTKYRLVPITDVTNGKVYIKGFTFRLQATDEVKGSVK
ITQYRINGGAWNTYEGPVKFYAPDVKVVEYYSTDVTGNQEKYNKMDFVNGTFEGAGSY
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CDS complement(3481418..3481579)

/locus_tag="EFAGFIKM_02974"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKELQNTSNNTVKQVWECPRMEVLDISETMNGGQGIWQYVWDGE
FWKLELMVS"

CDS complement(3481901..3482299)

/locus_tag="EFAGFIKM_02975"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVERRLGQEPGLKLTRQQKRLGEEAACQWLREHDYRIIRQNWR
CRSGEIDIISCEGLIVFEVRSRSGAAQYGTPQESVDMRKMQQVRSTASVYLQMTGE
TELQIRFDVIAVMLDQAGEIVSVNHIVNAF"

CDS complement(3482293..3482604)

/locus_tag="EFAGFIKM_02976"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MKDESSQPDLLSKKAVALKYVPGESEAPVVVAKGRGKVAEAILD
KARENGVAVQEDAALVEVLSKLDLDEQIPAELYQLVAEVLTYVYRADRMASGREENES
W"

CDS complement(3482601..3484655)

/locus_tag="EFAGFIKM_02977"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNIGSMIKGLMGDSKPGNAKPLELKEGQVVRGSVSVSDDGGEA
VLQIQGVQVRAKLETPLRPGETTLLQVQPPGENGITVMKPMGTGLAELPQASLNNLLK
DVGLPDTKGNRELLAMQRSGLPLTKDNVAMVQNMMTAKPAQVPVEEWVQATGIAFQR
GLPVTAETVKGLHQTTFGPPLHQLLSGLADQLETMLTQTTGKPLLPGEQSATLKPAVV
AGAPVLPNASQTEEGLAALGNRQVTGTGTPALSTQQGQAALAGSISMTDGGADDAGT
AVKGNVQTGGGTGNAEAGAKAIASNVETAGKGGAGIPSGTGIPGESPSGADAGQVGSR
PGTPGAAAESVAGRVIAGQPEAGAAVRIDGRAETPAAAGTPSAAAWAPAAPTAAQLAP
KLLALLDALRSASTAAPAQPGAAAQAAPASQGGQAAAAAGGVPQPLPAGADAPPAGGN
AAPAGAAAVHAPVTHEGDPWVGRVLKLLGAEHEQQAVHGAAAQPRVGDAASPANADT
LKGLLLQLASSEGAPAALKDAAGQAVQYLTGQQLLLTDRSATFAQMHWFIPTGPDG
EETASVQIQSRRGSRGELDASNCRLWFDLDMKSLGPTLVDVHVNNIVSLRVLNDREG
MGPLLESGREVIHQALDKLGYQLLTFKAEPWPVGQEPGAERKTRASDYSPEYKGVDL
KV"

CDS complement(3484686..3485501)

/gene="rnhB"
/locus_tag="EFAGFIKM_02978"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00052_B"
/codon_start=1
/transl_table=11
/product="Ribonuclease HII"
/translation="MLRETGCTEQKTEYLRLYYKKVSDTHAEKAWVEEMSIFENNE"

EIGNLLDTPIGPKKKKEASEPRDLLLYEREYWDSGFERIAGIDEVGRGCLFGDVVAA
AVILPKDLILEGVNDSKKLTEKKRDALYDIIMEKALAVGIGYADAETIDRLNIKQAAR
LAMKRAVEALGETPDYMLVDAEKVDVNPQLSIIKGDANSQSIAAASIIAKVTRDRLC
KEEWDTLYPEYGLSIHKGATKVHREQIMALGATPMHRRSFLGNLLGEQQSLF"

CDS complement(3485851..3486714)

/gene="rbgA"

/locus_tag="EFAGFIKM_02979"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31743"

/codon_start=1

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/product="Ribosome biogenesis GTPase A"

/db_xref="COG:COG1161"

/translation="MTIQWFPGHMTRARRQIQDKLKLIDVIELLDARLPVSSRNPMI

DEILLDKPRMILLNKSDLADAKVTQEWIEYFKKEGITAFPVDASTGTNVKDIPVQAKL

LLKEKIDRQIAKGINPRAVRGLIVGIPNVGKSTLINRLAGRSIALTGDRPGVTKGQQW

IKVGKEMELLDTPGILWPKFEDQNVGYRLAVTGAIKEEILNAEDIAFFGISYLMRYYW

DALEERYGLQEFSKDADDSDSVIAIMEQVGRIRGCVVSGGRIDLEKASRAFLRELRA

KMGRFSMEAPY"

CDS complement(3486745..3487365)

/gene="sipT"

/locus_tag="EFAGFIKM_02980"

/EC_number="3.4.21.89"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P71013"

/codon_start=1

/transl_table=11

/product="Signal peptidase I T"

/db_xref="COG:COG0681"

/translation="MEQEVQQDRGNPAEEKDSRSKKAKNEIVEWLKAIVIALVLVILI

RWLLFKPFVVDGSPMQPNFETGERVIVNEILYDIREPKRGEVIVFHVPSGRDFIKRV

IAVEGDTVEVQDDTVMVNGKKVDETYIQGAIDAAEANGGTYNVKDFPNEQFPDGKVPA

GHVFVMGDNRPNSTDSRMIGYVSLKDIIGRADVIFWPIGEIKWINH"

CDS complement(3487723..3488064)

/gene="rplS"

/locus_tag="EFAGFIKM_02981"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31742"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L19"

/db_xref="COG:COG0335"

/translation="MNIVQAITQEQLRKDLPSFRPGDTLKVHVKVIEGTRERIQLFEG

VVIKRRGGGISEFTVRKISYGVGVERAFPLHSPKIDRIEVARRGKVRRAKLYYLREL

RGKAARIKEIR"

CDS 3488422..3489387

/locus_tag="EFAGFIKM_02982"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKYWKKITLALLAMLTCITLYSYAVTHPTNALSHKACTSWDIV

KRKAFELSHTDFSNQSALDRSTFRIEQGTATEVPVLMYHYIEPKLNNHETDNKSIINL

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KYNFHASLFVIGSKIQDQPSVFEPAINSFISKPEMQAATDVFEFNSHTYNLHHKGFM

CGNSVPVGLDTSLLDDDIQMKETGIDTPYLAYPFGYTSTQMIYKLQQHGYRMAFTVK

SGFVHPGDHPMLPRLTVTTGTDLATLLQPESSPQNELPAENDQ"

CDS complement(3489391..3490638)

/locus_tag="EFAGFIKM_02983"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNHQPYEITRLDISEAGERCKMLLGDNLNGDGRLEMLLVQADGGI

DDRYVPHQVCCLTAFDLEGTLWQVGTDPDAGGPGSDYPAQIADWDGDGNNEVLCVM
DKQFLVLDGRTGEIKETRDLPGDEAHDCIILANLTGNQQRMDIILKDRYKTLWALDHD
FNLLWKHEGNPGHFPWLYDIDGDGKDEVMAGYDMLDHDGTLLWSCQNLDDHADCIWFG
DVDGNGQVEVVIGGSVTVMMDRYGNEKWRYEDSIESQHIALGHFCTGMEGLQIAGLDR
IVRGDEHGKDGFMFLDSAGKEIWKENRTTRGWLTIIIEPVCNWDEGGLDYILAYRRGGD
VLPSLVDGDMKTVTEFPKEGYAVHADLVQTGKEQIIYDAEEAVIYSSSPMTLSLTDA
KRAKPQLKRLYSSTLYPGGEVKI"

CDS complement(3490793..3491167)

/locus_tag="EFAGFIKM_02984"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTYNIIGLDHIQLAAPEFCEAEARLFFNNVLGWTEIPKPEILRK

RGGVWFECGRHQVHIGVQKDFIPARKAHPAFHVQHLDQLRDLLIHNQIHIVDDEARAD

EGVKRFYINDPFGNRLEFLEWV"

CDS complement(3491366..3492133)

/gene="trmD"

/locus_tag="EFAGFIKM_02985"

/EC_number="2.1.1.228"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q6GHJ5"

/codon_start=1

/transl_table=11

/product="tRNA (guanine-N(1)-)-methyltransferase"

/translation="MKVDVLTLPPEMFDGVFGASILGKAQTKGLVSLGATNFRNYATN

KHNTVDDAPYGGGGGMVLKPDPIFAAVEDVLEQRGEAAASKAPRIILMCPQGETFTQ

KKAEELVQEDHLIFICGHYEGYDERIREFLVTDELSIGDYVLTGGELPAMVAIDSIVR

LIPGVLGNETSAVTDSFSTGLLEYPHYTRPPEFRGMKVPDMLLSGHHLNIEAWRREQS

LLRTLERRPEMLETADLTDKERIWLKKIHSNRKHSTE"

CDS complement(3492135..3492647)

/gene="rimM"

/locus_tag="EFAGFIKM_02986"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P66656"

/codon_start=1

/transl_table=11

/product="Ribosome maturation factor RimM"

/translation="MADFMNVGKIVNTHGIRGEVRIMPLTDFPEVRFAKNAELFFFTP
DNHPVVVNVESARLHKNMYYLRLKEYGNINEVEKFKGGMAKVLKENLAELEEGEYYFH
QIVGCSVITEEGETLGTISEILTPGANDVWVVKTPAGKEVLIPVIDDVLDVDIEQQQ
VKIHLMEGLL"

CDS complement(3492949..3493179)

/locus_tag="EFAGFIKM_02987"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEELVSIIAKALVDHPEDVTVRTVEKDRLVYELTVHPDDVGKV
IGKQGRIAKSLRTVVTSAAVKMDKRVTVDIIS"

CDS complement(3493203..3493475)

/gene="rpsP"

/locus_tag="EFAGFIKM_02988"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P21474"

/codon_start=1

/transl_table=11

/product="30S ribosomal protein S16"

/db_xref="COG:COG0228"

/translation="MAVRIRLKRMGAAHKAPFYRVVSDSRSPRDGRFIEEIGYYNPVE
QPAVVKIDEDKALAWLQNGAQASDVRNLLSKAGVMKKFHESKLSK"

CDS complement(3493529..3494908)

/gene="ffh"

/locus_tag="EFAGFIKM_02989"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37105"

/codon_start=1

/transl_table=11

/product="Signal recognition particle protein"

/db_xref="COG:COG0541"

/translation="MAFEGLTTRLQNVFSKLRGKGKVSDEDVAEAMREVRLLALLEADV
NFKVVKEFIAKVKEKAVGKEVMESFTPGMVIIDIVNKELTDLMGGSQAKLAKANKPPT
VLMMVGLQGAGKTTTSGKLAKMLKQKNSRPLLAVAGDIYRPAAIKQLQVLGEQIKAPVF
TLGDQTSPVEIARQGLQHAKDNGNDYVIIDTAGRLHVDEELMEELRQIHSVVPDEVL
LVVDSMTGQDAVNVAEHFNQQLNLTGVVLTCLDGDTRGGAALSVKAVTGCPKIFASLG
EKLEDALEPFHPERMASRILGMDMLSLIEKAQLNIDTDKAKEMERKMRNAEFTFEDFL
EQMDQVKKLGPIQIMDMIPGMGKMKQAKDLKVDDKQMGRIEIVYSMTTEEKRNPD
INHSRRKRIATGSGTSLAEVNRLIKQFDEMRRMMKQFSDMMGPKGGGKNKAMKQLKGM
GKGMKFPFR"

CDS complement(3494971..3495321)

/locus_tag="EFAGFIKM_02990"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSQENRLEKTNRINLLFAFYELLLTEKQQTFLKYFHHDFSLGE
IAAEFEISRQAVYEHKRAEQVLENYESKLGLEKHERRNRNLEDLKNALERAGVSID
NNKQIHDIQAQLSE"

CDS complement(3495584..3496231)

/locus_tag="EFAGFIKM_02991"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P67153"

/note="UPF0073 inner membrane protein YqfA"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MANTYTYSRREEVANAVTHGIGAALSVAALVILIVFSSMKGTAW
HVVSFTIYGISM LLLYTSSTLVHAWKDGKVKDLFEIFDHSSIYLFIAGSYTPLLFIAV
RGTLGWTLFGI IWGIALFGVIFKAFFTKKFLFMSTIFYIAMGWLIVIAWQPLMAAIPT
GGIVLLVAGGLMYTLGTLFYVWRGFPYHHAIWHLFVLAGSILHFFMVLLYLTPLR"

CDS complement(3496378..3497391)

/gene="ftsY_2"

/locus_tag="EFAGFIKM_02992"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P51835"

/codon_start=1

/transl_table=11

/product="Signal recognition particle receptor FtsY"

/db_xref="COG:COG0552"

/translation="MSFFKKLRDSIASKTESVTKQFKDGLEKTRKGLVEKVSDLVIRR
KKIDEEFYEELEEILIGADVGVNTVMNLIEDLRVEVKKRKIEDAAELQPV LSEKLTGL
LRGEQNNELKMNP DGITVILFVG VNGVGKTTTIGKLAHRFKQQGKKVIMAAGDTFRAG
AIEQLEVWGQRAGVDVIKQQSGSDPAAVMYDAVQAAKQRGADVLLCDTAGRLQNKSNL
MDELNKIYRVIQREIPDAPHEVLMVLDATTGQNALNQAKLFGEKSGVTGLVLT KLDGT
AKGGIVVAIRQELDLPVKLVGLGEKIDDLQPF DSEQFVHALFAGLIQE QPAESAEEEE
ANS"

CDS complement(3497500..3501069)

/gene="smc_1"

/locus_tag="EFAGFIKM_02993"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P51834"

/codon_start=1

/transl_table=11

/product="Chromosome partition protein Smc"

/db_xref="COG:COG1196"

/translation="MFLKRIELGGFKSFADKTEMEFVRGITAVVGPNGSGKSNISDGI
RWVLGEQSAKSLRGGMEDIIFAGSDARKAVNFGEVSLTDNEDHALALDFGEVTVTR
RVHRSGDSEYFINKQSCRLKDITELFMDTGIGKEAYSIIQGRIEEILSTRSEDRRGI

FEEASGIVKYKSRKRDATRKLDETEQNLLRIHDLVTELEDQIGPLKEQSERAIHYKEL
RSQLKSQEISMYVYQIEQIHASWSKANERLQSLKQEEVGLAAIVSTHDAKLENDRNAL
RILETETEQLQAALLQFSEATEKSEGLGELLKERSHHLQTNQEQLKVTLAASEERHRE
RETELLALREKFGKLEHELNDVRNQLSQEEAKLIGVTGGISQQQEESLKGNLLELMNQ
MAQTRNEIRYVDQQKETLERRMNRAAEESGKWEDQKETLESRKADIEKKVVRGKEIS
DLRGGYITESERLQSLQKLEESRGTVRKWEQKREAQVSRRDTMKEMQDDFDGFMGLV
KEVLKASRKGTLSGVHGAVAEVLKVPEKIELAVETAMGASLQHVV MENESVSRQAI AF
LKQRQLGRATFLPLDVIRPRAIGAAERSMIEGMEGFVGIGADLVQFESKYASIIGSLL
GNVIAETLEVANKIAARQCQRFRVVTLEGDVVNAGGSMTGGSQHKKNVSLLSRKRQL
DQLDQDILD TENQIVKLHRSVDDVKVQLEQCQDKLDEL RQSGDDTRNAEQQASMEMKQ
VEHEL RHVLEQVAVAGQE KSGFTEEIKELDTARIVAVKKLEQLEEEEEKATHRAIHAAE
FARKANESAKEELQSQLTELKVREGKLDQERFSNGEQLRRLEREVESLVKDLRQNRTL
LASMEADLKKTQTESVKQIEDLNQYKLKKA EASQELDFKRAARSELSKKLEFAESETK
EQRTQLKAVEEQMRQTEISVNRLDVELENILRKLTDEYELGYELAKERYPVPEDVEHT
QAEVQKLKRSISALGDVNLGAIEEFQRVNERYEFLSEQKNDLVEAKTTLYQVIREMED
EMAKRFKITFDAIRREFGTVFSKLFGGGRADLV LMDPERLLETGIDIVAQPPGKKLQN
LQLLSGGERALTAMALLFAILHV KVPVFCVLDEVEAALDEANVVRFAQYLREFSEQTQ
FIVVTHRKGTMEEADVLYGVTMEEGGVSKLVSVKLEDEEAVIA"

CDS complement(3501480..3502232)

/gene="rnc"

/locus_tag="EFAGFIKM_02994"

/EC_number="3.1.26.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P51833"

/codon_start=1

/transl_table=11

/product="Ribonuclease 3"

/db_xref="COG:COG0571"

/translation="MPPLFSKNLKHKGLVRLSEDLKQLQHKLQIKFDNRQLLKQAFTH

ASYVNEHRFSQH QDNERLEFLGDAVLELTVSEYLYHLYPNRPEGELTKLRASIVCEPS

LVKFAEVLGFGQYVLLGKGEELTGGRTRPALLADV FESFIGALYLDQGLAPVRTFLDQ

HVFPLIVLGSKLQMSDYKTELQELTQH HNMGALEYRIVEERGPAHEREFVSEVHMGQE

RLGRGTGRSKKEAEQQAASAALDRLKLPEAGA"

CDS complement(3502198..3503436)

/gene="fabF_1"

/locus_tag="EFAGFIKM_02995"

/EC_number="2.3.1.179"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34340"

/codon_start=1

/transl_table=11

/product="3-oxoacyl-[acyl-carrier-protein] synthase 2"

/db_xref="COG:COG0304"

/translation="MKQRVVITGMGVMTSLGKDLETFWGSLMAGKSGISQIEAFDVSE

YTTQIAAEIKDFNPPEYMDRKDARKMDRFVQFAVAAGFKAVEDSGLKINENIDAERFG

VSIGSGIGGLGTWEDQHNALLQKGPKRVSPFFIPMMISNMASGQMSISLGAKGPNINV

VTACATGTHSIGDSFKLIANGDADAMICGGAEATIRPTGLAGFCAMRAMSTRNDDPAK

SSRPFDTERDGFVMGEGAGVMILESLEHAQKRGARIYGEVIGYGLTGDAHHMTEPD

GAARCMKMLRNAGIEPEEVDYINAHGTSTPVGDRSETLAIKKAFGDHAYKLAVSSTK

SMTGHMLGAAGGVEAVICGLSLTHQTLAPTINLENQDPECDLDYVPNVPRQTKVNIAM

SNSFGFGGHNATIILKKFEA"

CDS complement(3503614..3503847)

/gene="acpA"

/locus_tag="EFAGFIKM_02996"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80643"

/codon_start=1

/transl_table=11

/product="Acyl carrier protein"

/db_xref="COG:COG0236"

/translation="MSDVLERVKRIVVDRLGADEAEVTLASFKEKDLGADSLDVVELV

MELEDEFDLEISDEDAEKITTVGEVVNYIQSHT"

CDS complement(3504000..3504749)

/gene="fabG_7"

/locus_tag="EFAGFIKM_02997"

/EC_number="1.1.1.100"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P99093"

/codon_start=1

/transl_table=11

/product="3-oxoacyl-[acyl-carrier-protein] reductase FabG"

/translation="MSKPLEGKNALVTGASRGIGRSIALALAEAGANVAVNYAGSQAA
AEEVAEEIRAKGVKAITLQANVGVMDEAEQMVKATLEAWGNVDILVNNAGITRDNLIM
RMKEEEFDQVIETNLKGVFNCLKAVTRPMMKQRSGRIINISSVVGVLGNAGQANYVAA
KAGVIGLTKASARELASRGITVNCVAPGFIETDMTKELSQELVDGMLSGIPLSRLGQP
DEIAGVVTFLASQASSYMTGQTLHVDGGMYM"

CDS complement(3504787..3505719)

/gene="fabD_2"

/locus_tag="EFAGFIKM_02998"

/EC_number="2.3.1.39"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A5Z3"

/codon_start=1

/transl_table=11

/product="Malonyl CoA-acyl carrier protein transacylase"

/translation="MGKIAFVFPQGGSQAVGMAKDAYESVPAATEIFRTADETLGFSL
SNLVFEGPETELKQTSNTQPALLTASIALLEAFKEKGIQPDYTAGHSLGEYSALVAAG
VLSFADAVSTVRARGQYMEQAVPGGQGAMAAVLGADREALGVLCRDVSESGHAVELAN
INCPGQIVISGVKEGVAAVSERVKEAGGKRAIALEVSGPFHSSLMKGAAEKLAEKLT
VTFSPAAPVAVNTARPTEDGQVQDLLTAQVYSPVLWEDSVTWLIEQGVDTFIEIGS
GSVLTGLIKKTDKTVKLYNVNSLETLEATASALK"

CDS complement(3505745..3506734)

/gene="fabH_1"

/locus_tag="EFAGFIKM_02999"

/EC_number="2.3.1.180"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q6GIA4"

/codon_start=1

/transl_table=11

/product="3-oxoacyl-[acyl-carrier-protein] synthase 3"

/translation="MNNLRPVGIIIGTGKYVPEKILTNSDLEKMVDTNDEWIVSRTGIK

ERHIAAPDQATSDLAYEAAIKALESAGMTGSDLDLIIVATITPDSSFPSTACILQDKL

GAKGAAAFDLAACS GFVYGLASATSF IQSGMYNNALVIGADCLSRITDYDRNTCVL

FGDGAGAVVVGEVPEGRGFKAFDLGAEGAGGSLLQMEGGGSRLPATAETVENKKHYIN

MNGREVFKFVVRVMGTATIEVLRKAGMERTDVDLFVPHQANIRIIQSAMQRLELPEEK

VVVNVDKYANTSAASIPLALVEAAEEGRMKAGDTVLMVGFGGGLTWGASVLVW"

CDS complement(3506743..3507738)

/gene="plsX"

/locus_tag="EFAGFIKM_03000"

/EC_number="2.3.1.274"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P71018"

/codon_start=1

/transl_table=11

/product="Phosphate acyltransferase"

/db_xref="COG:COG0416"

/translation="MKIVIDAMGGDNAPASTVEGAIAAATEWADTQIVLIGDEAKLEP

LLSQSGVRPANLTVRHASEVIGSDDEPVKAVRRKKDASMVVAGRMLKEGEADAMISAG

NTGALMTAGLLVGRMAGIERPALAPMIPTIDDVGV LALDLGANMDAKPEHLAQYGLM

GSLYRQKVQGIQSPRVGLLNVGTEPGKGNELTKHAYPLLEQLPIRFVGNVEARDVLTG

ACDVLVCDGFAGNILLKSLEGTAGAIFALLKEQFSSSLKSKLAAAVLMPELRGLKRKL

DYTEHGGAPLLGLSRLVVKSHGSADGNAIKNAVRQARIAVQNQLVESISKEISGK"

CDS complement(3507735..3508283)

/gene="fapR"

/locus_tag="EFAGFIKM_03001"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34835"

/codon_start=1

/transl_table=11

/product="Transcription factor FapR"

/db_xref="COG:COG2050"

/translation="MIEENPFVTDQELTRQLKVSITIRLDRLELGIPELRERMKLMA
ELSYDQVRSLPLHEIIGDIVDLQLDKSGISLFEIKEEHVFSRTGIARGHYVFAQANSL
AVAIINDEIALTASADIRFVRSVHLGEKCIKAYVRSIPGQKGKAKVEVFTYVGEEMV
FQGNFVIYHSGGEDSGEGGHLE"

CDS complement(3508656..3508829)

/gene="rpmF"

/locus_tag="EFAGFIKM_03002"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P07840"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L32"

/translation="MAVPQRRTSKTRRDKRTHFKLAVPGMVKCEQCGELKLSHHVCK
VCGTYKAREIISQ"

CDS complement(3508897..3509403)

/locus_tag="EFAGFIKM_03003"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLMPFRKVATSDGPLKFNEQWEIKELVSNRQDITAVTPLTADLS
AEFREGDVVDVHGKLTGVDMCLSRCLKPINEHFHIDFHEQFKQGKQPEGLHEDDDL
YVDGDSVDLKGAAEEAFLDLPIPLCSDTCKGLCPKCGHELNEGDCGCDNEVIDPRL
AGLKDFFK"

CDS 3509867..3511102

/gene="hmp"

/locus_tag="EFAGFIKM_03004"

/EC_number="1.14.12.17"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P49852"

/codon_start=1

/transl_table=11

/product="Flavohemoprotein"

/db_xref="COG:COG1017"

/translation="MLSEYTIRVIKSTVPVLEVHGEAITRHFYETMFVAHPELLNIFN

HANQKQGRQQAALANMVYTAALHIDNLSSILPAVRQVAHKHRSLGIVPEQYVIVGTYL

LQAIKDVLGDAATDEIITAWGEAYNVIADAFIGIEQNMYTEAENQTGDWEGFRTFKVA

KKVQESEIITSFYLVPPDDGQPIASYEPGQYISIKIKPEAQSFQIRQYSLSDTPGKPY

YRISVKRERGVLERPDGVISTYLHDHIEEGSLVELSAPAGDFTLNADDKRPVLLSGG

VGLTPMISMLNTLVNLTNENRNITFLHASPNGQSHAFRDHVNSLAKRNQGVKAYCYTQ

PENADRENECFHKEGYMDAVWLRQVIDELDSTYYLCGPVSFMRVYTELQALGVASDN

IHYEFFGPKASLSPTPESV"

CDS 3511321..3512553

/gene="tmcAL"

/locus_tag="EFAGFIKM_03005"

/EC_number="6.3.4.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34513"

/codon_start=1

/transl_table=11

/product="tRNA(Met) cytidine acetate ligase"

/db_xref="COG:COG1323"

/translation="MKAVGVIVEYNPLHNGHVYHLQEARRLSGADAVVAVMSGPFLQR

GEPAIVGKRARTEMALHAGADLVLELPVAYAVQPAEWFAFGAVSLLHRTGVVDSLFCG

SESGDLDSLQRIARVLAVEPAGMREDIARRLREGASYPAAYAGAAAAALAPGGVDAHDA

AALLEQPNNLGLHYLIALQRLGSAIQPFTAARTGAAYHEATPGPGAIASATAVRLL

MADGPNAAPYVPAATLAILHREWQEGRAPIHWERFAQPLLHLAATRRASELERIAEV

TEGLEHRLSRALAQLPEPSVEALLNAMKTKRYTRTKLQRMLAHLNHTKAECSPQL

AAGPGYLRVLGFNTQGQSLLKQMKKTASLPVVLKPSTFTHNQLELDIQAQVAYGLAWE

HKDTRKMFSDYYESPVRL"

CDS complement(3512918..3513958)

/gene="ylbL"
/locus_tag="EFAGFIKM_03006"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34470"
/codon_start=1
/transl_table=11
/product="putative protein YlbL"
/db_xref="COG:COG3480"
/translation="MNRIRKSGGFRASIFVIVVALVYVAVYMPTPYIIYMPGSADEV
KPMVTVKGGDQEEHGVFMMTTVSATYANVLLGTSLFNKNAQVDKKEDRLRGKSEA
SAEQVWFMSDSQSSAMEAAEQAGVTYSIVPEHIFVFGLSDEPKPEGDIAPGDIILGV
NGTATPDNTVLSAELKDKKVGDTVEMQLERGGETISRDKLIQVKDSKTGETRPG
MIGTVQKVKAEPDKQISFTDTQVGGPSAGLMFTLEIYNQLTPGDLTKGHRIAGTGT
TKDGVVGAIGGVVHKIVAADRKEAEIFFVPKDNKEAAAKAEQIGTKMKLVPVSTVDD
ALAYLKTLSVKS"

CDS 3514210..3515547

/gene="ylbJ_2"
/locus_tag="EFAGFIKM_03007"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34765"
/codon_start=1
/transl_table=11
/product="Sporulation integral membrane protein YlbJ"
/db_xref="COG:COG3314"
/translation="MTLQSEVRDSGPLRTIMLSTGALMLVIAVVASPKAEFDASIQGL
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AVGMCG
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AAGYFLLV
VHWISGWIAAILATRLPAPGNQKDRVSSTAVQADNSSLDSQPASPTSSTAR
SSAPHH
ATNKRRSIWSDMMIAAREAHRRDGRGFGKLLGDTVSAVQTLMMTGGYMI
GFAVFIRL
VSLYLTPGSSAALWPAFFELHLGTYHLSQTSLTPLLMSLLAAVLGWGGLC
SHLQVSA
VLKTTGPGSKSMYFAGVRLTHGLIAFFISLFLWMPFSRYSTEVTTLQTNA
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PFGWLFIHSPGNTYINTIWSVFPAACMGLALLAVMVSLSGLTFFWNRFR
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CDS complement(3515525..3516040)

/gene="coaD"

/locus_tag="EFAGFIKM_03008"

/EC_number="2.7.7.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34797"

/codon_start=1

/transl_table=11

/product="Phosphopantetheine adenylyltransferase"

/db_xref="COG:COG0669"

/translation="MTEMIHRQERIAVYPGSFDPVTMGHLDIARASKQFDRVIVAVL
 NNMSKNPLFTVEERKELITEVTRHLPNVEVDSFRDLTANYVRQKEAQVIVRGIRSVTD
 FEYELQLASTNSKLNPDATIFMMTNPKYSYLSSSIVKEIAHYHGDVTDLVSPEVEAA
 LRQKISEKTGG"

CDS complement(3516033..3516653)

/gene="rlmI_2"

/locus_tag="EFAGFIKM_03009"

/EC_number="2.1.1.191"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01857"

/codon_start=1

/transl_table=11

/product="Ribosomal RNA large subunit methyltransferase I"

/translation="MTRQVRVVSGSAKGRPLKAVPGTGTRPTTDKVKEALFSMVGPFY
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 DAGRALKALAKRGTTFDLVFLDPPYRMKNGHELMMLTMHELELLEPEATIVLEYESKHD
 YPEQFGPFQTRKALYGETAVSIYYAPEAVEDGESITPEEEAPHD"

CDS complement(3516944..3517378)

/locus_tag="EFAGFIKM_03010"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MIIGKSIDTSGLTRVANLSDELQPVFDQAESKYQIVDIELFFVF
RCLPEEYERRSTVRHVKKENVIYFDLVSEDRYKALSKSKQRYVLSHEFYAFLSEKIP
KYKIEHLNVNEFIADMGMWLREIGWLQTEEQADISEFEEKYN"

CDS complement(3517506..3517790)

/locus_tag="EFAGFIKM_03011"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVDMYLIILVAILGMVLFYSLIAYFLIRFISKKAFLTLTKYEM
MEIITWLAVLFITFMMIKTGSINLLLPVLLIPLINLRLSNRKHRELNS"

CDS complement(3517898..3518203)

/locus_tag="EFAGFIKM_03012"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSKKAKTGIWVTVLVFLGIIVGCFIWYFNTASGERALKTMRSNN
SGGLERVVKVYSNNGELIQTYDGKIDVEDTEYGNKVLFDLNGKRVVIYNATIVVEEK"

CDS complement(3518374..3521421)

/gene="cbgA_1"
/locus_tag="EFAGFIKM_03013"
/EC_number="3.2.1.23"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P24131"
/codon_start=1
/transl_table=11
/product="Beta-galactosidase"
/translation="MKATKADINWLGDVSVFEVNRLHAYSDHRYQTMDEAVGSGAMS
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GYGEDSFTP SDFDLTPFLQDGENKLAVEVYQRSTGSWLEDQDFWRFSGIFRDVYLYTV
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NDGQVSLREDIGTVNLWSAEIPYLYRLYIRVYDAAGTLVEVVPQAVGFRTFEMIDKVM
HINGKRIVFKGVNRHEFNPRRGRAVTKEDMLWDVRTIKQNNMNAVRTSHYPNQSLWYE
LCDEYGLYVIDEMNLETHGSWQKLGAVEPSWVIPGDKPEWHDIVMDRAVSMVERDKNH
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PADIEEFLNANPTKPYISCEYMHAMGNSIGGMHKYTELEDKYPMYQGGFIWDYIDQSI
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AEYAVNTAFVLKEATMWADKGEEVAFGQFIFTQDQVND AVEVDLNLVSDVQVIEGDVN
IGVRAGKTHALFSKQFGTLVSLKLSGRETI AVPPTPLFWRAMTDNDKGMAMGFELGAW
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AGLPNLPIHALSFRTSPDFENVEWLAMGPEENYADRAFGARLGIHGSKVADTMAPYLV
PQESGNRTGVRWAKLTDNAGRGFKIEASGTPVELNVSPYTASELENAQHAYELPPVHY
TVVTVAGKQMGVGGDDSWGAPVHPEYLIPSDGELT FEFVIRAL"

CDS complement(3521579..3522409)

/gene="lacG_1"

/locus_tag="EFAGFIKM_03014"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29824"

/codon_start=1

/transl_table=11

/product="Lactose transport system permease protein LacG"

/translation="MAKAKAKRIFTYVFLSIVAFVSIFPFFWMLVSSTNASVDVTKGR

LLPGSAFIDNFNKLIDSTNLVQALGNSAII SVISTVLALFIGSMAGYGFEVYRTKSRD

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QNTKMFPKDLLEAGRIDGLSELGIFLKIYMPTMKTTYAAAAIITFMSSWNNYLWPLIV

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CDS complement(3522402..3523301)

/gene="lacF_5"

/locus_tag="EFAGFIKM_03015"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29823"

/codon_start=1

/transl_table=11

/product="Lactose transport system permease protein LacF"

/translation="MKAMNTGDSLQKKNNLTGWAFVLLAVVGIVAFYFYPMIQALLLS

FKSGVGANLEFSGLSNYKRLLVDTTFRALTSENTFIYLIQVPVMILGLFISVLLNDS

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WAKITIIIIVTWRWTGYNMIFYLSSLQNIQSIYEAAIDGANAFTQFFKITVPLLKP

IILFTSITSTIGTLQIFDEIMNITKGGPGNATMSISQYIYNLSFKYSPDFGYAATVSY

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CDS complement(3523434..3524990)

/locus_tag="EFAGFIKM_03016"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSEVNRVKSFLYYFKIKKLQNQKKLQKTKFNASGFCKGFHCGNK

MTNPYKIITNEWRYGNDKMNISKATAFRKRKQITHKEVEGELNVLKKMWWLMLVTVLL

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AQADIIQKLNTGLNSGTASGLPNVVLIEDYRSQSFLNAYPDAFKDLSSSITASDFADY

KLGPATFDGKQYGVFPDSGVAGLYYRTDLLEQAGYKAADLQDITWDDYIQIGKDVKAK

TGKELSLDPNDLGLIRMMIQTAGKWYSAEDGKTPDIANNAALKEAFITYKAMMDANI

VKLHSDWSQFVANANNGSVATIPTGNWFSPSVRQEASQSGKWAVAPIPKMAGQPNSVH

ASNLGGSSWYVMNNVPGADQAADFVAKTFGSDKQLYQDLLNNIGAIGTYKPAVDGEAY

AKADEYFGGQKIFTDFANWTKEIPSVNYGINTYAIEDILVVEMQAFLNGKSIDDLAD

AQKQAEQLN"

CDS complement(3525070..3526839)

/locus_tag="EFAGFIKM_03017"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MKKWMNQLSRLGLFPKLFLVMVVSIVLVSVLILWTTIHMSTNLF
TETFSITNSKVLNQIKTNFESFNEAIAAVSNNVTQSGSIRGFLSEGDADSLTMAKSFY
SMRETMDRIQSITESYEVGITIIGINGRSYSTNRAHLQLSVDELKQEPITMEEAETPS
RLIFDVYQNEATLGSQQMISATKALTDRTSRITYGTLYVTMREDIFRQFYSSFTSRGN
DWWIMNEKGEIVSSNREDWIGTTQLDLLSYAREMNNNSPRSINARVMDQDSVVLSEYL
PFYRFYIVNVVDKDLAMGQLIDMKTVALICAAIVVGALILVFLITSQITKSLRRLVKQ
MSNITKSDLDNYIPVSGSYESRQLGHAYNYMLDELHDYVDQLVQTQHEQRNAELAALQ
SQINPHFLYNTLASVKVLVQQGNKDRAAETINALIGLLQNTISDVSQTVTVEQEVENL
KNYVFINHVRYGGRIKAAFYVAPDCTHYHVPKLVIPFIENAFFHGFIKKETGTIHVM
VSRAGESLICEIMDNGDGIEGLVMGETLPNPKNNRQLFSGIGIRNVHDRIELLYGSPY
GVTIMSTVGEGTRVTVTLPLITS"

CDS complement(3526858..3528405)

/gene="cheB_10"
/locus_tag="EFAGFIKM_03018"
/EC_number="3.5.1.44"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00099"
/codon_start=1
/transl_table=11
/product="Protein-glutamate
methylesterase/protein-glutamine glutaminase"
/translation="MNRLCKVLIVDDEFLVRQGIIKHMMNWESEGFIIIVGEASNGEEGL
QQVNLLKPDIVITDIVMPVMDGETFVRTLKASNPQIEVIVLSSFSEFEYVRSTLQHGA
ADYILKPKLDTNELLQVLQRTAGKIPELQFEP SHD GWRLGQLMEKMLSGFTLDEDSEM
PIIRDTFPYESFRLLVYKPVGAGGNPLKMDQE QIESKL RSDLP EVECAMVPAEGTLPV
MLLNVD PARDEWMLERIRQLASENAAGEGSPGWVLSESFTSFEQMGVVYRERLIK LIE
YRFYYKDRSILVYGELPPMHPAGYQFNVMFLQHVKRNRVEAAREYLQEHA KTLGRDY
IADVFEIKSFLGNLIFNVTITLADMDVQSAGLEESKYTYFKNVDGASSLDEVMTVLDQ
FMTEVQECTVGAGGKRSDPNMKMLLDYMH EHF DQPLGLAEVAKHFHFNPSYLSSYFSS
HKKEGFNEYLNKIRIEKAEELLRSDDVTISEISSMVGYS DHSYFCKVFKKFTGLSPSR
YRRKFWA"

CDS complement(3528677..3531757)

/locus_tag="EFAGFIKM_03019"

/EC_number="3.2.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q3MUH7"

/codon_start=1

/transl_table=11

/product="Xyloglucanase"

/translation="MRTFMGKLRMMSLTVAVV TASLGGLAGTTAAAPSEAYEWKNVVT
GAGGGFVPGIIFNESEKDLIYARTDIGGAYRWNAADERWIPLTDFVGWDDWNKNGVDA
LATDPVDPDRVYMAVGTYTNSWDQNNGSILRSTD RGDTWQTTLPFKVGGNMPGRSMG
ERLTVPNDNSILYFGARSGHGLWKSTDYGV TWNEVTSFTNPGNYVQDPSNEYTSDIV
GLAWVTFDKTTGSAGQATQTIYVG VADKAQSVYRSTNGGLTWSAVAGQPTGYIPHHGV
FSDSGSLYITYSDGVGPYDGEKGDVWKLNTSTGVW TNISVPSSSTDNYFGYGGLAVD
AQNPGLTMVATLNSWWPDATLFRSTDGGATWTRIWEFEGYPNRKLRYTQDISAAPWLT
FGTNPAPPETTPKLGWMIGDLEIDPFDSDRMMYGTGATIYGTKNLTDWDDDEKINISV
MAKGVEEIAVLDLISPPSGAHLISGVGDVSGFRHNNLDQAPATIFTSPNYSSTESLDF
AELSPNTMVRVGKADYAADPNAKSMGLSSDGGTTWYKANAEPAGTTGGGTVAISANGN
RLVWSTSDKGVHYSTGGNSWTASTGIPAQAKVISDRVNSNKFYGAAGKIYVSVNGGA
TFTASSTTGLPMEGNSDLDAVPGVEGELWFAGGSEEEGPYGLWHSTD SGATFTKLANV
EEADSIGFGKAAPGQSVVALYTVAQIDGTRGFFRSDDGGANWVRINDDQH QYARVTTI
TGDPRLYGRVYLGTNGRGILYADRVGGNNGGGGGGGTPVTNSAITPVIAEFDRKAGNQ
VNIPVTLTNLNGNTLASIRNGNATLVSGTDYTLTGNEVVLSKNYLASLPNGAATLTFQF
SAGAPATLNLLIKDTTAAPVGTIRIEMFNSNTSATGSSISPKFKLTNTGTTALNLSDV
KIRYYTINGEQPQNFFADWATAGSANVTGTFSALNPVRTGADHVLEIGFTASAGTLN
AGQSTEIHTRISKNNWNTNYTQTDDYSFAGSQTSYTDWSKVTGYIAGSLQWGIEP"

CDS complement(3532160..3533041)

/locus_tag="EFAGFIKM_03020"

/EC_number="3.1.1.99"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0DOV6"

/codon_start=1

/transl_table=11
/product="6-deoxy-6-sulfogluconolactonase"
/translation="MSDVTVAVQTPALLGEGPSWDAENNRLWVDIESFKVHVYDPAT
GQDQAYDVGEHVGAVVPYRGDEVVVALRSGFHTYHLLTGELQAIEDPEQDKDTNRFND
GKCDAKGRFWAGTMSMNNESKAGSLYCLEQQGPVRTMVQGVSTSNGLGWSPDRQTMYY
IDTPTRSIDRFDLFDLTAGTIQNRTSVIHIPEEFGFPDGMTVDGEGMLWVAHWGGGRVT
RWNPHTSSELLQQIEVPADQVTSCCFGGPDLEELYITTARIGIKEERLKETPDAGSLFV
IRPGVKGQETHAYGSQQ"

CDS complement(3533054..3533719)

/gene="axe2_1"
/locus_tag="EFAGFIKM_03021"
/EC_number="3.1.1.72"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q09LX1"
/codon_start=1
/transl_table=11
/product="Acetylxylan esterase"
/translation="MKLQKNDKLLFIGDSITDCGREHPVGEGSSGLGHGYVAQVYALL
RSIYPELMRLRVQNVGNGGNTIRDLKQRWDRDVLDPDWLTIMIGINDVWRQFDNPLS
TDSHVFLEEYESTLRELVASVRPNLKGLVLMTPYYLEANPEDPMRATMDIYGEAVRRV
ANEYDAVYVDTQATFAPFWDHFYTSVLTYDRVHPDATGHMVLSKAFLDAIGFEWSSGV
KSE"

CDS complement(3533804..3534592)

/gene="axeA1"
/locus_tag="EFAGFIKM_03022"
/EC_number="3.1.1.72"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:D5EV35"
/codon_start=1
/transl_table=11
/product="Acetylxylan esterase"
/db_xref="COG:COG0657"

/translation="MTTTIPLWDHAAPYAAQGHEDEMPLIPFIQPGSESAVIVCPGG
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INPAKIAVLGFSAGGHLTATLGTLYDEGQPDHEDIIERQSSRPDRVILCYPVITMESY
GHAGSRENLLGSDASAEQIKAFSAEQQVRADAPEAFIWHTSDDQAVPVENSLRYALAL
GAHGIPYDLHVFEKGSHGLGLAEDNHAIRVWSDLCLTWLKNQGW"

CDS complement(3534736..3535569)

/gene="rhaR_27"

/locus_tag="EFAGFIKM_03023"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MFISPRHQRYFMTSRDHPLPLYIESLGYNGNQEKVSRPVGYPY
HWLQTVKGAGEFKFAGSTVVLGEASGILLPPNEPHEYVRAQGEWETFYITFGGSQCPA
ILESLSLGEAALHQWEQSSPFNDYGQEVLDSIRSDQDLGLEASADIYRFLILLKKHG
MTGNRSSISHAVERLAPLIAFMEQHYANPEIGLEHMADVTGISSRHLNTLFKQSFGMT
AYSYFILLRIRKAKEIMTGDTALTIRETAVRVGFRDASHFVATFRRIEGVTPEQFRNL
Y"

CDS 3535698..3537725

/gene="bgaP"

/locus_tag="EFAGFIKM_03024"

/EC_number="3.2.1.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q09HN2"

/codon_start=1

/transl_table=11

/product="Beta-galactosidase BgaP"

/translation="MISSKLPKMFYGGDYNPEQWDHETHLEDLRMFQLAGIDIATINV
FSWALIQPDEVYQFAELDQLINRLYEKGVYICLATSTAAHPAWMAKKYPDVLRVAD
GRKRKFGGRHNSCPNSPTYRKYSEKIADKLAERYKDHPAVLVWHISNEYGGDCYCDNC
EKAFRVYLKERYQTLEQVNKAWNTNFWGHTFYDWDEIVLPSNLSEHWGNNNSTFQGIS

LDYSRFNSDSMLDCYRLEYDAIKKHIPDSVVTNLMGFFKQLDYFKWAKYLDIVSWDS
YPGLATPISFTAMAHDLMRGLKDGQPFMLMEQTPSQQNWWQPYNSLKRPGVMRLWSYQS
VAHGADTIMFFQLRRSIGACEKYHGAVIEHAGHENTRVFREVAELGKELQILGDTTLD
ASVESKVAIVFDWDNWWAIEKSSGPTVALNYVDQIHKYAAFFRRNIQVDIVSVDTDM
SKYDIVLAPVLYMVKPGFATKLEKYVEAGGTFLTFFSGIVNENDLVTTGGYPGELRK
LLGIWVEEIDALLPEQKNRIVLKETYGDLQGEYGCMLCDLLHSEGAEVIAEYGDDFY
KGMPVVRNTFGQGEAWYVASDPDERFLDGLLQGLAAAKNVKSLLETPEGVEVSARTK
DGKPYLFVMNHNATTQSYDLGTAKAHDLLTNRELSGSVEIEARGVQLLEMK"

CDS 3538164..3539120

/locus_tag="EFAGFIKM_03025"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNRTNRLAAIVMALQGHETAHSLGEKFEVSRRTILRDIQSLSE

MNVPIIAISGPGGGFSLMEGYVLPPLQLDPVEAATLLFALEGLSRYADTPFHEKRWTL

MNKVKAIIPDDIMSRI DPMLKQLHHHIPDRNYILPHLDALLACIPEHGWLSVLRSAS

RQRWLHICPTRVYASSGFWYCEAYSLEHGEQRLFRVDRIIEVKAIEPQDAQMLNEQAE

QQQSKPIPEQPPTLVKAQLSYRGMIEAEQDEHIGEKMTIAPDLWELSFLCPPGEWD

WAVRFFYRLGREAEVIEPLQLRSEIRQHAEVSRRYLASTKS"

CDS 3539155..3539841

/locus_tag="EFAGFIKM_03026"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTYEAVTTYEEAVQRIQSIGLLPLAPLFTEYPSLSSLTPKEHWH

KDDELDPWLWRSRLAEEGIAAYGKFVKKKALLVSSEYFPWVHRLADSRTIKEQYEAG

LLSREAFKLHALVAEQEGIDGRALRSQAGFGAKEDKKTFDRGLLDLQGCAAIVISGTK

EKEGLAEGKVAWNSSAYETAGHWMERHGKPFEGSVAEARELLVTQLQQHASPAALSS

IAKALGIRGI"

CDS complement(3539943..3541457)

/gene="uxaA"
/locus_tag="EFAGFIKM_03027"
/EC_number="4.2.1.7"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42604"
/codon_start=1
/transl_table=11
/product="Altronate dehydratase"
/db_xref="COG:COG2721"
/translation="MNTTSTINDWIAIQPQDDVIALRDYAKGECITLPDGVSFLLD
DVPKGHKIAVHTLAPGDDVMKYGFSIGIAQEQIEQGSWIHSHNLKTGLHGLLEYEQP
GAQVQTDMPPEHLRSFDGYLRPNGDAGIRNEIWIVNTVGCINKVCEALARMGQSQFGS
RVDGVFHFPHFPFGCSQLGDDLKYTQQLLASLVEHPNAGGVLVIGLGCENNQVDEFREC
IAPEYRGKVRFLKAQETDDELEEGRLMEELVEIVEHEQRQPLPLSKLKIGLKCGGSD
GLSGITANPLVGAVADMLVAAGGTAILTEVPEMFGAETILMNRAANEQVFHDLVDLVN
GFKQYFVNHGQNIYENPSPGNKAGGITTLEESLGCTQKGGRSSVVDVLRyakrvtqt
GLNIVEAPGNDLVSVTALSAAGAHIVLFTTGRGTPFGGPVPTVKIATQSDLANRKKHW
IDFNAGQLLEGQTMDEVKVQLFSQLIDIASGRSHTLSEQHGFREIAIFKDGVL"

CDS complement(3541454..3542971)

/gene="uxaB"
/locus_tag="EFAGFIKM_03028"
/EC_number="1.1.1.58"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34354"
/codon_start=1
/transl_table=11
/product="Altronate oxidoreductase"
/db_xref="COG:COG0246"
/translation="MSASTKRPRLLKNLLGSDGQRKCKEIMERPVKVLQIGEGNFLRG
FADWMLHESARQGKFHGSVAVTQPRPGGKAKLEQIRDQDGLYTMITRGLSQGKPVERT
ELISIFSQCINPYEEWDAFLNLAELPSLEFVISNTTESGLKYTYADYIEGEPVQSFPG
KLTVFLHQRYLKFDGDPsrglihlpcellegngdvlrscvlrhseDygysegfrswie

NHNHFLNNLVDRIVTGAPTQEEADSLNRWGYEDQLINTAEPYHFWAIQGDSELDKKL
PLKQAGLNVHWVKDLKPFQVRKVRILNGAHTLMSSLGILQGKQHVRETMEDPHFGSWI
REAVHQEIVPALDMPDHQLDQYAEVFERFLNPYIDHKLQDIALNTIGKFKVRVLPTL
LSYEQNQGSWPERLIQGFAGLLCLYRPVNTPEGYKAQRLNGEDILLRDDPDVLAALAT
HWEGYDTLNRNQNQLDDRVA AVLSDTLIWGENLDAREGLRAALVREIGLLEGEK"

CDS 3543164..3544039

/gene="rhaR_28"

/locus_tag="EFAGFIKM_03029"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MERSPVRTTIQAESGIPFRLVYSDTKSPQNELPDHLHDWHEIY

VYRGQGSIFIDTGLENMQEGDLFIIPGSTVHRALPDAGNPVTSSALFFSPGLLASTAG

GAASSLLSLFERCRKQRVYKRHLNTEEQSQVAALIDDIQTEFQLGHHLSAHAALLRLQ

LLLIFLERLEAAGRANPGKSAPGPSWLSSTISHIDNLRNGLSLPELAQYASVSPAHF

SRAFKRYTGMTLTDYALARRVIMAKEHLVQSDETMAAVADACGFDSLPHFYRQFKKLT

GTPPAAYRRTMNSSR"

CDS 3544181..3546169

/gene="tetO"

/locus_tag="EFAGFIKM_03030"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P10952"

/codon_start=1

/transl_table=11

/product="Tetracycline resistance protein TetO"

/translation="MLNELNRRNIGIFAHVDAGKTTTTEHMLFESGVVRSPGRVDDGT

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AYQLHEDSFHGIDSLWNPQNQDSLSDGTPSIPGLVEILAELEEVMEAYIQETPLSQRD

LNESFLRYVHKGEMFPVCYGASGKGIGVTALLDAVLAFLPPPAQPVDSPVSGVVFKE

RDRTMGR TAYVRMYGGS LYNRDTIHNSTRELEEKVTQIRRM DGRKWADTGAVHAGQIA
ALYGLSDTHVGDIIIGNPEGVPPLPQMAVPLLT VQVHGKDPAQYPDLVAALQELTDEDP
LLDLQWLPEERELHLKVMGTIQLEILSSLLLSRFGLDWVFDPPSVIYKETPRTAGEGY
IAYTMPKPCWAILRFKIEPLPRGSGLIYASNVRTEDLLIRYQNEVERRIPEALSQGML
GWEVTDLRITLVEGEHHVWHTHPLDFV VATPMGIMDGLSRTGTTLLEPLLQFRLTVPE
EYGGKALS D LVHMRATFEAPVIGSGRCIIEGVMPLATSM DYPVKLRSETSGRGVLTT S
FAGYQDCPADANHTRKRRGVNPLDQSKYILSVRNAITS"

CDS 3546184..3546861

/locus_tag="EFAGFIKM_03031"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MLIKFLIFGLLWRIIGNPFIAILILLVILYFLDRRYVGVFPSFT

KPLKRM RNISRLRQQLAMSPNEVSSKLELARLLIERKRYSEAHALLLELERPYEQSAE

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QFQEIHSSSSEAYYLLGSVHRSLGRNADAKQAYEQSLNVYRSLPKYKKRQERRWAVRS

WFRKRGL"

CDS complement(3546975..3548036)

/gene="thrB_2"

/locus_tag="EFAGFIKM_03032"

/EC_number="2.7.1.39"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00301"

/codon_start=1

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/product="Homoserine kinase"

/translation="MQNIDSGSLHPSEQQRRISEVLALYGFTSDWKGERGKGGMNNSTY

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YYRIQDAYPLCSPERLLQLCTSPPEQLAACANELKQLRDALPDLFEALRGMELLPHQL

VHGDVNASNVLVDQQDGEICAILD FEFATWDLRVMELAVPMSDLLTMDKSEDWMWQAQ

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CDS complement(3548129..3548755)

/gene="lipC"

/locus_tag="EFAGFIKM_03033"

/EC_number="3.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42969"

/codon_start=1

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/product="Spore germination lipase LipC"

/db_xref="COG:COG2755"

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MGVNGLTSGEMLQMISSHPRVRQSLREADIITISIGGNDLIRTFKASNGIPNASKMTQ

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GNYACAQVYDRFEGRERELLFWDRVHPNARGYRVIAEQLNRTGYYPFS"

CDS complement(3548954..3552121)

/gene="smc_2"

/locus_tag="EFAGFIKM_03034"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01894"

/codon_start=1

/transl_table=11

/product="Chromosome partition protein Smc"

/translation="MRTILKARWWLMGLWVVLAAVLMFTAPNMSELIREKGQFSVPEG

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TGKGLIDEDTIESSQEGLKKSEYITVVFILLILFLVFRSFVAPFVPLLTVGISYIVSQ

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GVSGVRSMTPTGDEIKDFEVTQQVGTLS DGLGEGKTGLDKIRDGLSEASSQLSKNEP
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DQLAQANNQLLEAYRQAGAGVAALGDGTRELEQQ LNGVSTALTSLSSESFTALEERYPE
LQQDADYQRIKGTIGETGSGTAQLAQGLGQIKTKLGEAAAGINQANEGFASAAAGQKA
LADGLGQIVTGIGLLQSGLKQAADGQGK VISEIPSIQDGLGQLQGGQEKIQQGFSDLS
GQLTQLTDGLNQSV DGIKQVSGGLDSAQDYLTQLQNSPDS DLAGWYVPDEALNSKDFT
QVFDTYLSERKMTIDVIFAENPYGTEAIDRV PDIEAAVHRAVQGSTLEKADIAIGG
VTSTFADLQEISNNDYTRTVMLMLAGTFIILVLLRSVIMPLYLIVSLLLAYFTSMAL
TEVIFVNILGFAGISWVTPFFGFVMLIALGVDYSIFLMDRFNENKGMKVQDAMLYAMK
NMGTVILSAAVILSGTFAAMYPSGVLSMMQIATV VLSGLILYSLLFLPFFVPVMVKMF
GRANWWPFPNKEQSDSVDS DRTIGM"

CDS complement(3552118..3552576)

/locus_tag="EFAGFIKM_03035"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTPDAKSLV NRYLDASFMVNKRFDTRIREQVGLTITTDQFCAL

RLIEEKPSCTPSDLAELLCIGKSSITALVNKLVD RDLVHRAGDERDRRVVYLTLTDTG

RQVYRETEREIQQILEPYLVHFKPEEVRI FIESFEKLAALLSHEGGRENE"

CDS complement(3552797..3553234)

/locus_tag="EFAGFIKM_03036"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLINLKSRIQEPEVQELLSYS VFDPDPHLNRALQQYVEKDELQM

GGYEDEGQLIGLIGYEKGTSEVTIHHISVLPENRFKNYGRGMISQLLATYNPDRLIA

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CDS complement(3553298..3554284)

/locus_tag="EFAGFIKM_03037"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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/product="hypothetical protein"
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ILAGRYGPQDQAWIEQVLKYWNVASIRELAALGIAGFAENKQATNRKFGQMASMVTEA
ADRNIPLAVRVCGSAADTAVVGILMLASCFDQPTVSMTLTGSCSSPYMVEAVQKGLD
AANMREGKRIQYIPSNLPGVGGAMLDAYHLAQINVSDNISTVLQSELNRHTT"

CDS complement(3554353..3555066)

/gene="COQ3_3"
/locus_tag="EFAGFIKM_03038"
/EC_number="2.1.1.222"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00472"
/codon_start=1

/transl_table=11
/product="Ubiquinone biosynthesis O-methyltransferase,
mitochondrial"
/translation="MGNEQFEAARKAEAGYHSNFYQNNELFASGTWMSRPMPMVMMDML
ERLLAHKEELRVLDLGCVGVRHTIPIAQR LAKTKSEVIGVDLLDEAVDGLRKYAKEYQ
VDHIVQAVKADVEHYAVEPNYFDYIAACSCLEHVS NKQAFMEAIDRLQAGTRTGGIHC
ITMSTNVEEKEINTGKEIEPLIELNLPTAE AIAILEKAYKGWNILLQEHVTQTIEEEK
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CDS complement(3555084..3555434)

/locus_tag="EFAGFIKM_03039"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MARTQRKCSYCHEGMAEDEFKCKSCGNLVATKTALPEQPYMIEY
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IILFAGTGTLTNF"

CDS complement(3555492..3556454)

/gene="menH_1"

/locus_tag="EFAGFIKM_03040"

/EC_number="4.2.99.20"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01660"

/codon_start=1

/transl_table=11

/product="2-succinyl-6-hydroxy-2,
4-cyclohexadiene-1-carboxylate synthase"

/translation="MLFYVLAALVLIVLALLWTGGLYFFKTAIR RTPKTLVDNPNLM

PEPDNEIISSASDLKWLD AQPTEEISLQSHDGLKLYGTWLG SNKGSDQTVILAHGYSG

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TQGEILLHGISMGGATV LMTGGEALPTQVKAIVSDCAYTSVEEELTFQLKQLYKLPAF

PFIPVTSLISRWKAGYSFREASALKQLAKVNPVLF IHGEADM FVPTMVYRLYEACP

TKKELLTVPRAGHGTA FQVDRTGYEAALESFMKKNLSQPESVIN"

CDS complement(3556491..3558200)

/gene="rcsC_9"

/locus_tag="EFAGFIKM_03041"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00979"

/codon_start=1

/transl_table=11

/product="Sensor histidine kinase RcsC"

/translation="MSNESGEIQRLRRTIEQLSDQMIRSKEQEERTLTFSDMNNELV

TLQRLLAKNNNSLEAARQQA VDAGDSKIAFIAGISHDFRTPLNGILGMAEMLKLSPLS

EEQENSVSVIQDAAKLL LKLIQDLLDSKLEAGQMRLELGEVNLQETINYIVRLLEPQ

VRKNGNQLSIDCDPRISTL LEGDSTRITQILINLIQNANKFTSEGTVRIRVTLMKDDE

ITQMIRYEVEDTGIGISEEDQKQLFQPYVQTEQGRSSEYGGTGLGLSICKSLVTLMEG

QIGVDSQEGEGSTFWFELTDKKDGNQSANQSVASAEQQGQDMDDEAPSVSVLLADD

NVINRQLVMLQLKKLGITQVDAVVNGEEAIAAFLSKKYSLILMDYMPVIDGLEATRK
IRSIEMDEMRHTTPIIAMTGNVMQGEKDKCMEAGMNDFIGKPFTLEILSKMIEKWQQS
SEPTVLNMSIVHEIAELNTDGDRTLLGMLLDMYRTDTPGKIEVLR RHIVSGDHVAAT
EVAHDLKSGSLGIRYLSLTFARIEQFAKEGQSRKAEPLLDALLPAYQAACASLQQI
SKD"

CDS complement(3558216..3559310)

/locus_tag="EFAGFIKM_03042"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSHQEAGERLLQESANLADKITEKQYLRQPDLLERFGENGKMRT

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EIIEAQLEAGVTIRDIYRYIFQPTQYEIGRLWQCHRISVGQEHFCTAATQSFISRLYS

RWLIHTGQDKKLVATCVGSEQHEIGLRMLTDVFEMEGWDTHYLGANVPNGSVIEAIEL

HQGDVVAISVTMTYHLHLAKELIHLIRHHPATAHVKIMVGGYPFNIDQELWKTIGADG

YAPGADEAVAVAEQLLSQPATCNYLDMVRD"

CDS complement(3559596..3560057)

/gene="mhqR_1"

/locus_tag="EFAGFIKM_03043"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31672"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator MhqR"

/db_xref="COG:COG1846"

/translation="MLNTEDNRELSLQLFVVLVRAYNSVTSRSNRDIQSHGLNTEFG

VLDLLYHKGPQALQKIGEKVLMSSGNITYVVDKLQKNLLFRRPSKEDRRVIYAELTE

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CDS complement(3560073..3560672)

/locus_tag="EFAGFIKM_03044"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKELPIVDGELVLRCEKKDLKELYELIYSDDVPEWKQWDAPYY

PLKHESYESFEQGMLKRMDVDPGDSKPVSIRIIESDRQIVGTISYYIEDELSMWLEMG

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RMRKCRIVRGQYYDSIRMGMLREEWEQKLAPHTSRNVNN"

CDS complement(3560698..3561369)

/gene="rpiA"

/locus_tag="EFAGFIKM_03045"

/EC_number="5.3.1.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q72J47"

/codon_start=1

/transl_table=11

/product="Ribose-5-phosphate isomerase A"

/db_xref="COG:COG0120"

/translation="MNLKQIAAERAAEYVEDGMKVGLGTGSTAYYAICRIGERVERDGL

NIQAVATSEASDKLAREWGIPVPFDQIGRLDITDGADEVDPFNLIKGGGGALLRE

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ELHRS"

CDS 3561856..3563622

/locus_tag="EFAGFIKM_03046"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKSLSWKSMSFFSKNLLLSFTNIVIIGVALIASSYYFQKTVLVD

QLHGGQVEQITKKWAEDINPAEVQAAIAEGSYDGATQTKLRAYFDEMQEYYPNIAQAYI

FGVELGGDNKRLTSLVAMPTNLREAFQSENVNIGDMYEQPVVAVANALKEMLNDRPTF

TTYFYSDDFGTWTTIAYPIKDSNGKIFSYFAVDADASAVPAGLNSLLKNGIILVAFL
LFLIIQYLVVKNTLSPIRHLIKGIDDVSRGNLNVNIPTGKDDLGLVNEKFNTMVRKIN
DTIVKVQITSQEVNQSAKELYEVSENRSENADSINNNVTQITSNIRSSEQATRDSARA
MSEMATVIQTIASSSASVADEAYEMERRSQQGNVVRQVSEQMNLITESVKNTASAE
VLESRSQEIGDILNIISGISSQTNLLALNASIEAARVGEEGRGFAVVAGEVRKLAEQS
EQATSQVGVLIQEIQAGIKQAVRAMEQGTSEVDTGLSVADQTGQLFEDILEAAKKVSN
QIQEVSSATEEISAGTEEMTATADDLSSSVSKTANSSEQISSSVDEQKASLITLVDSS
TRLNSMSEELQELISHFNVSKQ"

CDS 3563669..3567376

/gene="lgrD_2"

/locus_tag="EFAGFIKM_03047"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q70LM4"

/codon_start=1

/transl_table=11

/product="Linear gramicidin synthase subunit D"

/translation="MIENQPSSSHSMESLPLVLIPLDFGRRQQSFSYQSAQITLHAS
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FSQLCHQVSEQLKIEYTLQNGGYPESFFMLNSVQLPQAPQILNWNVRDDQNMLILDLF
YDSSLLKESTVLRyAEYYQTLALLVRDGEKAIGTVDILSASDRLLYREMNDSVLEP
ENQTVHGWFEATAAAYPDSPAITSKSYTYRELNERANQVARVLLSNGLQKGEFVSI
FMDRSLETIISLLGILKAGGAYVPIDPEHPQERNYSYIVEDTASSFVLTEASYAQASS
LFSSIATVRQILAVDGRLAGFAASNPNDIQPDDLAYIYTSGSTGKPKGALIAHRGV
TNLGSVVQRDCDIQPGDVLTFATYSFDASVWDTIGALFYGAELYLLSAEERSVVEEF
ASAIERTGTIITILPTIFFNQLASYLSDEGFHKLAKVRIITVAGEALYGEQVRAFQR
KFGNQIDIVNVYGPTECTVATTTTHRISQVPEHVVNIPIGKPIHNYKVYIVNEEQQLC
PAGVPGEVYIATPALAKGYLNQPERTEQAFIENPFAIGEKIYKSGDIAKLLDTGLLEY
VGRSDSQLKIRGHRIEIGEIEDHFARLDQIQNVAVIPKESDGQNMLVGYFTSKDGST
LSVSDIKAELTEKLPSYFVPKWICQLDEMPIAPTGKINRKAMVSLPHMERHEDRPDRV
MPETETESIILDAWKEILQHDDFGVEDSFFNIGGDSLRVIHVLVILKPHYPQLKIADF
FAEKTVRALARREALSLSAAEVTDSVTEGMITQLSEHPVELTSQGYPLIREPEHV
LLTGATGYLGSHVLQQLILNSRTRIYTLVRRPSNGITAMERLTNVLEGYFGKQLTDQL

STRVEIIEGDLEQPNLGLSAEQRAYVQDRIDRVIHCAADVRRHFGDADQFAKTNVEGTV
ALLDLIRSKPGASFHHVSTMGIPEDLALSGQWESSLQYDRFPADLHVDNLYSDSKLEA
EKVLMIAAEQGVPSIYRAGNLTCHSETGRFQSNIDSNAFYRMIKAMLLLKGAPAADW
MVDFTPINYASEAIVHLALRQDTAGRVFHICNPEPIRYDELIRSVNRAGYEVELPFA
DYTRWLFDASISKEPEALQLAIAQLEGDGAKDSAYVYACPVTTAYVEPAGISCAKTDD
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CDS complement(3567491..3568111)

/locus_tag="EFAGFIKM_03048"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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YKHTRDVQKYIWRLFWIAIISQVPFMAAFNHYSLNVVWTLWSALLVLFVIDKLPSKLL

GIPIVIGAGWFMEISQMDYGMYGLLLVLFRYFQGPVLVVAHVLLNALYLLLHNSSVQ

MYSVLATAGIAIAQYYQAGFRMKGPRWVWRYFYPAHLAIIAIRWV"

CDS complement(3568189..3568719)

/locus_tag="EFAGFIKM_03049"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLSIPEELSEMQRIRQAGLLDSNEVGRLFNEYRMFYNQNADIE

AARQYIRERMEGHESVILVAETDAESDHGTDESNVMSLSKGLICTGFVQLYPSFSSVS

MGPVWVLNDLYVHPDYRQQGIARKLLQAAQLASERGVLRISLSTELSNKRAQALYEP

EGYAQDTKFMYYELNV"

CDS 3568934..3570379

/gene="gerAA_1"

/locus_tag="EFAGFIKM_03050"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P07868"

/codon_start=1

/transl_table=11
/product="Spore germination protein A1"
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MREAIVKPLLEEAARNEVGPDFITQVVSGETFSLENQHRDSAETLVDDIVTGNAALYI
EGMSGMIIFSIQNYQKRSVPESTNEVVVVGPEAFIEDINVNMSLLRHKIKHPDFKMI
KFTIGKYTKTEVFVIYIQGLCKPEILENVLTSLGDIDMDSSLGVSYLSEFLEDHPLSP
FPQYQYTERPDTVAAALVEGRIGVMQDGTFFSLLIPVTFFSLMQSSEDYYQRFHSASF
IRIIRLLFAVIAFLLPSVYVAVTTFHPEIIPNTNLLITIASARENIPFPALIEAFIMEI
TFEGLREAGIRIPKPLGQTVSIIGGIVIGQAAVQAGIVSAPLVIVVSITGIAAFIIPH
FELGLAFRLLRFPVLLMGGTLGLFGVVISYLLYWVMVSMRSFGVPYMQPFAPLVLRD
FKDTFIRVPWFMMKKRTKAYATDNERRQDTP"

CDS 3570376..3571524

/gene="gerAC_2"
/locus_tag="EFAGFIKM_03051"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P07870"
/codon_start=1
/transl_table=11
/product="Spore germination protein A3"
/translation="MIFRRPPLPIIVVIICLLCTGCWSKVEINERTFITTLYVDKAD
TPGEIEVTLSPMLPNRLSPEGGGTGKDPYAAVSATAPTIADAIERIQTDLTRKISWGH
TRVIVFGQAYAREGIEDTMEWIARQPLFHLSSYVMVANGKAKDVSDLTPVFEETPSDV
LREFSTEENLLKTQVLSIFTSDKMNQGFASSMLASKKTKMVSEEGESKKWVSQIGGTI
FRQMRMVGTLSADEARAVAWAGQNLDSTISVRTKKQKASMKLYRMHSDIHVKLQNGE
PHFVINLTGRAELNSVIPVLKAEDIVGIKDIEQAANEKVSAHLTQAIQTAKHQGSDIL
MLGYRLEWRYPQVWKKLRPTWINYVKNDLQFTVNTNINIQFVGSESSF"

CDS 3571562..3571768

/locus_tag="EFAGFIKM_03052"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"

/translation="MLAVLVFAGLYLLDWSSVKSSKKAIRRAYFILLGLFLVWNTLAV
SWSAWPNPNVDVIQLVFGWADHLIQ"

CDS 3571784..3572902

/locus_tag="EFAGFIKM_03053"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNHLTAGQAYRFMFVYLYSEPVAFLQRLFKMSGYQGWLSTIGG
FLISLIFLFFTYRLGSINPDKPWISYGEDIVGKVVHRFYIGLIVMLCIYLLSIDVENF
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GGGGNPGILLAMATHHDLGEIMMGFSSTMPWFSEWMFFLFLAPVVAFRPMLKSMLFA
GITVIVFVFWMF TLMNFGPYVAAGLRYPLLEMVRFARYGDFLDNLDPVLIAIWSTT
MFTRSSFLLYVASVCLSKLSGIRQQKSVVYLIGGTAAAIVLQYARDAASYELAIRSYA
VPLYTVLIESMPILYVLVYWLRNGKNKKATKASTAPSP"

CDS complement(3572907..3573380)

/gene="fucU"

/locus_tag="EFAGFIKM_03054"

/EC_number="5.1.3.29"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AEN8"

/codon_start=1

/transl_table=11

/product="L-fucose mutarotase"

/db_xref="COG:COG4154"

/translation="MLKNIPAIIPPELLKIMSEMGHGDELVLADGNFPAASHAKRLVR
CDALGVVELLDAILQLYPLDTYAERPAAVMQVVKGDQVPIIWEDYRRLIEEYEGITD
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CDS 3573636..3574058

/gene="slyA_3"

/locus_tag="EFAGFIKM_03055"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:B1JJ73"

/codon_start=1

/transl_table=11

/product="Transcriptional regulator SlyA"

/translation="MDYTLEQSVGFMLGFTHRKAVALLATRFKPYDITTEQFSVLFNV
DRGEGVNQKELAAARVFKDQPTTARIIDLLEKKGWVERRTSEQDRRAYLLYLTTTEGKAL
IDILVPIEREMNKELAEGIPEDQMEAFKHTLSLINRNL"

CDS 3574089..3575429

/gene="yfcJ"

/locus_tag="EFAGFIKM_03056"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_02091"

/codon_start=1

/transl_table=11

/product="putative MFS-type transporter YfcJ"

/translation="MKEQSTQVRLWTTDFILLMLCNFLLFLQLHMIVSPLPSYVQERF
HANAFEVSLFTCLFALSAIAARLYSAKALEKGLRNAMIYIGLSVALLATLGYYFAAGI
AVLLLLRMLFGIGFGMSSTAFPTMASDIVPVKRMGEGMGYFGLSTSLAMSMGPIIGVT
LLQGAGFVTLMLCTAGVLAVIYPLSYSLTRKKEVRTDNSTTIMPQATTSASGSNPKQK
TPFNRLKILPSVLNCLLSITYGGLVG FIVLYGKEANLANPALFFLFNALAVLLVRPFA
GRIYDNKGPKALLIPGAIFVAVGLILLSYATSM SVLFIAAFIYGIGYGS MQSSLQTWM
IQVVSPTQRGMANGMFLNSLDLGIATGALLLGAIAAITSYTD MYRYSVMFMILFLLIY
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CDS complement(3575584..3576885)

/gene="ymfD"

/locus_tag="EFAGFIKM_03057"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31762"

/codon_start=1

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/product="Bacillibactin exporter"

/translation="MNDKKWDLVALASIPLIMTLGNSMLIPILPQIERELKVSAFKVS

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LAVWLWYAPFMAIPILCVLSVLVIFLVKTPRKKEKPPTFSEFVASIRDVLKEKGRWL
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GKNKTRMKWLGFAGLTLTVSLGVIGLFDNIYVVVGLFTLGSAGIGATLPCLDALITE
GVDDKKQRGITALFSSMRFIGVSLGPPVVSLLIGSHHFLFLFGVLAASGAVGGLTLFA
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CDS complement(3576968..3579916)

/locus_tag="EFAGFIKM_03058"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKEYHQYPMWDASLSLEERLDDLIARLTTEEKIRLIPTREAAVP

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ATLKHFFANNNEKDRLNCSSSIDPRNLREYYLKAFETPFVEGGALSMMTAYNSINGTP
AIESPYVNDVVKGWAMRGFIVCDGGDLSQTVNYHGYHTSHAESASGALKAGVDCLTD
EVDLVVSALEEALDQNLLEIADLDRAIRNIFGVRMLRGQLDQSGLNPYASIPESVLCA
SEHAKLSYRAAAESIVLLQNDGLLPLQPEVLQKISVIGPLADVYTDWYSGTLPYRVS
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SQLPDMMDYDIIQNGMTYMYHEGPVQYAFGHGLTYSEFEYEAIRVSRDTTAEATTTDQ
LKIEVEVHNTGQHDSDEVVQIYGSSHTSRVKRAQKQLLAFRRVHVKAGTRVTIRFEVP
VQKLALWDVTRDRYCVETATWAILAGRSSTDIRQSADIEIEGETIPDRPLHLLTFAEN
YDACAGVLLDECLEGRSAVRRAINREEPLYREAQLSWIAFNHNAVQEVQGFEARVAAFG
EEGRLEIRSGGLEGELLGVCEVSGPGGSGVNGKDIKWTTVQCSLVAPHKVNELYIVFLG
GAALRHFRL"

CDS complement(3579936..3580946)

/locus_tag="EFAGFIKM_03059"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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QVTRPVLVHNDLWEANVLVHVENGELNIAAIIDGDRSMFADREFEAILSSESA AFHEG
YDRPLDSSAEGQARRLAYRILSSYFNAYVHEHQVNQPEDGQKYRQRTLDLLEQWKQLG
LN"

CDS complement(3581022..3583340)

/gene="yicl"
/locus_tag="EFAGFIKM_03060"
/EC_number="3.2.1.177"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P31434"
/codon_start=1
/transl_table=11
/product="Alpha-xylosidase"
/db_xref="COG:COG1501"
/translation="MKFTDGFWMTREGYQIQNPTDIRDIVQKDNSVTVYAATKYIRSK
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YGLGERFTPFVKNQIIVDTWNEDGGTSSEQSYKNIPFYLSNKGYGVFVNHPERVSYEI
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TDYDEATVNH FVDGMAERDLPLSVFHFDCFWMKEYQWSDFWDEAMFPDPEGMLARLK
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VNWYKSKLEVLLDQGVDSFKTDFGERIPTDVVYFDGSDPVKMHNYTTQLYNKAVFELL
EEKIGKNEAALFARSATAGGQQFPVHWGGDCSSTYESMAESLRGGLSLGLSGFGFWSH
DISGFESTASPDVYKRWWQFGLLSSHRLHGSTSYRVPWLFDEESVDVVRDFTKLKIS

LMPYLYNSAVESTVKGIPMMRAMLLDFPEDPTTYSLDTQYMFGDSILVAPIFNKEGDV
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DVSLHLFELADGQTAQAVVVNQAAEQELTVNVTRNGSVLDVRAEGAGKPWNIVLRGIE
SVSSVEGGSQVSGANGVVVTAATGANALTIQL"

CDS 3583513..3584433

/gene="chbR"

/locus_tag="EFAGFIKM_03061"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P17410"

/codon_start=1

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/product="HTH-type transcriptional regulator ChbR"

/translation="MERERLREDRIHG NAMYPVSVYPDIQQLNGDSILDCHWHDEMEF
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TFDTVQEKF IGPLVRKTVIPPSHIKADEDWGQEILDHLKRIFADHATRTETCEMSTKA
YLYLIFARMFEHMRPAPLKGT VATGSHDKVERLKS VLG YIHKRYPEPLKLKELADEAN
MSEGHFCRFFKQMVQKTPVDYINYYRVQQACVQLENTD HKIVDIAMDVGFEHLSYFIT
TFKKHKATTPSQYRKMFYENVGMESALVQV"

CDS complement(3584601..3585521)

/locus_tag="EFAGFIKM_03062"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKSKRGYRFILL SCLILCASTACSSKAIADGSVDSYATI HGKL
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IAVDVMDGRSAWGLTESREQIASFLDWIEEYQAQALPNEKFAGIHL DIEPHVHPQWKI
NQASVITQWQGNVEYIVERASRMKMPVAADLPFWLDNYKIPGSTMAVSSWMIRKFDSI
TIMAYRDTAAAIYSVAKDELA EAALLGKTISI AVETKQSKEGDFITFYEEGSAYMEAQ
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CDS complement(3585907..3587766)

/gene="ade_2"

/locus_tag="EFAGFIKM_03063"
/EC_number="3.5.4.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q72EX7"
/codon_start=1
/transl_table=11
/product="Adenine deaminase"
/db_xref="COG:COG1001"
/translation="MNKSSFERPLMADCVPDLVATARGDLPATLVIRGGTLVNVISGE
ILPEMSIAVQGARIAYVGKDVSHITIGEHTRIIANGKYIAPGLLDGHCHIESTQMKVT
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CTELGLDTRRMMLVTDDRSESLLKEGHMDFVVR LAISQGVKPVTA FQMATINTAERF
GVARDIGAIIPGNIADIILLDGR LADVRVGMTIAAGQVVAENGKMTAVWDSFTYPEEA
LNTVKLEANIQPEDLELAAPIAEGTIGAKIIHVTENHVD TNEKHLPVTVENGKV VVST
SGEVCKIAVLERHKQTGNRAVALVGGIGFKSPA AIAMTVAHDSHNLLIIGNDDALMAE
AGNRVIRMQGGVAVVTAAGVTEFPLRIAGLMSTESFEVVA AQSAVSEALQSAGCTLN
NAFM TSL L LALVVIPELR LSDKGLVRISAEGIELVSLFDEVVDNTPVALSGNE"

CDS complement(3588078..3590453)

/gene="helD_3"
/locus_tag="EFAGFIKM_03064"
/EC_number="3.6.4.12"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32215"
/codon_start=1
/transl_table=11
/product="DNA helicase IV"
/db_xref="COG:COG3973"
/translation="MSTDQQWNEEQQRVNTVTDQIERKITTLEDEVGSFRDEVVGMRK
DFWDEV TMNFSEADDVGETSTSMRQQSQVLSDRERSHLNTAAALDKMKRLHHSPYFGR
IDFKEDGY PNAERIYLG IASLLDEKEESFLVYDWRAPISNLYYDGAPGPITYHTPSGE"

ISGDIEMKRQFVIRDGRIRFMFDGTIGDELLQAVLSRTSDAQMKSIQKEQNR
IIRNDRTRMLIVQGAAGSGKTSALQRVAYLLYKYREHLQADQMVLFSNPMFNSYVS
TVLPELGEENMLQTTFQEYLERRLGREYQLEDPFIQLEYVLTGTEDPDYDVRMSSIRF
KSSETFLKVITRYKESMLSGGMKFKPVRVFQGRAIVTSEAMAEKFYSFESSVKLVSRLE
MLRDWMLKELSAFGKGELDAPWVDQQLDLMEPEDLQRAYQRLKRKQKGKTHTFNDFEQ
ERGILARMVVSRLKPLRKWIKSLRFVDIRQLYAHLFNDQAQMERLLGDEVLPQWDE
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RLFPRAKITALGDFNQAIYAHSSVLSGTGPLTNLYGPDNTEVIELTRSYRSTREIVEF
TRGMVPGGEEIIPFNRSGEKPVKVIVSSDSERHMNVITDLKHLIKEGYESVAIICKTA
EESRDVHAALSKALPTAPKLIKTTLAFEQGVHVIPAYLAKGVEFDAVLIYDGSAEQY
AQEHERKLFYTACTRAMHLLHVYCVGTPSPFITAQSEEKYDLGKVSAAQVD"

CDS complement(3590699..3591160)

/locus_tag="EFAGFIKM_03065"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIIIEELDAELMEWLSGTNLEHKQHEAMQLLTVSKDHWPHQAMIS

MGEVIAINPHQLRLALWQGTQTSMNMSKTGKATLIAVQGHRLHIRIEVERLPKMGGA

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CDS complement(3591341..3592408)

/locus_tag="EFAGFIKM_03066"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSFGARVLKTGIAVTLALYLSSLFLNPQSPVPAAIAAIFAMQPS

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TLVTVVSIMEASGDWHFALNRFLLTLVGIVSAFLINITVFPPKPKVQFVKQIHSVFSG

MSLLLRTSISDEIKEVVFREEKSNLGGSIKSLSDKYNLFEEEQKKMKRSTFSETRQMV

VYQMMLLSLQKGYEVLDSVERHYFQAPRTTAMDQFFDSHLELVIKFHEHALLKFEDKL

KPNGEEAAQFVLNDNDRFMEQAITQFDIDKEGMLRLSIVAAAIYDYGQLERLNRLAEH

VHSASEDKESQDKILNWLKWP"

CDS complement(3592709..3593431)

/gene="yedJ"

/locus_tag="EFAGFIKM_03067"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P46144"

/codon_start=1

/transl_table=11

/product="putative protein YedJ"

/db_xref="COG:COG1418"

/translation="MSENPLQPGGNLQELGHMHNIDGITAGEAVLRAARSFVQGDSSK

HSDGHDWPHIERVTALAVELAHRMGADPFVCELAALLHDVPDEKLNESLEAGMAKLND

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QRHDYMVQFVDQFKREWEGTDR"

CDS complement(3593433..3594872)

/locus_tag="EFAGFIKM_03068"

/EC_number="1.1.1.38"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P16468"

/codon_start=1

/transl_table=11

/product="NAD-dependent malic enzyme"

/translation="MNQRNLDGNSIIIRLEMTTKDIKFGEVASAISEAGGDIIAIDVI

STNQDVSVRDLTVAVTDAQDNSKIEGVRQLKGVSIINVSDRTFLLHLGGKIEVTPKT

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AAMPVMEGKAMLFKQFAGVDAFPICLDTQDTEEIIRTVKAISPGFGGINLEDISSPRC

FEIERRLNEELDIPVFHDDQHGTAVVLYAGLINALKLVGKSIEDVKIVVCGIGAAGVA

CSNILLSAGASRLIGVDREGAIVRTQTYENEVWSDYAARTNPELETGSLRDVIRGADV

FIGLSRGNLLTREDVQTMEDPIVFAMANPVPEIMPALVEDIVAVMATGRSDYPNQIN

NVLCFPGIFRAVLDCRATEINEEMKLAQAIAITDEERTRYIIPSVFNDKVVKS

MRSRVIEAAVKTGVARRIPREQAREGGES"

CDS complement(3595083..3597155)

/gene="bglY"

/locus_tag="EFAGFIKM_03069"

/EC_number="3.2.1.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C8WV58"

/codon_start=1

/transl_table=11

/product="Beta-galactosidase BglY"

/db_xref="COG:COG1874"

/translation="MTYKFPPVSSKAPHMLHGADYNPEQWLRYPEVLEEDIRLMKLAK

CNVMSIGIFSWVSLEPEEGVYTFEWLDQVLDRFAANGIYAFLATPSGARPAWMSAKYP

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MNLDWRRFVTDQTADFIVHETKPLKAQNPDLPVTTNLMEFYGGLNYWKFADILDFLSW

DSYPTWHDADDDAKQASRIAMMHDIRSIKGGQPFLLMESTPSSTNWQDVSKLKKPGM

HLLSSLQAVAHGSDSVQYFQWRKSRGSSEKLHGAVVDHVGTEHTRVFQDVTDVGTALE

GMEAIVGTAVPAEVAIIFDWENRWAVNDSQGPRNIGVKYEQTVEEHYEAFWKKGVAVD

VIDMDADLSKYKLLIAPMLYLVREGVGERIEKFVEQGGTFVATYWSGIVNENDLCFLG

GFPGPLRKTLGIWSEEIDGLHDRDMNGIIEPKGNELQLNTAYDAIELCDLIHLEGAKS

LATYRSDFYAGRPALTVNQLGSGKAYYVATRLKAPFYDDFYAKLIADLNIERGLETEL

PAGTTAHTRTDGTADYVVFVQNYTPDEKLVELDGQSYTDLLSGDAVEASLSLKPYPICV

LRRPAARK"

CDS complement(3597245..3598330)

/gene="ganB_2"

/locus_tag="EFAGFIKM_03070"

/EC_number="3.2.1.89"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q65CX5"

/codon_start=1

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/product="Arabinogalactan endo-beta-1,4-galactanase"

/db_xref="COG:COG3867"

/translation="MSNLTEKTFILGMDVSMDEIEQHGGSYSDVDGKEQNLLSILKI

NDANAIRLRIWNDPVGGFCNLERTVEIAKRIKEQGLKFLLDHFHYSDRWADPANQWKPK

AWEHLSYEELQRAVCMYTADVLRTLKEHDALPDMVQVGNEITPGMLWNEGRVGGEEHD

TDEQWERFAGLVKYGIAAVKSVDADIQIMIHIDRGGDNAESRKFYDRFEALGVEFDII

GLSYYPWWHGTLDALRDNLHDLAERYGKPINVVETAYPWTLEQPEGIEWILNQEDMLL

PGYPASVEGQTKYLKDLLQIIREVPGGLGHGFYYWEPAWIPSKEEWSVGHPNNWGNLT

MDFDKGRKLESFTALATAEESDVVTYV"

CDS complement(3598363..3599241)

/gene="ycjP_5"

/locus_tag="EFAGFIKM_03071"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77716"

/codon_start=1

/transl_table=11

/product="Inner membrane ABC transporter permease protein

YcjP"

/db_xref="COG:COG0395"

/translation="MYHKSLPYRVFNIVNTCFLILIAIMCIIPMVHVLAVSFSTKAAA

DANLVNLWPVGFSLEAYKKTMMNNPIFLNSLWISLLRTVIGTAITLLITFLAAYPLSKE

NSEFKGRTIYSWIFVFSMIFNGGLVPFYMVVIQKIGLMDSFWVLVLPGAVNTFLVILML

NFFRGIPKELEEAALMDGANHFRTLFRIFLPISMPSIATIALFSMVFWNSWFDGLLY

MNNAKDYPLATFMQTVIIGRDMSSMSMNPKEMEALSQTTVRAAQIFIGSAPILIVYPF

LQRFFVKGMTLGSVKG"

CDS complement(3599271..3600161)

/gene="yteP_24"

/locus_tag="EFAGFIKM_03072"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system

permease YteP"

/db_xref="COG:COG4209"

/translation="MRTLKRTWPFHVMLLPAIIFLIIFSYPVMGGIVMAFQNYKPWLG
ISGSEWVGLDNFRYLFEREDSLQVIWNTLIIAVLKLIFNLFVPFVFAILLNEVRKMAI
QRTIQTLVYLPHFLSWVILGGILIDLLSTGGLVNRVLGTFGLGPYFFLGDNSWFRSTV
ILTDVWKEFGYNMIVFLAALAGINPALYEAAEIDGAGRWKQTLHITIPSLVPMLMVVG
TLALGNVLNAGFDQIFNLYNPLVYQTGDIIDTFVYRSAMQNGEMGFATAIGLFKSVIS
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CDS complement(3600351..3602036)

/gene="lipO_9"

/locus_tag="EFAGFIKM_03073"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37966"

/codon_start=1

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/product="Lipoprotein LipO"

/db_xref="COG:COG1653"

/translation="MRAQSTKKRFLTLLATTLSLTVVLGCSGGSGGGDSATPSTSGT
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EQDPNVWNQYSRDGKRMGIPVLDYAYNNDYLLWIRQDWLDKLNMKAPKTIDELEAVME
AFKNNNPDGLAPDKVTPLSIGFKTSMNTWMGDPSWIFGAYGTLPFQWNLGEDGKLEYG
SINPGMKQGLTKLSEWLKKGYPQEAALWDENKTAEPVAVAGTAGIIPGPYWMSGWPLL
DTVKNVPSAVWKPIEPTGPEGKAMRHGTQFVNGVTLIKDMAHPEAFFTYQNYLFDN
YADPAPGSQYDNLGAFGYDYQLDADGKQMPIDEIEGGYVNVVRYLLVRD GARIPDAQM
KALMNLANGKEPETKLEKDVAVNYGKETPAAAKVLLSQEEISFKNMFTGPTTQTMKSK
LDYLNKIENQAFNEIYGKNPVDAFDTFVQTWKSGGGDQITQEVNEWYDSVKK"

CDS complement(3602160..3603788)

/gene="rssB_7"

/locus_tag="EFAGFIKM_03074"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00958"

/codon_start=1
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/translation="MIDILLVDDETYVTESLELTIPWGELGVTTVLRAASGKEALEIM
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ITARALREQLQQYEIHIDPEQSAVMMLIRLTGRFSSMDQQSLDLMDFAVGNI AEEVLG
EQFNVWFGRGPHECLVMFLQNQDQIEAPQMDLETLRISAETFREHVIRYLQGDLSMVV
TPSPFPNELTAAYRKSLSGLVLSGPPEHQIYMDMDQALSKRPENDATQALEELYKPP
VLPQLLETQKWEAAARKLNTVFDAAEQVRLSREHVYEMYLSVTNAFMYIAHKQGHLVH
EIDHAGFDLLLAHQLIQSPEKLRRWATEMLAKLQEELSDQEGVQSRRHVIKQVQELVT
RDTGQDLSVKLIADKVYLHPVYLSKIYKAETGEGLDYMIRMERMERALYLLKNSNKKI
YEITSELGYQNPQYFSKMFKKHYGMTPNEFRDQA"

CDS complement(3603862..3605616)

/locus_tag="EFAGFIKM_03075"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MSYRTNLFSKMVILILIMLIPVLLYWYSNHKTTAVLRDELNRS
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RFMFSWITVSPYGIKDPANNAETIIKLEFSDNIRDMLDKFKDDGRHDPFYFREESGV
IYNRTSDRSLTNQLMEELSIHKLQDVDNRTVVIGNEPYMVNTVKSSTTGWYLV DY MPL
SDILKPIHQSNMLFYSSMICLLLSFGVAYLFYVQVQVPVKQLIRGFQRLKQEDYSVR
IKPKGRNEFSFLSERFNL MVEQIQQLFEHVYLEQIHVREARLKQLQSQINPHFFYNCF
SFITSMAKLKRMDAVVAMSHNLSRYRYTTRQERDVVPLTEEIEFVSCYLEIQRMRMD
RIHYKIDLSDEMLRQEVPLIVQPLVENAVIHGIEADAEAGEIRVSGEKQGGVMVLVW
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CDS complement(3605915..3606613)

/locus_tag="EFAGFIKM_03076"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSRTRLVFSGALLLFAIIFTCNHHLGFSVGDMLSAIGISPYTT

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SYKFKDDPLLEALQSVQLRPVHVEIKRHGFTTGKLEFYGKAESPLFVNGKLMDIVLDV

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CDS complement(3606795..3608324)

/locus_tag="EFAGFIKM_03077"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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GVPTNKELAATRGLVLRKDLADKYKDLTAVKTWADLEPLLKTIKENEPAITPFYMSN

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NSDAATSNVFPKDQAKAGKAFLWTDGMKPGKDKEEGYVGFPLTQIEMTQPTITTGDA

SGAMLAISRSESEQPEKAMQVINLLHSDKEINNLLNFGIEGTHYVKKDGQDNIIALPDG

VDANSRTYNPGAQWQLGNQFLNFLWDNEDPQKWEKFKEFNAKGVKSPALGFTFNSQSV

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/locus_tag="EFAGFIKM_03078"

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/inference="similar to AA sequence:UniProtKB:P94530"

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AraQ"

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CDS complement(3609384..3610370)

/gene="yteP_25"

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/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

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/product="putative multiple-sugar transport system

permease YteP"

/db_xref="COG:COG4209"

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CDS complement(3610551..3612164)

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/locus_tag="EFAGFIKM_03080"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

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QRITLTEQRLQELAELYGAEIDPHARVLPVISVEEWVRDFDLRDEEVLEYALRNAAK
EMLLSDKPGEVFQDQSGLNIVLAYEQDGIIPSASEVAQRCQGYIQECGYFYCRLSCY
VGAPVAVTELQGMLNELMDMERRNIKEEEVFYDERGRDQEDRFLPIPWFSLSILF
ETGKVGDLRERVDEIFELLAAQEGLSPEMLHLYYHAMLHVYPLLHQKNVSIRSLYPG
EREPEESMVTRSLPQLKQWTADLIDRVIPVLYPDDHSPMTIVDQLCVYIETHIGEELM
REELAAFAGFNPAYLSRLFRKEKGMSLSEFILQGRVAKAKTLLSQSTVKVTDIAGKVG
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CDS complement(3612139..3613938)

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/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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STLNTAQIQLAAAHLPGLKNPYQVISEVVNKGARQYLMLGASAMSQMNYIVLLPEE
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DPPSSSELEFMTRSFNQMTSEIRHLKIDVYEEQLRTREAEFKQLQMGINPHFYLNLSN
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RFDFFELDIEPNLGHYVIPPLTIQPFVENAIIHGFQRRRTQAFVIRIVARLGQKSSGQVD
GTVLQLMIVDNGVGFEELLGRLQHGQYAEDPSGQHIGIWNVAHRLLVKYGDQASLQF
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CDS complement(3614148..3614285)

/locus_tag="EFAGFIKM_03082"
/inference="ab initio prediction:Prodigal:002006"
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/product="hypothetical protein"

/translation="MHVKIGRSWSPGLAAAFIFREKLLSNNEGFFLQLENLLLHEACY
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CDS 3614337..3615779

/locus_tag="EFAGFIKM_03083"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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HSPNAISGTVSTEPSSSSEAVSTSLPTDQPVERQAMSLRLQKAFALLIPLLFAVDVIL
MFVLKLQGGDATALIGGTAVVILIAVTAAHRHAGPEETTNYLIEGFQFGFKVFGPVI
PIAAFFYLGDAAITELFINPLPEGSHGIVNDLGVALAGLVPLNDTVGAITMTVTGAVT
GMDGSGFSGISLVGSIASMFAGSADSAPVLTALGQVAAIWVGGGTLPWALIPAAAIC
GVNPFELARRNLKPVLLGLTVTTIVAIFLI"

CDS complement(3615799..3616392)

/locus_tag="EFAGFIKM_03084"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MVQGGEMSTEVMAHLASGNTRQQDAYHVLQSSGLLDILADYHPY
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CNLQVGHWPEIFAQSVPVYRQNAYLHMIVEWRLLQLWGDAGHREIRRLKQVGWKTEP
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CDS complement(3616395..3616601)

/locus_tag="EFAGFIKM_03085"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNGQQRVNIKPGLEVDIVLKQDQATGKLTRGIVKDLLTKSPTHP

HGIKVRLTSGQVGRVKQVITGGSN"

CDS complement(3616816..3617604)

/locus_tag="EFAGFIKM_03086"

/EC_number="3.5.1.104"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81AF4"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0726"

/translation="MNLKAARFIGMFTLIILLGSSSAYAKPVQKNRQYYEERGEIVWE

VPTQDKLIALTDDGPDPIQTPQILALLQQYHAKGTFFVLGKWADKFPKLIKQEQLEG

HEIANHTYAHTYAVRSTRADKYMKDMNEAESSIIKAGAERPLLFRPPGGYYNDMVIQA

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KTILPKLQQQGYQFVTVSELLAVKAREAAKDGTSPSSSLKNVKP"

CDS complement(3617546..3617671)

/locus_tag="EFAGFIKM_03087"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSSGESGNANREFTYEDKVRTPHEPEGSPIHRNVHANYFAG"

CDS complement(3617671..3618609)

/gene="iolS_2"

/locus_tag="EFAGFIKM_03088"

/EC_number="1.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P46336"

/codon_start=1
/transl_table=11
/product="Aldo-keto reductase lolS"
/db_xref="COG:COG0667"
/translation="MAEQQIRLGKTDLIVNPIGLGANAVGGHNIYPDMLNDETGKEVV
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SPAFLKTAVDEALKRLQTDYIDLFYIHFPDEHTPKDEAVDTLKQLKDAGKIRAIGVSN
FSIDQLREANKDGYVDVLQSEYNLFKRDAEKELLPYTAEHNISFVPYFPLAAGLLGGK
YNRDITTFQDGRAKNPLFTGEAFIENLDKVEQLRSIAQSKDVEVAHLVLAWYLTQPSID
ALIPGAKRPEQVINNLQTLNVELTAEIIVVDQIFR"

CDS complement(3618719..3620743)

/gene="nhaK"
/locus_tag="EFAGFIKM_03089"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32212"
/codon_start=1
/transl_table=11
/product="Sodium, potassium, lithium and rubidium/H(+)
antiporter"
/db_xref="COG:COG0025"
/translation="MEIFIAVLVLLVLIGLSNINRFVPIPIPLIQIVLGVAIALLP
AGVHLPLNPELFFVLFIAPLLYNDGKRTPRNELWNLRAPILLALGLVFVTVVAGYA
IHWLIPSIPLPAAFALAAILSPTDAVAVGAMAGRVHLPKGIHRLLEGEALMNDASGLV
AFKFAIAATVTGVFSLANATFSFILIAIGLLAGALLSFLIRLGWWIRRLGMEDVTI
HMLLQILTFFIYLVSEEIGVSGILAVVAGGIIHAIERDRAESVQLKMQVVSASTWSV
ILFILNGLVFVILGVQVPDVLSTIFENVSFNNLQVLGYVGLISVLLLILRFLWIYLFW
QGNELLRTKSSIGRPRFKDITIISLSGVRGAVTLAGAFSIPYVLQDGSPFPERDLIIF
LAAGVILFSLIAASVFLPVLAADDGKSTEETPQKSERKAHDIMLNAAIRAVKSEMND
NKAALAVVSDLSKYIRQAAGQLTADKRKDIQKQETAINLIATRAERKEVEVMLDENA
IASDAAFKCDSWLDRKEMMLANRTNTQFMTSISEIGRVLGHLFTNRSQKPNQPFMLEN
AELFRQVKLRTSEAAIKAIRAHMNDGNRVVALSVIAKYERVIKLRWTWNQGKTEDPFN
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CDS 3620945..3621244

/locus_tag="EFAGFIKM_03090"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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CDS complement(3621341..3621823)

/locus_tag="EFAGFIKM_03091"

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/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSPDTERNSQLANVDQLLEAFFRYKNKVLDQQQKTETNCKLNPT
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CDS 3622094..3623209

/gene="oxyE_2"

/locus_tag="EFAGFIKM_03092"

/EC_number="1.14.13.232"

/inference="ab initio prediction:Prodigal:002006"

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VGIHVPQDHLLEAIVSHAQQHSSYEQVLFNTIMTGLLRDKNQVVGINIRQNGVPASI
EASVIVGADGRYSAVRKHSGMTPKVRKHGYDLLWARIPAPVGWEPVRMASMDGQQLA
LFSQFGGYVQIGWNIPEGAYSKLREQPIAPFVDKLVSAFPCLSDSVAANIQSWSDFVL"

LSVESSYCQLWAQENVVLIGDAAHTMTPTGAFGLNAALEDADVLSSELLVQMAVDQFSS

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CDS complement(3623327..3623554)

/locus_tag="EFAGFIKM_03093"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSFVFYPEMVIFILMLILLIIGIVYIVRKSKQVLRRLSNLEKAV

YEKDNISSYPKDVDTVQEALREDTFAPRKRK"

CDS complement(3623768..3626344)

/gene="lacZ_4"

/locus_tag="EFAGFIKM_03094"

/EC_number="3.2.1.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01687"

/codon_start=1

/transl_table=11

/product="Beta-galactosidase"

/translation="MKTYNSSQDISGQWKIQHFVGEKRAMDVAAAALDDRFWIGAEV

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SSYTKERPWLRKAAMNFGWDWGPRMVTVGIWGTVRLEKRTIAKLENVYARTESVSSEL

AVLHVTADVKSVLSYRSRQKREQAVVATCNVRLDRSGHEVAGVTELPVEGGKADTIL

NVTSPQLWWTHDLGEPYLYTLEVTLLADGVEVDYSEPYGLRTIELALHNERGEDAFT

FILNGVKVYAKGANWIPADHLIGAIPNSRYRELVELLVEGHMNMMLRVWAGGIYEKDV

YDECDRQGVLVWQDFAFANALFPDFNRDFMNNVRQEVENNVRLRLNRASLALWCGNNE

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TLEKNMPAGQFYWGSPMAYRNKDTNHQKGILLMEGYTGIPQNIEEYMNYSMLTQADG

LRYGIEHFRRINHRNSGALVWQLNDSWPGTSWSMIDYELLPKASFYYGKIFFHPVLLS

LEHEPGEPLALWVVNDTQDVLKGELRLNVYALNGEKIYSSSHVVEVTSQSSRCIAELT

EVEVLQGRRAEEVMVELVSEGFAAPSNRYFLRDPKDVTLPESQLSVHVNEEEQSVTVT
ASGAIALVKLELPLGRVRFSDNYFDLLPGESRTVRLRHPEQSSLPLTELRSAMNGR
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CDS complement(3626435..3628021)

/gene="rhaR_30"

/locus_tag="EFAGFIKM_03095"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

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/product="HTH-type transcriptional activator RhaR"

/translation="MRLLIVDDEVIIRTGLASVIAWHELGIELLQPAASAEALTRMA

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FLRSDAGKEAGVGDLNDEQILRQVIILRAEGWDRSSDALLRFAVQNTLEDMLPGAIAH

VEKQQIICVSWPPVEHETFRLESALRRVEQLLKCTLRAAVGLAMRGYADLHESYST

ASAAFRYRGLMDYKVWHYEHIQDRQGGKTVLTHEEETRLGTILLDNDSVTLTTWTREL

VANLITEPEVTPDSFSACLHSAIIAGHRWLTRTMRATGREEPARLEPWLPEPDAEAGD

LGDMLFHHLGLMHVYHSRMGQGQAAHVQKAIGYIESSLAHDINLQLVAGHVHLHPGH

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CDS complement(3628018..3629799)

/locus_tag="EFAGFIKM_03096"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MARWLTSSLQRKLSVVVTASMIVPLLALGLFAFLISSRITEQKT

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AGIQNVITLVRPIRSIHDIRPIGWLAISLDEKAISKGWAALGLGRGQGRLELIGSSGE

ILSSMDKSRLGLKLEGVEPGISTLIQDGGSGTTTYGSGDDKRTLTYPEELTGWTLVG

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PLPLFRSESDDEIGRLGESYNLLGAHIQLLKEEVIRGEARKKEADLRVLQAQINPHFL
YNTLSSIHWIALMSEEKRIADMVEGLSDFLRISLNNQDYCPVEQEIHIRHYVRVQS
IRFPDQFVLHYIVDPALEKRMMLKLLLQPLVENAMIHGIQPKAGVGTITIMIRKDPDN
EQMNVLVLDDGIGMEPDRLEQLRISIREWKQKQPEKQLNQGGYGLCNVNERLLLHYGA
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CDS complement(3629830..3630705)

/gene="ngcG_4"

/locus_tag="EFAGFIKM_03097"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O50501"

/codon_start=1

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/product="Diacetylchitobiose uptake system permease
protein NgcG"

/db_xref="COG:COG0395"

/translation="MRVTPVSMSPQSSSGHPIRRRLRSGIVWTLTVYGILTLYPFYW
LVISAFKTNEDFYSRPFGLPENWNVANFSAWESSRLGTAFGNSLIVSVGSLILTLFI
AALASFILARFQFRWKGLIMTFFVIGMLIPIHSTLVPLFILMKQMSLLNTYWALILPY
TAFALPTAIFVLTAULTSVPRDIEEAAFIDGTGLWGLFTRIMLPMSVPALSTVTILSF
LHAWNDFSALVFINKTGLKTLPLAIANFADGYQTDYGLTLAAMTLSVIPTIILYLIF
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CDS complement(3630724..3631602)

/gene="ngcF_3"

/locus_tag="EFAGFIKM_03098"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O50500"

/codon_start=1

/transl_table=11

/product="Diacetylchitobiose uptake system permease
protein NgcF"

/db_xref="COG:COG1175"

/translation="MNALRSRRFIMLGLAPAVIIYALFVFPVVWSAYYGFFNWSGIG
ASKYIGVDNYVEIWHDPVFWRALKNNVIFVLASVFGQIPLALMLAVILHKS NPLQRFL
RSAVFLPMVLSTVVIGMIWQYIYHPQIGILNFLLDALGLESWKLQWLSDDKIAIFSLV
PPLLWSFVGLYLIIFISALQNIPGEIHDAAKIDGASGIRKLVSVSLPIIWGTVQVAII
LCISGSLKSFDLVYIMTKGGPAHATELLATYMYNSTFTTYRYGFGSAISTTIVLISLL
LIGTSQWLTSRKRKEN"

CDS complement(3631704..3633017)

/locus_tag="EFAGFIKM_03099"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLKKWLSGFLAITLFSIILAGCAGGDTSEGGSGNDKVTVTLWHN
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DAMTKEFVKGDLLQPINAELDAKPEWKDNFIPNALDGYTLDGNIYSVPMNLAPSSFIY
YNEALFKQYNVKVPETWAELEQAIATFNQNKVIPMALGNKANWVAQSTIFSTLADRIT
GTDWFLKAAAQEGASFTDPQFIEALNKMQELGNTKAFQDGFNSIDETQMMQLYFQGKA
AMVMNGGWALANLVNNAPEEVLNNTHTILPPVDGGQGEPRTSGVVGTGLGVSKKLS
GAQKEAAMELFYALAGPDGQKATLDSSTLVSYKIDLDKTKAHPLFVELYDLMQEVKIT
PVYDSKLG SATVEVINNALQELLMGGKAEDIAAKIQAAQANAVSQ"

CDS complement(3633275..3635359)

/locus_tag="EFAGFIKM_03100"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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LTALRGDIVSGVLYISNWWWYIFHNVS YFESFGPPSPFGHFWSLAVEEQFYLIWPLLLI
AAIVVFKRKGWL VVFI VAAELSAGAMAIMYNPDLDPSRVYYGTDTRAFALLAGAALA
VVWPSRKLSNSLSGMNRLVLDVSGLAALALLIYMLNSSEYDPFLYQGGMVLQAIATT
LLVAVLAHPSSFLASIIGAKPLRWIGERSYGLYLWHYPVIILTNP AVDTGGAHPVR II

LQVAATVVLASLSLKYIENPIRYNGFRDSWSRLWGRGRSSIGIRNVWWKRALMTIL
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HTHKPAAGTKDDPGKNEKPTGEPAPDSKPDDQDNSVNPBGDQSEDKPADDSTNEND
TPDDAGANQSDDTDDAPDSSQDNEETAPPAQDGKVHYTVIGDSVILDAKPYLEQSISG
VYVDGHVGRQMWQAGDVLEGLKQNNQMGSKVVLELGTNGSFNSKNLNAVLDYLDKEDR
VYLVTVRVPRPWERTVNRALNEAASKYSNVSLIDWNSASEGHDEYFEKDGVLTTQGS
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CDS complement(3635935..3636495)

/gene="flr"

/locus_tag="EFAGFIKM_03101"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9KIT1"

/codon_start=1

/transl_table=11

/product="Flavoredoxin"

/translation="MRQPIEEPIFYSPGMVAVVTSRHEGIQNVMASGWHTYIGSSPG

VYGISLRKETYSYELIEKSGVFGVHFLPGHRSEWIQAAGTFSGRDTDKFTRFGIPYEE

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IPMYTGRSAYRIMDARTEEKIHPFHL"

CDS 3636727..3637374

/gene="cat"

/locus_tag="EFAGFIKM_03102"

/EC_number="2.3.1.28"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P06135"

/codon_start=1

/transl_table=11

/product="Chloramphenicol acetyltransferase"

/translation="MFNSIVLDQWDRKPYFDHYLNQVRCTYSITANLDITLLINELKL

KGLKFYPALIHMISTVVNAHREFRTCFAEGKLGWDEMSPSYTIFHEDDKSFSTIWT

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TYLLIPTMGKYVQQNDKVYLPVSVHLHHAVCDGYHAGVVFNELQSLADRCQDWC"

CDS complement(3637457..3640096)
/locus_tag="EFAGFIKM_03103"
/inference="ab initio prediction:Prodigal:002006"
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VESTADKRATWESKFRSVLEDWKLVPGGRIAAGAGASDELTFNCYVIPSPQDSRGGI
MRTLTEMTEIMARGGGVGINLSSLRPRRAVVKGVNGSSSGSVSWGG LFSYTTGLIEQG
GSRRGALMLMMNDWHPDVLDFITVKQTMGQVTNANLSVCVSNAFMEAVKQDGDWDLVF
PDTNDPDYDTEWNGDMQQWKAAGHSVVHYRTLKAREIWH TIIESAWKSAEPGVVFM EY
YNQMSNSWYFNPIICTNPCGEQGLPGWGV CNLSAINLSKFYDET NHDVAWDELAETTR
ISARFLDNVIDATPYHFEENRLNQQRERRVGLGTMGLAELMIKLRIRYGSPESLAFLD
KLYGFMAKEAYLASAEIAAEKGAFPAFEAPYLQSGFMKNMVATYPKVGEAIRKRGIR
NVT LITQAPTGSTGT MVGTSTGIEPYFAFKYFRQSRLGYDEQFVPIAQDWLDEHPGEA
LPDY YVTAMDLSAENHIRVQAAIQWVDSSISK TANC PADFTVEDTAELYELAFDLGC
KGV TIYRDGSRDVQVLSTSKKEATQAEDQNTAEAE EKT VVSAIENPNNAEVQASDGTS
NSQVGVRTHSSDQTPSSSTVLDKQYRSRPQVLRGATYKINTPFGMAYITINDLEGTPG
EIFLNVGKAGSDVFAMAEALGRVCSLFLRYGDHGHKVELLIKHLKGIGGSGAIGFGAN
RVESIADAVAKALESHVQSNVQENETGALQEQNQVESKYPEVEDQKTFTESRDLCPS C
GSASLMNVEGCKTCSNCGYSKCN"

CDS 3640558..3642321
/gene="rapA_1"
/locus_tag="EFAGFIKM_03104"
/EC_number="3.6.4.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01821"
/codon_start=1
/transl_table=11
/product="RNA polymerase-associated protein RapA"
/translation="MNRKNPHHTNQPV AELPVPLEFDRTWINQLESRLDKGGPWGDYR

LFQLGIAEETNLIPNFDEIQCLKHLQGLTPLPHQMDTARRVLFEMSGRAILADEVGL
GKTIEAGLILKEYMVRGLVSKVLILVPASLVLQWVRELNSKFGIPAIAQKKAYSWQNE
VVVASMDTAKRDPHKDMLLNTDYDMMIIIDEAHKLKNKKTNYQFMLKLRKKYCLLLTA
TPVQNDSMSELFNLINLLKPGQLGRQGDFAAANFVVDKRVKPNQEQLKNELSKVMIRNRR
GEGPVQFTKRNVSNNVLQLSPEEQALYDGVTSFVKDQYQEAGGNLSSMLSLVTLQREV
CSSRDAVFVTLVNLSKKLPLDSPLRDKIWELVAHIKAIENTKAECTMELVRNMNEKV
IIFTEYRATQEYLLNYFRNNGLTAVPYRGGMNRGKKDWMMDLFRGRVQAMIAEAGGE
GINLQFCHHMINFDLPWNPMRVEQRIGRVHRLGQQNDVNIFNLSTTGTEEHILLSLLH
EKNMFEMVIGGLDVILERLEKKESIEKSLYKIILESQTDEDIRRKMDSLGQSLNSIQ
REVSDEGPAVSGLLDLRKGGs"

CDS 3642325..3643524

/locus_tag="EFAGFIKM_03105"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTMSPHEVQAYVLTYLEALDCQIMERSPAHVTVKLSPEADKALT
NRPPYYWGFVERTGAPAETMSFTFIFDPDSYQQAIEAAEIAAQASPPAVPNPDGTNGV
TNGSPQGEPPKETILGRYFGITPSLPQLGPGRILREEVVYGSRRLLQQIFGAAREGGAF
VNLFEQAAKRQLRATAPAVYEPWLGVCFKVEFACDLKREELHFLGISLRSGEIIEKFG
TKLNRRDLSPRLAENMHVQTAKVSLFDAGAALESHLTNRLLDYSWAIEKAQERLDLE
LDVLDITYYEAVLREDMPEVESPGNKTSNTENENVHSDRTPPAPLKVVVDITNAKPIGA
DVELAAEAAPIDSETDAEEEEKAKQAVIDREAMKLQYETRRTEMIWQYEPKVKVTAIS
SGMFHLR"

CDS 3643678..3644685

/locus_tag="EFAGFIKM_03106"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRFFHTCWNNAAQKTTCTLGLLSCLALFSFWSIANAEQKTSS
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GLHSWLVAEFEGKPIGYMIIRATEQQQLMLSEYGHGEQSPYNNELLGQALDRQHVN
EALLAGGGELHLGYALPLLAYWKVEQPNHSALYIDATNGDVLPSFLDLLEADSKQNS
VSITDLSTTPSLSDPLHLRPVFNPADNLLWLTSPVAADRAQDVIQHGENQEIVFSA
GDRNVVYGGPLPVSGYQLWHTDQVAESILYVSLGGKSSIQRVPLSTLQQGGLFYIV
P"

CDS complement(3644841..3645059)

/locus_tag="EFAGFIKM_03107"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAKSDELVKYITQRVVHYIDTPKDERKGRTRKEPWAMKWFGMI

PFAVSLWVGKKEKEFDTKSHKRSSSGKG"

CDS 3645254..3646000

/locus_tag="EFAGFIKM_03108"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYKLLTASVALLISFHCLPILPHHVAHGEEAAPSQNSPSMLPVTD

GDAYRSSHHAFAPVILLDVGHGGIDGGTSAQGVLEKDINLAISQKVYLLLRSGYAV

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VVLHQKEGRSYLLAQSIQDAMNKLYGTEHGVVWGKPFYILNYVKQPAVIVETGFLSNA

ADRARMNDPAEQKRIAQSIANGIIYYLSVV"

CDS complement(3645975..3646814)

/locus_tag="EFAGFIKM_03109"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P44863"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/db_xref="COG:COG2861"

/translation="MMKVQRKIYRFIAGIMALLIVFYAGISAGGPTAAASESTSNQKR
LAIIDDVGNDMKGTAELAMPVKLTAVAMPFLPTTKKDAIAAHEKGMDVIVHMPMEP
KKGRPEWLGPGAITSNLTDEEVRSRVEKAIDDVPHAIGMNNHMGSKITSDKRIMSIVL
DVCKERGLFFVDSRTNFRSVVGELAVSKNMPPVGNDIFLDDQNSKQHIRKQLDLAAQR
AIDKDICVVIGHVGHSGMNTSAVIRESVSRLQNQVQFVGIGDLVRDVWQWQSAPTLPT
DNK"

CDS 3647233..3648918

/locus_tag="EFAGFIKM_03110"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKFKLKKTINVLLACLTALPLMLTPTNVSAANDANINLSSEKQL
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IEKGAIVFASPWNPPSSMVETFNRRNGDTNAKRLKYDKYTAYAQHLNDFVTYMKNNGVD
LYAISVQNEPDYAHDWTTWTPQEILRFMKENAGSIQGTKVMAPESFQYLKNISDPILN
DPQALANMDILGAHTYGTQISNFAYPLFKQKGAGKELWMTEVYVPNSDNNNSADRWPEA
LDVSYHMHNAMVEGDFQAYVWWYIRRQYGPMKEDGTISKRGYNMAHFSKFVRPGYLRV
DATKNPDTNTFVSAYKGDNKVVVVAINRGTSATSQKFVLQNGNASTVSSWITDSSRNL
ASGTSLNVSNGAFTAQLPPQSVTTFVANVTGGNSGGNTGSGTTYEETGTSLTEAAIE
TIYPGYTGSGYVNFNAMTGSAIQWNGINNTTGTKNVKFRYALESGTRNLDIFVNGTK
VISNEPFPATGSWSTWVEKTIQVPMNTGTNTLKVVTTGSEGNIDSVNVTAAQ"

tRNA complement(3649053..3649139)

/locus_tag="EFAGFIKM_03111"

/product="tRNA-Leu"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Leu(cag)"

CDS complement(3649315..3650268)

/locus_tag="EFAGFIKM_03112"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MKAKKIITFVLACTMVFSAVGMAVLPVGTVSAADASGTTASISD
ILKNQLPDGGWRKDYKQTSGEWAKSTIDNKATYSEIRRLAKEFKKTNDPRYSTAAIKG
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ANRSKNSVAKGVEAILNTQVVSGGKLTAWGQQHDSSSLKPASARIYEVPSLTAGESVT
IVKFLKTRPANAKITASIKGAEAWFNKVKITGYKYERANGDSKIIADSKATPIWARFY
EIGTDKPIFIGRDGVVKYNLSDIDKERRGGYAWYGNWPSKL"

CDS 3650832..3651296

/locus_tag="EFAGFIKM_03113"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKLIISIFGA AVLFTSGATSTEASSINSVNNMTGIPYKWGGT
TVAGFDCSGFMRYLFNKYSIELPRTSQQQAKAGTPVSKSNVRTGDLVFFNTTGKGISH
TGVYIGGGQFAHASSSKGV SITKLSNPYFNDRYVTARRVTGQFMYDKMLGKM"

CDS complement(3651370..3651699)

/locus_tag="EFAGFIKM_03114"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTLMNDKVHAYKDQIGALSDVLPGVVKS YHEFTGECFQPGVIDA
KTKQLIALGIGLFANNEVCTFYHVEEARAKGATDQEIMETVAVAGAVGGGHALSQQGAM
RVQKALH"

CDS complement(3651841..3652059)

/locus_tag="EFAGFIKM_03115"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MISDTELDALRLSGEKVRVVRDELESNDVKGI VAWDGEQVLIR

RQNRRVVKLDRGYSYQLFSEPRQSPLSE"

CDS complement(3652179..3652508)

/locus_tag="EFAGFIKM_03116"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGNQPATEQQFNDKLAESKVHFERALDCKHTEFDDLYPYMIEHP

QFFWYKRYVAWSELLTIVGLCEELSFWSKEQFTPHQVEYLEERVMSAKVLDFWFEKND

SKEHAQR"

CDS complement(3652606..3653187)

/gene="xpt_1"

/locus_tag="EFAGFIKM_03117"

/EC_number="2.4.2.22"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42085"

/codon_start=1

/transl_table=11

/product="Xanthine phosphoribosyltransferase"

/db_xref="COG:COG0503"

/translation="MELLKQRILQEGVVISDQVLKLDGLLNHQIDPALTMEMGREFAA

RFRESGVTRVITVESSGIPVAFAAAYELGVPLVFARRKKTLLADPDAYCERVPSFTKG

IVTDIMVSREFIHENDRILFIDDIIANGDAARGVIKIIERSGAELVGFGVVVEKSFQA

GARTIREQGIPVEALVRIRSLNDGTVQFDDNEM"

CDS 3653392..3654447

/locus_tag="EFAGFIKM_03118"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKQAFRVLQIAFTYIGTVVGAGFATGQEILQFFTQYGKWATITI

GLSTMLFVWLGTKMMLIAHDTGSRSYEDLNKHLFGHKAGKWITWVTLILIGVNSVML

AGAGSVFVEHLGLHYQTGLIVTLVGTYLLLGRGIQAILQMNSIWWPMMLLLSLLMITS
TIHHPGASRFITLTDSNPIQVWLSPLLYTSFNLVLAQAVLVPVGNQIRSRNVLKWGG
VLGGIGVGFMLMAAHFAMSAQMPGIIQFEIPMGSIQFQLGWAVQSVYVSLIFMEIFST
FVADIYGMTLQLRQHIRVHPRFITLTIMLLCYSLSQFGFSSLLSILYPIFGSMALFWA
AKLVLNRWGAFRRRNNI"

CDS complement(3654583..3655713)

/gene="mshA_2"

/locus_tag="EFAGFIKM_03119"

/EC_number="2.4.1.250"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01695"

/codon_start=1

/transl_table=11

/product="D-inositol-3-phosphate glycosyltransferase"

/translation="MKLLQALFFPEQPGGVSSMIPYMQERFTTPRWEMDLFSLPKRI

RNKGREEVQFETFDWTEYQDSPVVQKYIQTYPDYLWWTKLRIQKPYDLIAHHPIAGL

AMRTVFPDTPLIQTIHSSYERELILNGRIETDGPENRFLAIYGELEHQAERLLTVSD

SFRRLAPYVKEPDVIGVIPNGFDEKRFKPIPHDNAIPQLVTVCRVPAKGLDILFKA

CAELKGRGHDYVLHIIGDGPDPDLEELAQLGIYNETIFYGYTLHPEEFMPFFDIFV

LPSRAEAFGSVFAEAALSCLALVGTDVGGIPEQIENGSGNLLVPAEDPSALAEALEKV

MLDPAYRYELARSACEKAKTHYSLGRSVNELKKMYLQFPGKA"

CDS complement(3655907..3656458)

/locus_tag="EFAGFIKM_03120"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMHSFRIISQYINDGFQAVQAKPEDTEDVMSLLVETAEWLQSQG

SSQWNALLKGEDSHDTAGAIRRGDVVFVKKGADVAGMVILLVQSPWDIHLWGSKAHA

KDGAIYHLRLAIRRYAQSGLGRSILQWSSSGIHFEGKHTVRLDCGASNATLNSFYAR

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CDS complement(3656563..3657603)

/locus_tag="EFAGFIKM_03121"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKYDVELVADLRTSGGEVQDVMVNGQYAGSLFLVYREGDRLSGS
LQIEQESLPDDTEEFIVEKVHAYVRS LADALEAAYEVLVSCGSLHTVLHMPESETVW
PSEEMNHDEGSYDDIGSSGSKVIPV SQAESFTYEDRDQVLEMEMVSAGRSISTYIFND
VEGQELAEASLKQYGADVQGEIHWYDEPEENQLEAAAELLVRELEDEDIIDTITIRMWH
QGNELETLEWVHRDFSEDLED TDES DLDELEAAEETCYVMLKRKDREFRVYELFLQER
GGLPVG TATIDTSHSDLTGYIDYEVPGTSIQRKSLVEVLMQELDKEMEFDTLH LTM L Y
RNQIIDEARIDG"

CDS complement(3657700..3658536)

/gene="ywpJ_1"
/locus_tag="EFAGFIKM_03122"
/EC_number="3.1.3.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94592"
/codon_start=1
/transl_table=11
/product="Phosphatase YwpJ"
/db_xref="COG:COG0561"
/translation="MRLTDEDEARMTYKLI ALDVDGTLLNDHHELTEWTQETLIQAS
RQGAEIVLCSGRGPANTIPFMEQMGLDGYVITHNGAVTAQVDTREV VHHFALDGQGLE
PIISYCRTNGVHFDINTAFGLYVDQPEGLGLQVREMYYNFMAEPLKLPKWVDMTEPLA
KFTAFGPIEQMDAVLQEWSTWNLPYYMTRSGDFFIDLMHPEASKGAALKRLAESKGIM
PSEIMAINYFN DITMLTFAGKGIAMDNSPDEVKVADEV T LSNNEQGV AHAIQKYVL
SV"

CDS complement(3658848..3659594)

/gene="rluB_2"
/locus_tag="EFAGFIKM_03123"
/EC_number="5.4.99.22"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P35159"

/codon_start=1

/transl_table=11

/product="Ribosomal large subunit pseudouridine synthase

B"

/db_xref="COG:COG1187"

/translation="MSGKGKQTLRLDKILSHMGVGTRSELKKMVKQGRIHVDGKAVKD

SGVQVNPEVNVIEADGERIVYREMIYMLHKPPGVVSATEDNRDKTVLDLLRKEDRVF

NPFPVGRLDKDTEGLLILTNDGPLAHDLLSPRKHVPKTYEARVLGNVDEADVQRFKAG

IQLDDGYETLPAQLTILGQEETEEGTISSISLIIEGKFHQVKRMFQAVGKRVVYLKR

VAMGELELASDLAIGSYRELTADELSLLRK"

CDS complement(3659591..3661288)

/gene="rsmF"

/locus_tag="EFAGFIKM_03124"

/EC_number="2.1.1.178"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01579"

/codon_start=1

/transl_table=11

/product="Ribosomal RNA small subunit methyltransferase F"

/translation="MGVKLPLIFAERMKSLLGDEFEQFMRSYEQSPHAGLRVNTLKIS

MEQFDEIAPFDLRPIPWCEYVPHGVKPGVHPYHAGLYYIQEPSAMAPVELLQVE

PGDRVLDLCAAPGGKTTQIAAKLQGKGVLTNDIHAERTKALAKNVELYGVRAVVLN

ESPERIANAFPHYFDKVLIDAPCSGEGMFRKDEDMVKSWEHHSVEKCVLMQRDILETA

ARLLAPGGTIVYSTCTFAPEENEAMIAEFLNVNRDFVMDIPEETGFAPGRPEWVRQM

MPEKAEETEAVLDQTRGTARLWPHLLEGEHGYLAVLQHRAGQEVETDQPGVVKEGAME

YGQVVDVSRIEVEGNKDHSIAASSIAMTKADRKKERLLRIESRESHDRQAGGGKNSGR

QSKKGKDHGGRKSERGQGRGADSASIDPVAIYSQFMKEQLKIETGETVCYGDRVYQS

SVGAARLEGLKVIRPGWFMGTIKNGRFVPSHPLACALNASEARRSVNLSSADGEAVRY

LKGETLNIEEERVLLKADTVAKGYVLVCVDGYAAGWGKWLDGVLKNEYAGWRWTSV"

CDS 3661510..3662058

/locus_tag="EFAGFIKM_03125"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKS KKKKKSAAILIFLGILIIIMIAALVVVDQQSKKQMDSVENAY
GIAASKLN PATRELLSDPNYQQIIVPTDLKAKIDNKDSFFVYFFASDCSHCRATTPQL
MPLVDSEGIELPQFNLRFEAGWTDYNI EFTPTLVYYEAGVEKDRMVGG LQENGSDQG
YTLDDYKQFFQKYKGSATPSAS"

CDS complement(3662276..3662758)

/locus_tag="EFAGFIKM_03126"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSIYEPLYVDYLIYFN RDQDYFECHEVLEELWLERNRDSFYKGL
LQIAVGLYHFRNGNLRGGTMM LQSSLDLLEPYPATILGIDLGALVRNVQEIVKQLSQS
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CDS complement(3662745..3663560)

/locus_tag="EFAGFIKM_03127"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDGRDWGTFLLPYEQAVEELKV KFKTMRAELKKREEYAPIEFVT
GRVKKISSILEKSRRNLN VSLDDVETGIEDIAGIRIMCQFVDDIRRV AEYIRGRKDLTV
LIEKDYITNFKESGYRSFHM IIEYPVQTALGQKKVLAEIQIRTLAMNFWATIEHSLSY
KFREGLPDEMRTLKKTAEAA FILDNEMSAIRLQILEAQKAFEDDSNIVSRTLNIHQ
LYFYHLVSEAIEAQKR FNDYWERHDM EGLKDLLDDVKLLNNARKGENPDEHL"

CDS complement(3663696..3664793)

/gene="pyrD"

/locus_tag="EFAGFIKM_03128"
/EC_number="1.3.5.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P9WHL1"

/codon_start=1
/transl_table=11

/product="Dihydroorotate dehydrogenase (quinone)"
/db_xref="COG:COG0167"

/translation="MLYRSLAKPLLFKMDPEQAHHLIIGGLSGVGSIRPVPSGLRVMY
GVRETSDLAVDMFGCHFPTPVGLAAGLDKNGQAVTGFSIGFGFMEVGTVTPLAQPGN
DQPRLFRLPPDEALVNRMGFNNLGAEAMAGELARLQDRRIPVAVNIGKNKATSNEEAH
LDYSKCIQALYDYADLFVNNISSPNTPDLRNLQHGNELKELLAAVMNEMNVQHARAGG
ATKSVLVKIAPDVNDQELEYMVRTIADSGVAGIATNTTISRGLSHQHAKETGGLSG
KPLRDRSTEIRQIYRQTEGKLPIIGSGGIFTSEDAYEKIKAGASLVEIYTALIYEGP
EVNRRIHAGLRELLRKDGYRHISEAVGAEHR"

CDS 3665049..3665186

/locus_tag="EFAGFIKM_03129"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAPKRKPPALQQKKEEVNRKAIAWTAASVGGLIIIGALIIIAN
M"

CDS complement(3665229..3666671)

/locus_tag="EFAGFIKM_03130"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQNTHLRTYVKKHPDNKMAWYLLGKEYLGEGQEAKANYCFQQAG
EVEAFERSKAPADIWVDYQDKLVEMSEQKEKKQRRRKMWLTLLMLLVLAGLPADAP
GFSREAADALSAALESTDDIEAPVEADKQVGTASIAPSNVFTAAAFGGGNHGEAALAA

AWSGSGPKVETSAVLGMQTSDDWSLWKRNPVKYIVQTNNTSGKLTAQSYDAKQCNCPE
PEITPKIKKIALAWTAKQEAAASLSSAIVAYRKKNDAWPKSVTQMAQPFNNILGETA
SGMTEMFPKLLALHQGKVQEGKNDSSGKENGSTTSNSSQSKNAAFADTLGGQPFLQEP
LEIVIDKDKHKLALISGDTIVRMYDVGLGGDRTPEGSFIITDKVVNPNGRSNGEFGSR
GMQLSNTNYAIHGTNEPDSIGLDESLGCVRMRTGDVEELFALAPQGTPVRIGEDVLPD
LTLVPEAKQRYQH TLV PKQNNPNKTYHWLN"

CDS complement(3666892..3667134)

/locus_tag="EFAGFIKM_03131"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P10245"

/codon_start=1

/transl_table=11

/product="Ferredoxin"

/translation="MSKYTWVEKDTCIACGACGATAPDIYDYDDEGLAEVIFDGDANH

GVKAIPDDLFDMDQDACDGCPTDSIKVADEPFNKEG"

CDS complement(3667251..3668555)

/gene="dinB_3"

/locus_tag="EFAGFIKM_03132"

/EC_number="2.7.7.7"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q47155"

/codon_start=1

/transl_table=11

/product="DNA polymerase IV"

/db_xref="COG:COG0389"

/translation="MMSSDGNPPANVDQYYPAAGRVILHVDMNAFYCSVHEAEEDLY

RGKATAVAGSSELRKGVIVTCSYAARNRGISTGMVVHQAMKKCPDLIVIRPDFHLYRQ

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GIAPNKLLAKMASDLKKPNGISILRMRDVPRILWHRPCNEMFGIGKKTAEKLLKLGIE

TIGQLAKSDENMLTELFVNGAWLKNSANGINHSVHAEREANKSIGHTTTLPADVSD

MNEIHRVFLNISDQVARRLRKHEMFSQGIQITIRTPDMKTITRSRLMEVPTEDAKVIY

REACKLFEKHWGSGKPVRMLGVTLQNLIPREESAVQMDLFEYEQKPKKDNLIRIMDQL

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CDS 3669084..3670703

/gene="cimA"

/locus_tag="EFAGFIKM_03133"

/EC_number="2.3.1.182"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q74C76"

/codon_start=1

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/product="(R)-citramalate synthase"

/db_xref="COG:COG0119"

/translation="MSKAISIFDTTLRDGTQGEGVSLSADDKLKIAKKLDDLGVHYIE
GGIPGSNTKDIEFFKRVKELNLNAKVVAFGSTRRKGSVASEDANLKMIESGAQAATL
VGKSWDFHVHTALQTTLEENLSMIYDSIAYLKQNGMEVIFDAEHFFDGFKHNPEYAQA
VLTKAHEAGADWLVMCDTNGGTMPNEVHEIVSTLHRSLPHAHLGITHNDCELAVANT
LSAVQAGARQVQGTMNGYGERCGNANLASIIPNLQLKLGYESVTEDSMRQLTNVARYV
SEIANVNMPINQPYVGNAFAFAHKGGIHVSAILRDSRTYEHIVPELVGNKQRVLVSELA
GQSNIVSKAQELGLEFDPSSANSRQIIEKIKDLEHQGYQFEGADASLELLIREANGDM
KELFTFESFKMLVEKTAGKSVVSEAFVKVNIAGTSAYTAAEGNGPVDNALRKAALV
QYFPSLANMHLSDYKVRVLDEKDATAAKVRLIESKNTENTWNTVGVSENVIEASWEA
LVHSFRYALLQEKLQDEPGTLPIPAHGISH"

CDS complement(3670824..3671375)

/gene="resA_4"

/locus_tag="EFAGFIKM_03134"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81SZ9"

/codon_start=1

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/product="Thiol-disulfide oxidoreductase ResA"

/db_xref="COG:COG0526"

/translation="MKRNIYILLGVVLLVGIALAQNAGDGIAAVFKQEPMPTETGPR
AGLLAPAFSLTAMDGKTYSVGAKDKATFVSFWASWCEPCKQEAPELNRMAAKYKDKL

DMYGVNVTSYDKLKDAKAFVDEYQLTFPIPLDEKGTVYAQYNGVAFPTNVLIDSRGVI
QEIVLGILPEKELERKIKKLIAN"

CDS 3671602..3672093

/locus_tag="EFAGFIKM_03135"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAALHGQQNAFYIPSSVEEEMSKHMFSLPQEACGVMLGETAAG

GIRISRFQPIRNVAPDPLHHFTLDDAEWIRCVFSEPMLIGIFHSHPHTRPVPSLEDIQ

ALPAFAGLLQMYLIGSPDLTSGLRSHMHLNGYLISSKESQDPAQHVVP SYNLLPVPL

CVT"

CDS complement(3672079..3672816)

/gene="dinG_2"

/locus_tag="EFAGFIKM_03136"

/EC_number="3.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_02206"

/codon_start=1

/transl_table=11

/product="3'-5' exonuclease DinG"

/translation="MREPARGNTGFWNSLRQGGVPSAIASIMGAPTAQHMAFIRSM MR

EQRRPEVLHTPLNELDAVVFDETTGFSPQHGDEIISFGAVRIHGGVVLEGEQFYTVV

QSKTAVPEHITELTGITQEMTLDAPTLLEGLHDFMSFVGGNVLIAHASAH DRAFLNAA

LWRTSKVRLTHRLIDTMMLARWLEPSRPGYGLDELLESRGIPYGRHHALEDSKMTAQ

LWSCYLEDMTRKNVETLGDLYTQLSHA"

CDS complement(3672813..3673898)

/locus_tag="EFAGFIKM_03137"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MEPISYTNYSWSYQGIDGAMSSQELRQARVILQNELQELLSASL
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QDNGMIISDTPHEGKEEYFAQLGQRM TDMLEELGYAKCEGKVMCSEPLWRKTQAAWKQ
QLADWSSDLNWEPIRNLIASDMRFVAGEQSLAEWITSFYEQFRLIPELSDAVLRNT
VKHKATLNLVGRVVTERFGEHAGGFDIKYGLYIPLVNSARYLALQHGIRESSTLKRME
RLTSLEAVPFTLLDACQRAFLAALRFRRSTPVVIQGD LQHSSGFLDEKQMKQKQLHYE
LRDTLGLVRRVHRALQRQLRFAERRRP"

CDS complement(3673940..3675340)

/gene="nrgA_1"
/locus_tag="EFAGFIKM_03138"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q07429"
/codon_start=1
/transl_table=11
/product="Ammonium transporter"
/translation="MRKKWLVSMLVMLTLFAFPVSAFAAAEGPTNIELQSGLNSAFTF
LAVLVFLMQGGFALLEAGSTRMKNAGHIAGKTILTLGISVIAFWALGFGLGFNGNS
FFGTTGFFLSGDKMAASFESLAFSDVPLTIKFV FHLAFAAVSLAIACGGMAERAKMSV
YIVFGTLYTIIMYPVVAHWVWGGGWLAELGMQDFAGSTVVHLTGATAALVATILLKPR
IGKYNKDGKPNII PGHNQVYSVLGVIIWIGWFGFNP GSTLSAMGDGFFGYVALTTNV
AAAAGGVAALLISWAVLGKSDIPSMLNGVLAALVAITGACAFVEPWAALVIGALAGII
TFFTAQYFDRKGIDDPIYAFSVHGIAGMWGAISTGLFATPELAENAGVGQAGLFYGGG
FHQLGVQLLGLAGAFV LVMFSFIILGGMKAIMGIRVTEEEETMGLDISEHGTGYYPE
QMKNVDSKSNGGTFSS"

CDS 3675692..3676120

/locus_tag="EFAGFIKM_03139"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKLFRIGELAKTAGVSERTIDYYTKLG LIAPEERTQKNYRLYSN
ETLTRLERIVQMKEKYS LDEIKQSLEKWRLVSTEEQVASKLTTLELHVQQLEREVNE

LKPLLGEMKPVQARKMMAGLLTKSAGTMEALKILLENTMM"

CDS 3676149..3676829

/locus_tag="EFAGFIKM_03140"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSFNNGMFVLIIIAFLLSLWAQFRVKGTFRRWSEVPNQNGMTGY

DAARQMLDANGLHDVPIEPVRGTLSDHYDPINRVVRLSEPVYYENSISAVSVACHEVG

HAIQHKESYPMLALRHRIFIVNFASGLAPFLLIAGFIFNAMNLVGIGIIFFSVTVAF

QLITLPVEFNASNRAREIMVSEGYIRNEEEKGVAKVLNAAALTYVAAALISLLELIRY

IGIFNSRD"

CDS complement(3676874..3677785)

/gene="gltC_4"

/locus_tag="EFAGFIKM_03141"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P20668"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator GltC"

/translation="MELRQLHYFLKVAQKEHVTQAAEELHVAQSAVSRQIHQLEELG

VDLFMQKGRNLQLTAVGQLFCKRIEGILKDLDKAVGEVHEFLDPEHGEIRIGFPHSLG

IHLIPSVAAFRQRYPNVKFRFKQGMFPTLIRDVLSGEVDLAFISPFPEKHDQVDGDI

VLTEELHAILPPNHPLAGEETIALEQLKDDKFVLFSGYSLRPIVWHACLEAGFTPPI

AFEGEETDIRGLVAAGMGVSLLPEMALFQTNPLQPAHVAISHPKVTRTIGLIHRAHD

KLPLVAQSFRSFLLDYFGLQQNNTPSD"

CDS complement(3677855..3678481)

/gene="gluP"

/locus_tag="EFAGFIKM_03142"

/EC_number="3.4.21.105"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54493"

/codon_start=1
/transl_table=11
/product="Rhomboid protease GluP"
/db_xref="COG:COG0705"
/translation="MIFIRYENWKGYLKYFPLTSLFLIANVVMFIVLTVNGGSTNNMV
LLKFGALTNHELFAHEWWRYITSMFLHAGFSHLLFNSFALIVFAPPMERLLGSVRYGV
LYLGGGV LGN ILAVAWYNSVGSITISVGASGAIYAVYGAFlyVALFQRTMMDEASRKT
MYTLLLFGIIFSFAMSGINWMAHLGGLLGFFIYGLLIRLWKPRSLKR"

CDS 3678630..3679148

/gene="tpx"
/locus_tag="EFAGFIKM_03143"
/EC_number="1.11.1.15"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P80864"
/codon_start=1
/transl_table=11
/product="Thiol peroxidase"
/db_xref="COG:COG2077"
/translation="MTQERTGAATFKGNPITLIGPELKVGDQAPDFTLSKNLVEDASL
KDFAGKIKLISVPSLDTGVCDQAQTRRFNVEAGELGDNVVVLTVSVDLPFAQARWCGA
AGVDRVVTLSDYKTRSFGEYGVLIKEFQLDMRSIFVLDAEDRITYVEYLPMTDSPN
FEQAIAAVKALL"

CDS complement(3679221..3679613)

/locus_tag="EFAGFIKM_03144"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTLKRTLVGIIIRSMEGTSDRAKDPKLKTRYYNLSKDRAWEVSS
TLKKIPGYKVLHEVPSVGEVILEKRTTFGRITMDITVSIISVSPVRSVDMYSASRGS
LGDLSNYRTIMNLFVLDKKLSKYKAND"

CDS complement(3680039..3680851)

/locus_tag="EFAGFIKM_03145"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEFKGAMGGIYRLTEWITRLAATNLLWAICSSPFLFFLIMKLLV
MQQNLANESLQMNWAIAIVAPLTLFPATSALFTVVRKWNMGD TDVPIFR TFFVGYKEN
YKQSLIGGIFYTLLFAIMYLDYTVYMTQFRNMQLVGII MLVLLLLLVSLFNFFSMVV
HYHMSIGLIIKNAVLLTLIRPFRVFSTLLGSGLLFYIGFRYPVLVFFIISIIAWFAF
FNFYATFNKMQE QMEKMQLKKEEEEEAAALAEQSAENGETSEPSDDKNITLQK"

CDS complement(3681069..3682667)

/gene="cshA_1"
/locus_tag="EFAGFIKM_03146"
/EC_number="3.6.4.13"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P96614"
/codon_start=1
/transl_table=11
/product="DEAD-box ATP-dependent RNA helicase CshA"
/db_xref="COG:COG0513"
/translation="MTNLNFTDFNLEPLVLQAITE LGFEEATPIQSKAIP LALEGRDL
IGQAQTGTGKTAAFGIPLISKISK SDEKIRALIMAPTRELAIQVAEEIEKLTRFKGLR
SLPIYGGQDIVRQIRALKRKPQIIIGTPGRLLDHINRKTIKLEDVQTVVLDEADEMLD
MGFMEDIQSILKQVPDERQTM LFSATMPPNIQKLAQQFLNNPEHISVIPKHVSAPLID
QSYIEVPERQKFEALSRLLDME SPELAIVFGRTKRRVDELAELQKRGYSADGLHGDL
SQNQRD AVMRKFRDGSIDVLVATDVAARGLDVSGVTHV VNF DLPQDPESYVHRIGRTG
RAGKEGAAWSFVTPREIDHLHFIERVTRHRIPRKPLPTMAEAVEGKQRLTAERLLEIV
QSGELNEYKGIAIQMLEQYDSVQLLSAALKLLTGDKKDAQVDLTPEDPIRAKRRKPDV
RSGGRKPSGYSGNRTSGSGGSGGGYNRDRNSSGSGRGGYNRDRNSGSSSTSGGSREGG
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CDS 3682973..3683794

/locus_tag="EFAGFIKM_03147"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPKIIWHSLVILGAAAIACGFNWFLVPHQLLSGGVSGISMLLG

YFTTLNLSIMYFVLNIPLLIAGWFILGRRFITLSILSVAATSWFIALLPVFAVATDPL

LSSVFGGVLIGMGTGVSRVGGSTGGLDIVGSIFTRKRDFPIGTVMAGMNGTIIMLAG

YLSDNWNTALASMVSIYITGKVLDLIHSHVKVTLYIITNETEAMLKLLVRPRGVTK

IKTQGAYTDIEKDMLMTVTTRYELVEIKRIIKDTPNAFVNIVETVGVMGSFRRS"

CDS 3683954..3684157

/locus_tag="EFAGFIKM_03148"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIIVDMETVKLFEIVNRWCPEMLPFLKPNELDSLIVLRDGLGIL

EQGDAMEIIQYSICEHQNEIYIQ"

CDS 3684321..3685502

/locus_tag="EFAGFIKM_03149"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNMFWALLAMAFGSFGGAPAVADQGNPQFQSLTNSFNTAIIQSQ

KDQVVIDADNPPAKIDPQPDAPVVKGIYVTAYSAGGARMKELLELDSTELNAMVIDI

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NPELSFRNKDGSVWANGKGDSFVNPYSKEVWDYNIEIAKEAAKLGFKFIQFDYVRFPE

GFETRADILKYTKSDKSRVDVVAEFVQYARKELAPLGVRSVDIFGYAASVPAAEGIG

QDFVKISENVDISPMVYPSHYSTGWYGVKDPDKDPYTTIKGSMEDTHKKLDPTKELK

PVIRPWIQDFTASWLGS GHYIKYGKKQVEDQIRAMKMDVHEYLLWNASNRYTSGVQY

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CDS 3685699..3687057

/gene="mdtK"
/locus_tag="EFAGFIKM_03150"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37340"
/codon_start=1
/transl_table=11
/product="Multidrug resistance protein MdtK"
/db_xref="COG:COG0534"
/translation="MNMNTTSFSQKVKQFLIIFLPIFTTQIALSAMSFFDTNMSGKFS
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SLVVIGAGALLLGPVLNGMPLEPRVAQVAFYFLCALAFGIIPLFGYTVLRSFMDALGQ
TRTTMFITLVSLPVNIFLNLYLLIFGRWGFPQLGGVGAGVATACTYWLIFLISLFFVHR
VEPFAKYGIFRQWTRVSLSKWKELLKIGVPIGFATFFETSIFAATLMMSRFDTTIA
AHQAALNFASTLYMLPVSICMALTILVGYEAGAGRLRDARQYSLLGIGGAIGLSLLTA
IVLIVFGEQIAGVYSNDREVIALTQHFLIYAIFQISDAIATPTQGALRGYKDVNPAL
IITFVAYWIIGLPVGYLTATYTSLGAFGYWIGLIAGLAVGATALLWRLFLVQKQAALR
KA"

CDS complement(3687141..3688112)

/gene="pfkA"
/locus_tag="EFAGFIKM_03151"
/EC_number="2.7.1.11"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P00512"
/codon_start=1
/transl_table=11
/product="ATP-dependent 6-phosphofructokinase"
/translation="MTAVKKIAVLTSGGDSQGMNAAVRAVVRSGLFHGLEVFGVQRGY
QGLLNNDIFPMDLRVSGDIIQRGGTVLQSARCKEFYTAEGQQKGADILRARGIDGLV
IGGDGSYNGANKLSKLGINTMGLPGTIDNDVSFTDYTIGFDTAVSIVDAVNKLRTM
SSHERRSSIVEVMGRHCGDIALHAGLASGAETILVPEVPFDMDEVADRMKANFAHGKRH
SIIIVAEVGVKGEDVAKELMERCPTYEPRVTVLGHIQRGGTPTPFDRNLASRLGDFAV
RSLIAGETDKGCGIIKGELTLTDIDKVNTKKDFDMVTYELAQRLSQ"

CDS complement(3688166..3689245)
/gene="ytpB"
/locus_tag="EFAGFIKM_03152"
/EC_number="4.2.3.130"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34707"
/codon_start=1
/transl_table=11
/product="Tetraprenyl-beta-curcumene synthase"
/translation="MSQSNRKRHQYPRGPLALMRGVYKYTIPETRKALNGWRAQAEI
PNEELRTQALASLKDKQFHCEGGTVYALADLPNRHILIPLIVSYQTISDYLDNLCDRS
TSMDDPDDFRLLHQSM LDAVDPEAIPVNYALREEQDDGGYLRNLVTTTCQELTRQLPGY
ASAKPQIQDLAGLYTDLQVYKHIPKELRETALLEWWSEHRHRT PQFRWNEFAAATGST
LGVFMLFLAASDDQLTEEQAASIHTAYFPHVCALHIMLDYLIDQDEDRIGGDLNFCNY
YENVETMLDRIAFIVEMARSDVQKIPGSSFHRMIEGLIAIYLSDPKVSEQQEVRVVS
KRLLKNSPITRIFFFIFSRWIRKNNM"

CDS 3689425..3690765
/locus_tag="EFAGFIKM_03153"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MSSSESLSWRRLFSFFVPLGISASLVTISHVIINSTLARSAPHE
TVIASYAIAGSLLTLTERPSTLLRQTCSALVRDRLSFQALTFVTKIFLACVLLIGFLI
VYSPVGTGVFKYLFVSPDLLTKVIDVYEILMYVSIFSVIRNIYQGIIITNNRTKWLT
IGMVFRLAGMYGLSLYFIYTD SIDSGRVGAIIFAAGMMIEALVSFLEGNSIKRKMPAK
LEDHPVESKGDVFRFYKPLLSSFVALFIGPVINIVLGKTTGIALAISSFAIASSLMQ
LMLSFFTYIHQIVLNFYLVDAKLVRKFALVTGFIPFAMMVSIAYTPLGPWVLENVMSV
QGELLQQSLWTLRAFLVFLPLIFPFLDFSNGLILLRGQTKTMFRSQTANAICTVIVLLI
LVSIFPAWNGMIGAVAQSLGLLAELIIVWLVRRTKQEPTMSVVPKARKSTSLKG"

CDS 3690806..3691978
/gene="yegT"

/locus_tag="EFAGFIKM_03154"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P76417"
/codon_start=1
/transl_table=11
/product="Putative nucleoside transporter YegT"
/translation="MKLSHNARPDQNWLRALMFTIFGSTVLVWSYFQLYFSHLGFSRA
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VLVTLFYFFYPVYPLSDTMAITASKYGRNFTSIRVFGSIGYAFFALSIGYFLGSFG
PVWTIWVCVGLAATLLISFQLKDQPSGSSSKMDLSGLWAILKRRDVLTFFGCVFLLA
MGHRMNEAFLTITLKDLGASEGLIGWSLLISSVSEIPIFLLLSKYGNRYKELPLIAFA
ALMYTVRLLLSVSDTPAAVVAIQTMHSVTFGIFYVTAVRYIIRLVPDGYRATGMALF
TIVWSSASGLLSGTLGGLLLEHAGRQTFYLTAMAFSLAALIGFGLKLWSSMANRVS"

CDS complement(3692134..3692331)

/gene="cspD_1"
/locus_tag="EFAGFIKM_03155"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q45099"
/codon_start=1
/transl_table=11
/product="Cold shock-like protein CspD"
/db_xref="COG:COG1278"
/translation="MKGTVKWFNAEKGYGFIISVEGGEDVFVHFSAIQGDGFKTLEEGQ
AVEFEITDGNRGPQAANVNKL"

CDS 3692493..3692726

/locus_tag="EFAGFIKM_03156"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIKKHEIYKTDKWNMMTVEVQGKYLVLREISEEWGEECHTFLSR
PALMHWAERRFPKADFENREDEWRQLMAAFKGV"

CDS 3692730..3692915

/locus_tag="EFAGFIKM_03157"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQLDSSNVVIFILAFSLGIVLILGRNSIPDRLRRGMALIATLL
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CDS 3693129..3694919

/gene="pepF1_3"

/locus_tag="EFAGFIKM_03158"

/EC_number="3.4.24.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54124"

/codon_start=1

/transl_table=11

/product="Oligoendopeptidase F, plasmid"

/translation="MSQLLKRSEVPAEHSWKLEDLFADQKAWDQEYEEVSSLTKKASE
FQGKLNQPDVLKSCFEFEDEISLKIERLFVYARMHQDEDTANPTYQNLSQKAQKLVR
VGEALSFTPEILSLPDDQLDAFIANEKLSAYTFTLEEMKREKAHVLSQAEEALLAQV
GNLSQAPQTIFSMNNADLKFPRIKDEHGNEVELTHGSYIQFLENPNREVRERAFKAV
YETYAKQKNTIAAALNANVTKNMFYANVRKYPVMSLYGDNIPDVTNLVDTIHE
SLPLLHRYMDLRKKLLGVDQLHMYDLFAPLVDEYKMDITYEEAKQTVKDGLKPLGKDY
ADALQTGYDNRWIDIYENENKRSGAYAWGAYGTHPYVLLNHKDNLSMFTLAHEMGHA
LHSHYSDTTLPYRDAQYTIFLAEVASTTNEALLMDYLLNKSTDPKEKLYLLTYADQF
RTTVFRQTMFAEFEKIIHERAEQGDALTPQLLSEIYYDLNVKYHGEGMAVDKEIEMEW
ARIPHFYNSFYVYKYATGFSAAFSFSKQILEEGQPAVDRYLGFLKSGGSDYSINILKK
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CDS 3695052..3695432

/locus_tag="EFAGFIKM_03159"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
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ILGCTLIGGIIVGSYGIYRQYRLQRENKQLKLRVSELESSTTNKSTLDSFKSMDSLDS
NESDSLLENDISIQSQRKGNPTGTL"

CDS 3695545..3696585

/gene="ysdC_2"
/locus_tag="EFAGFIKM_03160"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94521"
/codon_start=1
/transl_table=11
/product="Putative aminopeptidase YsdC"
/db_xref="COG:COG1363"

/translation="MSFTIDESYVLSFLKKLLDTPSPSGYTHHIIEMIRKEAAALGIA
CELNNKGGAVLTLPGQDSSKTIALSAHVDTLGAMVRSVTSYGLKLTSGGGFSMQSIE
NEYCSIHTRDGKTYTGTLISLHPSVHVYPDARTFERSESHMEVRIDEVVSSKEDVLKL
GISVGDFISFDARAVITPSGYIKSRHLDDKASVAALFGILESAREGWKPLHNVSLLI
SNYEEVGHGASYIPAEISEMIAVDMGAMGDDLSCKETDVSICAKDSSGPYDYDMTSRL
IELAKQDGM DYVVDIYPHYGSDGSAALRGGNNIRAALIGPGVHASHSMERTHKDAVLN
TARLLAAYITTK"

CDS complement(3696702..3697640)

/locus_tag="EFAGFIKM_03161"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MYKEINQQLAALKEKGRIYEKWKRLKLEKLQTEESEWEAKVKRRL
EHLQKEQKDVDRNLNSMTLSAFFYQLIGKKTERLEKEELELMESKAAYDTACRMLQDVQ
EQRIHVEQELEGGRQYQYWQSDYNALWGKKEGRLLDQDAELQHMAENREHLASELQEL
DEAFREGEYLLYALERA EKALASAGNWGVYDMMGGGVISTHIKGRMDDAQVAIMDAG

KRLRRFQKELEDVEMAVHADLHLGGLLSFADYFFDNLFVDWMVQDKIRKAERQVKDGL
SAVRKTMHVLNRNEMRDHKAEEILDRKYHAYVEQAD"

CDS complement(3697804..3699726)

/gene="taeA"

/locus_tag="EFAGFIKM_03162"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:BARRGD:NG_063829.1"

/codon_start=1

/transl_table=11

/product="ABC-F type ribosomal protection protein TaeA"

/translation="MTVEQIAKSYGEKILFKDASFGMADQDKIGVGVNGTGKSTFLR

VISGMEPADAGQISIGNDVRIQFLAQNPDPDNTVLQQVFEGDSMEMKTVREYTETM

ELLELNSSDPALQERLLRLNQQMEQLQLWQMESEAKSILSKLGIRQFDALMGTLSGGQ

RKRVALAAALHPCELLILDEPTNHIDNDSVWLEQYLQKRRGALLMITHDRYFLDRV

ANVMLELDHGRILFRYEANYTRFLELKAEREEREASSEQKRKNLLRTELAWIRRGAKAR

TTKQKARIDRFEQLKDQQGIQRSGSLEVSVGSTRLGKKILEIEHLSKSVGGRKLIEDL

SYIAVPGDRVGVGPNPNSGKSTLLQMISGKLEPDAGVVDVGPTVNLGYFTQEHQEMDE

TLRVIEYIKEVAENVKTADGSLITASQMLERFLFTPASQWTPISRLSGGEKRRLLYLLR

VLMAAPNVLLLLDEPTNDLDIQTAVLEDYLDFFPGVVFVSHDRYFLDRTVDKVLSE

GNGAVRVHVG DYSEYAEWMLKNAPGANQESDTGAAKVKQSSEKTPAVSAAKPKLKFS

FKEQREYDQIDENIEKAEANLVRINKEMEESFSDSARLQELMAEQVEAERHLDLMER

WTVLNELAEQIEQSKS"

CDS complement(3699796..3700374)

/gene="fadR_2"

/locus_tag="EFAGFIKM_03163"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94548"

/codon_start=1

/transl_table=11

/product="Fatty acid metabolism regulator protein"

/translation="MSTVQGDKSEAILDAAYGIFGSKGFYETKMSDIADEAGIAKGTI

YLYFKSKEQLFIAVSKRDCNSFISRLEYALNSYENTGDKLGAIKTHLTYYYERRNHT

KLFFMAPNNDPDLMKFMKAFMNQYMSMVCEVLESASVPEPVLLAEAYIGILDRKMDI
MLNPEFNEEHLNKRIAFAAALFLDGCRSFLQV"

CDS complement(3700387..3701196)
/locus_tag="EFAGFIKM_03164"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDWIIGAVCASMVAGAAAYAKKSLTSGCLAAIMMGTIYYGAGNL
FWFGTLLFFITSTLLSRFRKDRKQELEKSYAKSGNRDAGQVMANGGMGMFLCLGYWI
FPHPAWVYAFIGVMATVTSDTWATEIGSLSRKPPRSVLTWKVLTPGASGGVSLLGTVA
AAVGGALIGAGAFLSWIAGIEGLGLFSWTFVGLAGGLAGAFADSYLGATVQMMYRCT
VCGREVEVHEHCGHPTVPARGWAWMSNDLVNVLSSVIGGCVAIGLGNILAL"

CDS complement(3701425..3702198)
/gene="ssuC_5"
/locus_tag="EFAGFIKM_03165"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P40401"
/codon_start=1
/transl_table=11
/product="Putative aliphatic sulfonates transport permease
protein SsuC"
/db_xref="COG:COG0600"
/translation="MKWLEKKWVSIPLLWVTVILIWQLGALIYGPDPVIPGPWHTILGA
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PPIAFITLFLVWFGIGEQQKIALIMYATFFIVVLNLTGVLVSVEEDKIRSARSMGANE
RQILLHVIVPATTPYIFTGVRLAMGTSYMAIIGAEMIASNEGVGYLIWNSRLFFRTDW
IFVGLISLGFMGFLTDRLFNWFGRKVLYRYGVIGGAKRV"

CDS complement(3702216..3702992)
/gene="nrtD_1"
/locus_tag="EFAGFIKM_03166"
/EC_number="7.3.2.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P38046"

/codon_start=1

/transl_table=11

/product="Nitrate import ATP-binding protein NrtD"

/db_xref="COG:COG1116"

/translation="MSLPATQHTIHIEQLRKTYHAPTNGDVHYIIKDVDLVIKGGEFF

VLLGPSGCGKSTLLNMIAGFISKSGGQLKVDNKEIDRPGRDRAMVFQQADSSLFPWLT

VRENVEFGLRMSKVPKTQRREISDRYIQLVGLSAHEGKFPKELSGGMKQRVQLARVLA

NDSAILLMDEPFGALDAMTRRTMQKELVNIWKETHKTVIFVTHDIQEALLGERIGIM

SVGPSSNITDIYHNTLPYPRNIASSEFNTLYDRIQGHFEE"

CDS complement(3703020..3704075)

/locus_tag="EFAGFIKM_03167"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTRSNGVYIVRKPSIVTGILILFLATALLSGCSSNAAGSGAKD

ATGKNTDNVKIRIADTSTNPTFRVAIAKGFFENRGIDAESITFGSPAEGVNALFIKQV

DIAYGADFPVLNALSKEYSVIASAGQTTDEAAAAWKLYARENIQSGADLKGKKVSFI

RGTFIPYLWDEYLDQGVALSVDVTQIGQGAFDEAYIALKQGDLDAAWVIGSALTDKFD

ALEGVHQLTMSQTPIRLGMGLVSSNEFIQANPEKISEFLAALDEASTYAQAHPEEVA

DLMYQETKQPKDATLKDLPINPWEVGFTQAAYDSLQKQYMVDTGIIQDFDLDTKL

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CDS complement(3704088..3705536)

/locus_tag="EFAGFIKM_03168"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGHSTIYPTGATLYNPDKAWGGYTVYQAGEEGVVLIDMNGKEVH

LWKGLLGFPKILPGGYVLGSTGRRDPKFGIQDNVDLVQVDWDGNIVWKYNSYEHIED

PGYEPLWYARQHHDYQREGNPVGYYAPGLAPKTKSGKTLILAHKNVSNPQISDKPLLD
DAIIEVDWEGKVLWEWLPNEHFEELGFDEAARNVLFDPNTRSFHGLGGGVGDWLHIN
SASYVGNRFYEEGDERFHPDNIIWDAREANIIAITDRQSGKIVWRLGPDYTSPEVKH
IGTIIGQHHAHIIPQGLPGEGNLLVFDNNGGWAGYGLPNPASPFGLKHAIRDHSRVLEI
NPVTLEIVWQYTSAEAGFSVPTDSYKFYSPYISSAQRLPNGNTLITEGSNGRLFVTA
EHELWVEYVSPYTDGRNTNMVYRSYRVYPYQWVPQLEKPQEVAIEAIDVSTYRVQGAAP
KGSASIVSVETTLPPFVEGAACVATSDEGKSGG"

CDS complement(3705595..3706152)

/locus_tag="EFAGFIKM_03169"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSDRDWEALERTDWLFRKMVRRFVKERDRISVEGISLPGMLILH

KIIREGEQRLGDLAEQLDFTSGAITALTDKLEKKGLTIRRRKEDDRRTVLLDITSSGR

EMYARNSNIGARCITLLFEGFTSEELEQQSQFYERVVANLEGFSDTVLELAESNGIQE

HDRSSTSLEQKQRDNTGKRNYLSY"

CDS 3706539..3706946

/locus_tag="EFAGFIKM_03170"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNMKRVIIIGTMIVTMSFAGTAWGQSAISPIPTAKWSIVDLDR

EGSSDELALDNLQASEVDLYQELYNGKSLRTITEENNGNLDEVIAIQVRQLREQLDER

LANGSISSEQHAAQQAELEELVTQSANTAYSLA"

CDS complement(3707069..3707701)

/gene="ycgM"

/locus_tag="EFAGFIKM_03171"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P76004"

/codon_start=1

/transl_table=11
/product="putative protein YcgM"
/db_xref="COG:COG0179"
/translation="MLTNIRNVYCVGRNYKLHAEELGNAVPEPMIFMKPSHAVVPLN
GETLELPATKGEVHYEAEVVQIGRSYEPGMAVDELVDAYAFGIDFTLRDVQTVIKKK
GHPWTAAGFRNSAPVTAFQAFPGAAALLEKDFTLTKNGEEVQRGNIRNMIFSLQDIV
DYVGHHYGLGPGDVIFTGTPEGVGPTQAGDVLELAWDGESLGACTIGAAQ"

CDS complement(3707749..3708501)

/gene="glpQ_2"
/locus_tag="EFAGFIKM_03172"
/EC_number="3.1.4.46"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37965"
/codon_start=1
/transl_table=11
/product="Glycerophosphodiester phosphodiesterase"
/db_xref="COG:COG0584"
/translation="MNNLCVAHRGFSSIAPEMMAAFLMAMERPEVQWMELDVQLSRD
GVPVVIHDFTVDRITNGKGLVRETDWADLQRLDAGSWKNKSYKGERIPALSELLDRSC
GRVRLNIELKTQGDMYPGLPAAVIHEVRKRHMQNDVVITSFEPALIEVKKLAPEIQT
GLIIDARPGDLLTALRQMNCTFLSIGYTNVDKSLMNEMRSAGIRVMAWTVDDKTIMKK
LAAVDPELMLCTNRPDWWELAFQETSSRFFRP"

CDS complement(3708526..3709947)

/locus_tag="EFAGFIKM_03173"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MYPPRSERSVKKKKGSKRTRNTITIIWTVNIVLIIAIGLVGIFY
VINTRQQQADQPVKQEIVDQDQPSIGDDAKGGDQVSSPDSEDETSEEPKATDEETT
ADADKTSGVATPETSSNTNSEKTESGTTKPAADSTPSGKGNAGVDQESGMSKPSNSA
KDVTINFVGDIQFSGKVAELLDKNGYDYPFAKLGRLFKDDDLTIGNLETPITHGGTSA"

ADKTYVYKSSPKALAAMASAGFDAVNLANNHILDQGVGLVDTLTYLKEYGIAHTGAG
MNRDEAYAPAYLERKGMKIALLGFSRVVPETSWKAEGNRAGVAEAYDSTGAVKAIQEA
RKKADLVIVVAHWGEERVSTPNSDQTRLAHEFVDAGADLVIGGHPHVLQGLEYYKGKW
IAYSTGNFIFSRSTTEETWKTAVFQARCSQDAACSMKVIPYEAGLGQAIPMIDEANKL
LLEQMAKLSPGIRYDGNGVASPN"

CDS complement(3710133..3711557)

/gene="hemY"

/locus_tag="EFAGFIKM_03174"

/EC_number="1.3.3.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P32397"

/codon_start=1

/transl_table=11

/product="Protoporphyrinogen oxidase"

/db_xref="COG:COG1232"

/translation="MGDKKRRVVVVGGGLTGLSAAFYIRKHYREAGVEPMITLVEKSS
SMGGMIETLHRDGFVIEKGPDSFLARKTAMIDLAKELEIDHELVSQNPESKKTYIMQR
GKLHPMPAGLVLGIPTELRPFLRSLVSPAGKLRALMDFVIPPRRTTEDESLGYMIER
RLGAEVLENLTEPLLAGIYAGDMRRLSLQATFPQFGEVERDYGSLIRGMMTGRKPAET
HTGTKRSAFLNFRQGLQSLVHALVHELQDVDQRLNTAVKSLQRLDGAQTRYRVELGNG
EMLEADDVVVTPTYVASELLKPHVDTAALDAINYVSVANVVLAFEKKEVEHVFDGSG
FLVPRKEGRNITACTWTSTKWLHTSPDDKVLLRCYVGRSGDEQNVELPDEALTNLVLK
DLRETMGIEAVPIFSEITRLRKSMPPQYPVGHQLHIAALREELGSKLPGVYIAGAGYEG
VGLPDCIRQAKEMSVQATQELAAD"

CDS complement(3711557..3712480)

/gene="hemH1"

/locus_tag="EFAGFIKM_03175"

/EC_number="4.99.1.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81U22"

/codon_start=1

/transl_table=11

/product="Ferrochelatase 1"
/db_xref="COG:COG0276"
/translation="MSYGTPENMESVEAYYTHIRRGPPPEPEQLKELTDRYEAIVGGV
FPLRENTDNQVKALQETLNRDERGTDVEFRCYQGLKHAYPFIEDGVEQMAKDGIQTAI
GIVLAPHFSTMSVGSYIKRAREKAEELGVHMSFIESYHLHPKLIQALSTRVSAKLDAF
EEAGAKRGDVKVLFSAHSLPARIVEMGDPYPQQLLETSEVIASRVGITNWQFTWQSAG
RTAEPWLGPDILDTLQELSREQVEDVLVAPIGFVSDHLEVLYDLDEAKSIAKEIDMR
LMRIDSLNSDPLYMETLSDVIISQWQQGSDE"

CDS complement(3712500..3713564)

/gene="hemE"
/locus_tag="EFAGFIKM_03176"
/EC_number="4.1.1.37"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P32395"
/codon_start=1
/transl_table=11
/product="Uroporphyrinogen decarboxylase"
/db_xref="COG:COG0407"
/translation="MSYNDRLIRASFKQQVDRVPVWYMRQAGRYDPEYRKIKEKYSLL
EICKQPELAAEVTLMPPVRKLGVDAAILYSDIMNPVASLGIDFIDIVKNIGPVIDNPIRS
AADVDRLRPIDVEGDLSHILETIRILDKELDVPLITFAGAPFTIASYLIEGRPSKGYI
RTKTMMYSEPEVWHKLMQKLGDMVITYVRAHIANGGKAFQLFDSWVGALSPKDFRTYV
LPTITRIFTELSDLNVPKIYFPGVASGELLPALHNLQADVIGLDWRVSISEGRQRLGG
KFAVQGNLDPYLLTAPMELIKEQAKVIIDEGIKEPGYIFNLGHGLFPEASLEKLRELT
AYIHEYSAEAMKSGVTVTND"

CDS 3713770..3714981

/gene="sbnD_2"
/locus_tag="EFAGFIKM_03177"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q2G1N0"
/codon_start=1
/transl_table=11

/product="Staphyloferrin B transporter"
/translation="MKTWKVNLIVLWFGQFLVNSGMTMITPFLSLYLARDLGVVGEHE
IGIWAGFIFAANFLTSFLFQPLWGLSDKYGRKVMLLRSGFGMAIVIALMGLAQNPWQ
LLLLRLLNGTISGFNPAAVALISGTPKDRMGFAMGISQSGQVAGTILGPLIGLLAD
AVGFRPIFYITGGLIFVASMLAMFLVREKFDRQEAAKLPAQSVLSGLKELNKSPQLPA
LFAVTFLQFAMISPMSLLPLYVQKLHASDVNNAFWAGLVGAVTGLSNMAMSPILGKL
SDRIGPHKVLTFSLIGTGLMLIPQAFVQTVWQLILVRFMMGVFMGGLPSVNALIRSY
TSDSMISRAFSFNTSTLALGNMLGAIIGGFAMAGFIGIEGLFIVSGLLLLNMVWVRFK
LYNKPASIRES"

CDS complement(3715093..3716295)

/gene="yjiB_2"
/locus_tag="EFAGFIKM_03178"
/EC_number="1.14.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34374"
/codon_start=1
/transl_table=11
/product="Putative cytochrome P450 YjiB"
/db_xref="COG:COG2124"
/translation="MKQAPRKYANYIPIRELETLEERLSPFKVYAEIRDNTPVRYDEH
RECWDVFGYEDVKYVLKNPKLFSSARDRANTSMLTTDPPKHKQLRDLVNQAFTPKAIE
ALAPRIQEITDELIAPHLSEGHMELIDDLATPLPVIVIAELIGVPAADRQKFKDWSDV
LVKGARD DSEQAFQELLEKKRNMQELHIYFTGIMEERRLQPKDDLISLLAAEIDGQ
QLTSDEVVGCILLAAAGNETTTNLITNAVRILSEQPELQQELREQPERITSAIEETL
RYYPPIVAIGRVAKETVELNGQMIQAGEQVISWVGAANRDSAQFENPEDFISDRKPNR
HMGFGFGIHFCLGAPLARLEARVVLHTLLQHMGNIQLVPGTALQPIQSAFVFGVKHYP
IQFNLINK"

CDS 3716782..3717993

/gene="ansZ"
/locus_tag="EFAGFIKM_03179"
/EC_number="3.5.1.1"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34482"

/codon_start=1

/transl_table=11

/product="L-asparaginase 2"

/db_xref="COG:COG0252"

/translation="MSKTSNLRPWAVWSTAALTALTISLSPIGTAAHAATVEVKGT

GAVQTATTTPARNTSIPAIPDSSKQSALPNVLVIGTGGTIAGQSEDATSFQNYKAGTL

PIGEMVDALPDKQKIADVSTLQFGNSGSGSYSMTDLYDLSQTVDKALAMYDSVVVTTG

TDTMEEIAYFLDMTVQSDKPVVITGSMRPWTVIGSDAQANLYNAIKLAGSGRTTSFGT

VLMLNDTIQLARGVTKTNDYRTDTFETPMLGAVGYIDEENIRIYRAPARALKPEGTAK

PVFDLSKITKADLAKVEIAISYQEAGGGAIEGFVSSGAKGIVTSGTGAGGISRAMGQA

RTKAIEEGVIFVTTTTRTGSGSVYGGGKGIIAGDNLSPQQARVLLMLGLSFSDDFDTIK

KWFETYGTPEV"

CDS complement(3718048..3718260)

/locus_tag="EFAGFIKM_03180"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRPLFIFLSLLLISGFVFHFLNVYTPFLILPVYIVLIATLVFFV

VYLFRFYLTKKIIKSENTQRRDDTP"

CDS complement(3718504..3719136)

/locus_tag="EFAGFIKM_03181"

/EC_number="2.1.1.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07431"

/codon_start=1

/transl_table=11

/product="Catechol O-methyltransferase"

/db_xref="COG:COG4122"

/translation="MNLTPDEYVNQLFQEDELLLVKEAIRSNGMPEVSVAAAYGRLL

TFLAKTSKAEAALEIGVLGGYSGICIARGLRESGTLTSLELKEEYAAMARGHLEEGGF

GEKVEYRIGPAADSLEELEQEGRTFDFFFIDADKENYPVYLDYAIKLARPGAVIVGDN

CFLRGRTLNPDKQGPVLAVRRFNEQMASDPRLVTTMLPDYDGLVLAWVK"

CDS 3719229..3719354

/locus_tag="EFAGFIKM_03182"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHHFERGVHTFTAFLIVSFFTESGKAAPLLYSREKDFPSPA"

CDS 3719367..3720530

/gene="rlmL_2"

/locus_tag="EFAGFIKM_03183"

/EC_number="2.1.1.173"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9K0V4"

/codon_start=1

/transl_table=11

/product="Ribosomal RNA large subunit methyltransferase L"

/db_xref="COG:COG0116"

/translation="MNHMAQLQLIATSAMGLEAVVARELKQLGYEDVTIDNGRVFFTG

DYIDICRCNLWLRSSDRVLVKMGEPATTFDELFEGTKALPWEEWIPADGEFPVEGRS

QKSQ LSSVPASQGIVKKAIVEK LKLT YDEWFPEDGSRVIEVILLND RALLTLDTTG

PGLHKG RGYRKL VTEAPLKETLAAAL IQLSRWNVSRPFYDPCCGSGTMLIEAAMIGWNI

APGLRRTFNSEDWAVIPEELWEQAREEAFDAVRDDVPLQISGSDIDPEAIEVAMAAIK

SAGFAKDIEVSVLPAHRARPQGQYGVII TNPPYGERLSEEKEVQKLLRSLGRSYLDMP

TWSFFAITSTKAFEEYFGHKADKRRKLFNGRIETQYYQYLGPLPPRNKTPQSS"

CDS 3720745..3722745

/gene="ltaS2_2"

/locus_tag="EFAGFIKM_03184"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34952"

/codon_start=1

/transl_table=11
/product="Lipoteichoic acid synthase 2"
/db_xref="COG:COG1368"
/translation="MVVTRPTRSAMPRGLLNHPLTLYLIFLVMLLKLMWLHHNLHAY
NITMGLLDKVIAGSLLLLSFWTWLLPRRGMILSLAVLNLLLTALIYADMVYYRYFQD
FLTIPVLLQARQVDALGDSIATLIYTSDLWFFADWLVIPFAAIVLFSRRYRSKHSST
SVTGYGSYLYNDGKARLRRRLTAGSIALVLGLGLAVGPIYFYSKTWAKGLFDNNWWNV
SMYNVTGLLAFHGYDLNYAKDHIGSGPQADPADVEQAKAFFAERQEAPQNDALFGK
YKDSNVIIVQGEAFMFMIGQSIGGQEITPHFNELMKESQYYSHFYHQTGGRTSDAD
FGANISLHPLPVGSFAVRYADHTYDSLPSILKDNGYSTNVFHAYESGFWNRYTMYQNM
KYDKFYSKNDFAQDDPLGWSLSDSEFFRQSVEKMSSDVTEPFYSFLITLSSHHPYALP
KEKQQLDVGEFQGTMFIGNYLQSVHYVDSALGKMVEDLKNRGLWENTIFMFYGDHDNSI
KEQSQYEQFLGRSLNELDMAQIMNEVPLLVLHPDGAAAGTMDEPSGQLDITPSVLHLL
GVSDQSYHYMGNDVYDGSSRTVWLNRNGAFSDGSVFYIPSDDIYENGACYDLSTRDKT
DINACRPGHDEAAKRLHVS DTVITYDLIQRFREEDSSTATPQ"

CDS 3722822..3723250

/locus_tag="EFAGFIKM_03185"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTSHTGPFNIEQQLFDAAAKFVKQRYPPQGWGGAGAVYTEAGSLL
ISVAPEVINDATHLCMETGAYLEAHKLKERVTHSLCIARDDEHSEFKVLTPCGVCQER
LFYWGEENVKAAVYDPSGQLVFKRLDEIQPYHWSKAYRDKK"

CDS 3723333..3724058

/locus_tag="EFAGFIKM_03186"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNIEIWSDFLCPFCYIGKRRLENVLEQFPHRDEVKLQFKSFELD
PNAALNPGKTNSEYLAAYNMSVEQAKGMNAQMNAARTAGLEYNIDAMIPTNSFSAH

RLTHWADTQGKALELSERIFQAVFIEGKHSGDPEVLAQLAEEIGLDRNAATAVLSSDQ
FTDNVRADQAEGEQLGIRGVFFVDRKFAVSGAQPDEVFLDAIQKAWDERSPFTMVE
SNTTETDGSGICTDDGCEVPKKN"

CDS complement(3724355..3725185)

/gene="yvgN_2"

/locus_tag="EFAGFIKM_03187"

/EC_number="1.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32210"

/codon_start=1

/transl_table=11

/product="Glyoxal reductase"

/db_xref="COG:COG0656"

/translation="MTKHITDCTILNNGVTMPWLGFQTYKAKGKEVQQAVETALEVGY

RSIDTASIYGNEEEEVGQAIASSGVARNELFVTTKLWNEDQGFDSLRAFEASQKALGL

NVIDLYLIHWPGRDQYKETWRAFERLYSEGSIKRAIGVSNFQVHHLQDIIDEGGTVPV

NQVELHPGLIQQELQDFCGAQQIGLEAWSPIMKGKLNQESTLKALAKYKTPAQIIL

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CDS complement(3725360..3725641)

/locus_tag="EFAGFIKM_03188"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPKRYDSSLQADTTVSQAQNAVKNLHYAVSQALSHPTAQTVQA

ERRLAHTEQAMRQAELSLGGQGVELAEEMFIEEKRRRLNSIQSQHGQGDL"

CDS 3725791..3726189

/locus_tag="EFAGFIKM_03189"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MKKILLTLCMLPFLIWVQGCPATYEIEGYTASSMNPDI VPSN
AKLIKIITDSGNRNIKEGV MYELKHIGGEQGLYPPLDYFQKLADTGWVELEEERMGHV
HFLKKDTTVIAIEIREDAFEIYEMVKGAME"

CDS complement(3726291..3726512)
/locus_tag="EFAGFIKM_03190"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MANDIRVCEKCNHVR LKSIVPKLQKMAPDTEIKIGCKSYCGPCA
KRA FVFINGRYISAPTEEEVLVKVAKFVK"

CDS complement(3726534..3726836)
/locus_tag="EFAGFIKM_03191"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNCKITRNAAKVLKLELDK PENEGKNLRVVITHAHGDHAHYGLD
IDTPKENDTVVSTDKEIDVILANDQPLLNGVKIDYLFPEEGFVITNPSQGNHGDH"

CDS complement(3726979..3727236)
/locus_tag="EFAGFIKM_03192"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKWRSLLSFKRWTQVFKRLPRLLRAPQIPLGEKLLFIIPALLYW
VLPDVMPFMPIDDIGVT LILMNWFVSRAERKYPVLQEGAPS"

CDS complement(3727432..3728643)
/locus_tag="EFAGFIKM_03193"
/EC_number="3.4.19.11"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q03415"

/codon_start=1

/transl_table=11

/product="Gamma-D-glutamyl-L-diamino acid endopeptidase 1"

/translation="MDLQWIIVQRGDTLLRIASAHHMTKEFLAALNPEVASQPYLLAG

QMLRIVPGTGRRYAVPPGERVGEIAGRFGLEDDEVLQRQANPEITNITDWVGRCIHIPAS

NGKTIVKIQGEYGYRELIRDIDKLENQYPFIETGSIGTSVMGKSLPYLRIGQGSRIH

VNASVHANEWLTTAVLMKFIEEYAEYSAHRTWHQYQTERWMQETTLWAVPMVNPBGV

ELVQEGVNVNQHHPHAQQLLAWNADRSHFTHWKANIRGVDLNDQFPAHWDEEAARRGVTS

PGPRDYAGTAPLTEPEAQALAQWTQQHTFDVAVSLHSQGQEIYWNRYDLEPRESGPLS

RRLAKASGYKAVKLGGSDAGYKDWFIQDFGRPGFTVEVGLGVNPLPVEQFDDICIEVG

MLLAELLSNGQ"

CDS complement(3728872..3729687)

/gene="murl"

/locus_tag="EFAGFIKM_03194"

/EC_number="5.1.1.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31332"

/codon_start=1

/transl_table=11

/product="Glutamate racemase"

/translation="MFVQQAIILDSGVGGLTVAKEVMRQLPREKIIYFGDTARTPYG

PRSSSEQVKQFTEQIVDFLIQFDPKVIVACNTATAAALEYIRGKVNMPVIGVIHPGAR

AAITATRTGRIGVIGTTGTIGSGAYTTALKQLSPYIDVVSQACPALVPLVEQGEFRSE

HTTHTVEQSLGEIKQQPIDCLILGCTHYPFLMDTIQEVMGQEVKLISADETAREIST

ILYDKRKLASGDETPVHQFFCTGDPRMFQNITRRWLGEQISKTPVWVQVTQLS"

CDS complement(3729901..3730278)

/locus_tag="EFAGFIKM_03195"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKDSNKSLLWGALIGSVVGSVTALLLAPKSGREL RQDITEGARQ
VSEKGQELAGIVGEQSSQIVSKVKETADVVIQDIQSWRNCAEGKEIRISAAIVDNDID
KTVDEPGIDIVAKLPADESKDDN"

CDS complement(3730464..3731378)

/locus_tag="EFAGFIKM_03196"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTNESKEFNEVNTESNETNETPSGFHPVYMVELLFRKRPEVDRL
RLQEAMIRHTGQVRLDVKQESGGQKHEMLVFYHLDHKVSFQEGDIPAQTCMLPVNEIA
DRARFGGALQQA WYWPEVGQVVEASRYSIRIHDMFTAAMP RKQRLELFQKTVLAIMES
LTCDALYWYGSDKLVEPEAYTQAQEREEHLYAAMNVRMYQAGGTEEQRGLVMDTVGLS
ALGVPDVQCHFVGLDPDTVAQTLLGAAYYIFDQGDVLQDGQTLGSSGGRRWRCEHQAA
LIAPGRYVIDLDPGDEHAAADLEPARQN"

CDS complement(3731389..3731850)

/locus_tag="EFAGFIKM_03197"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32126"

/note="UPF0331 protein YutE"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYYVNREQIARRLAAVPEVAEGLRGAAEAWDGSMLGMVQERCL
HLAIEIVTDVGSYLIDGFIMRDASSYDDIIQINYEKVF DNPTYEILRQLVTLRKPLV
QDYITWERSELHPLSVELPSILEHFTTQVSAYVEKELGPFNTAQAE GQRKE"

CDS complement(3732024..3732311)

/locus_tag="EFAGFIKM_03198"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIKHIVLFKMKDRSAESIETAAQVLRNLEGKIDVLSLEIGIDV

LRSESFDISLTAEFASLEDLQAYQVHPLHQEVIKYMNEVREQSIAVDYEI"

CDS complement(3732432..3732980)

/locus_tag="EFAGFIKM_03199"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHLSVNTFAVISGAFVTFAFGGWDQLLSLLAVAMAVDYITGLAA

AVRTGTGLNSNIGFWGIARKGLMLTVVLLAHRIDLIMGTDFIKGGAIYFYLVNELISI

TENYAKIGLPLPAKLRQAI AVLKKQEDQEDLMNREWSKPQQTPDNIKQQAETGQTLQD

ESAKQTEDGSQKKSESKNGSN"

CDS 3733430..3734026

/locus_tag="EFAGFIKM_03200"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPNQPEQHSIQAWSLINRKYLGKGVVRVKRFRKPTRCQIRNRVLL

AVLMANDIKLSQLAEDLSISSRSVSAWVYEGRIPGSTNLDKTCQLLGYPRHILFNEEV

VRNSPVICQPESSRFMKRTVTRSPVSNRILTGLCMVHDLSVTDVSHWIGVHPGTFRKW

LHQGTLPAAAFQEQAQFFRIPKILFADVILKDRRNN"

CDS complement(3734250..3735404)

/gene="egsA"

/locus_tag="EFAGFIKM_03201"

/EC_number="1.1.1.261"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94527"

/codon_start=1

/transl_table=11

/product="Glycerol-1-phosphate dehydrogenase [NAD(P)+]"

/db_xref="COG:COG0371"

/translation="MNMNERIAAWNEEAQQCACGHQHRVVDMLIHLEAGAIQRLPGYL
SEQGYRQVTVVYDQHTFRAAGSDVLSSIREAGMHVDEIALPENRTGDIIDEAAIVQV
MLGVRLESQAVIAVSGSTIHDLVRFVCSKMKNKPFISIPTAASVDGFTSAGAPLIVSGI
KQTFQAVPPEAIFADMNILEQAPQVMTAAGFGDMLGKYTSLADWIVSRDLGGEPFCPV
AYRMTEEALNTCIDHVQAIAEGRAEGVAVLMDALIVSGISMLIIDHSRPASGGEHHLS
HILEMDLMQAGERPVLHGAKVGVACALLTVKYKELAQTSGEPVFGIYDQLPEASQLIA
WLEQVGGPVTTEQLGVTPEMVEHAFNTAHTLRPRYTGLRYINEVLNTRLG"

CDS 3735563..3735748

/locus_tag="EFAGFIKM_03202"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLTKELGISLGFLAGTTFGSGIAFLFRLQSFEVVASVTLFGIA
GAIAGIITAVILRQRQH"

tRNA complement(3735852..3735938)

/locus_tag="EFAGFIKM_03203"

/product="tRNA-Leu"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Leu(cag)"

CDS 3736163..3737155

/gene="iolG_7"

/locus_tag="EFAGFIKM_03204"

/EC_number="1.1.1.369"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01671"

/codon_start=1

/transl_table=11

/product="Inositol 2-dehydrogenase/D-chiro-inositol
3-dehydrogenase"

/translation="MKTTHLCFIGAGFHASTNIYPSVVEAGAIIQAIATRSMERSEAA
LLRFGSNGKAYDNAQLMLQQEICDGVVVAQPVDTALVLECIKAGKNVYVDKPLGWN

AAEAATVAEAAEQAGVVVMVGFMKRYAPIYMKLKEIDSGSLGKVRSFQMKFAVDSTP
FCKDEEQFMKLAAIHMV DLMRYLFGEVIRVTGTTVKDGEHINQSSILIFENNVGSAY
FTGMSAWSRESESVLVTFDNGFASAEFNTLTVHQSRSTNLPWKSLEEQDTVYTPSG
SPMSGAYRDLYLRGFVGEMAHFIACCQNQTPHSSAKDNIATMALCDSILSSLK"

CDS 3737379..3737741

/gene="yybR_3"

/locus_tag="EFAGFIKM_03205"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37486"

/codon_start=1

/transl_table=11

/product="putative HTH-type transcriptional regulator

YybR"

/db_xref="COG:COG1733"

/translation="MKKDATKLCPAPYGCSVEVTL SVIGGKWKGAILYHLFSGPLRFN

EIRKLFPDITQRMLTLQLRELESSGIVHREIYPQIPPKVEYSLTPFGETLRPIIFSMR

DWGETYTNEVLARSSQEV"

CDS complement(3737792..3739408)

/locus_tag="EFAGFIKM_03206"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIAQIKRSRLRRKIKNIKKISLTALLGGLVTISVIMTLTLMVIS

SYTSQKQSLIDNTLSLNYASAVQMSQTLDSLFSYMQESLKYAATYFPDMDNSNTKELN

STLDLVRNSSNFFNSVSLVNKEGVIRSTSPYSQASVGHVSSNAAKEAVKL RASYISE

AYQTPRTKRRI VFVSEPIFDSAGEYQGTIGGNIFLQENNILSLSFGSQLKTSNGSYFF

IVDKKGTLLFHPNTNRIGENVSKNEVVQKLLVNKHGKEQYKNLAGVDSL AGYYKVPST

DWGVVIVSPTQTVYDQLNHHIRM LLLYSVPFLILT LIVRVARKLASPFAMLADLVN

QVDKGQVDLPVMKPHWNREADLLTRAVVGALANFRKQTNQLVYDARTDVL TGMNNRRT

FEEVIQEWIQDEV PFSIIVLDIDRFKSINDTFGHHAGDEV LKHIANIIQLSVRPEDVC

ARFGGEEFVLLRNSESNVAYEIAERIRITVEESVLPIDRSVTISAGIAEY PKHSTTS

TELFHLADNALYQAKEEGRNRTVTIQSVIK"

CDS complement(3739573..3740310)

/gene="speE_1"

/locus_tag="EFAGFIKM_03207"

/EC_number="2.5.1.16"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00198"

/codon_start=1

/transl_table=11

/product="Polyamine aminopropyltransferase"

/translation="MRVLYRNKSEQHELTVDTKKLYGEKGQFRVLEFSNAAVQGAMD

LDEPARMVLEYPRAMVHLMETNDPEFDTVFVVGHGIGTLPTYLSDRQVKVAELDAEVV

ELSRTFFGYEGSPVLIGDGRELLGQEPATYDYIIIDAFTATGTPEQFISSDFFAMVK

DKLSDSGAVILNVFGRAGNDRLVNAIYTLQAQFAYTRAFALPTETADEVQNRILMGS

HHPIEFQVRQMAGFVEQEPEEGYIIVD"

CDS complement(3740466..3741161)

/locus_tag="EFAGFIKM_03208"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISBth8"

/codon_start=1

/transl_table=11

/product="IS3 family transposase ISBth8"

/translation="MMAIHFENREFGYPRMTTALWEAGLNVNHKKVWRIMRELSIQSV

IRKKRKKSSYTPSVIYPNRLKRQFHATAPQQKMVTDITYISDGNSFVYLSVIQDLFNN

EIVAWQLSKRNDVQLVLDTVEQWTQKRDVSEAVLHSDQGFQYTSQAYNTRLEAFGVKG

SHSRKATCLDNACIESFFSHLKTEKLYLNQCNSEAEIRQAVEDYMYNYNYRRFQAKLK

QRAPIEYRCALAA"

CDS complement(3741326..3741646)

/locus_tag="EFAGFIKM_03209"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MAKKGQTFQTYTEEFKLNAVRSYVEGSSSYKVVAEREGIRNCSQ
LKVWVKKWKKGAEFDERKNSVPNPLKGRPRTAFGSVEEERDYLQAQVDYLKKRYPNLV
KEKR"

CDS complement(3741776..3742678)
/locus_tag="EFAGFIKM_03210"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTLQQLKYVIEVATRGSMNEAAKRLFISQPSLSNAIRDLEQELR
ITIFERTNKGISLSKEGVEFLSYARQVVEQAELLENRYLNAKPSQHFVSSTQHYAFA
VNAFVRLVQQYGQDEYELALRETKTYEIIQDVKSLRSEIGILYLNENAKVINKLLKD
AGLVFTSLFTAKPHIFISVKNPLAKQESVAIEQLQDYPYLSFDQGEYNSFHFSEEILS
TLSHPKSIQVNDRATLFNLLIGLNGYTISTGVLSADLNGDEIIPVPLECEESINVGWI
SHKSTSLSNLGVAYVQALHEAIGS"

CDS complement(3742738..3743475)
/locus_tag="EFAGFIKM_03211"
/EC_number="1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7A3L9"
/codon_start=1
/transl_table=11
/product="putative oxidoreductase"
/translation="MSNVKKGKVVITGASSGIGESTARLLAQHGAHVIGARRMERLE
ALASSIRLEGGSVESCHSLDVTRLEEMQTIVDLAQTRYGRVDVILNNAGVMPLSPLESL
KVDEWNRMIDVNIIRGVLHGIAAGLPVMKKQGFGQFINIASIGAYAVSPTAAVYCATKY
AVRAISEGLRQEVGGDIRVTLVSPGVTESELADTISDEEARDLMKEYRRISIPASAIA
KSILFAISQPAEVDVNEIVVRPTASMA"

CDS complement(3743500..3743760)
/locus_tag="EFAGFIKM_03212"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGDQQEPKHPYVGMWVTKDGYIRHELLPCGRYDEARGDRQSAYQ
GRYVVHGHKHEIYVDDTGFTADGNFRDGVLYHAGMILYRENVQ"

CDS 3743936..3744871

/gene="rhaS_27"
/locus_tag="EFAGFIKM_03213"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1

/transl_table=11
/product="HTH-type transcriptional activator RhaS"
/translation="MLIKTNETDTSITEQQQQLAQLEHFTPSDGIHPTAIPSLALIR
ASEISQPIYSVYQPSLCIVAQGSKLVLGRESYTYDLSQYLVASVNLPISGQVVKATT
EHPYLCIRLDFDSGQIFDLIQDTPSAQPKPDHSTQRGLFVSSTKPSLLEAVIRLVRL
DTPEDIPVLAPLFIREILYRIIQDEHGHSIKQFAIQDSHAQHIAEVIEVIQSDYAKPL
RIEQLAAMINMSSSSLHHHFKAITAMSPLQFQKQIRLHEARRMLLAGSTDAANAAFQV
GYESPSQFSREYARMYGLPPKSDIKRLRLTLDIKN"

CDS complement(3744936..3745373)

/locus_tag="EFAGFIKM_03214"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MMSENEVFSIKETSEQAGLSEDTIRYYEKIGLLPRAERKANRHR
VYRSEDIHTMKLITCLKKTGMSLEEMKPYLQMSMDSLDLDFPDEREMLVNHRKKVEAQ
IASLQQVVD FIDEKLEKRSMYPDECPITGENQMSVFQKQNLFS"

CDS 3745543..3746421

/locus_tag="EFAGFIKM_03215"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNIQNQLRTALITGSTSGIGLELTRLLAEGWQVIGLNRSFRS
EDTDIQNALRTGQLRWVQANLTNYDSLRTALDQIKSDTNSIDVLFNNAGGSASELRFS
DQGHELFELQTVVPYIYMELVELLLKGQMKTVINTSTTSFNMVRQFDLNILERPAE
FKKLFGPYATSKLGLSLWTREVAKSASADVIQLLSVDPGGNNTLRGNKTSGLPFYIKP
IMKWFFPHPSHGASLLYNAALSPTGHESGTFLVKNKATALRFTEQGPVAVLKRVNEIYE
QRFRTTQSGKTIITRS"

CDS 3746529..3747692

/gene="oxdD"

/locus_tag="EFAGFIKM_03216"

/EC_number="4.1.1.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34767"

/codon_start=1

/transl_table=11

/product="Oxalate decarboxylase OxdD"

/db_xref="COG:COG2140"

/translation="MTKGQQPNEKPFIPQPIRSDGAGGPD LGPRDIMRDIQNPDM LV
PPATDNGLLPNLRMSFS DTHMQLNHGGWSREITVRDLPIATTLAGVNMSLTPGGVREL
HWHQQSEWAYMIWGTARITSVDQNGRNFIADVGP GDLWFFPKGLPHSIQGLE DGCEFL
LVFDDGSFSDLNTLSISDWFAHTPPEVLSVNFGVPESAFQSMPKEQVYIFQDTVPGSI
ESQEVQSPYGTVPLTFKHRLLAQEPLITPGGSVRIVDSTNFP ISTTVAAALVEIRPGA
MRELHWHPNAD EWQYYLTGQGRMTVFGGNGIARTFDYRAGDVGYVPVAMGHYIQNTGT
DTLWFLEIFRSDRFEDVSLNQWMALT PRDLVRDNLNAPPELLDALRKVKWPVV"

CDS 3747772..3748911

/locus_tag="EFAGFIKM_03217"

/EC_number="1.1.1.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07737"

/codon_start=1

/transl_table=11

/product="putative zinc-binding alcohol dehydrogenase"

/db_xref="COG:COG1063"

/translation="MRAVTFQGIKDIQVKEVEDPKLQQKDDIIVRITSTAICGSDLHI

YQGALPAAKDYVIGHEPMGIVEEVGPEVTRVKKGDRVLPFNIACGECFYCNHDMESQ

CDNSNGNPDIIHTGGYFGFTERYGNHPPGGQAELLRPYGNFTPFVIPESCELEDEALLF

LSDVLPAYWSVENAGVKPGDTVTVLGSGPIGLMTQKFAWMKGAKRVIADVRLPYRLE

KAKRLNDAEIFNFEDYDDMGEHIREITQGGTDVVIDCVGMDGKKNMLEEIGQKLKLHG

GSLSAIEIGMKAIRKFGTLQLTGVYGSSYNMFPLGNLFERNINLKMGPVVIHYMPEL

FRKITAGEFDPTEIISHRISLENASDAYRIFNDHEDECTKVILKP"

CDS complement(3749050..3749838)

/gene="ycgJ"

/locus_tag="EFAGFIKM_03218"

/EC_number="2.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31474"

/codon_start=1

/transl_table=11

/product="putative methyltransferase YcgJ"

/translation="MSDVIKSQVQKQFAKNAGKYVTSAGHAKGEDLALLVASSQATPD

MNVLDIATGGGHVANALAPLVQRVTALDLTEEMLQVAEAFIQNGHRNVDFVAGDAEK

LPFDDDIYDLVTCRIAAHHFPDVSSFVHEALRVMKPGGRLLFIDNVAPERDENDQFYN

EVEKCRDASHVRAWRKTEWIIHMLEYAGFRMETMVSFQKRKFEEWCNRAALPERERRE

LEASMLSAPSIIRKFFNFVTTNGKLDSFQGESVYIQAIPTHV"

CDS complement(3750038..3752005)

/gene="fruA_1"

/locus_tag="EFAGFIKM_03219"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P71012"

/codon_start=1

/transl_table=11

/product="PTS system fructose-specific EIIABC component"

/db_xref="COG:COG1299"

/translation="MRITDLMIQETMIMDLQATTKAEAIDELIASLNRSGRINDPVLF
KEMIIYKREAESSTGIGGGIAMPKATTAVNEPTVVFAKSRKGLDFEALDDQPAHVFFM
IAAPEGAGNTHLRTLAAALSRLIDSDFISQLMSTDTPAEVSALFDAQAEAAEKEAAK
EKAKAEKEANAASASTTGQQQNTSGVIVGNANSEDFVAVTACPTGIAHTFMAEDALK
KKAQEMGINIRVETNGSEGAQNVLTADEIARAKGVIVAADKNVEMARFDGKPVLRPV
SDGIRKSEELIRKAVNGDAPIYRSQGGNAKEEGASTGKISVGSKIYKDLMNGLISHMLP
FVVGGGILLAISFLFEQLASPENPIVQLLQTIGGGTGAFHFLIPVLAGFIAMSIGDRP
ALMPGMVGGMLMAVNSNAGFLGGLAAGFLAGYVVI GLRKLFKGLPKAIDGLKPILLYPV
FGLLIVGAISFYVFDPIFGSLNTWLVDALGNLGTGNAVLLGLLLGGMMSIDMGGPFNK
AAYTFAIGVFTSSGNTDGAWMAAVMAGGMVPPALAIALATFFKSKFTEQERKSGLTNY
VLGFSFITEGAIPFAAADPLRVLTSCILGSAVAGGLTQLWSINVPAPHGGIFVAALAN
HALLFLLAVAIGSVISGLILGLWKKSPTLVK"

CDS complement(3752096..3753007)

/gene="lacC"

/locus_tag="EFAGFIKM_03220"

/EC_number="2.7.1.144"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q833W9"

/codon_start=1

/transl_table=11

/product="Tagatose-6-phosphate kinase"

/db_xref="COG:COG1105"

/translation="MIYTITLNPSIDYIVEVDELKLGGLNRMNRDLKLPGGKGINVSR
ILNQLGADNTAIGFLGGFTGRFINDKLQEDNIRTDVFTIADDTRINIKLKHGEETEIN
GLGPAIGAEAEAEQLLHKLSSLEKGDIVILSGSVPPSLGTDIFYDRLIKVCKQTGAEFVI
DTTGPALEALEHAPLLVKPNHHELAELFGVTIDTREELVLYGRKLLEAGAKHVLISM
AGEGALFITKAEVHHANVPKGTVKNSVGAGDSMIGGFVGTYYVQSGDLLEAFRTGVASG
SATAFSDDLATRELIDELRNQVTITTI"

CDS complement(3753010..3753756)

/gene="glcR_1"

/locus_tag="EFAGFIKM_03221"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94591"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional repressor GlcR"

/db_xref="COG:COG1349"

/translation="MLTEERYTAIIERLHLQGIVKLQELVDVLGASESTIRRDIDLE

SRQMLKRIHGGAAALVNEKTLEPGMEEKTFKNIQQKTTIARLAAQEIENGECIYLDAGT

TTLAMIPFIEAKDVTVVTNGLSHVEALVSKRIRSYLLGGMMKIHTKAVIGSIALQNMD

NFRFDKCFGLSNGVDPEMGYTTPDPEEALIKRRAHQLSGKSYVLADSSKIGEITFAKL

FDLEEADLITEQMPEHWRPGIAQKTKIIEG"

CDS complement(3754022..3754507)

/locus_tag="EFAGFIKM_03222"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNEMNYEQFRAHLKKASRKRNVPLIKIVAFQERYMKIEEVQFYD

VEQNHMSVQACNTLWMHLENKSFRNMVSQHLQFYRDMENLGRHSFENLIKELYDTSVP

VLLDYNPADYYTSGQLAEILVMDEERLIEQLEMGRFKGAFINEEGKWLKPKPDEMVE

S"

CDS complement(3754642..3756072)

/gene="hpyO"

/locus_tag="EFAGFIKM_03223"

/EC_number="1.14.13.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8PDQ6"

/codon_start=1

/transl_table=11

/product="FAD-dependent urate hydroxylase"

/db_xref="COG:COG2072"

/translation="MSLEALNERVKNDLAYLSFDGANWVRPREHADGHVYDVVIVGGG

QSGLGAAFGLLRERISNIVVIDENASGLEGPWETYARMVTLRTPKHLTSIDLGIPSLT

FRSWWEAQVGPEGWEEVDKIPRGDWMNYLRWYRKVLNLPVLNEVELTLVEPIENGIHR
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/inference="similar to AA sequence:UniProtKB:O31818"
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/inference="ab initio prediction:Prodigal:002006"
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CDS complement(3764987..3765508)
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/inference="ab initio prediction:Prodigal:002006"
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CDS complement(3765748..3766560)
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/inference="ab initio prediction:Prodigal:002006"
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/gene="yfiY_4"

/locus_tag="EFAGFIKM_03229"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31567"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0614"

/translation="MVRQRAATMILLALLVLVTACSKASEVTEATPPQQDTPVEESG

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LAGIPTVGSADSPNLEAILQIDPDVIVIESRTAESTYDQLEKIAPTIVLGTEWLDYVD

DTTYWTQDLLTIAGMYNKVDLAKEKIAEVEQQAKQLKAKIEQLDQKKLAYLRVREKTL

QIYAAKGHPTNTLLYHDLGFVPTTVTPAEQREDLSMEKIADVDADFVVLEIDPNADEY

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CDS complement(3767649..3769250)

/gene="rhaS_28"

/locus_tag="EFAGFIKM_03230"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

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/translation="MEENDWIKQLEQLHFSAVHVCHYSSNPGAVQRRIWKRFAICRVI

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/locus_tag="EFAGFIKM_03231"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01819"

/codon_start=1

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/product="Transcriptional regulator SlyA"

/translation="MTRIVSKEEQIINLLNVLGNKISPKFERCTGISSSRFEILHELD

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CDS 3770130..3770780

/gene="yodC_2"

/locus_tag="EFAGFIKM_03232"

/EC_number="1.-.-."

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P81102"

/codon_start=1

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/product="Putative NAD(P)H nitroreductase YodC"

/db_xref="COG:COG0778"

/translation="MSTIQSKFQKTNDFNEITYGRRSVKLYDPEVKISREEMTEILSE

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GYDTNPIGGYEKQIAEAFGMDKERYQPVMLISIGKSAKEGHPSYRLPVETITTWA"

CDS 3770878..3771174

/gene="ycnE"

/locus_tag="EFAGFIKM_03233"

/EC_number="1.-.-."

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94425"

/codon_start=1

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/product="Putative monooxygenase YcnE"

/db_xref="COG:COG1359"

/translation="MIIHHAHLQIKPDQEQAFSLASAKELITATRQEEGNISYDLAKST

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CDS complement(3771334..3772254)

/gene="qorA"

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/EC_number="1.6.5.5"

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/inference="similar to AA sequence:UniProtKB:P28304"

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/db_xref="COG:COG0604"

/translation="MRAIICTKYGSPDVLQLKDIAPSPKDHEIQIKIHATTVTSGDC

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ILDAVGKVSQCRHLLAPNGTYVTVEGQGIARVTAKDLILLKELMEAGEMQAVIDRR

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CDS complement(3772348..3775038)

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/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P06993"

/codon_start=1

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/product="HTH-type transcriptional regulator MalT"

/db_xref="COG:COG2909"

/translation="MYAPILSTKLTPVQRSHVDRPRLYVRFGEGMHAKLILVSAPA
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CDS complement(3775224..3776573)

/gene="yvdP"

/locus_tag="EFAGFIKM_03236"

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/inference="similar to AA sequence:UniProtKB:O06997"

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/db_xref="COG:COG0277"

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GPGGFYFLNWGGAVSRKSPRSTAFFWRKEKFYVEWTSTWLKPSHAAKNIALARNTRKK
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CDS complement(3776765..3777292)

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CDS complement(3777340..3778149)

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/EC_number="3.1.1.23"

/inference="ab initio prediction:Prodigal:002006"

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/db_xref="COG:COG2267"

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CDS complement(3778425..3785957)

/locus_tag="EFAGFIKM_03239"

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GQLVLKDVANKAVTFDGIFRNPNNQQFISNSEVGFVSFNNGSSTSN SGHVEIPKGSNG
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tRNA complement(3790729..3790803)
/locus_tag="EFAGFIKM_03241"
/product="tRNA-Ala"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Ala(ggc)"

CDS complement(3790988..3791455)
/gene="nrdR"
/locus_tag="EFAGFIKM_03242"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P67318"
/codon_start=1
/transl_table=11
/product="Transcriptional repressor NrdR"
/db_xref="COG:COG1327"
/translation="MKCPYCGYMGTKVLDSRPANEAKSIRRRRECEQCARRFTTFEMI
EETPLIVIKKDGSRREEFSRDKILRGLIRACEKRPVSVETLEMMVSEVEKSLRNTADAE
VESRQIGELLMEQLFPVDEVAYVRFASVYRQFKDINMFMKELKSLLSKDNLED"

CDS 3791572..3791793
/locus_tag="EFAGFIKM_03243"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P22065"
/codon_start=1
/transl_table=11
/product="Small, acid-soluble spore protein alpha"

/translation="MAQSNNGNSNNLVTKASAALEQMKYEVAQELGISIPQDGYQG NM

TSYENG SIGGYITKRLVTIAEQQLAGQYQ"

CDS complement(3791876..3792439)

/gene="mltC_2"

/locus_tag="EFAGFIKM_03244"

/EC_number="4.2.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01616"

/codon_start=1

/transl_table=11

/product="Membrane-bound lytic murein transglycosylase C"

/translation="MRILRKKRVLLLMFVSFVLVFLNTNWMWAFYPIHYKEEIRAQS

QSYEVD PFLIASIIKVETNFKTSKESKRG AIGLMQLMPDTANWILEQAKIPDTSLEEL

KHEPERNIQLGTWYLRNLSDQFDGNEAVMIAAYNAGPGKVNSWLRDGVWDGSFDTVKD

IPFGETRH YVQRVIYYYNQYVKIYNTF"

CDS complement(3792436..3793032)

/gene="coaE_2"

/locus_tag="EFAGFIKM_03245"

/EC_number="2.7.1.24"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P63831"

/codon_start=1

/transl_table=11

/product="Dephospho-CoA kinase"

/translation="MNIGLTGGIATGKSSVSAYLASKGALLIDADVIAREVMMPGHPV

LAAAVKRFGQAILNEDGTLDRKKLGSIVFQQPEERKALEAITHPAIRREMRERAAAYE

LQHPDKLVVSDIPLLYESGLEDFEEVMVVYVPRSVQRDR LMSRDGMTAAQAEARMDV

QMDIERKKQLADIVIDNSGLWPETEQQIDTYLQRKGLL"

CDS complement(3793042..3793815)

/gene="ytaF"

/locus_tag="EFAGFIKM_03246"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SP79"

/codon_start=1

/transl_table=11

/product="putative sporulation protein YtaF"

/translation="MLHHFISLLALALALSLDGFVGITYGLRRTKIPLLSIAVISIC

SGLVIALSMQVGVLLSHVSPDIASIVGAVILIGAWSLQLIRKQGKEQQETDTGT

GGVTEATVTGMGEARERLSDSKGRNQVLALDLEQSASSGSLERMVFTLELRKLGVVIQ

ILRSPSKADMDSGSISAEAMWLGIALSLDAFGAGLGAALLGFPTLWTALIALFSG

AFLSLGMNVGLRFSALRWMRRLSVLPALLLMIMGIMKLL"

CDS complement(3793958..3794785)

/gene="mutM_2"

/locus_tag="EFAGFIKM_03247"

/EC_number="3.2.2.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42371"

/codon_start=1

/transl_table=11

/product="Formamidopyrimidine-DNA glycosylase"

/db_xref="COG:COG0266"

/translation="MPELPEVETVRRTLNLIVGKTIDHVTVSLPRIIQRPDIDAF

MELAGHTVIGVERRGKFLRILLDGLVLVSHLRMEGRYGVYEQHEDVEKHTHVIFHFND

GTELRKDVQRQFGTMHLFNAGEELVSKPLLKLGLEPLDPAFTVTAFREAVGKRRTKIK

AVLLNQAYVVGIGNIYVDEALFRAGIHPETIAKLTAEQTLVLEAIVATLQDAVNAG

GSSIKSYVNGQGEMGMFQHQQLKIYGRKSEPCTTCGTLEKTVVGGRGTHFCPNCQLL"

CDS complement(3794904..3797558)

/gene="polA"

/locus_tag="EFAGFIKM_03248"

/EC_number="2.7.7.7"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P52026"

/codon_start=1

/transl_table=11

/product="DNA polymerase I"
/translation="MDKFILIDGNSIIYRAFFAMPPLTNSKGLHTNAVYGFTTMLLRL
LEEHPKTHVMVAFDAGKITFRHEGYQEYKGGREKTPPELSEQFPLLKELLKGLGIAQF
ELAGFEADDIIGTLTKRADEAGRQVLVVS GDKDMLQLASEHVHIGLTRKGVTDIELYD
PAQIKERYGLTPLQIIDLKGLMGDASDNIPGIPGVGEKTALKLLHQFGSVEDVLNGTS
ELKGKMKIEAHAEDARMSKQLATIHREVPLEQTWEDMQFAGLKEEHAGPALAKLEF
KSLLERLSFGSIGSEQEAVPAAEVES SATEDNISELFSS LDSIDVLHVETHGDNPH
QAKLIGLAVGSAGTYTFISPELLHSEAAAPVRAWLGNSDQPKRGYDLHRVDLALHAHG
IEFAGAAFDVQLAAYLLDP TESNQTISGLTTKYGLPSLVEDDTVMGKGAKYKVP EMEI
LGDFLCRKAAVA AIIPLQE QVLETDEMNSLFHELEMP LSRILADMEKQG IKANTADL
QALGSEFEEQISRLMAEIYKLSGTEFNLNSPKQLGEILFDRLGLPVVKTKTG YSTDA
EVLEKLAPYNDVVKHILQYRQLAKLQSTYVEGLLKEISNRDGKVHTYYRQTIAATGRL
SSQFPNLQNIPIRMEEGRKIRKVFVPSEPGWSILAADYSQIELRVLAHISDDERLKEA
FVNDMDIHTKTASDVFGVNPEDVDGDMRRSAKAVNFGIVYGISDYGLSQNLHITRKEA
AQFIDQYFEVFQGVRRYMDDIVKEARQDGYVKTLLERRRYLPEINASN FNLR SFAERT
AMNTPIQGTAA DIIKLAMVQMDEALRERKLKSRMLLQVHDEL VFEVPADELELMKELV
PSVMEKALELSVPLKAEVSFGDNWYEAK"

CDS complement(3797792..3798451)

/gene="phoU"
/locus_tag="EFAGFIKM_03249"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q97ID9"
/codon_start=1
/transl_table=11
/product="Phosphate-specific transport system accessory
protein PhoU"
/db_xref="COG:COG0704"
/translation="MIRRKEFDQELEELRTLLKQMGEHVGAALDGAIESLQTMNAEKA
QVIIKNDANLNALEDKIMELGSKLIITQQPVAKDLRRIIVAFKISSDLERMGDLALDV
AKVTLRMDGQKLIKPLVDIPQMAEIVKSMIDESIESFLKENTDLAYKMAQTDDQVDQL
YSHMISDLYTLMSEHPNQASQAMLLMMVGRYIERIGDHATNIGESTVYLV TGKRPDLN
Q"

CDS complement(3798515..3799270)

/gene="pstB3_1"

/locus_tag="EFAGFIKM_03250"

/EC_number="7.3.2.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A2V9"

/codon_start=1

/transl_table=11

/product="Phosphate import ATP-binding protein PstB 3"

/db_xref="COG:COG1117"

/translation="MKDLIHIEENLNLYDTHHALKNISMDLPEKTVTAFIGPSGCGKS
TLLRTLNRMDMIPGVRVEGQVMLNGSDIYSNEIEVETLRKRVGMVFQQPNPFPKSIY
DNVAYGPRLHGVTQKAELDQLVEQSLVHAALWDEVKDVLLKKSALSLSGGQQQRLCIAR
ALAVQPDVLLMDEATSALDPISTLKIEELVKELHHKYTIVMVTHNMHQAARVSGRTVF
FLNGEVVEAADTETLFTSPQDSRTEDYISGRFG"

CDS complement(3799501..3800682)

/locus_tag="EFAGFIKM_03251"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPMLLEVKPDQPHVVLHNEELTPIMEQTEVALVAEESVIHLHD
YYRQVPVAGVHTTCGEAATMMNQDQEHPCIVLCDEQMKPTGLLMRETLRMLNGRFAA
DLFYRKPVIVVNTSPVIADIHMEAATIIDIALGRNEQHFYDCLLVTDQGRLLGVLT
RDVMSLSRRLQQA/TEEGIRTVTESRQEISKINNAVTKLVNAANQTVHEAREIMALSK
QGEESLKHVDASYNRVHQMESQGQHADHMLDSIKTGSGMAHSIRSLADQSGLLALNA
SIEAAHAGEYGRGFQIVAGEIRALAKQTREVAGNMSSLLENIGGLTLQTVELVKASGA
EIDDSSVHVTTAGGATFRQLNSAVRDLSRIAEEIAMEGGKAGEVAEHIRTKLDEMVTNS
E"

CDS complement(3800835..3801563)

/gene="phoP_3"

/locus_tag="EFAGFIKM_03252"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P13792"

/codon_start=1

/transl_table=11

/product="Alkaline phosphatase synthesis transcriptional
regulatory protein PhoP"

/db_xref="COG:COG0745"

/translation="MAQRLLVIEDEPTLSRLLTYNLTQEGYDVTAEDHGSAGYDRALS
QEFDLILLDLMLPGMNGLDILSKLRIQGVSTPVIILTAKNGEAEVQGLKSGADDYIT
KPFGVSELLARVDAVLRYSNGEDLPQLEDKDGSRILGELEIYPLKYEVTLGGQSSIS
LRPKEFEVLLYLAKKPGVVLTRDDLMNAVWGFYIGGQRTVDVHVSSLRKKLELDPES
VHIDSIRGVGYKLVVKRKTPHHSS"

CDS complement(3801680..3803500)

/gene="phoR"

/locus_tag="EFAGFIKM_03253"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P23545"

/codon_start=1

/transl_table=11

/product="Alkaline phosphatase synthesis sensor protein
PhoR"

/db_xref="COG:COG0642"

/translation="MRPFRIRLAIIMMVLIGVSVIVAGYTMGRVFKTTHITALEQTMV
REINLLKATFPFHDASDPTSEATRKYYSDRAELDRLTDSRVTFINKDGMVIGDSED
PATMDNHLNREEIKGAVGDGYGQSIRYSETLGQDMLYVALSVNSDQSDMIEMPSGKFD
GYIRLSMSLHAVDQGLQRGWMIMFAALGLLFLIVAFVSYRVARGLTSPIEHITKVAHR
ITKLEYDARVDVTRRDEIGQLGLAINGMADSLQSQLKTIRDNEALLQSVLANMTGGIV
MIDAGQSIALVNREAERMLGIQAGKVTGKPYTELKRHYELTRTIEESVALKERMHEEV
SVFNPEEKLIRIDGVPMSEDDGGYRGMLFLLQDVTAIRRLESMRSEFVANVSHELKTP
VAAVKGFAETLLSGGVQDKETERSFLKIYDEGDRLNRLIGDILELSKIESKRAPLQC
SPVHVHSFFEMVLGTLSKVAEKKQIRLEMHVPEELYIEADEDKMKQIFINLLSNGINY

TPDGGRVKLQVTMDNDDEVVFAVSDTGIGIPKKDLPRIFERFYRVDKGRSRNSGGTGL
GLSIVKHLVELHHGKLSVESELGMGTTFRVILPFIQEEEM"

CDS complement(3803532..3803891)

/locus_tag="EFAGFIKM_03254"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKMSKQNATHYIWGAQCDGWHLVQNETLSIIHERMPAGTAEIRH

YHSVSRQFFFILSGEACMELNGETFVLETHEGIEIVPGMPHQMMNRSNEEVEFLVISN

PGTRGDRIELDSMLSES"

CDS complement(3804185..3805054)

/gene="ydaD_1"

/locus_tag="EFAGFIKM_03255"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80873"

/codon_start=1

/transl_table=11

/product="General stress protein 39"

/translation="MSTTPQNQKTMPAQHQDQRPGIESEMHPRPEFEKPEYKAAGKLT

GKVALITGGDSGIGRAVAVTYAKEGADVAIVYLSEHEDAKETKRQVEQEGRKCILIAG

DIGDDAFAKKSVQQTVDELGKLDIVVNNAAEQHPQQNLEDITPEQLERTFRTNIFGMF

YVTQAALPHLKKGSTIINTTSITAYRGSPTLLDYSSTKGAITSFTRSLSMNVIEKGIR

VNAVAPGPIWTPILPSTFDEKKVSEFGATQPMKRPGQPDELAPAYVYLASDDSSYVSG

QVMHVNGGEVNG"

CDS 3805444..3807003

/locus_tag="EFAGFIKM_03256"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MESHINTYITLVATSAVLNVFLCLYTYFRRSEIPSSKIFILYTA
ALSIYTFGYAIELASNTLGQMKFWTTVEYIGMPFSASLGLMLMIKYTGKTLSSKKVTAS
LFVIPSITLGMVATNDFHHLFYKKVWLREDSVPVPLMDIAVGQWYVVHGAFTFSCLLCA
CLILIGQWRHTKKMYRRQLLTLTSQIIPMVA AFLYLLGLTPGGMDPVPVLMCITSAM
YIWAILSSRLLTIVPIAKDSIFESMREGVIVLDSFNRLVDYNRSLRDMLPELNTTMIG
QPLDDIWLTLAGKTFPVEYGREGLQTDLYWQLNGETVCYQVRTSYVYNKDAQTVGSLI
MLIDITEQRFLQEQLKQLAYFDGLTKIYNRTQFLHRGREILSEAQLNPQPVSFILFDI
DYFKRINDTYGHDVGDQAIHVVSVCNRYLSPEMLFARYGGEEFVIALSNTSLQEAEK
LAEQLRVALLNDPLDVKGVPITLTSSFGIAQYNGGSDSLESLLRDADTALYESKRNGR
NAVRAYSVSTT"

CDS complement(3807267..3807692)

/locus_tag="EFAGFIKM_03257"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTMIMYLLHIVGALAMGFYLILPFVVGKIRTLNAAAQEGAFASL
RSLNKVAQYGLVIQLLTGGYLMTKGEYSHVWMAVVVVLLLAIAAIGGIMGKPLRLAAE
GVKNKRVDVGPEQSKIRMFSTLLAVFLLIMVYLMVNNQVI"

CDS complement(3807828..3808769)

/gene="mdh"

/locus_tag="EFAGFIKM_03258"

/EC_number="1.1.1.37"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q6HSF4"

/codon_start=1

/transl_table=11

/product="Malate dehydrogenase"

/db_xref="COG:COG0039"

/translation="MTIQRKKITVVGAGFTGATTALMLAQKELGDVVVLVDIPQLENPT
KGKALDMMEEASPVQGFD SHIVGTSNYEDTAGSEIVIITAGIARKPGMSRDDLVNTNAG
IVKSVCEENVKKYCPDSIVIILSNPVDAMTYAAYQTLGFPKNRVIGQSGVLDTARYCTF

IAQELNVSVEDVRGFLGGHGDDMVPLVRYSSVGGIPIDTLIPADRIESIVQRTRVGG
GEIVNLLGNGSAYYAPAASLVQMTEAILKDKKRIIPVIAYLEGEYGYNDLFLGVPTIL
GGNGIEKIFELDLTVEEKAGLDKSADSVRNVISVVNL"

CDS complement(3808785..3810077)

/gene="icd"

/locus_tag="EFAGFIKM_03259"

/EC_number="1.1.1.42"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39126"

/codon_start=1

/transl_table=11

/product="Isocitrate dehydrogenase [NADP]"

/db_xref="COG:COG0538"

/translation="MKLEKFAHPTEGEKIQIDNGTLQVPSNPIIPFIEGDTGRDIWK

ASKRVLDAAVEKAYDGNKKIAWYEVFAGQKAFDITYGEWLPNDTLEAIREYIVAIGPL

TPIGGGIRSLNVALRQELDLYTCLRPVRYFDGVSPVKRPELVDMVIFRENTEDIYA

GIEYAEGSEEVKKVIQFLQQEMGANKIRFPETSGIGIKPVSSEGSKRLVRAAVQYAI

HNRKTVTLVHKGNIMKFTEGAFKNWGYEVAEEEFADKVFTWAQYDIKENEGTDAANA

AQKAAEDAGKIIVKDAIADIALQQVLTRPGEFDVIATLNLNGDYLSDALAAQVGGIGI

APGANINYVTGHAIFEATHGTAPKYADKDVNPGSVILSGVMMLEHLGWQEAAANLIYK

GMETSINNKTVTYDFARLMDGATEVKCSEFADQIIKNL"

CDS complement(3810225..3811337)

/gene="citZ"

/locus_tag="EFAGFIKM_03260"

/EC_number="2.3.3.16"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39120"

/codon_start=1

/transl_table=11

/product="Citrate synthase 2"

/db_xref="COG:COG0372"

/translation="MTATKGLEGIVATTSSISSIVDGVLTIRGYDIDDLAEHASFEEV

AYLLWFGKLPTTDELKSLRKSLSDYAPISELIAQIQLYPKNVSTMAALRSVLSALAL
YDEQADEMTTEANENKAVKLQAQLPTIVAAIARIRQGKEPVAPKEGASIAENFLYMMT
GEEPSETAVKALDQALVLHADHELNASTFAARVTVATLSDIYSGVTSAGALKGPLHG
GANEAVMKMLNEIGTPDRLEAAIQEKLNNREKIMGFGHRVYKNGDPRAKHLQKMSKEL
GEMNNDTRLYDMSVKIEELVTGQKGLKPNVDFYSASVYTQLEIEQELFTPIFAISRVS
GWTAHILEQLADNRIIRPRAEYTGPTQKYVSIELR"

CDS 3811868..3812986

/locus_tag="EFAGFIKM_03261"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0A1W5X0D5"

/codon_start=1

/transl_table=11

/product="Sodium-lithium/proton antiporter"

/translation="MDRIIMKRLFRGLWVIAAVLIAVAIYLLFLLYPFAIAWIIAY

AMNPLVKLLQHRARFPRWLAVTSLILYFGAIAVVLSSAATRMVKEVISLTTSDLHV

DEIKDTFVRWTQNDTIQSLTAQINEFYKENPNYQETINSNISKTTETVGTAVTDLVTG

FFNMILSLTSLPNMGAVLIVVLLSTFFISKSWTRHNITVSGWVPSSIRKPISDIWTD

LKKALFGYARAQLIMISITALFVMIGLLILQVNSAFTIALMIGLVDLLPYLGVGLVMV

PWAAAYLFMNGDLYLGIGISIIYLILLIARQIIIEPKVLASSVGLDPLATLVGMFVGLKL

FGVLGLIIGPVSLVILDAFNANVLRDLRTYIINGRVR"

CDS complement(3813089..3813487)

/locus_tag="EFAGFIKM_03262"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRKWMWALLLIIPVIELFGFILMSDWIGAGKTLMLTSLIGI

AMLQFEGRKVLVDKSEMERGKVPGRKMVDGLFIFVGGFLLIPGFVTDLIGFTLVFP

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CDS complement(3813495..3814031)

/locus_tag="EFAGFIKM_03263"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNDRAKEADNVREQSNGNWYAARLRVRYQESDQMGVVYHANYLN
WFEIGRTEMIRQMGYTYRKMEEQGLLLPVTGLDVKYHKPARYDDEIIIFTRIAAFSGL
RLNYEYDVRRMSEEPDEHMAIGERVWSTDEALPGERLVTGSTQHVWVNGDWKPVRLDK
AASELYSALEKVWLSGKG"

CDS complement(3814133..3815560)

/gene="pyk_1"
/locus_tag="EFAGFIKM_03264"
/EC_number="2.7.1.40"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P80885"
/codon_start=1
/transl_table=11
/product="Pyruvate kinase"
/db_xref="COG:COG0469"
/translation="MRKTKIVCTIGPSSSELENTKKLIMAGMNVARLNFSHGDFDEHG
GRIIAIRQACEELNKTVAILLDTKGPEIRTGKLEVEPIELVQDEYITLTTEEILGTKE
RLSITYTDLPN DVEPGSTILIDDGLIGLTVVEVQGTEIKCRIVNGGSIKSKKGVNVPG
VAISLPGITEKDANDIVFGIEQGVDFIAASFVRKASDVLEIRELLEKHNAGHIQIISK
IENQQGVNDNLDEILEVSDGLMVARGDLGVEIPAEVPLVQKRMIQKCNVAGKPVITAT
QMLDSMQRNPRPTRAEASDVANAIFDGTDAIMLSGETAAGKYPVESVLTMSRIA EKAE
SALPYQELYLKQ RVAQQTTVTEAISQSVALQAQDLNAKAIITSTESGHTARMISKYRP
ESPIIAVTTEDRTSRRLALAWGVTPVKGR LVDSTDALFENAIEGGVKSLVKEGDLVV
ITAGVPLGRSGSTNLIKVSQIPNNA"

CDS complement(3815666..3816697)

/gene="accA"
/locus_tag="EFAGFIKM_03265"
/EC_number="2.1.3.15"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q6GG07"

/codon_start=1
/transl_table=11
/product="Acetyl-coenzyme A carboxylase carboxyl
transferase subunit alpha"
/translation="MAGELPYEAPLVEMRKKIDELVQFGQEKGIDFTDEIARLEERYH
RLEEEIYTGITAAQKMHLARHQQRPTALDLIQLIFTDFIELHGDRMFGDDLAVVGGLA
KLNGKTVTVIGQQRGKDTKDNIARFFGSAHPEGFRKGLRLMKQANKFGRPIITFIDTK
GAYPGNTAEERGQSEAIARNLMEMAKLSVPVIVVVIGEGSGGALAMAVGNRVLMLLEH
AIYSAISPNGAASILWKDASKADQAAEAMKITAKDLLEMEVIEEIVPEPRGGAHRDYE
ASAAFISEALVRHLDDMKGWSGDQLKQDRYEKFRKIGSVTFEPQASNEAPQELVKVDV
ASNLSGNAE"

CDS complement(3816698..3817591)

/gene="accD"
/locus_tag="EFAGFIKM_03266"
/EC_number="2.1.3.15"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:C0SP93"

/codon_start=1
/transl_table=11
/product="Acetyl-coenzyme A carboxylase carboxyl
transferase subunit beta"
/db_xref="COG:COG0777"
/translation="MFKDIFQKKRKYATIPSERALPGEGQEVLERPKREIPEGLMNKC
SKCGTIQYSKELEKNLKVCPACGYHMRLNAMERIAMVLDDQGFVEFDADMISVDPLGF
PGYSNKLEQQRLKSGLKEAVITGEGTIDGLPVVVAVMSFDFFTGSMGSVVGEKITRAI
EHATEKRLPLIIFSTSGGARMQESILSLMQMAKTSAAALSRLDEQGGLYISVITDPTTG
GVSASFASLGDINIAEPGAVFGFAGRIVIEQTIRQKL PDDFQTAEFNMQHGQLDMVVH
RKELRATLGKLLDMHSEKGGV"

CDS complement(3817655..3817909)

/locus_tag="EFAGFIKM_03267"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MHVLYAAVLPSFFVRTRTDLVAPGDPTKIDSNIGATIFRFLQVT
SIVLTEAGDPCPVPADFFVFNAGQGPWQVRGRKFTVTRG"

CDS complement(3817997..3818185)

/locus_tag="EFAGFIKM_03268"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MWTVIYIAPTAKVADKIKTKLSEEGFLVQTRPISLSKQQFEIRV
PSGELEEVQEVLNSILHS"

CDS complement(3818470..3818961)

/gene="ypjQ_2"
/locus_tag="EFAGFIKM_03269"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54173"
/codon_start=1
/transl_table=11

/product="putative protein YpjQ"
/db_xref="COG:COG1267"
/translation="MSYEIVEAMLARRGVRIDAIAAIVYRLQKGYHPELTLD DCVTSV
KSVLQKREVQYTLTYGIALDELA EKKLLPQPLQAIMEADESLYGVDETLALGITHVYG
MIGLTSFGYLDKEKIGVIHDLNEHTTAIHVFLDDL VAGVAAAASARIAHKNIKAKKYP
SDL"

CDS complement(3819168..3823277)

/gene="dnaE2"
/locus_tag="EFAGFIKM_03270"
/EC_number="2.7.7.7"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01902"
/codon_start=1

/transl_table=11

/product="Error-prone DNA polymerase"

/translation="MSSFVHLHVHSEYSLLDGAARIPDLVDKAADLGMTTLALTDHGV
MYGAIPFYKACVERGIKPIIGCEAYMTAGSRKERGSRKDQPIHHLILLAKNMTGYRNL
MKLCSIGHLEGFHYKPRVDMESLAHHEGIICLSACLGGEVPQHLLHGREEEARRAAL
RYKNIFGDDFYLELQDHGLSEQKRVNPQLIKLAAELEIPLVATNDAHYLSEEDAELQD
VLICIGTGKTVDDENRLRIGTNQLYLKSEEEMARLFPHVPEALANTVRIADSCELKLE
FGKSILPEYRPLPDGLSPSVYLRQLCEEGMEERYAQSTRWTDALRSELEQRLAYELG
IIDSMGFSDYFLIVWDFIAYAHKQGIVTGPGRGSSAGSLVAYTLHITDVPKYNLLF
ERFLNPERISMPDIDIDFSDERRDEVIDYVAHKYGKAHVAQIITFGTMAARAARVDVG
RALNVPYGEVDKAAKLIPAQLGINIERAMEATPELKALYETKPKTRELLDMAMKVEGM
PRHASTHAAGVVISRDPLTDAVPLQEGSEGTALTQYSMENLESIGLLKMDFLGLRTL
IIERCVRWIGEHEIPDFRLIPDDDPLTYEMLGRGDTMGIFQLESAGVRRVLKEMKPS
SFEDVISVLALYRPGPMEFISKYIQGKHGQIEVDYPHVDLEPILKDTYGIIVYQEQIM
QIASRMAGFSLGEADLLRAVSKKKREVLDLGRGHFVQGSLLKQGYSEEEADLVYDMIV
KFANYGFPRAHAAAYGVLAFTAYLKAHYPVHFMASMLTAVMGSHRKVAEYVVECRM
DMEVLPPDVNESGILFTPVIVPSGSAGAGDQSSASQQTAGADAESDAGSPAEEHAANG
NGSSFREDRVHEHDGHSGQAEYGEAPLPDDPGPGPEEDGGGYEWQAATTMPASDNRK
EPGLVSASSLENGNDDGQEASSSREEHGELSSAEKNVAVSNDSPDEEKLTAIRFGLA
AVKNVGTQAMESIMIVRQERPFDSSLDFCRRVDLRVCNKRVIESLIQAGAFDTLPGHR
AQLLAMLDETVEAALKWRKEREDLQIQLFDFVETPNWEIYPEIPPYSSGQQLERE
LLGLYLSGHPLDDYEDVLESSGADRIMELTEAADTMTVAAGMVSVKSITTKQGKAM
AFMELEDQIERCEVVLFPVWRRSQQHVGKGELLVVRKVQQQDEGFKLLAEVPLS
PAALEQQLRSRDRRVKPGSGSSSRPAQAASPRRPAGAGAEARSSAGGDASAVRSSDA
AGTGAATAAASRPGGAAEAAGSPEQSREPRAVEQRFVVKIAPHAEKPELLARLKQLLQ
EHPGPVATVLFYEQQQKLLALSDAYRIKPSPTLFSEMEKMLGEGTVKIK"

CDS complement(3823440..3824024)

/gene="ydjA_3"

/locus_tag="EFAGFIKM_03271"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ACY1"

/codon_start=1
/transl_table=11
/product="Putative NAD(P)H nitroreductase YdjA"
/db_xref="COG:COG0778"
/translation="MKNTQSNSVERVIRERRTVRSFSNRPVSEDKLLLELEAAVWAPY
HSKQEPWRFIVFMNEGRKMFSNAVLSTYTPQELEQFGQSAAKDYCEDTPVHVCVVRQ
GTD RWKNEEALLATAGLIQNLQLLAWEEIRGLVWKTNEYNR EDTFAARIGLNSGERLV
GTLHLGYLRDDAVSRPVSRKPAEQIITWIRHEEG"

CDS complement(3824026..3824943)

/gene="yfmC_1"
/locus_tag="EFAGFIKM_03272"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34348"

/codon_start=1
/transl_table=11
/product="Fe(3+)-citrate-binding protein YfmC"
/db_xref="COG:COG4594"
/translation="MKHSNKWFGLGMILTLLLATACAGTNGEKAEPNAETEPQTQAQR
VVATSVTYPDFLYVLGVTPVAAENYHSDYPDYLEGKFDSVPKLGNGSNMEGILATDPD
IIIPKWRDEKLYDQYAKIAKTVLLPDRDNWRDELKDMGEALGKQKEAEQAIQDYDKK
IATARDELKALVGDETFIYLRIMPKESYVMGELSNRGMVIHKELGLKTVAAYPKNEGS
VPVSLELLTEYQADHIILQIDGGDDNTNAQKLYDEM KESNIWKGMKAVKEDQVYLVGD
KEWMNFGYSSVATLNAVEDIVSVIRERNH"

CDS complement(3825063..3826733)

/gene="rhaS_29"
/locus_tag="EFAGFIKM_03273"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaS"
/translation="MNLETKYGLLFRDWTMVLKDAVQVSLLAGEKYNFGTGVAVRSAA"

VSGVELVLGVSGEGEVELEEGIHRSIRPHDLLLIEKGQSTFLVNRCSTPLVCYIIQCHR
VRLTQELAPTEDPWDKQNDGDDHKLEQSNFVALQHAAVEDVKKIVEAFQHTDLHDPMW
CHLLFQQWICTVVEHIRREAEPVHSQQPDQAVQRTIDYLDEHYDDPVTVQQLAQMAN
VSRKWYTVRFREITNQNPSDYITELRMKRAKELLNLTGDSVYEIARKVGYEDEHYFSR
RFKQKVGRSPRLYLHNRRYLGTMTAPELLYTLGMTPIAAQAPFCEPHYLKESFKQV
RKWERSHALNLEEIRRMKPDLIASAWQDSMDYEQLNRIATTVLLPERSNWREELRDL
GELLGKSKQALQVISNFDVGLDQAREQLHTLIPDETIVYIRLTREGITLYGEQSSRGS
MLYRELDLNMPKASLFSGEGTLVSVEHLAEIQPDHILLQMEDGVEARLHLYDHPMWNR
LLAVQNHQVYVLSNTEWYNFSFSPLATQYAIHEMLDLLKRKRLIRRMT"

CDS 3826905..3827234

/gene="ytrH"

/locus_tag="EFAGFIKM_03274"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0H3P8"

/codon_start=1

/transl_table=11

/product="Sporulation membrane protein YtrH"

/translation="MSTFLSKAILDFFIAFGIVLGGAMIGGIGAVISLQPPTQTMLDI

SGKIKIWALAAVGGTIDPMRVIESNFLDGNLSPAVKQILYLISAFMGAHMGTELVKW

VCGGGRN"

CDS 3827256..3827744

/locus_tag="EFAGFIKM_03275"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRVPPFSRYRPLMRMTAVFVLGMIAGCVVYNGVFHLSYNALWLN

NQELQLQLHQNEEDIKTLKKYSKRQTVIKEIKVRAEESDKGPDEASLKVMLQKLGDEL

EVLGRDVFNIDEYSKMTRIMLNQKVYSVREKEYTVQVKTMLVMEGVLQVWVQIRMHV

PA"

CDS 3827827..3828168

/locus_tag="EFAGFIKM_03276"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFIDVLKYALIAIFAVAMVFAALNSIRSHRSSDATSAGLHRSWT

NIWMGGMLVVLALILMFVFTGSTLSVIVEALFLIMGSYNVFAGIRNRSYYARLQQRSS

NGSGKTSGQSA"

CDS complement(3828312..3829646)

/locus_tag="EFAGFIKM_03277"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDGQEENVTKHEQLLQHIEQLKVGSKISVRGLARELGVSEGTAY

RAVKEAENFGLVVTKERIGTVRIEKRPRGMSEQLTFADVVTIVEGHVLGGNEGLAKPL

HKYVIGAMKEQAMARYIDAGSLLIVGNREDAHSLALEQGAGVLITGGFGTSREVRIMA

DELGLPIISSRHDTFTVASMINRAIFDRLIKKKIMLVEDIIGQKPRLQVLKVTSSAAD

FHMLVSETGEHRFPVVDENNRVIGIVSLKDVSSELKEDQSIEKCVIRRPITASLQTSLA

SAAQIMTWEGIDFLPIVDRNRKLIASVTRKEVLQAMRDAQKQPQLGETFDHLIWNFGA

EERGEQNELLFHGFIIPQMATDLGTISEGVLLNVMTQAGRRAAWDVTGNDHVVDNVTT

YFVRPVQIEDQILVRPLILETSRRTCKMDIVVTREGSVVCKAVMTLQSIDHA"

CDS complement(3829858..3830145)

/locus_tag="EFAGFIKM_03278"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVKRLKKAKHVYLLIALSMLVIALPRISFAGGMDWVNIFGIVW

VLFSLLIVGAHLHFILGVDEEKKRALEAVRRAKLRQWEMKLLDKQERSESV"

CDS complement(3830339..3830686)

/locus_tag="EFAGFIKM_03279"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07542"

/note="UPF0342 protein YheA"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNIYDKANDLAKALRESSEVEEITSAMKLEADPDAMLDNFR

DQQMELQQRMMMSGDMPAPDEMEKMEKLFVLSLNLNIRRLFDAERRLSVIIEDVKNII

ADSLGHLYGGAEA"

CDS 3830924..3832291

/gene="yheD_4"

/locus_tag="EFAGFIKM_03280"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07545"

/codon_start=1

/transl_table=11

/product="Endospore coat-associated protein YheD"

/translation="MSTKKVTIQVTGSGILQDDVIMLGEGVLKALKIPSGRPLQLQFG

SFRREVTVIPVPTRYDGLRINQTVASKTGLVPRSVLRVSYRSASRTLRLGPYISVLVSQ

DYPDQPDPRPFGSITMFCQELVNACRKQGAYVSFFTPEDIGAVTGYMKGWVYDDGWKKT

VLPVADVNNRLTSRKLENKPSVQHFMKEVKSLYGTQTFNEKFLDKNEVFDALKSIST

LKRVLPESHLLKTSAMLKTM CNRHPVFLKPVRGSLGKGIIRVSRQIDGSFLTATGV

GGTRKQTYTSLDKLYASMSGKMKTRYQIQGLTLIDNSGRPVD FRALVQKNRTGKWS

VTSIVARIAGGSHYVSNLARGGSLSTVKDAVAKTQLSGSAKASAYAGLHTAALDIAGK

IESAIPAHFGEIGIDLALDTTGRVWLLEVNSKPSKNDNTPLSESKIRPSVKAMLEYST

YLAGF"

CDS 3832342..3833532

/locus_tag="EFAGFIKM_03281"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFPPSQTKMAILVRATEGSPPTDELFCRRLSLGSMYPYALQII

VIPISTDAVHLPLQWGYAYHKGKWNSVPVPAVDLIMDRCLRPISRYVRQQLKEWIPTN
GTDQHRYWSASLPGKWEVHRVLSRNPELRSQ LAPTTRIGSHIPWETWLD RWPRGLFFK
PVSGTHGKNTFRLSRGTPSTWIVEGRNEDNEPFFLT FNHTQAVSSWTLHQAERKMI
VQPYLELSHHGRAFDIRALMQKNGQGRWTLTGCMVREGPEGSLTSNLHGGGKAYPAHA
YLLQRYGTIRTETLLKSIRQTATLIPTMLESRFGR LAELGLDFGADAEGQLWLIEVNS
KPGRTSFAEAGDRRMHTLT YTRPLAYARYLLQQHVLTDVIRPMKLPNTSSKAGLKPIQ
IHGG"

CDS 3833593..3834966

/gene="yheD_5"

/locus_tag="EFAGFIKM_03282"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07545"

/codon_start=1

/transl_table=11

/product="Endospore coat-associated protein YheD"

/translation="MSLTFCNLHFTKQPDKVYISNALMKSLNLSGKKT VHLRFGRDR

VPATIKPIKKAGKHL YLASGIRNMMNVPKRGS IYLRNLQNDEVQLG PLIGVLSDGPAT

STNPFGSRTGFIKQLLREGSRKSYIYAFTPRDINWQNETVSGFFLNDNGSFTRRTVPL

PDVVYNRLPSRRSDFSPAINQLRERFVRRKIPFFNWSFFNKSDIYTLLEN EPAAGRYI

PESITNPSVEQMKEMLERHQFVYYKPTAGSLGNGIYRLTYSPKRGYFARYRKKGGNAL

LRFGSFNSLMRMLQGRHGKQLRGYVVQQGIRLIEIDECPIDFRFHM HKNGNNQWVVVG

IGAKKAGRGSVTTHIKNGGSLMTPEQALSRNFGDRAGEVLQHAKSVAITLAQAIETQH

QHLIGEIGFDLGIDQEEHVWMFEANAKPGRSIFRHPSLRVEGKSSVEHILEHCLYLSK

FRKKEEI"

CDS 3834966..3836072

/gene="yheD_6"

/locus_tag="EFAGFIKM_03283"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07545"

/codon_start=1

/transl_table=11

/product="Endospore coat-associated protein YheD"

/translation="MTLHDDFKPVI AVLTMHDKQRMFRGNHQNFQDILQTGESMGYVW
YIVTVRDLNVSGPTVKGYTYNKGSGKWVSQPFPLPHVLYNRIPNREDEGKPSVQRKID
ECMQSGIELYNPFFFNKWDLFEWLRKSKSTQQLIPYTRRMRSASSLGAVLRAYPYLYL
KPESGKAGKGIMMLKFQEKERLPYRLKIQTTRRSTTYKASTLAKLWARIRKETGHTPY
IMQQGIELASSRKRPFDLRVLVQKNTKGQWSVTGVGARLAGSRSITTHVPRGGSVEDP
EKLLTELFGEEMSTNLMKRVKSTSLMIARQVERGSGYTLGEMSMDLGIDDLGELWFFE
ANAKPMKFDEPQIRRRSLERIFHYSAYLARQSKR"

CDS 3836108..3837286

/gene="yheD_7"

/locus_tag="EFAGFIKM_03284"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07545"

/codon_start=1

/transl_table=11

/product="Endospore coat-associated protein YheD"

/translation="MSSPVLGIMTLYLNEHRALEERSVYRRMILEGRKRGLDIYVFTP
ADVHPGGKQIEAMVFHEGKGWSREWRSFPDLIFDRCRIQRNRRFQQLLAFREKYGHLL
FLNRPLRNKWTIHQTLLQKANFREHLPETALFQDMSDVNRMLKASSLVYLPINGTGG
RGILRIERSSSEANTVLVQGRDQKRRIITPRKVHLSRLGALLQHWNMKDKYLVQKGIQ
LQLPNGRVHDYRMLVQKNGEGQWELTGCAGRMGAEKSVTSNLHGGGQAIAMDRLMKQW
IEDDDLRAKINTTAEKFGIDVASFLEDTYGDLCELALDLAIDRSGRIYLLEVNPKPAR
EVFARIGERDIYYKAITQPLEYALWVYRNRPPGTARKPAIPRPVTQKSPRVKRKRKLK
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CDS complement(3837353..3839275)

/gene="hepC"

/locus_tag="EFAGFIKM_03285"

/EC_number="4.2.2.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C7EXL6"

/codon_start=1

/transl_table=11

/product="Heparin-sulfate lyase"

/translation="MSDFYLSATDLQRAAQYYEKHFPEEARNSLTIANRAILNEFIVP
YTNDLNRWIPMGTPVDWLHNPTNDLEFTWGINRHHWMLDLGKAYLMKGNPLYVTAFID
HYRSWRQQNPVPVNLVYDEAVFFQKPGPWRLLETGLRVQSWISAYKYMEASSLIDEGF
QAEFQQGLEEHAFLTRYLGSTEINHAIMHMQGLFMIATFYHQHPRSPHWRQVAMERL
ELCLLHQLGEEGIQVELTTHYHNASIEMFGTPYRLGEISGHPFSTWYASCLRQMAAFT
EALIRPDHQSTGIGDSDWVGDRQRLTLLGAILDDDDLMMARGTDSSECLWLLGVEKYE
RCLRLQASSSPALSSRAFPQTGYVVMRDKYQYLFFDAAAMGGAHGHADALNVEWMWKN
QLFFDTGTRYTYEEGEWRRYFKSTRAHNTVTVDGLNQTPYLSTQQWGEPEAQATTLRW
ESNDSYHFIDASQDGYTHLPDPVTHRRWMLAGVEIPILLIVDWLEAETEHTLEQRFHL
HPEADIALRMNEAGELTADMSYEASSITLTMQWVTAGIGKGAFELTEQPGWVSEVYGS
KSETSVIQGKTDFSGKVGILTCLPVDHIDQVSVTTCQLEPDLMLRLALSIVQGEEKG
YIVIDNDTLQWTKEQK"

CDS complement(3839272..3839607)

/locus_tag="EFAGFIKM_03286"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIINHASTDAYIINETSSRKILGMGGTMMMEVTFAGGIGVVH

SHDAHEQVSYIVKGSFEVQVGEETRILKAGDSFYAGFNVLHGVKALEDSVILDVFTPF

RQDFLEASQ"

CDS complement(3839676..3841073)

/locus_tag="EFAGFIKM_03287"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVKKWMVTTLSALLALSLAGCSADSGTSANNESGTSGENAGGKT

KIIYWTPDRHDADFMKSKIDEFNQTNKDNIEMVTVMGDNYPQAVDIAFASKQAPDVL

QVNDFTQYYQKGYLTPIDGYMSDEMKTVEKDSLIENKNTIDGKIYSLPNTGQVWRLVY

NKDIFKKAGIESPPKTLAEMVADAKKITEVGKSEGIYGFASPFKSSSGFWRAANTIAG

ASSNVGIDGYNYKTGQFDGMYKDIAMALRQMNQDGSMLPGVESLDIDPLRAQFAQGK

IGMYINHSGEPGVYKDQFPTKENWAAAPVPTNDGTIKGASQVIGGSYIGINADSANKE
AAWKFMEEVYSTDLQSEYYEKGYGISLIPAVLSSDKKPSIPGIEGFLPKRYDAIFPAN
PSVVTESLEGTKWGEAFSIFVFTGGDLDAVIKDLTRYNAALEKTKAAGLTNITADP
SFDSSKLQGKLSTED"

CDS complement(3841207..3842811)

/gene="rhaR_31"

/locus_tag="EFAGFIKM_03288"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MGQLTMCVMDDIQAVVKGISSTIPWEDHQVRIVGTASNGESGWS
LLEEQQPDIVISDIRMPKLSGLDLMKRALDAGLRAKFIFISGYSDFQYAQEAIKLGAS
DYLLKPFTPPEILGAVLKVRQVIKEEQAQCKQLEQLEQKVESSSQYERHSYLLGLLRH
EIGGFLNESRWNELHIDLDSSNLLVMVIEVDGYTRYGYTMHLDAEIVPFAVQNIVGET
LNRYTKGVVLRENRYRLAAIFNTPSQIDVSELLEQCRQNVERFSKKTVSIGVGITIAHR
PQEIWTSYAHADQAISYRFYSEGNCILKYAELENQACVAPVYPLEKEKELFYALKCGN
ESTCHRIIDEILEEWQVSEGFPEPLTMIRLLSGLAFIYRAFCDEITAEERLRLEADL
TVLEAMRSLTFEGWRGYIKHFSSMGCEIMDKKRLTDVKQAISKAQEYISLNLAENLTL
HACAQSVHLSPSYFANAFKKETGITPIQYITKMRMEKAKELLVAGVQVQEICQRLGYE
DRPYFSGLFKKYCGMTPTCFRQMYEN"

CDS complement(3842780..3844573)

/locus_tag="EFAGFIKM_03289"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIFNFYKMSLKKRIQLLYIFLVVLCISVTGICSYLFAARSIEQN
ALELKQSILNKSVQVMDEHLRHIVVSSFSFMLNETFTQVMKDVGKNNTSHYYQNLSLL
QTSFAQLKLVEPLIDTAYLTTPIGDFFSTKDFPNRNNSFNREYGRYVKLQGWNTMWFG
SHQSQLFQSQGNVLSLLLKPIVIDNHTYSNVYMVVNMKEEAMRDILTQDLMNNQIQLF

LLHKNGNEVIRPRSRNYDFIMEPDFTQQFSRGDAGDFTYRNDQGEDMLVNYSALSMNE
DWVMVSVQSKADLLSPLQKIRWLIILIMLFCILLALGLSKLLASALLKPLNKLRRMLV
EVESNDLDVRFRRSKYDDEVSAVGHRFNRLMDQIQILFEEVRTTEQDKRRFEVKALQAQ
VDPHFLYNTLNTMFWKSESGEKKDVSEMIVSLSLLFRLGLNDGKDITSVEQEIKHVEQ
YMLQKQKCYEDLFVYRIEVDGPSCYAVDILKILLQPLVENSILHGFNDKEDLGVILIR
IDRQGDTLRLEVADNGCGMDVASIYAEDAPDGGRGYALSNLHGRLSLHYGDVASIVF
HSSTDVGTTVVITIPITEEGQYGPIDDVCYG"

CDS complement(3844678..3845550)

/gene="araQ_21"

/locus_tag="EFAGFIKM_03290"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MMTQNVLAPSGSPQLIRWTKRTVLWLFLIAIALLSLFPILVLL

GSFKTNQELTGGATIWPKIWQFSNYAQAWKTANFSGFTMNSLFVSISTTVGTLLVASM

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AHAATYFILIGFFKSIPRELDEAAMIDGCNFFTTYWRIILPLLRPGLAVAGLGVFQSS

WNEYILPSVFTMSNPDLQTLPVGLANLRYGIGAAAEVQLMMAGACLSILPLLIVYIFA

NKSFMQVTLGAVKG"

CDS complement(3845570..3846460)

/gene="lacF_6"

/locus_tag="EFAGFIKM_03291"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29823"

/codon_start=1

/transl_table=11

/product="Lactose transport system permease protein LacF"

/translation="MKPSKIHAYMFIFPSLFTLVFGIYPLLWALRYMFYDYQGIGTP

VFIGLDNFGRILRDGQFWDSVGNTGVYALGKLVVTIPLSLTLAIILNRKWRGRSLFRA
IYYLPTIFSASVMAIVFFIIFNSYNGILNQLLLKYHLISESISWLGAEHAMLTIIIA
IWGAVGNMYMLLFIAGLQSIPEELYEAASLDGASEFQKLRNVTIPLLGPVLQMIIMLAI
TTALKGYESIMVLTEGGPYGKTEVMYLYLFKLLFPVSADTQSLQQLGYGSavgfttal
IVGAVTLIYFRISKKLNDVY"

CDS complement(3846666..3847352)

/gene="gph_4"

/locus_tag="EFAGFIKM_03292"

/EC_number="3.1.3.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00495"

/codon_start=1

/transl_table=11

/product="Phosphoglycolate phosphatase"

/translation="MNKEKVLLKPEAMIFDMDGTLFQTETLLLPAYQQLFDTLRAEGH

FEGETPPEERMLGSLGMLLEDIWKVVMPEASEAAHRRADELLLQLEIEGLDQGSSQLY

PGVKETLQALKQQGVRLFVASNGLEDYVKGVAFAHEIMPFFEGVYSAGQYKTPSKINL

VQILLEKHRIQDAWMVGDRESSDVEAGKMNGQAVIGCAYAGFGRDEELAGSDVLISDFT

ELLRLYDEAE"

CDS 3847648..3849366

/locus_tag="EFAGFIKM_03293"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKRKTFKIFYKIGLGYLLVLAVLAGCILLIQNSTSQLQRELDF

LVDHDMRVHALTYELERNMVDMETGQRGYIITGQDNYLDPYTQGKEQLITLRDELAAL

ISDNPAQLALLEDIHTNMENWVQVAGEPVVALRKANNTQAIRDDFFADDPGKRDMDQIR

TALDTFRTNEHTLTDNRTEALKQKNTLLNLELYGALIVVAIISFITALVLSRAIVRNI

RTVKQALNDIGSSNGDLTLRIATPMKDETRELAEAAANTMLTGLQQMMLDVQSNAMILS

TASDRLDKGVADSHLAGKEVATAMERVAEGADEQVALTQTMVAAMQQSLNGLNRVASS

ASDVAGRAVRTESIAVDGQQRIDNAVGMSSIEQSFLSVQEAINESKMSDQVINIAD

SMSGIARQTNLLALNAGIEAARAGENGRGFAVVAAEIRNLADQSATSAKEITSILETV
VTGVQSTVQVDESTLHVNEGLRTIEDAGNAFSTITQHIHNLSGEVLEVS AVVEELTS
GSEAVMKSINEVSAVVEDTASATEEVSAMTEEQ LASLQEMSDTSKQLNEMSDALDQLV
KRFKLA"

CDS complement(3849545..3850516)

/gene="iolG_8"

/locus_tag="EFAGFIKM_03294"

/EC_number="1.1.1.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9WYP5"

/codon_start=1

/transl_table=11

/product="Myo-inositol 2-dehydrogenase"

/db_xref="COG:COG0673"

/translation="MTVIKMALIGLGKMGLHMHVHLIDNTKMDTEIEIVAVCDANEEGL

ASFAASHRGVRTYTDYKQLMNEHQIDLLYVAVPPKFHYPVMEALERKIHVFCEKPLA

NSVEEAKKMLEAAEQAGVVHAIHFSMPHEPSVLKLQEMIEQGTVGAIKIDLILQFPQ

WPRSWQQNAWITSREQGGFILEVGIHWHMIQKVFGTIRVVSTQVQYPENGDCLELVQ

AAMELEDGTRIQLNGISQFAGEERVSMVVYGAKGTIALENWEELKTGLVGQPLSPVEV

LESASELPVLKHVIARIQGKPAKIYDFNDGYQAQLVLEALRNTEQSR"

CDS 3850930..3852561

/gene="ilvB1"

/locus_tag="EFAGFIKM_03295"

/EC_number="2.2.1.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WG41"

/codon_start=1

/transl_table=11

/product="Acetolactate synthase large subunit IlvB1"

/db_xref="COG:COG0028"

/translation="MRTVADYLAETLRNLGVTHVFGIIGKSICPAVLKMVDYGLEFIP

GRHESSSGFAASGYALQTGKLGVAFATSGPGGTNLLTAAAHAKANNLPVLFITGHQSI

QELGLPQCQDSSSYLADLAEMFRPATLFSKLVERGDHFGTLLNHALSIALGPNKGPVH
LCIPFDVQTELLSQCRIVPEPEPLLSISNLNRIFPLIQQSNRPLIAGKGVSRARAH
DELLQLAESFNIPVITTPGGKGAIWDHPLYHGPCGVGGFPHADDMLNQSDLYIVLGS
RLSDMTLCNLKPEHHPAHLIQFDADPTFVGKILSAQTLHITGDLKDNLQYLLGTLEDL
PTPVRTTAPMDYTVPLPDLSQLSLASVLDGMSDLLPYDHLKFVDDGSHGFHAVQRYKV
KKPGSFVFDAYFACMGNAIGMAIGAKAASPEETVVCITGDGCFMMLGTEINTAVCNNL
NVIFIVVNNKQLDMALKGMEKTTGRIDGTYEVPMDAAKFAESLGAVAFRAETLAEFS
SALNTAQTNLNQVTVIELLTDRDEIPPTAHRTVNLN"

CDS 3852574..3852942

/locus_tag="EFAGFIKM_03296"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSEHVAQGLDRFAKLSGEYGARALAPIKEHFPELSEFIMGTAYG

DIFQRTTITDQWKEVAISSLITQGQYEQLGVHYTMALSVGVTVTDQLKGILLHLAPCV

GAPRIISAFNILLATLDEIQ"

CDS 3853129..3853479

/locus_tag="EFAGFIKM_03297"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGNFILKTDVPNKVLNIELEGSFSQEDGLRSISAYQDTIASINT

KEYDLNIDCKKLNVTAPEIVPLLEGCLQLFKKDEYKKVVLLENNAILKMQLSRLGRS

VGLDNLEIISTVTT"

CDS 3853534..3854526

/gene="fabH_2"

/locus_tag="EFAGFIKM_03298"

/EC_number="2.3.1.180"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O67185"

/codon_start=1
/transl_table=11
/product="3-oxoacyl-[acyl-carrier-protein] synthase 3"
/db_xref="COG:COG0332"
/translation="MAGIRIVDIDIYHPATKVHNDFYIEHFDARGVDIRGLLQALGRD
TRYKIDNDDENSLSMAYEAASNLLKKTGLTGADIDLIAYASQTPEYIFPTNSLMIHRL
INGASHTICIDSNANCAGMTAAFEQVSRQMLGNPRIRRALIIGSDYVAPHASPDDPVY
FANFGDAAAIVIVERDEHAVGFIDSİYQTDTCVYGNSLFP AEGLAKLGKTGVDAGAFH
VKFIPFDD SICVDAASESIRTLTRNEIGPDEIK AACFSQLSISNIRAVSENVGIGDD
IAVYIGDEFGYTSTSSPFIALHRAVTTGQIQRGDKVLFWTVGAGWQNVAMVVEY"

CDS complement(3854737..3855306)

/gene="ydbD_3"
/locus_tag="EFAGFIKM_03299"
/EC_number="1.11.1.6"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P80878"
/codon_start=1
/transl_table=11
/product="putative manganese catalase"
/db_xref="COG:COG3546"
/translation="MWVYEKKLQYPVRVSKCDPRMAKLLMEQYGGADGELAAALRYLN
QRYTIPDKIIGLLTDIATEEF SHLEMIATMIYKLT KDASVDQLEEAGLGP NYAQ RDSA
LFYTNSSGVPFTAAYIAAKGDPIADLYEDIAAE EKARATYQWLIDLTD DDV DLQDSLKF
LREREIVHSLRFREAVEILKDDRETKKIF"

CDS complement(3855403..3855678)

/locus_tag="EFAGFIKM_03300"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEPEGAKACDTQYYELLEELQALDFVLVELNLYLDTHPGDYQSI
EQYNKFTQERTRVAQEFQQLYGPLMNFGHAFSKYPWEWSQTPWPWQV"

CDS complement(3855668..3855907)

/locus_tag="EFAGFIKM_03301"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKDPQLRAYAPFVGPFDCPPVAIRTYLVPPQLFIPFQPMGWPQ
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CDS complement(3856186..3857538)

/locus_tag="EFAGFIKM_03302"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WFP3"

/note="UPF0053 protein Rv1842c"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDIHTEFHLGQLVFNLCVFLVFLNGVFVAAEFSLVKVRQTRL
TQLQSEGNRMAGYALKVNSKLDSYLSATQFGITLTSGLGLGWLGEPAISELLVEPLMFK
LGVGDTGLISTVSVIIGFCIITFLHIVLGELAPKSLAIQKTDGVALFLSAPLLLFYKI
FFPFIWVLNVSANALLRLAGIEPASEGEAHSEDELRLMKQSAKSGVIDKDEIKLMDN
IFDFSMDLAREVMLPRTDMDCLYTHMSLEENLEIINATKHSRYPVAVEDKDEIIGFIH
ITDLLLAKPEQQHDLASLVRPILNVPESMEISHVLRLMQKKHSQMTLVVDEYGGTAGL
LTAAEILEEIVGDLYDEFEDERPHMERSGDSFSIDGRSLIEEVHKWTGAIIEDEEVD
TIGGWLFKELGGNPTKGKTQELNGYVFEEESTRLRITRVRVYKQSV PQDMNSEENPAE
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CDS complement(3857585..3858688)

/locus_tag="EFAGFIKM_03303"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPLSPMNDPWDPISLRTYGRHVLTSVEMTVTHLCNMRCEHCAV

GDMLTMREAPALPLPLMLKRLDEVEHLQTISLTGGEPSFSRKTVDEMIPLLKYAKER
GIRSQINSNLTLDISRYEQLLPYLDVMHISFNLYLNADDFHQVGFANSSRPVKREVAVK
MYEKMIENSRLSEAGMFISAESMINFRTHDKLDGIHQLIREMGCVRHEVHPMYNSNF
ASSLPVLSLDHMRAAIHRLLDARDKDMWMLFGTLPFFACSAEQDRELINRLYSEPNV
TVRNDPDGRNRVNVNMFTGNVYVTFADIPAFGNIRDRKLDDVFHEWSAEHPLNQTVN
CHCDIASCCGPNLLVADMYKGVDFKSRKAITR"

CDS complement(3858942..3860063)

/locus_tag="EFAGFIKM_03304"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRLVHINLLQPGMKLGKRIYSEGLVLLSEDVELTSRLIGRLKD

LGVGYVYIKDAATEDIIVPEMLQEETRRKALVEIKQQFQSMGLKTKNRIPHFGKALS

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GLGALLHDIGKTQIASEILHKPSRLSDEEFKIIQQHTTYGHRILKDEPGIPLLSAHCA

LQHHERIDGSGYPFGLKDKEIHEYAKWIALADSYDAMTTNRVYKQALLPHQAVEVLYT

GSGTLYEQRMLEKFRDCVAIYPVGISVKLSTGEVGVVASIHSRVPQRPLIRVIKDADG

QTLSSPYEINLSTALSVMITGVEGVEDIPSAAQSEQVES"

CDS complement(3860137..3861567)

/locus_tag="EFAGFIKM_03305"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTREKQTLTILHTNDIHSFSGSMSTIAAMINEERDQGGNFLVL

DIGDHMDRMAVETEGTLGTANVDVINLTGYDAITIGNNEGLTFTPDQLSQSYAGLLCP

VVCSNVVEQDTGLAPVWMKPSLIVEKGPFRVGLLGATAPFTTFYELLGWDVLDPVESL

RVQVEALRDEVDVVVILSHLGLSTDRRLAEQITGIDVILGGHTHHVLEEPLVIGQTVL

GAAGKFGQWLGVVLERLSVGEPLQLVSSGCMAAKSILLDDQVSLAIATNRTEAERTL

NQTAVITDRVLPITYDRESPFATLLAQAVRHFTGAQLSLVNAGQLLGELPQGNITKGM

LHSLCPSPINACTICLSGSHIREALEQSLLDEFSGKPIVGFGRGHILGTLCMDGMEV

QYNPDAPAYQKIQTISINGEPMDEQCEYIVGTLDMFTFNVGYPPLAHGTRTLYHLPEF

IRDLLETEIKRPGALDDSLRARWNQS"

CDS 3861688..3862434

/locus_tag="EFAGFIKM_03306"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLTIQLFAGIAERLNTSLLEFEYIGDIPTAADLKEKLSLAYPE

AASQIRTSFLAVNQYAPADTILSSEDELALIPPVSGGDGTDISDEKLRSSVREHRTE

DGLFLITESTLSVEATTALVITPNHGAALTFVGT TREMTGEQRTVHLEYEAYVPMALS

QMAAIGVEISDRWPGVLCAISHRIGKVDVAEISVVI AVSSPHRND CYDASRYAIERLK

QTVPIWKKEIWEDGSEWKGDQLGPWNPMEN"

CDS 3862559..3863608

/locus_tag="EFAGFIKM_03307"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRVHVTDLKTGDLLKNDVYNSSGLHMLMKGSTLSEDDL SKLLQH

GIEYADVEHTTSDLHSDAQTLPDQTRLLTNLFNDTIKGTESLFQQAMEKGFIDETQV

DEILFTLTEQLEKQKDVVSLLLMLDGDSDYTYNHSLQVGMLAFYIAGWMGYNPEECLT

VAKAGYLHDIGKSKIPSEMLHKPGKLTTEEFDEM KKHTFYGYDIIKESTQDEILAMVA

LQHHEREDGSGYPHGLRGDEIHPYARITAIADV SAMTTNRVYQTKQELISVLC ELYS

LSFGQLNAEATQELIKHMLPNFIGKRVLLTTGQTGLIVMNNPADYFRPLVQTSTAFID

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CDS complement(3863741..3863881)

/locus_tag="EFAGFIKM_03308"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSEVGYGCGGNVGGVGGVGGYNMFTNTGAILVLFILLVIITKAF

CV"

CDS complement(3864032..3864751)

/locus_tag="EFAGFIKM_03309"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSVNPFEgyRITSSFGYRIHPIHGGQTFHRGIDLVTWPWNGPVY

AFMEGRVRFASEGVTGSGFGGYGLTVALQDHRGYLHCYAHLSWIAVTVGQRVKGQLI

GTQGSGTGQSTGPHVHYEIRKTSAPSYGYTASEDGVTEPGAYLQAEYGTASQEQEAPPM

TNEQKKVFEAMQKTLEIQGGWIQQEQLSNMDCPAWAQQAfDYRPFIMNDKGSYEFW

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CDS complement(3864960..3865652)

/locus_tag="EFAGFIKM_03310"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSENGLRDPWIDLIRGGSIPADGDALMDASNINGPNYEIVDKIL

YRGSKALSLNAQSYRLENQTFVDPGKQLSDHYPITAEFVYSTSSQYQLSSTIGGSGG

TGFNDLNQIPDARPSSVVLNSGNRVDGISTLYRDGTNLAHGGQSNIVTLNLADGEYLT

EATIGQGTRNGDKRIFYVELSTNLGNKVEGGQKTSdQIKLEAPAGWYIAGFYGRAGQE

LDQLGVIYRPLN"

CDS complement(3865946..3867343)

/locus_tag="EFAGFIKM_03311"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A6L4"

/note="UPF0051 protein SA0778"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAKKAPEMEEYKYGFRDEHKSIFQTGKGLTAEVVTEISKIKNEP
EWMLEFRLKSLKQFEKMPMPKWGGDLDGLDFNEIQYYVRASEKQGKTWEEVPSEIKET
FDKLGIPAEQKFLAGVSAQYSEVVYHNMQKELEDQGVIFMDTDTALREHPEILREY
FATVIPPADNKFAALNSAVWSGGSFIYVPKGVKCEVPLQAYFRINSENMGQFERTLII
ADEDSFVHYVEGCTAPIYSTNSLHSAVVEIICKKNARVRYTTIQNWAPNIYNLVTKRA
VAEENATMEWVDGNIGSKLTMKYPAVVLKGRGAKGSVLSIAVAGKNQHQDAGAKMIHL
APDTTSTIVSKSISKHGGKVTYRGLASFGRQAEGAKSNIKCDTLILDNESTSDTIPYN
EIMNDNIMLEHEATVSKVSEDQLFYLMRGLTDAEATQMIIMGFIEPFTKELPMEYAV
EMNRLIKFEMEGSIG"

CDS complement(3867364..3867795)

/gene="sufU"
/locus_tag="EFAGFIKM_03312"
/EC_number="2.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32163"
/codon_start=1
/transl_table=11
/product="Zinc-dependent sulfurtransferase SufU"
/db_xref="COG:COG0822"
/translation="MQLDDLYRRVIMDHYKNPRNRGTFDNDNAVTVNLNNPTCGDRISL
QILLKDGIVQEAKYTGEGCSISMSSASMMTEAVKGKTMEQALDIANRFSSLMKGEEVD
FDDYEDLEALSGVKNKFPARIKCATLAWNALRKGIDEENKVQ"

CDS complement(3867785..3869005)

/gene="sufS"
/locus_tag="EFAGFIKM_03313"
/EC_number="2.8.1.7"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32164"
/codon_start=1
/transl_table=11
/product="Cysteine desulfurase SufS"
/db_xref="COG:COG0520"

/translation="MNPSIREQFPILHQEINGHPLVYLDSAATSQKPHAVIEAVKHYY
EYENSNVHRGVHTLGS RATDAYEGAREKVAKFINARRTQEII FTRGTTALNLVASSY
ARANCKEGDEIVITQMEHHSNLIPWQQVAKETGATLKYIPLQPDGHIELADVEKTITN
NTKIVAIAYVSNVMGLIHPVKQIAEIAHRNGAVIVVDGAQSTPHMKVDVQDLDCDFYA
LSGHKMC GPTGIGALYGKKALLESMEPIEFGGEMIDDVGLYESNWKELPWKFEGGTPI
IAGAVGLGAAIDFLEQIGMDEIAHHESVLAAYATERLAEIDGLTIYGPAKRHVGVVTF
NLGDVHPHDVATVLDASGVAIRAGHHCCQPLMRWLEVSSTARASFYLYNNEQDVDRLV
SALIQTKEYFGDAT"

CDS complement(3869002..3870306)

/locus_tag="EFAGFIKM_03314"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A6L4"

/note="UPF0051 protein SA0778"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTTQTILPVESEALRALSESNNEPGWLTEQRLEALKLASGLALP
KLEKQKIERWNVSEYGYKTSEAISSLTEVPASIKDLVQDQAEGSLVIQRNSGTVYSK
VSADLAAKGVIFTDLATAVREHGDLVKQYLNTAVKADEHSLAALHAALWNGGVFLYVP
KNVEIEVPLQAVLLTDDASATFAPHVLVVVEANSSVTYVDNYVSGELSAPVFHNGVVE
VFAKSGAKVRFASVHQLSVNVTDVSFRRVLENDASIEWIVGEMNNGDTASNTMTVLK
GNGSSSDSKVIAVGSGSQKINYTTEARHFGKNTPSQMITRAVMREEASAIINGITKIE
KGATKADGQQTEKVLMLSPKARGDANPILLIDEDDVTAGHAASVGQVNAEQIHLYMSR
GINRTDAERLIYGFAPVVADIPLEALRTQLQSLIEKKLGQ"

CDS complement(3870332..3871114)

/gene="sufC"

/locus_tag="EFAGFIKM_03315"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80866"

/codon_start=1

/transl_table=11

/product="Vegetative protein 296"

/db_xref="COG:COG0396"

/translation="MATNFVIEGLKATIEGKEILKGINLEMKGGEIHAIMGPNGTGKS

TLASALMGHPKYEVTDTITLDGEDVLDMVDERARAGLFLAMQYPSEIAGVTNSDFL

RSAINARRGEGNEISLIKFIQMEGKMKELDMNPEFAHRYLNEGFSGGEKKRNEILQM

MLLDPKIVVLDEIDSGLDIDALKIVADGVNAMKSEDRGFLIITHYQRLNYPDYVH

VMMQGRIVKSGGPELAHRLEAEGYDWVKAELGITDETVGQEA"

CDS complement(3871493..3872068)

/locus_tag="EFAGFIKM_03316"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLEPKIPALKEWASAIKALETGRQIMVMRKGGIVEETRHFEKLS

PAFYLYPTYEHQRKELIKSSDQSYVEESLAEWVPEASTIRITAYAEVTQDLEIRDQEM

LDRLDFHMTADFAEDRLKWKRKDLHLVLRVYLLKEPMEIPVLPEYNGCRSWISI

PNGPVPREMPVVDVDFDEQVQKINEMKLK"

CDS complement(3872194..3872655)

/gene="dps2_1"

/locus_tag="EFAGFIKM_03317"

/EC_number="1.16.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8RPQ2"

/codon_start=1

/transl_table=11

/product="DNA protection during starvation protein 2"

/db_xref="COG:COG0783"

/translation="MATKNKTDQAKSVEQVLNRQVANLNVLYVKIHNYHWYVKGPNNF

TLHVKFEEFYNEVTVMDEIAERILTLKGSPAATMKEYLELSSIQAAGGEDAKTMVQ

NLIEDFATLSNEYQEGIEVADAAEDQPTSDMLTGFKADLEKHMWMLRSFLG"

CDS 3872952..3874169

/gene="mtnK"

/locus_tag="EFAGFIKM_03318"

/EC_number="2.7.1.100"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9F0P1"

/codon_start=1

/transl_table=11

/product="Methylthioribose kinase"

/db_xref="COG:COG4857"

/translation="MSQYRPFTPQDAIELAKTLPGPFAADANLDCHEIGDGNLNLVFH
ITDQNSDKSIIKQALPYAKVVGESWPLSLVRARIEREILQEEYRLCPGMVPEVYHYD
DDLALTVMEDLSDHVIMRKGLIEGVSYPLFAQHIGEFMARTLFFTSDLGMDQQLKKEQ
QGRFINPDQCKITEDLIFDEPYRIA EKNNYDVSIEDEAESLRTDGELHLEVALLREKF
LTHGQALLHGDLHTGSIFVTPESTKVIDPEFAYYGPMGFDVGAVLANLLLNYASLPGW
IQDETALRERKTLNLMVRDVWTEFESRFRALWVNDLVDPMAKTPGYQDLVYVQQLFRD
SIGFAGAKMVRRIVGLAHVADIDTIPNATEREHAQRKALSIGKALIKNNRRLNTIGEI
LDIVSTAVTTTKV"

CDS 3874193..3875266

/gene="drdI"

/locus_tag="EFAGFIKM_03319"

/EC_number="5.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0DTQ1"

/codon_start=1

/transl_table=11

/product="5-deoxyribose 1-phosphate isomerase"

/translation="MTTPDYQPLSSLIWKKDKLEMLDQRLLPETILMLKLYTPEEVWE
SIHSMKVRGAPAIGIAAAGVVLGAKSYDGTTVQGWLDHVKSICAHLATS RPTAVNLF
WALDRMMQKANEVVESGLSLDDGNDALEVEALLIQKEDEEVC RMIGENALPLFEDGMG
VLTHCNAGGLATAKYGTATAPMYLAQERGIHLKVFADETRPVLQGARLTAFELQQAGI
DVTLLCDNMAGMVMSKGWIAVIVGTDRVAANGDVANKIGTYSVAVLAKAHNIPFYVA
SPLSTIDLSTPSGDLPIEERAAEEVTEGFGKRTAPQGVKVYNPAFDVTPNEYVTAIL
TEKGVVRAPFQENLAALFAKEEA"

CDS complement(3875406..3875708)

/locus_tag="EFAGFIKM_03320"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVTMEPIVVGEHVLVGVEVKLPKTTLLINTSKGYIMCGALDVG
LLNEKLGDRKIIAARAVGVRTLLEQLLHAPMESVTTEAEAMGITVGMTGVEALLKMI"

CDS complement(3875931..3876536)

/locus_tag="EFAGFIKM_03321"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKLVLSFLALLLFVVTTTYAPAPATAATKYDFKNVNWGMTVNQ
VKKKEKSKILETVKSKDFTYVVYKTKGFRKNANLYLFYKNKLVRAMYVFDPNNTNGT
TMHLIGEYFSLKRDLFDTYDRSINNRDILDRSGKRVTMYDGEEKDLAAGKISYQCYWI
VDKKKTHISLSLSIFGNFLINRVIYSDNTLDFDIDKVMDSM"

CDS 3876674..3877198

/locus_tag="EFAGFIKM_03322"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNSIYKVSFFITVLVLIMLSFILFTDIRIPLEGTGRFYTKETMN
FGMVLCISITGLLGVLSGLAALEEKVLVHASLLYNFTGWLFMMAVHYRVAYNNDLFD
GLLLSILKWTTLFIVIHIFASFFIRIDKKRRKQEEKKRKGSIEKVGKNYVYTFGDG
SKITVTQEDFQKKD"

CDS complement(3877399..3877659)

/locus_tag="EFAGFIKM_03323"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MHQEDSVIEQIMKQKRLKPIKPETTTVQVKPIHKKKLAQEPLSE
LDVQFKKSVAESIDRSVLHRRVLGIRDLTEIRRLKNGEHMF"

CDS 3878124..3878696

/locus_tag="EFAGFIKM_03324"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKETLSNQEDIGFLFNVDILIKSRSNALALQSLLEFINNEEQIA
DFRIQSGIELGKII EATLQSKKDSFVTLHNERKKANAAQKASTAAQTPASPAPVKTQN
QQEKPVSEKKPATQTSNVSDGNSFDAWIDTLIKENKLTRIVVNNKNGKHQSIPCRILN
FDRDTSIVSIYHVDEKQVYTFRTNEIDFL"

CDS complement(3878821..3879207)

/locus_tag="EFAGFIKM_03325"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39619"
/note="UPF0382 membrane protein YwdK"
/codon_start=1
/transl_table=11
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CDS 3879540..3880010

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CDS 3880116..3880964

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/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9X1H9"

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/db_xref="COG:COG1307"

/translation="MSRIKIFADSTSDLAPEWIIQQHDIGIIPLYVVFGEESLKDGAEL

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IYNTVL"

CDS complement(3881159..3881938)

/gene="pdaA"

/locus_tag="EFAGFIKM_03328"

/EC_number="3.5.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34928"

/codon_start=1

/transl_table=11

/product="Peptidoglycan-N-acetylmuramic acid deacetylase

PdaA"

/db_xref="COG:COG0726"

/translation="MKRMVLYILLGLLSISMVPAQTEASPTGAYHFGFKKSQNGQLP

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CDS complement(3882201..3882608)

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/inference="ab initio prediction:Prodigal:002006"
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CDS 3882816..3883454

/gene="cysC"
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/EC_number="2.7.1.25"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34577"
/codon_start=1
/transl_table=11
/product="putative adenylyl-sulfate kinase"
/db_xref="COG:COG0529"
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CDS complement(3883615..3885435)

/gene="btuD_9"
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/EC_number="7.6.2.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01005"
/codon_start=1
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/translation="MISELRYFMRKLHHVTGPILYWNLLGMICISLMEGIGIYMLVPM"

LSLIGIFEMGSTGLNIPWIGEVNRFSENSQLLLVLFTFVLIVSGQAWMQRLQTIRNT
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LIFTGIQIGLAFWLSAKLTALVLCGLLLFFVLRKFKRAKQIGDQTSEFSQSYNGI
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FIYLSLRVMTVPPASLLLIIFSRLWPRFTAIQSNLEYISSMLPAFRVVRELQAQTA
KSREISEEIASAGDVGTDIEIQPMELKESITCEDVCYRYEGSDTYSLRNVQASIPARGM
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CDS complement(3885432..3886628)

/locus_tag="EFAGFIKM_03332"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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TERGKV"

CDS complement(3886618..3887103)

/locus_tag="EFAGFIKM_03333"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMLRKIKAYLSLPRSMRRLVWEAYILLGWARIQKAMPFAKIAPG

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CDS complement(3887105..3887404)

/locus_tag="EFAGFIKM_03334"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTATTPMNVEDRVTRKEGNLVSDMGSEKVMMSISSGKYYNLGST

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CDS complement(3887401..3888348)

/locus_tag="EFAGFIKM_03335"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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GTCMAVIMMQRGILPLHGSAVVIDGWAYAFVGHSGAGKSTLSAALASRGYPLLTDDVV

ALTWDAGGRAIVSPGYPPQKLWQPSLDGFGMKEQDYATVHAEITKYAIPVQHYFHEMA

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CDS complement(3888487..3888624)

/locus_tag="EFAGFIKM_03336"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQMEKKEWQAPALEVLEVNQTMAGTGYRQIDWVTVHDADLYDPT

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CDS complement(3888654..3890585)

/locus_tag="EFAGFIKM_03337"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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LMNP LLGLEGVHKELDET WLSEFLAIPDMHDSADINSTVYRGISQLPSAHTLVFRDGR
LELKQYHRWNEVEPLKLKSDGEYVEAFREVFGQAVGSRLRTHRQVAAALSGGLDSGAV
VGFASGTLRSQGKRLQAYSYPVPDFTDYTSKTL LADERPFIRSTINHVGNITENYLD
FEGRSPLSEVDTWLDIMEMPYKYFENSFWIRGFYEKASQQDAGILLTGARGNFTISWG
PALDYYASLLKSGRWYRWFREMQQYSERTGMPFSRIAKITGKKAYPEWFKAQSKGASQ
AASVQLIHPDFAQRTGVLERLKSIIVLQGGAQADALKVRAEFNNLAIANKNGAVATK
CSLRYRAWERDPTSDVRVIRFCLSVPIEQYVKHGTDRSLIRRATSPELPKVRLNQRV
RGVQPADWLHRIIPNWDAFTAELRALCSDSKVAGILNTERIRSALANFPSPRPELASH
PDLRLMMHSLIVYRFIRKF"

CDS complement(3890582..3891850)

/locus_tag="EFAGFIKM_03338"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIDAQGNGLVFLLCVPRSGSSLSTV MLQNHSRIFATQEMWFLMN
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KSVDLTGLMLRLNDYFAKPHSNAYELQYERLVSNPQEELEKLCAFLGIRYEQGMEQYG
QFLDSAKS DMFYSMGVGDPFLSSHQEAHQGSVNNWKNILEPHEVELYCRVMGADLFHR
MGYSEQLAEAEQWTGVHYDASPDQEVIDRITHQLTAATGCQWQPQYRMQPADSVVHDP
LGNLNDQVVEEPEKTDPTLAALVTIRQLQAALRAADHRLERGYSERERLKVQLASAQ
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CDS complement(3892274..3893608)

/locus_tag="EFAGFIKM_03339"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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AASYLAYTHSIGMLCVALLTPLLGLTADLSGRKGDFLRVFAIIGVLATLGFS AIGEGD
WFLASALLVISTIGFAGGNTFYDAML PDLVPVERRDMISSKGYAYGYIGGGLLLAANL
LMIQQPGWFGLSSTLAGTRLAFISVSLWWLLFSIPIFRHAPRRPASPDLP GTWKGYAA
VGVRRLRQTRFQMRRFPQLIRMLVAFWFFNDGINTIILMATIYGTSIGIGTADLMLAL
LLTQFIGFPCTLLLGAWAQRWGAKQVLIVSLSVYICIVILGYFMTQAIHFYVLAGLVG
VVQGV SQSTARSLFSNLMPAGRTGEYFGFVNITGKFSSIFGPFVFGYVGQITGSTRWG
ILSLIFFFVAGIAVLLTVKVQKGMQDATRADQEEERN GSVGAPGKSSNVRFT"

CDS 3893863..3895032

/locus_tag="EFAGFIKM_03340"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P45742"
/note="Stress response UPF0229 protein YhbH"
/codon_start=1
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/product="hypothetical protein"
/translation="MSNSHQPYSFVVS KEDWSLHRKGYQDQQRHQKVKDVIKQNL PD
LITEENIIMSDGKQIIKVP IRS LDEYRFVYNYQKQKHVGQGDGDSQVGDVIGRDPSAS
QKPGKGEKAGDQPGHDIVEAEVSIEELEDMLFAELELPDLKQKDKDLIETHTVVFNDI
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MDTSGSMGSFEKYCARSFFFWMTRFLRRQYEKVEIVFLAHHTEAKEVTEEEFFTRGES
GGTICSSVYMKALDIIDSRYPSSYNIYPFHFS DGDNLTS DNERCVKLIGELMKRSNM
FGYGEVNQYNRSSTLMSAYRHIKMDQFMYYVIKEKGEVYKALRSFFQKREGGSVR"

CDS 3895029..3896465

/locus_tag="EFAGFIKM_03341"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
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RIIRELDLNSEDTIEFAKLNSSVVQPSKQSLNPYYLGLKIFEDIERRWDNPTREEQER
WGRKPGQGRAKMFVREFSDTSFIRNYMTKQLTEDLDLYVFEKKGPDWKITDKSWEN
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CDS complement(3896605..3899085)

/locus_tag="EFAGFIKM_03342"
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/inference="similar to AA sequence:UniProtKB:Q9I310"
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/db_xref="COG:COG2200"
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FFFRYHQSRHTWVYKMGSGLIMGIGISGMHYTGMSAAHFHHSHGSMVSSGMQIEPGIL
AYLIASGTFIALGLTLFGIFINQRMSQKDRRIHENEQWYQALYHNHSDAISVNKEGI
VKGINAAVTTITGYPEKEVMDRSIDEIAQQIDIEWISEFDSIDWDDHGLEQAHYMAKM
RDVQGELLDLSIVVPVVIDGRHVGSHILIKDVTEEKQAQEKIRHQALHDPLTGLPNR
RKLDDVLACTINDSAEKGNSFAVMVMDIDRFKMINDSLGHSIGDVFLREVSNRIMKAI
EASDPLAMENVMLARMGGDEFTLVVTQGQATEVRVAELAKQIVEAIQLPYRLKENDFY
VTASIGIAMYPDHGVGVDALLKHADSAMYEVKKNKGNAFQFYTAQLDSELYERIELEG
YLRKALERDEMVLYYQPQIRTEDSRMIGVEALIRWNHPLKGLLAPNVFIPLAEETGMI
YEIGNWTLREACRQMKLWHASGGPLIPVSVNLSSQQFHQSNLVEQVKNALLETGLDAR
YLELEITESMMMDAAVSTAILNELTALGVKISLDDFGTGYSSLSYLKHFPIHKLKIDR
SFVTDITESHSDQAIVATIISMAQNLKMEVIAEGIETKGQLDILMQNDCREIQGYYS

RPLPASEVEHDFVPLRLQGNGTPPVQS"

CDS complement(3899351..3902173)

/gene="xynC"

/locus_tag="EFAGFIKM_03343"

/EC_number="3.2.1.8"

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/inference="similar to AA sequence:UniProtKB:O69230"

/codon_start=1

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/product="Endo-1,4-beta-xylanase C"

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PEENSGITGFRMYVETPWKTSAEVTPADTISFYVDDVLITAAQKIEIEKEIPNLVDIV

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VKFAEANDMEIRGHTLLWHSQVPNWFFTPNDASKPATREQLLARMKTHIQTIVTRYK

GKVHTWDVWNEVISDGGGLRNEASNSKWRDIIGDVDGDGDDSDYIELAFRYAREADPD

AVLVINDYGMENGNKVNDMVKLVEKLLAKGTPIDAVGFQMHVSMYGPDKLIREAFE

KVIALGVNVQVTELDVSIYSSNSELEMPVTDELMLQQAYRYRELFDLFDELGKRGVMD

SVTVWGLADDGTWLDNHPVKGRKDAPLLFDRKLKAKPAFWALVDPTTLPIYRNEWTAL

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EKLYVLADVVDPLRSKLSSNAHEQDSIEIFIDPSKDQTTFYQEDDAQYRVNFDNEAS

FGGNARKESFKSATRLTSGGYTVEVAIPLDSVRAEGQRWIGFDLQVNDDGAGDGKRSS

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CDS complement(3902447..3903451)

/gene="ccpA_4"

/locus_tag="EFAGFIKM_03344"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P25144"

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YSFDGGSKAARRLLALQDQPTGIVCASDMSAFGAIHEIEKHGLSVPEDISVVGFDNTY
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CDS complement(3903581..3904588)

/gene="hemAT"
/locus_tag="EFAGFIKM_03345"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07621"
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/product="Heme-based aerotactic transducer HemAT"
/db_xref="COG:COG0840"
/translation="MSSISATRQKQLDYMGLTAGDLTLLAEHRPVFKKVNEVVDHFI
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HQLADDQQHTLQAITQITQELTGMISEL NESAMAISVAKETAASQDQAQVMLTELGT
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CDS complement(3904832..3906727)

/locus_tag="EFAGFIKM_03346"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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KEERERYLNFIALARKEYDELAKKEVQKAFVYSFEESARTLFENYLDNIEAFCNWSKI
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CDS 3907090..3907935

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/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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STGKI"

CDS complement(3908048..3908674)

/gene="azoR1"
/locus_tag="EFAGFIKM_03348"
/EC_number="1.7.1.17"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O35022"
/codon_start=1

/transl_table=11
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/db_xref="COG:COG1182"
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TVPAPLVNYIAYLSQAGKTFKYTAEGPVGLAGDKKVALLNARGGVYSEGPMAAAEMSL
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CDS complement(3908866..3910089)

/gene="lysN_3"
/locus_tag="EFAGFIKM_03349"
/EC_number="2.6.1.39"
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VRPKLLFAAPSFSNPTGALWSMERREAVLELCSRYGVLLVEDDSYGELHFDGLEPTEF
YRKYP SLFALDTADQGGHVLYIGSF SKTVAPALRTGWAAGHPALIQAMASVKRIADGQ
SSPMNQRLLYQLLAHSPFRWSDHLSMLNREYKTRLKLMLELLKRPGWKGCQYNIPEGG
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CDS complement(3910226..3910882)

/locus_tag="EFAGFIKM_03350"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P24908"
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/product="Putative transcriptional regulator"

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/translation="MKKVWQVVIIDIHPTSM LGTKLILEEQQDLTVRGMTSTGTEGLE

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GMLSKQASPSQLIHLISGLREGHVSIPLSWLNSAEWAQPVESPTEARVIELTETETFI

MERIVQGV TYDKIANEINVSRRSIDNYLRKIYVKLEVSSRAQAIERYALHARQVKTGS

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CDS 3911323..3911733

/locus_tag="EFAGFIKM_03351"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKPSAPSSDIHHTRS AKGKAGSSIKLFLVMWIVLIALGVVGTYY

YSNRLQQQMINQLQAHNQQQIAALKTDYENQLTTISKEVEDLQGQVQSFNELLTFTKD

NASDKTDNSNKLYTQLSEVKKQLETLQKKMDLLK"

CDS 3911730..3912794

/locus_tag="EFAGFIKM_03352"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MITPVKQVNRFFMLALAPFVGLILCLLLLRPPLEPGGLMPTELS

EDTITPRTQAISQELAGAKDAAVQTSSSIKRTTQLYNKTTSTMSTLVQKASTQAVRPE

TIYNKRIS SKLGVPFERVDSDRLTIEMYRVNPGSYKGYAMKIKLKDPTAMQMALDSEP

GRSETTMQAVKRNGAIAGINAGGFADSGGKRYPLSTTVMDGKYVNGFQASFKDLFFVG

LNDTGKLVGGKFSDKNSLDRLQPQFGATFVPVLLQNGRKTPIPDKWKVSPKRAPRTVI

GNYKDDQLLIIVVDGYNEGGSSGATLEELQGRLYKLGVIDAYNLDGGGSSSLILNNRV

VNNPSDGS LRPVPTHFLFYK"

CDS 3912880..3912984

/locus_tag="EFAGFIKM_03353"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MSFSLTFWIIAIVLTLFITGILTSSYNNDKTKGL"

CDS complement(3913102..3914118)

/gene="rbsR_3"
/locus_tag="EFAGFIKM_03354"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0ACQ0"

/codon_start=1

/transl_table=11

/product="Ribose operon repressor"

/db_xref="COG:COG1609"

/translation="MVSIKDIAKQAGVSISTVSYALNGSNKVTDETSSKILAIAKELN

YVPNAAARTLKKRESKILGVFLTDFRGDVYGDLLSGMKAVCNAQGYDLIVCSGKQSHR

MLPERMIDGAILDHTFASEELMQYADRGHKIVLDREMDHPNINQVLLDNKAGATLA

MEHLIEQGHKKIYVVTGPEGSFDSVQRLKAQRQAEREADVEWIEITGDFEKSNGGEQA

ADQIVQVYDGPAAVFCLNDEMAIGLCDRLADSGALGVGHEIDVIGFDNIELSKYVQPR

ASIDYSKRKWGSLAAEQLIKIAGEPVDHERIYVTLVEGGSVSGPIPSDSVISMNR

AVSY"

CDS complement(3914196..3916361)

/locus_tag="EFAGFIKM_03355"

/EC_number="3.2.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:T2KMH0"

/codon_start=1

/transl_table=11

/product="Beta-xylosidase"

/translation="MNNEQLLDLVKQMTLEEKTAQLLQLTANFYEGTNVEGQITGPME

EMGITEQSVDASGSILGLSGAQAIIDVQQAYMKKSRLGIPLLFMADVWHGFKTIFPI

LAIGCSWDTELAEKSAEIAARESAVSLHVTFAPMVDLVRDPRWGGRVMETTGEDPYLN

SLFAAAFVRGYQGDSLKDEPDRLAACVKHFAAYGAAEGGRDYNTVDMSERNLREYYLP

AYKAALDAGVEMVMTSFNTVDGIPASGNEKLMRGILRDEWGFDFGLISDWASIREMIA

HGAAEDDREAAYRAIRAGVDMEMMTPCYVHHLP ELIESGEVDEKLIDEAVLRILQLKE
KLGLFDNPLRAADPEREREIVFSKEHRQVSYELATKSAVLLKNDDSVLPLQPDANVAL
IGPFAQSPDILGWWSCGKEDAVKLG TALQERLTGGKVQFAQGSNVHTITAEQIAEA
LEVASKADLIVLALGEDSEMSGEGGSRTDIRLPAAQMELVKQLKAAGKPIASVIFNGR
PLDLHGVIDESDAVLEAWFPGSEGGA AIADVL TG VVNPSARLTMSFPQSVGQIPVYYN
HFNTGRPLNPEKTEERYVSKYIDSPNEPLLPGYGLSYTSFSYGDLEVSSNEMTTEES
LSIQVRVTNTGERAGVETVQLYVRDVTGEVVRPMRELKGYVKLALAPGESGTATFTLN
EEQLRYHHSDLSYRSDRGEFHILVGANSRDTQKKS FRLV"

CDS complement(3916460..3918055)

/locus_tag="EFAGFIKM_03356"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKTNKKLSVRALFAITLSVVMLMVTACSSQGASGGNEKDAEGNY

KDNLTISVANLTEIKNGNLDNDFHKFWTDKFNLTWDYNYIDWDSWGEKLRLWINS GDL

PDVAWVNYVHGDAINSIEQGLFYKFPDDWKERWPNVAAAYNL TGLGDKLEELTGGTYV

LPRPIYFENKPADPLTNQIGVIALRKDWAEAVGFELKDAYTTTELNEYAALVKEKDPG

KVG NKL VPLSYNAADAMTNMIMPNSVHAMTDS PFYKGEDGQFHWGPADPETLTGLKLM

QKAYKDGLLNPEFYTWKNNEGQNNFKVTGTA AVTSLGGLASYRQGLDS DMKKNLGVDS

DELVHTAIVVGDDGKYRNMEQANFWSALIFNPEISDEKFERIMDLIDYSATKEGQLLI

NMGFEGKDWKYDENNELV SLLPEGTVLEDKYPARFEGLYLLGDDFSV VNP A I K K D Y R D

RAVKLFEEKAKLGTEGKSLATYDWDVNLYDSKAKSQASFDYQNEYANLILKNGDLEAN

WKEWVNSKMSLVQPYLDELNDKF"

CDS complement(3918108..3919010)

/gene="ngcG_5"

/locus_tag="EFAGFIKM_03357"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O50501"

/codon_start=1

/transl_table=11

/product="Diacetylchitobiose uptake system permease

protein NgcG"

/db_xref="COG:COG0395"

/translation="MSKKANKKPRIGTEKMTLLDYIIFAVLLVLALMILIPFWNVIMI

SFATQKEYADNPFLMFPKEWTLDSYKALFADGTILTGYKNTIILLVIGLPLSLFLTTS

MAYGLSRNKFPFKKFLFFLVLFMTIFNGGIVPLYLIMKSLHLTGTLWSVILAGSFSAF

NMILMMNYFYTLPESLMESARLDGAGEWRILFSVVLPLATPIMATITLFYGVAYWNSW

YDAMIFLRKADQLPLQNVLRNIIVTSTTNASNASSVDAAQASNFSMGMKMAAVFVTMV

PIMCFFPMLQKHFAKGVLTGAIKT"

CDS complement(3919029..3919988)

/gene="yteP_26"

/locus_tag="EFAGFIKM_03358"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system

permease YteP"

/db_xref="COG:COG4209"

/translation="MKPAAEGPSKKLKGNVKGNSLWTEIWKHRMTYTLLIPGLVWLIL

FAYMPMGGLSLAFKDYKANLGIWGPWSGFENFKYVFRDPTFIDAVWRTLYINILKLI

IQFPFPIILALLLNELRMRRGKKLFQTVLTFPHFLSWIIVSGVVINVLAYDGLVNSAL

GLLGLPTINFLGSESNFVPMLLLTDIWKSSGWGAIIFLAAISGIDQDQYESAQIDGAS

RMQQMFKITLPNILPTITIMFILSVGGLMSSGFDQIFNLANAATKNVSEVLDVYIYRI

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CDS complement(3920000..3920782)

/locus_tag="EFAGFIKM_03359"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRGVTFMAHITIETGSPTLCMNTSIHVSSDSGETSGGTLYLLH

GAGDNASTWQRLTTIEMYAAQYGCTIIMPEANRSYYTDMYGLNYFHYITQELPEICK

RLNLNPDPEKTYVAGLSMGGYGALKCGLTPERYRKVVSLSGVTDIQTRLHDPHMPA
TMIKEMKAVFGERLQVKADQDIYALSAKLLEQGVALPDILSCCGDSDPFVEMNRDYAK
YMQGTAFDFRYVETPGAHEWKFWEHHLRTMFDFLYNDKIIVE"

CDS 3921238..3922155

/locus_tag="EFAGFIKM_03360"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSEQLKGFHTITEQQLNVFSIRILQKGHLLAHWDRDKDQRRVQ

HSISKSFTCMAVGLALEEGLIHLDATLGDYFSYDHPVTAQRNLPSPQELKLSDLLRMS

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TVKDYLTPRLFDPLGIHDVEWETSPLGVTLGACGLWISNEELSRFGQLLLQEGFWEGR

QLVPADWIRQATSQQIETTGDGDWKGKGYQFWMCSHDAYRADGAYGQLCIIPSKEA

VICINSEENMQGILNAVWNEVLPLYTQR"

CDS complement(3922256..3922510)

/locus_tag="EFAGFIKM_03361"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKPAGVVRKVDQLGRIVLPKSLRKRYQMNEGDPVEILVQGDHII

LERYRPKCIFCGSIEEVNEFKERYICAQCLDEMTQLPQHG"

CDS complement(3922678..3923145)

/gene="trmL"

/locus_tag="EFAGFIKM_03362"

/EC_number="2.1.1.207"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AGJ7"

/codon_start=1

/transl_table=11

/product="tRNA (cytidine(34)-2'-O)-methyltransferase"

/db_xref="COG:COG0219"

/translation="MALHIVLVEPEIPANTGNISRTCAATGTHLHLVRPLGFRTDDAT

LKRAGLDYWHAHVHIEYHDSFAEVQEKYPEGRFFYATTKAKNRYSDNFQDGDFLVFGK

ETKGLPPELIAANPDTCMKMPMTGDVRSNLNSNSAAIIVYEALRQLNFPGLEG"

CDS complement(3923285..3924394)

/gene="serC"

/locus_tag="EFAGFIKM_03363"

/EC_number="2.6.1.52"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q59196"

/codon_start=1

/transl_table=11

/product="Phosphoserine aminotransferase"

/translation="MERAGDFVTKRAYNFNAGPAALPLEVLERAQAEFVDFRNTGMSI

MEMSHRGAVYESVHNEAQERLLSLLGNPKGYKVLFLQGGASTQFAMLP MNLLGAGQTA

SYVMTGSWAKKALSEAKLIGETHVAASSEAEKFMKLPDVS NLSLPERTAYVHLTSNET

IEGTQKFSFPDTGSVPLIADMSSDIFCKPFDLNQFGMIYAGA QKNLGP SGITVVIARE

ELVSESPKTIPTMLRYSTHVDNNSLYNTPPSFSVYMN EVLKWIEEQGGLAGIEQKNT

KKAELLYNTIDASGDFYRGCEPEDRSLMNVTFRLASEE LEKKFIKASEEEGFVGLKG

HRSVGGLRASIYNAAPYESVKALTD FMSHFQKTNG"

CDS complement(3924771..3926195)

/gene="glnA_2"

/locus_tag="EFAGFIKM_03364"

/EC_number="6.3.1.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77961"

/codon_start=1

/transl_table=11

/product="Glutamine synthetase"

/translation="MSVENVLKSIQENNI EWVDFRFDLAGRAHHISLPASAVDADTF

VNGVAFDGSSIQGFRGIEESDMVMMPDPEATYVDPFTA HPTLNVMCDIFTPDGERYER

DPRSIAVKAEAFLESGVGTTAFFAPESEFFIFDDVRYESG TNSSSYFVDSEEASWNT

NRQEEGNNLGFKVVRTKGGYVPVAPVDTQQDIRSEMCRLLLEEAGLSIERHHHEVATAGQ
AEINFRFDTLKKTADNLLAYKYIVHNTARQYGKVATFMPKPLFGDNGSGMHVHQSIFD
GDSPLFYDKAGYANLSEMALHYIGGILYHAPALIALTNPSTNSFKRLVPGYEAPVNLV
YSKGNRSAAVRIPVAAVTPKGCRIEFRTPDSTANPYLAFSAML MAGLDGIKRKINPTE
LGYGPLDKNIYDLSDADKENIRSVPASLEEALDALAADNEFLTEGGVFTKDFLDNYIN
LKRDEAKAVAIRIHPHEYSLYFDC"

CDS complement(3926609..3927832)

/gene="aroF"

/locus_tag="EFAGFIKM_03365"

/EC_number="2.5.1.54"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9WYH8"

/codon_start=1

/transl_table=11

/product="Phospho-2-dehydro-3-deoxyheptonate aldolase"

/db_xref="COG:COG2876"

/translation="MCTLTQSDNYGIFTLTDKSLKANKRLSMTEFLYLIRRTLNDCA

LIQGRMGINMIVIAGKATPEEQIQDIVAVIEKEGLQVHISRGKDRTIIGLIGKVEPKM

QEHLRQMKGVENVVKISKSYKLASRDFHPEDTVISIKGVDIGGKELVVMGGPCAVESA

AQIDEIAGLVKAAGGQVLRGGAFKPRTGPYSFQGTGVEGLIMMAEAGKKHDLITITEV

MTPEYVDICAEYADILQVGTRNMQNFDLLRKLGECKPVLKRGFSATYDELLNAAEY

ILAGGNPNVMLCERGIRTFESYTRNTLDLSAIPVLQSLSHLPVISDPSHGTGRRELVE

PMTKASVAAGANGLIEMHTDPDNSMTGDGVQSLFPDQFANLLQDLEKLAPIVGKSFS

TAKQPAEFFPARVGV"

CDS complement(3927958..3929040)

/gene="ispH"

/locus_tag="EFAGFIKM_03366"

/EC_number="1.17.7.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00191"

/codon_start=1

/transl_table=11

/product="4-hydroxy-3-methylbut-2-enyl diphosphate

reductase"

/translation="MEKEPPLSGCRLSLLRLSNKGIIDRTAITSATLPRKKAGGNQV

EVLRI SPRGYCYGVVDAMVLARQAARNLDLPRPIYILGMIVHNQHVTDSFEDEGIITL

DGPNRMDILSQVESGTIIFTAHGVSPEVRKLARDKGLTTVDATCPDVTKTHDLIREKT

AEGYQIIYIGKKNHPEPEGAVGVAPDLVHLIEKEEEEIEELNVSPGKILITNQTTMSQW

DIKHIMSRLLLEKFPGAIEHNEICLATQVRQEAVAEQAGQSDLVIVVGDPRSNNSNRLA

QVSEEIAGVTAYRVSDVSEIQQEWLKGVNKVAVTSGASTPTPITKEVILYLEQYEHDK

PETWEIKRTVNMSKLLPPVREKTRTP"

CDS complement(3928979..3930439)

/gene="sasA_12"

/locus_tag="EFAGFIKM_03367"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"

/codon_start=1

/transl_table=11

/product="Adaptive-response sensory-kinase SasA"

/translation="MSIRLRLTAWYSGILAAVLIFWGVVIYAFVYFNSYQEVEQQLKV

KSTRITEQIGVNPLSQSLDLPFTESQLQEAQIYIQLWDYQSRSGRISGNMEKLQIQF

PVLKANEILKERGISKIYVDGTPFLVNQLPLSLQGTNEVRGILQVGANVSSQERLLEA

LLNILVFGWLAMALAITSGVLARKSMRPLVTVIDAANQIQSGDDL SVRIQYAGPKD

EIGRLIETVNNMLERTELSFRGLEETNAAQRRFVSDASHELRTPLTTIRGNVDFLKKL

WDQEGTDRPNLDEETVKQMSLEAIEDMADEGKRMSRLISDMLSLARADTGQKIELNPI

PLQILVQEVARRAQFLDRQADWLPGDFSILNGIYVNGSKDYLLQQLFIFIENAFKYTP

EGSVTLDAVLYKGQVGLRISDTGIGMDRDEVPPFIFDRFYRADES RGATPGIGLGLSIA

KWIIIEHHGSVEVVTRRGEGTTFIWLPVVFAPPIE"

CDS complement(3930441..3931130)

/gene="mprA"

/locus_tag="EFAGFIKM_03368"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0R3I8"

/codon_start=1
/transl_table=11
/product="Response regulator MprA"
/db_xref="COG:COG0745"
/translation="MRSTILIVDDDEKIVSMLRRGLAFEGYEVQTASNGAEGLSKLM
KEPDIVVLDMMPQIDGFEVCRRLEAGSKVPVLMMLTAKDEVQSRVTGLDTGADDYLV
KPFAL EELLARVRALLRRKSDSAGTPDNRLMYEDIILDNDSREVLRDGRLELTAKEF
ELLNLFMQNPRRVLSRDLIMDKIWGYDYSGESNVLEVYIAMLRQKTEEYGGKRLIQTI
RGAGYILRGDS"

CDS complement(3931307..3932971)

/locus_tag="EFAGFIKM_03369"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDERNYRSNRQDEENETKQTENRNSSGTDESSYYYSYGPFQSVN
QEDTANHMGSTNQREEGNVEITKPDVPVPPTYYNSESSEQA KRSSAGGGNGSGNGGD
QGNNGGKGNWYNNRKRPRSSVRSLLFSFIAGMLVITVLMYTADRTNMFTPETALTNTDN
QSSGQEASTNTGGGNNVTASLLPTGKEDVSSVVTSTSPAVVKIETLAKQSSRTGLGQG
GSNTSDPLYQYFFGNNGGTEGNQGQSQQPQSGNQLVPMGIGSGFIFDKEGYILTQHV
VQGADVIVQVTLNNSKPYEAKLLGSSFDLDLAVLKIEKNSGDDAFPVAPLGDSNSTQV
GEWLVAIGNPEGFEHTVTAGVLSAKERTISIPDEETGKTREYSHLLQTDASINPGNSG
GPLLNLNGEVIGMNVAVSADAQGIGFAIPSSVISEAVKYLKENKEVPKEVPFPGASL
MALTPEVAKQMGTDVTEGSVVASTIFQSPAYQADLRAYDIITGANGTPYATSQDLIDF
IKKQEIGSEVTLNVRDGGKMDLKIKNKNDFDTSQTTDTQQQQP"

CDS complement(3933120..3933782)

/gene="liaR_2"
/locus_tag="EFAGFIKM_03370"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32197"
/codon_start=1
/transl_table=11

/product="Transcriptional regulatory protein LiaR"

/db_xref="COG:COG2197"

/translation="MSGKVNVMIVDDHDMVRMGLKTYLMLEPTFHVMGEAGHGQDALD
QLRKLNDSEMPDLILMDLMMPIMNGAEATKAIMTEFPGMKIVMLTSFLEDDLTVVQAIE
AGAVSYVLKTVSAEELIYALQGAYRGMPVMTGDVSQALTRGIRQRTARESESGLTERE
KEVLLLIAEGKTNKDIGEELHISIKTVKTHVSNLLMKCEMDDRTQLAIYHRQGWWKT
KG"

CDS complement(3933801..3934826)

/gene="liaS_2"

/locus_tag="EFAGFIKM_03371"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32198"

/codon_start=1

/transl_table=11

/product="Sensor histidine kinase LiaS"

/db_xref="COG:COG4585"

/translation="MIRTILKANKWELMMYFALTGLITLGGFYLLYGEVLMGAGRQRA
WTYVAVVVLATVITGYIAALRLQRKIDLLDLNMLKVSKGNLAVRMPEADDASFGRVYQ
EFNVMMSDIEKKMRLLQRLGEQEVEIEKEQASERAVLEERKRMARDLHDTVSSQQLFAMH
MSASSLPRLLEMNPEHGGKVLQQLIQMSHIAQRQMRGLIAQLRPVELEGRDLTAALDS
WFPDYCRQNGLKGVKELELDGGISDAIEHQLFLVIQEAVANVVKHAEAGVVSLSIRE
EHQISMSISDDGQGFLQQAERPGSYGLSTMRERAELGGQVQIISKPGAGTTVRVLIP
KFPNVPE"

CDS complement(3934830..3935858)

/locus_tag="EFAGFIKM_03372"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRSTRDRWWVGIIPIAIGAMILFRQLGYDIDVGYIFRTYWPLF
LIWWGVKGISEIRRNGGYTFIGPVIVLAIGGYFLARNLGWIDYSMGEFIRYLIPVMLI

GGGLFVLIGPRRRDRKHHDKMQPPPAPEQPYKPLSPEDLEMPSSFDEQFEKTFGKPKQ
EQKNDAGHPHFTGSTDSSSQGQYKKKHQSYNSNDTEYGENYDDGYGNGYGDYGSNT
INKSAFIGDLYMGQEVFSLKPMNISAFIGDVTIDLTAKAIPYGETKIVISSFIGDVKV
FVPEDMDLGVTVTNSFIGDMSLLNQKRGGLSSAQAEAHYHEASKKVRIIVSVFIG
DVKVNVKVG"

CDS complement(3936057..3936272)

/locus_tag="EFAGFIKM_03373"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAKKSQGYQTPNEKYNAEFGEENAAAKVKQSAQNKVQDNFQTPD

EKYNAEFGVENTGQTGQGQKASKYKK"

CDS complement(3936382..3937173)

/locus_tag="EFAGFIKM_03374"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKQFSIQKKHIRGLLVGCVIFAGMMINLNQADAYTFEEESTVL

HVESQSSGIEGPIIETSSKSDQEFPEQVSHQYSDEAQLTTMVYMA LLWSPQPMVIPRP

ELPEKQVADPSPV LAPRSEQILGTQKV TATGYTAGVESTGKGPKHPQYGITYSGVKV

RRDKETVSTIAADPKLFPMGSILYIPGYGYGIVADTGSAIKGNKIDLYFPTTKQVYKE

WGKKDVEVQVIRQGAGKCTEKM LSELADAIDVYKSVPDSWLDKAI"

CDS complement(3937350..3939287)

/gene="thrS"

/locus_tag="EFAGFIKM_03375"

/EC_number="6.1.1.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P18255"

/codon_start=1

/transl_table=11

/product="Threonine--tRNA ligase 1"
/db_xref="COG:COG0441"
/translation="MAVNIKLPDGSVREYADGSSIEDVAASISSGLRKNAVAGKLDGI
VVDLSTTLHEGALVEIVTLDSPGLEVMRHSTAHLMAQAVKRLYGNQEVRIGIPVIE
DGFYYDMDLEHALNPEDLQKIEKEMERIVNENLPIVRKEVSREDAIKTFEEVGDPYKL
ELIRDLPADSVITIYEQGEFFDLCRGPHVPSTSKIKVFKLMNVAGAYWRGDSKNKMLQ
RIYGTA FVKKAQLDEHLHFLEEARKRDHRKLGKELEMFTFSQLVGQGLPIWLPNGAKL
RRTLERYIVDLEESLGYQHVVYTPVLGNVELYKTSGHWEHYQDDMFPKMVMDNEELVLR
PMNCPPHHMMVYKSSMHSYRDLPIRIAE LGMMHRYEMSGALTGLHRVRAMTLNDSHIFA
RPDQIKEEFARVIELIQTVYKDFGINEYRFRLSYRDPKDTEKYFQNDWMWEMSQRMLR
EVVEELDLPFYEAEGEAAFYGPKLDVQIKTALGKEETLSTVQLDFLLPERFELEYVGD
DGQKHRPVVIHRGVISTMERFTAFLLENFAGAFPLWLSVPVQAKVIPVSGNFDDYAREV
EAKLK RAGISAEADLRNEKLG YKIREAQLEKMPYMFVVGENERNAEAVSVRKRGE GDL
GMKPVDEIIAQLKEEIATRLV"

CDS complement(3939703..3940647)

/locus_tag="EFAGFIKM_03376"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MELFAVWTDVSGQEAAQFYRCVKEKTKGLHISKRGFRLTFKH
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DGRATWVCRGNENHEDFQQWLPRISDLSLGLADFIMETQERSMVEDMIAKACSVMD
E
HEVEKVN RICMPLLLNGDLDQPGLRERRRTLASGLRQDLEDVHFFHLEGIINFRIR
P
YKQELQELVEYALDEFWMDRQYEEFMGLLKYFVFFQEAKVPLVHLVHKGMHEFQVLDA
GLNLLPVQKDEQVVVEMPGLELEMDIEDMIVSTLISISPEKVMLHTRTPDLPIISTIC
QIFEDKVQICHHCPECEVLRSGLLTGLDASDLGNYNNC"

CDS 3940828..3941232

/locus_tag="EFAGFIKM_03377"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MRQQPRLHYTIIILCVFQALCFPIPMQSESAVGVSVEATSNK
EVLLQIPESQKPKVIRKYPQVMSKLIAVTHNKPVFLVLALLMLRIPTTGLSFKPWYC
LFKRRLFLLPIKFTSMYVSLTPIAPKYVNALH"

CDS 3941527..3942021

/gene="khtT_3"
/locus_tag="EFAGFIKM_03378"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07535"
/codon_start=1
/transl_table=11
/product="K(+)/H(+) antiporter subunit KhtT"
/db_xref="COG:COG0490"
/translation="MDVRETDLPGIGKKFQIETSSGDKIVIIHDDGRREMYHFEYDD
PDQSISMITLDDYEARQIAAIVGGLTYKPKQLENIEVTFDDLIIEWYKIEPSFGSIGK
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TGRG"

CDS 3942026..3943264

/gene="khtU_2"
/locus_tag="EFAGFIKM_03379"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07536"
/codon_start=1
/transl_table=11
/product="K(+)/H(+) antiporter subunit KhtU"
/db_xref="COG:COG0475"
/translation="MDHLIFEVGLALVLIAAAGLLSAKLRFVVPFYILIGMAVGPHA
MKIWHLDLFRFIESQPFIEFMGRIGILFLFYLGLEFSVGRLIKSGRSIAVGGSIYIGI
NFTLGLIFGFVSGFPVAEALIIAGITISSSAIVAKVLVDLKRTANPETEMILGIIMF
EDVFLAVYISILSGLVLSDDSSSIGGVIMSALIALGFMLIVILGRKATPLLNKLLKIR
SNELFSLVVFGALFLVAGFSEIHVAEAIGALLVGLVLAETEHAKRIEHLILPFRDFF
GAIFFFSFGLSIDPLSLGGDAVWLALIAVVITLFGNFLAGMLAGRSAGLSPKASANIG
LTIVSRGEFSIILANMGKAGLLPMIQPFAALYVLILAILGPLLTKEKSHVFRLLDKI

FKFKDPRKKKEEPKVLQKEG"

CDS 3943378..3944283

/locus_tag="EFAGFIKM_03380"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKAPLISANPVPNTAKTRISSTRRWLNLFVIAGGILASVGLEL

FLHPNKIIIGGITGISSLFAHWTEMRIGLFLFLFNVPFIFLSYKIVQKKFVLVTVLGL

VVFSIGAIVLHPMPPLVEHPLAAAMFGGLCLGLGIGLVVRYGGTLDLTLEIGDPSSRPP

ERVFSGKRMLIEKIIMLLNLLILTAAGVVFQWDQAMYSVIAYLIAYEMVYIAFRGFSS

KRKVCILTQSSQVEKAVRKRLRREPGILEATSDSTQLAMAEGWIRQIPGALYYEVHV

LEMIWLKSIVRHIDPHAGIVTNPEK"

CDS complement(3944370..3945383)

/gene="lgoD"

/locus_tag="EFAGFIKM_03381"

/EC_number="1.1.1.414"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39400"

/codon_start=1

/transl_table=11

/product="L-galactonate-5-dehydrogenase"

/db_xref="COG:COG1063"

/translation="MRAIVCEEIDQLKLQDLPQPERAEGEALVAIRRIGICGTDLHAY

KGNQPFFTYPRVLGHELAAVIEEIGPNEAGLQPGDQVSIIPYLHCGHCIACRNGKTNC

CASMQVMGVHVDGGMREKISVPVSHLLSAEGLTLDDETAMVEPLSIGAHAVRRAGIKPG

EHVWVIGAGPIGLGVMAFAKQAGARVIAVDRNLDRLELSRTWAGADDLVQANEHTVQQ

VAEITGGDYATAVFDATGNVNSMNEAIQYVAHSGQLIFVGLVKADITFHDPEFHKREM

SILGSRNATREDFEQVLSILRQKKLSMDGYITHRVEFDELPTAIDQWLLPDSHVVKAI

VEL"

CDS complement(3945380..3946357)

/gene="fdh"

/locus_tag="EFAGFIKM_03382"
/EC_number="1.1.1.122"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q52472"
/codon_start=1
/transl_table=11
/product="D-threo-aldose 1-dehydrogenase"
/translation="MKRRILGKTELDVPVLSFGASSLGSVFRDIDRDEGIRTVHAAVD
AGMNYIDVSPYYGLTKAETVLGEAIRSLPRSSYMLSTKAGRYGENEFDFSRQRILDSV
QESLDRLHTDYIDILFLHDIEFVPAEIIIEEAFPTLLRLKEQGVIRHAGICGLPLPLF
EKVLPQIDADAIISYCHYSLNDTSLLSLLPLEKKEIGLVNASPLSMGLLSTRGAPAW
HPADDRVKELCLKAARFCAEQGSDIAKLAVQFSTSNERIPTTLVSSASQRNILNNAAW
IEEPIDQSLLDEVHLHILAPLHNETWSSGRPEYNTKPSNTTAEASKGEQR"

CDS complement(3946590..3947810)

/gene="mqnC"
/locus_tag="EFAGFIKM_03383"
/EC_number="1.21.98.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9K864"
/codon_start=1
/transl_table=11
/product="Cyclic dehypoxanthine futalosine synthase"
/db_xref="COG:COG1060"
/translation="MLPPELASLEQVGTDRYIISLHEGGFFTMSTVDRILDKALRGER
LDLEDTIQLFESNEVDKIGAAANVIVKRMHPEPYRTFVIGRNVNYTNVCDVYCRFCF
YRRPGSDEGYVLPDEVIFQKIQETEDVNGTEILMQGGTNPPLPFSYYTDLLKAIKERF
PNITMHSFSPAIEIMKMVEVSDGLTLEEVVRAIHEAGLDSLPGGGAEILDDRTRRKISR
LKGSWRDWMQTAHRIGMNTTATMVIGLGESMEERALHLLRVREAQDECIANKYDS
EGFLAFIPWTFQPDNTNLKLERQTPEEYLKTVASRLVLDNIKNIQSSWVTMGPEIGK
KSLEFGCNDFGSTMIEENVVSAAGATYKVNIESILRLIRESGYIPAQRNTRYDIVRMF
DEENSVHEDFVMQN"

CDS complement(3947968..3949140)

/gene="metC"
/locus_tag="EFAGFIKM_03384"
/EC_number="4.4.1.13"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31632"
/codon_start=1
/transl_table=11
/product="Cystathionine beta-lyase MetC"
/db_xref="COG:COG0626"
/translation="MSESNNKPNSLKFDTKLLHFGDEIDKTTGASSVPIYQASTFHH
FDIFNPPQHDYSRSGNPTRQALEDYITLLEGGARGFAYSSGMAAIISSVFMMFSAGDHM
IVTEDVYGGTYRLLTSILSRMQIETTFVDMTNIDEVKAALKPNTKAVYMETPSNPTLR
ITDIAAVTDWSKEHDLITILDNTFMTPIYQRPIELGVDIVVHSATKFLGGHSDVLAGL
AVARTESLGVQLKQLQNLGTVLGAQESWLLMRGMKTLGARMAHSERSTAKLAAWLNE
RSDITAVFYPGLEDHPGREAHHERQSTGYGAVVSFDVSGSDRAKAVLNRVKLPIVAVSL
GAVESILSYPAMMSHAAMPADVRRDRGITDGLLRFSVGLEDIEDLIVDLEQALQES"

CDS complement(3949137..3950324)

/gene="metI_2"
/locus_tag="EFAGFIKM_03385"
/EC_number="2.5.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31631"
/codon_start=1
/transl_table=11
/product="Cystathionine gamma-synthase/O-acetylhomoserine
(thiol)-lyase"
/db_xref="COG:COG0626"
/translation="MEDNNKLKIESRLAQIGSINEPVTGAINFPIYQSTAFRHPKLGQ
STGFDYIRTTNPTRKVLLEAAAALES GDAGFACSSGMAALQTIFAMFGQGDHLIVSLD
LYGGTYRLLERILSRFGVTASYVDTNDAALEKVRQPNTKAVFIETPTNPLMMITDVE
AVASWAKSYNLLTIVDNTLLTPFFQRPIELGADIIHSATKYLGGHNDVLAGLIITKG
EALSAEMAFLHNSIGAVLSPSDSYQLMKGMKTLALRMERHEHNALTIAKYLLLEHPAVV"

EVYHPGLSDHPGYEIQNKQSTGNTGIFSKVKDARYVEPLLRHIKLI AFAESLGGVES
LMTYPAVQTHADIPLEIREAVGVDDRLLRFSVGIEHADDLIADLGNALTA AQQEVEGG
VHS"

CDS complement(3950349..3951266)

/gene="metAA"

/locus_tag="EFAGFIKM_03386"

/EC_number="2.3.1.31"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0A0D8BWP6"

/codon_start=1

/transl_table=11

/product="Homoserine O-acetyltransferase"

/translation="MPIKIPDTLPAKEVLEGENIFVMDETSAYQQDIRPLRIALNLM

PTKETTETQLRLVGNTPIQVDVVLVHPKSHTSKNTSQEYLDLFYKTFDEIEHRRFDG

MIITGAPVEQMDFEDVNYWNEIQEIFEWTKTNVTSTLHICWASQAGLYHHFDVPKVAL

DEKCFGVFPHTINKPHVPLLRGFDEVFNVPHSRHTEVRREDIEKNENLEILAESEEAG

IFLVATKDGKQIFATGHAEDPFSLKWEYDRDAAKGLDIALPRHYYPNDDPSRVPPAT

WRAHANLLFSNWLNYVYQETPYDIGPQI"

CDS 3952078..3953013

/gene="corA_1"

/locus_tag="EFAGFIKM_03387"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9WZ31"

/codon_start=1

/transl_table=11

/product="Cobalt/magnesium transport protein CorA"

/db_xref="COG:COG0598"

/translation="MKIRLVNNGVFIPVDDIQQALTPPAEGFYWIDADVDDLAVLQPL

FLMHDLAVEDCLSDEEQRPKIEIYENHYFIVINSIRFDDEEIFLRAVNLFGRHFIIS

VTKHKVSELRTLKPILWEQEISTPDRLLYLLVDLIVDNYFTVGDRIEARIKLEEDIL

MHTKKSHLNEIIGLRSEILWLKKVLGPQKEVINTLNKKDLRLIDDQLQKYFSDIYENA

VKISETFETYRDLMGNLREAYQSSIANRANEIMRVFTAITTVFMPLTVITGIYGMNFT

NMPELNWKYSYFVVIGLMVTLGLSMFFIFRKKDWV"

CDS complement(3953084..3954085)

/locus_tag="EFAGFIKM_03388"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEVIFMNRFSRMSDQNAEYAQLWIGEEEDSWQLGWSRYEEGERE
DSIWYEGTSWEELLHIYRHQLAIQMSEGYRPQLQGLFHENDDLKRSYGGQRLHCYSE
LYGNEQLYTDLCTWRRKRAVSDRKAPYFIATNRLLRLISAFVPQSLDELMQLPGVGES
KATEYGTEWMEITNGLERSTTFPLDWVYTALKEEEYESWLYKQREQKYQELDKFTTR
KQVLEGMKEGYTLEEIVNRSGLSRRELVELLEALDHEGYDTCLLDVELAVMPENEQE
AVWSAYEELGDTFLKPVLHKVYGGEKPDGGSLEQVYERLRMIRIRFRRHAETEKNVG"

CDS complement(3954262..3955140)

/gene="gmuE_2"

/locus_tag="EFAGFIKM_03389"

/EC_number="2.7.1.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O05510"

/codon_start=1

/transl_table=11

/product="Putative fructokinase"

/db_xref="COG:COG1940"

/translation="MTILGAIEAGGTFKFCGIGTENGEVLERSFPTTTPEETMAQVI
SFFEGKGIEALGVGSFGPIDPIEGSPTYGYITTPKPHWGQYNVIGKLKEHFDVPMTF
DTDVNGAALGEATWGAAQGLESCLYITVGTGIGAGAVVGKMMVHGLSHPEMGHIIVRR
HPEDTYEGFCPYHGDCLGLELAAGPAINKRWEQPAYELPADHKAWIEAHYLAHALMNY
VLILSPQKIVMGGGVMMKQEHLFPMVRSKLQELLAGYVQHPALQSDIDQYVVPGLGDN
AGLCGSLALAKLALNK"

CDS complement(3955213..3955899)

/gene="yiiM"

/locus_tag="EFAGFIKM_03390"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P32157"

/codon_start=1

/transl_table=11

/product="Protein YiiM"

/db_xref="COG:COG2258"

/translation="MTLTSDRKPGEGNTAVLAINVGLPQPLPGQKREVLSGIVKHPVS
DAVFLSFTGMTGDAQADLVHHGGPDKAVCVYDYSRYPALEQLMDRKLNWGACGENLTV
EGCAEEDVRIGDVYELGEATVQVSQPRQPCFKLGARYDYKELPVYFQESGYTGFYFRV
LQEGEVGPSSIFRRISTDPASMTVFEANRVMHQGKENVDGIQALLAIPALSDSWRQTL
VKRLSKLENK"

CDS complement(3955930..3956994)

/locus_tag="EFAGFIKM_03391"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MALVLALPVILSGAVSAPQTVDAKAAISTKVQKVKAAGRNFVQ
TVSIPKGTPTVGLAKKQVGQTATLPSIVKAYGAQAANGAFFEAYNGAPDPYGMLIA
NGKVIHIGRYGTSIGFKEDGSAIMDSLQVSLTGKVTDTKGKSRSWYATFINRTPSANA
SITMLYTPERGATVGFKGGTAVVMEKGIVTKKVPNTNVAIPKNGSVLVFTGNQKSSSD
RFTVGSTVEMNYKYTNAAGKEIPWQDVVTAVGAGPRLVKDGKVAVNPTSEGFKDAKIL
NASGARSGIAIMADGSVMLATVSGATIKEWAAVMQKLGAKQAMNLDGGASSGMYAGGK
MLTSPGRLLSNTLVFGGSVR"

CDS complement(3957042..3957935)

/gene="ypcP"

/locus_tag="EFAGFIKM_03392"

/EC_number="3.1.11.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54161"

/codon_start=1

/transl_table=11

/product="5'-3' exonuclease"
/db_xref="COG:COG0258"
/translation="MNQRNEPTLLLV DGMVLFRAFYATSASGYIRRTKAGLPTNAVY
GFIRYFWDVAVQTFGSPSHVCCWDMGGKTRGEEYAAYKGNRAEAPDDLIPQFALIREV
MDSLGI PNIGAQGFEADDCIGTLAKYYTEETDMNVMVLTGDHMLQLINDRTSIIIMK
KGHGNYMVYNPETLMAEKQLTPRQVIDMKGLMGDASDNYPGVRGIGEKTALKLVQEYG
SIEGILSNMDKLTPSVRNKIENDLDMHLHLSRKLAEIHCAVPVACALDICELRLDPDMV
MDKFEQLEMKSLGSWMGVAIG"

CDS complement(3958129..3958494)

/gene="mgsR"
/locus_tag="EFAGFIKM_03393"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54503"
/codon_start=1
/transl_table=11
/product="Regulatory protein MgsR"
/db_xref="COG:COG1393"
/translation="MSNLKVYQYAKCGTCRKAVKWLEAQGHELELIPIFDSPPESEL
TELIQKSGLEVKKFFNTSGEVYKEQQLKDKLPGMSADEQIRLLASNGRLIKRPIVTDG
EKVTVGFKEETYEQEWNNNA"

CDS complement(3958892..3959875)

/gene="rluD_3"
/locus_tag="EFAGFIKM_03394"
/EC_number="5.4.99.23"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P33643"
/codon_start=1
/transl_table=11
/product="Ribosomal large subunit pseudouridine synthase
D"
/db_xref="COG:COG0564"
/translation="MSQYYSPIVYTVTEQEDGWLLKTVLQRRLLVSRKLLSKIKLTEQ

GVMLNGERVYISVKVAAGDVVEVRMEQESDDILPEPIPFTVLYEDEHLLIVNKDAGI
IVHPTHGHYTGTLANGVWHYWKSKGERFRFRPIHRLDQETSGVLAIKPNPYVHQHVSE
QMIAGTVDDKKYIALVHGSPVPEQGSVDGPIDRDPEEPHRRIVTPDGYAARTLYTTVTR
WSGGSASAI SLKLESGRTHQIRVHMTSIGCPLIGDRMYKTLPVHEIDEQTMVREERD
SWIERQALHACELTFEHPI LQERITFQAPFPADMAALEKRLNDEAAPREEL"

CDS complement(3959872..3960447)

/gene="yvqK"

/locus_tag="EFAGFIKM_03395"

/EC_number="2.5.1.17"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34899"

/codon_start=1

/transl_table=11

/product="Corrinoid adenosyltransferase"

/db_xref="COG:COG2096"

/translation="MGIYTRTGDEGQTSVIGGRVIKDDDRVEAYGTIDELNCFVGQAI
SLIDSAQGEFEDLREHLLEVQQELFDCGSDLA FVKISETKYKVRDEMVT RLEQWIDQY
DAENPKVERFIIPGGSQ LSSALHVCRTVCRR AERRTVTLGQHTDINPSVRRYLNRLSD
YFFVVARTANARQQVADIEYVR SKKVFR RKE"

CDS 3960596..3961207

/locus_tag="EFAGFIKM_03396"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WP09"

/codon_start=1

/transl_table=11

/product="putative membrane protein"

/db_xref="COG:COG0586"

/translation="MQNWITDFMEQYGYIGIALIALENVFPPIPSEIILPFGGFMTT
YTSLTLPGVIIAATIGSVLGAVLLYGIGLLIDVERLEKIVERWGHVLR IKKEDIHRVD
AWFDKYGMWTVLFCRMVPLVRSLISIPAGMSNMKFGLFLLFTTIGTLIWNVILVCVGA
ALGASWESILHFMDVYSIVVYVILAIIVIGCIWWIRRSKKQK"

CDS complement(3961293..3961835)

/locus_tag="EFAGFIKM_03397"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLITVTGGIGSGKTRFALKYAAGISREGVYLSTGDHDPVPELP

SAHYRAIHAGNGQHLTEVITQINRESNLFADQRIVIVDSLTSWMAAGFRATEDLDHQ

RSETQLLLDALLSYQGKLLVITNEMHGTLHPTEERIFTARMASVNRMLQMHAEKMYL

LVSLAIDLKSQGMRNEDER"

CDS complement(3961873..3962424)

/locus_tag="EFAGFIKM_03398"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRFWGLTAIISIVFLLAGCGGKDGFISIFIIDNQGNPSVISEQL

QANLQQKLGEPEKVEVITSAMYDVQKIMVEYAAGGHDIFILPESDMKQYGSNGSNVPL

DDTFDPKKFERGVFEGGVLVEKGECDGGSDLKQESHLYGIPLEDMMKMKDVEYAASNL

FATIPVSSSNVEESKKVLKALTE"

CDS complement(3962594..3962860)

/locus_tag="EFAGFIKM_03399"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFCVEYDLPTNRGHYLAEGDHGDRWSVKPDNASLHDISLEDEIH

MLRRKMEQIFLEEKSTSDIVIEISSLLDLKINEYMKANPIKAK"

CDS complement(3963004..3964212)

/gene="dapX"

/locus_tag="EFAGFIKM_03400"

/EC_number="2.6.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P16524"

/codon_start=1

/transl_table=11

/product="putative N-acetyl-LL-diaminopimelate
aminotransferase"

/db_xref="COG:COG0436"

/translation="MIVNEQTTGNNKKMTSYLAPLVQQIPPSGIRKFFDLVGDNKDII
TLGVGEPDFVTPWHMREACVYSLERGMTSYTSNAGMPKLREAISEYLDNQFDTKYDPK
DEIIVTVGGSEIDLALRALIVPGDEILPEPSYVAYSPIASIGGGIPVGVETYAKDQ
FKLTAEALEAGITPKSKVVILCYPSNPTGAIMTYEEWLPIAEVIKKHDLIVIADEIYA
ELTYTQKHVSFAAIPDMKERTILVSGFSKAFAMTGWRIGYMCGHPELIAAMLKIHQYT
VMCAPAMGQVAALEALTNGLGEKDRMVESYNQRRRLIVQGFRDIGLDCHEPQGAFYAF
PSIQKTGMSSDLFAERLLTENKVAAPGNVFGPQGEGFLRCSYATSVTQLNEALERIG
NFVYKLQKEG"

CDS complement(3964226..3964726)

/locus_tag="EFAGFIKM_03401"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKDLNDLQLKVLDLLKEDARRTPALLSTLLGESEDKIKNAVAQL
EQDHVIVKYATVVNWSKIDDEKVTALIEVQITPERGRGFEGIAERIYLYPQVKSVMYLM
SGAYDLLVEVEGGNLREVANFVSEKLSPIDSVLSTKTNFILKKYKQDGIIFEDHQEDN
RLMISP"

CDS complement(3964887..3965282)

/locus_tag="EFAGFIKM_03402"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYSQSPSSNGAFMQEQDLLKSILADLRRTSREYTTATTEASCPM
TRRMFTDLTNDTLRLQGELFNLMQQNNMYSVSSKALRQDVKQIQSAHQTTQKQCFI

QEKNTQNSSYSQAPNVPQHQPNYGNPYYM"

CDS complement(3965314..3965550)

/locus_tag="EFAGFIKM_03403"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQNHTMQALSPKELNYIADSITNEELLIKQCAATASITHNPQIQ

QALNHYARSHEQHLNTLVNALQQHQSLAPAQVSN"

CDS 3965648..3966868

/gene="puuB"

/locus_tag="EFAGFIKM_03404"

/EC_number="1.4.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37906"

/codon_start=1

/transl_table=11

/product="Gamma-glutamylputrescine oxidoreductase"

/translation="MDLVYSTPFWPSTFNSTINYSALQEDISCDCLIIGGGMGGALTS

KLLTEQGVNTVVIDKRDIAGSSSANTGLLQYTNDKTLTSCINTFGEATGVRFYELCC

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ISQHFPFSKPAALYTMGDAEVNPYRFVHALFESANKRGARIYGQTEMIHCEYDEDGVI

CHTSNGKIRAKKVIFAAGYETQDIKKDRGAYLKTTYAIATKPLSDLSEWFEHSMIWET

ARPYLYMRTTPDGRIIAGGLDEETPREDQREIRAYHRGDTLLEEVRSYFPLDDLEVDY

AWGAVFGNTNDGLPLIGHPDYPHSYFVEGYGGNGTVYSMIAASLIVDAITGKQNPDM

DLFSLTRTSKPSPV"

CDS complement(3966964..3968178)

/locus_tag="EFAGFIKM_03405"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKITLGRQSILLLGVNGLFALAGALSGTFLNVFLWKSYPDYAML
GWFTLSQQLAIGLTFWLAGKWVKEHNKMSALRLGTALSGIFYMIVLWAGSKAVDWIWP
LGMLLGCSLGLFWIAFNVVYFEITDRENRLDFNGWVGLLGSMGTGIIGPWFSGLITRM
TDNTGYRLIFTVSLVIYVIAVVSFFLKKRKVSGTYRWSEPWIQLSKRDSPWRTLGLG
LFAQGAREGVFAFLIALLVYLATAQEYKLGQFSLITSAVALVSYWAAGKWYKPQYRSK
GMFIGALILLIVLLPLLWKVTYGTLLIMGIGSAVAMPLYVLP MISAGFDMMGTSGENV
EKRVELVVLRELCLMLGRLSGLSIFIVTVLNAPSLRMLTWLIIVLGASPLIGWVFMRK
LLNRTEGQEPLA"

CDS complement(3968308..3968874)

/locus_tag="EFAGFIKM_03406"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="METTVCPWCQTEIVWDEELGPEEECPYCHNELKGYRTLINIDDD
EENDEAEDDIYDVEDVTNEKQTTDLSDLWGDEVELKLPRLTLTKYADEGNDLIQYEQ
GVQKQLDHFQEEVPECPNCREFMILAGTQAATQDNFTPVANAASGEGSLLASPFKVLT
VCSGCFQVQYSLSEEDRLRLIKNLSTQE"

CDS complement(3968994..3969413)

/locus_tag="EFAGFIKM_03407"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIESIDQLLSHPLGMVLGFFSVAIMELLVFLACFELVTKYKCWT
EIKKGNVAVAMATGGKIFGICNVLRFCIQAKSSVYEAMTWSFVGILLIAYFLFEFL
TPVFSIDKEIESDNRAVGLISMIISVLSFVIGASII"

CDS complement(3969485..3971851)

/gene="mutS2_2"

/locus_tag="EFAGFIKM_03408"

/EC_number="3.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P65496"

/codon_start=1

/transl_table=11

/product="Endonuclease MutS2"

/translation="MDTKILHTLEYRKILNTLLSFAQTTMGKKKAEQLEPSSELEEVK
RLLQQTDEAFTFDRLKGPSFSGGIVDITASIKRAEIGGTLPHELLGISNTTFAARRL
KRQIGTLHEDEPIESLFYISDQLSEQKTLEDSIKICIDDNAEVADSASVTLAQIRREL
RGGEARIREKLDSMIRSSTVSKMLQDQLITIRGDRFVIPVKAEYRSYFGGIVHDQSGS
GATLFIEPESIVAMNNKLRETRIREEIEIILQKLTALVSEQGEWLLYDVDLLGSLD
FIFAKARLARELKATLPRMNDRGFLKLLKKGRHPLIPIENVVPIDIELGNDYTSIIVTG
PNTGGKTVTLKTIGLLSLMAMSGLFVPAEDGSQLCVFDIAYADIGDEQSIEQNLSTFS
SHMTNIIRILKNMTPKSLVLLDELGAGTDPAEGSALAISMLEHMHRTGCRMVATTHYS
ELKAYAYERKGVINASMEFDINTLSPTYRLLVGVPGRSNAFAIAERLGLPGYILDYAR
GEVKEEDQRIEHMIASLEENRLTAEQEREKAESLRQDMEKLRSRHQTELEKLEQQRDR
RIEKAEDARSIVDKARTEAEKIIADLRLLAMEEGASVKEHKLIAARKQLDEAEPEKR
RKTVKKTATAPKTRAIGPGDEVLVYSLNQKGHVEMAGSKDAMVQLGIMKMKVSLDDL
ELQQSAPAAKPKQKPVTGMKRTRDDNVKSELDLRGTNLEEALMETDRFIDEAFLANLG
QVYIIHGKGTGILRSGIQDYLRKHKHIKSYRLGNYGEGGNGVTVAELE"

CDS 3972039..3972398

/locus_tag="EFAGFIKM_03409"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNFLGHVVRFVIAAIVLMVSWIVPGFAVGGFWSALLLALVIAL
LGWIVEGIFGKRVNPFGRGIVGFIVSALVIWLGQYVVDHVEVSLLGAILAALVIGIID
LFIPVSTPFDAGRSSKS"

CDS 3972619..3973011

/locus_tag="EFAGFIKM_03410"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MKKGITWLAACMLILVLTACGGAKQSAESGSNGSDADAGVTASE
ELVIKASNYEFDKPEYHLKKGVVPVNIYKNENGNHGILVPELNLQLDTRNSSKVITPD
KVGFEFEMSCSVFCGSGHSSMISKIIVEE"

CDS complement(3973116..3975824)

/gene="zapA"
/locus_tag="EFAGFIKM_03411"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_02013"
/codon_start=1
/transl_table=11
/product="Cell division protein ZapA"
/translation="MTTPDRTRVTVEIYGTSYKLVGSSADYMKQVANLVDERMGAISK
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ELERRDEALADLQQLKIEAEQALQKSESDKNSEIAKLNKLLEQERAQATERVQKLQAAQ
ATAQLKEAEAKGTKQLKEMEEKVANQLKNAQAQAASQLKEAQNRSAELQQAQAKAAA
QYKELQDKTAAQLKEVESRAVAERQQIEAKAAQQVRTAKEEAESAILSELEQAESNLK
KAQEEAALQYNELQQQMELRLQQAEEKALQQTQELTDQANQERADLQEAEQKRLTEI
NQLNAEFKALSEQLELEWMEKEAALEEQLQQAKEAAASQAKEAEAAAEALLQEEQGKL
KQQLEEQRKQAEARLLDVEEQLEEVMQTLISAQDLVAEQEQQLQHERGQLESLRHEHG
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VDRETSLTAQLRKLQEQHAQLEQEVQKLREAEVKSEEEQRRLLQKVLEQAHAAVRTLQN
EIGTLTEREQSWKDLAEQRLAEIGDLENQILEVAEQNETLESGVQSLHDELSVVKES
RFNHEEAVQYQKDAELLEKRNQLEVELNVVREELNRLQDNYKQIRNDYSDVLQREEN
YSSKLDELSKEKQEIVSVLEEARQSSAKLSERYSEQENRLAQTEEEALEWQIKHEELS
AKQTELASRLEQLTRREEELRSSVEQAEQNDQVWQRRADEWAAQEQSWQERWAALENE
LTVWKRESAASSELLEGLEQERQQLDKLRAEATQEKEIMETELLEMGERYELAAANQLR
LLQVEREMEKEAEQLNTEYRQLHDEYTKLQTEYNEWIELIEQDQT"

CDS complement(3975963..3978416)

/gene="pheT"
/locus_tag="EFAGFIKM_03412"
/EC_number="6.1.1.20"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P67041"
/codon_start=1
/transl_table=11
/product="Phenylalanine--tRNA ligase beta subunit"
/translation="MRVSTDWLSDYISLEGVTPQELAEKITRAGVEIDVVENRNKGVN
KVVVGYVKSKEKHPDADKLNVCVIDAGQEEDLQIVCGAKNVDAGQKVVVALVGAKLPG
GLDIKKAKLRGVVSLGMICSAKELGMNDKLLPKDQQEGILVLPEQTEVGTPI SQVLGL
DDHVLELDLTPNRSDCLSMRGAAYEVGAILGREVKLPSPKDLVEIGDAAANHISVEI
KAQEQCIHYAARYVTGIKLGASPLWMQNRLMAAGVRPINNIVDITNYVMLEYGQPLHA
FDADKLEKGHIEVRMANEGETIVTLDGQERKLEPHMLLITDGVKPVAIAGVMGGENSE
VSEGTVNLLLES AKFDGGTVRKTSRQLGLRSEASMRFEKEVDPGAVITALDRAAELIQ
RYAEGEVHQGIVEAGAEAAEKRVQLSLDRLNRYLGTDL SLLEVKTIFARLHFACGDA
DQGLLDVEVPTRRGDITLDVDLSEEIARLYGYDNIPTTWIEGPTTPGAYTRSQAMRRT
IRGLLSGSGWQEMISYSFVHPDKATLFPALTQGSKAVKLAMPMSEDRSVLRTSILPQM
LDGAVNYMNRKQDSLAVFEVGNVFFTEEDQLTKQPHEIPVLGLLLTGNRASQQWNVGA
EKVDFFDLKGALEHLFAYVGLEQRIRLVANSPEGFHPGRSASVYLEGKDGGEGTLIGT
LGQLHPELQQQYDLNDVYIAEIALESYSEADADIRYRELPRFPAMERDIAVVVNEDV
EAGDMLRAIRESAGEWLQNVQVFDVFTGSKLGENKKSVMALVYRNRERTLTDEEVTE
VHARVVARLEEQFGAELRK"

CDS complement(3978499..3979533)

/gene="pheS"
/locus_tag="EFAGFIKM_03413"
/EC_number="6.1.1.20"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q4L5E3"
/codon_start=1
/transl_table=11
/product="Phenylalanine--tRNA ligase alpha subunit"
/db_xref="COG:COG0016"
/translation="MKERLEALKIEALEQLSGVNDPQTLSDLRVKYL GKKGALTEILR
GMGALSAERPVIQVANDVRAAIEEVIDSKQDQFQKEETAKRLQSEKIDVTLPGRRG

RQGGHLPLTKVVQEIEDIFIGMGYRVAEGPEVEMDYNNFEALNLPKNHPARMDMQDSFY
VTEDLLMRHTHTSPVQVRTMQSMKGEVPVKVICPGKVYRRDDDDATHSFQFNQVEGLVI
SENIRMSDLKGTLLQFVREMFGSHTEIRLRPSFFPFTEPSAEVDVTCVQCGGSGCRVC
KQTGWLEILGGGMVHPKVLEMGGYDPEKYSGFAFGMGVERIAMLKYGVD DIRHFYNSD
LTFLKQFGRL"

CDS complement(3979472..3979831)

/locus_tag="EFAGFIKM_03414"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPLDREEAPWIESVSVEQGCRNSLRSGSLNLFVCRHRGNSRGKR

LTVVIPYKVRQNQLQARRATQQWMSNKGTTVFSSLQGREGLFLLQKHHKKGAITHER

TFRGIEDRSAGAVVWCE"

CDS complement(3979944..3981836)

/gene="uup"

/locus_tag="EFAGFIKM_03415"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P43672"

/codon_start=1

/transl_table=11

/product="ABC transporter ATP-binding protein uup"

/db_xref="COG:COG0488"

/translation="MMTLVRLHEVSKEWNGIELFTGLNLEINEGERLAILGRNGCGKT

TLLRIILGEEHGGGRIERHIPQQEWGFMRQRSEIETGMNVLDVRRRESGQIYEVKRNL

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HSLSGGQKTKARLAGLLVSKPKFLILDEPTNHLDEGSMRWLEEWLSSYEGTLLFVSHD

RTFIDQVATGVIEFSPDALT KYKGGYSDYKIHKERELREQETIYRRQELERKALEETI

RNYQEW FHKAHNSATDVEVKITQSFYKAKANKNISRYHAKQKQLERLERERVDKPREA

AKLNMELQMNPLAARQLLALEEVSF SYTGDKSLLRNLRITVERGDRLAVRGPNGTGKT

TLLKLMFGELEPSQGVTRHPQLKIGYFSQELEGLPENLTLLDSLLTLPSMTQSAART

ILGCFLFSRDDVFKRIGDLSMGEKCRVAFLRLYFGGANLLVLDEPTNYLDIDTQEVME

NVLKQASGALVLVSHDRMLTKSLANRLCDLEAGGTATLFEGGVSDWEQSTKLREVALE
TRESDDERLRLEMRLSELLSPVSTAGKESLTQPEHSNERAVEAAEIREIQQRLKQLKD
KGASIN"

tRNA complement(3982356..3982426)
/locus_tag="EFAGFIKM_03416"
/product="tRNA-Gly"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Gly(tcc)"

CDS complement(3982586..3984712)
/locus_tag="EFAGFIKM_03417"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKVNLQDQRKISWWAVGGLLCFLASQWFRSSSSSDLIISGYPVL
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IQEWSMLPSMLDGEVLGGIFTRVHLMVGLLYGIIAVLLFVQWKKNKDGDLPILCGIL
CFFFGECYFVSATGVNDLNLLLGLLSNCMAYFFIQKGLYTSVVDTPFLQQQVAEAKMN
YIAHDDVTGLPNRRRLSQQLKMMDDAVVQEQLVGVVLNINRFKTINDSLGQQAAN
RVLRQVGQRLKQLSLPGEEVFGLRDEFALTMTDFSSTDALRRTRSILQLFEKPVLV
DGNEYHLLTIGMAIFPHDGESPLEIIQNADTALHSAKEQGMELNRFAHAMQMKAQER
LQLENDLRKALDRGQFYLVYQPQVNLQSGLVGMEALVRWQHPQRGSVSPADFIPLAE
ESGLIVPLGEWVLREACAQNKQWQEAGYRKLCVSVNLSMRQFRHSHLLDNINGILKET
GLEPVWLELEITESMTFDKDRSFEQLRKIKEIGVHISIDDFGTGYSSLHYLKDLPIDR
LKIDRSFVNEVMEDSNNAIVSTITMAHHLQLKVTAEGVENEDQMVFLRNQHCHEAQ
GYFFSKPIKAAEFKQFLRDVDKPTG"

CDS complement(3985003..3985959)
/locus_tag="EFAGFIKM_03418"
/EC_number="4.1.3.39"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q53WI0"

/codon_start=1
/transl_table=11
/product="4-hydroxy-2-oxovalerate aldolase"
/translation="MKTNHCKIVDCTIRDGGLVNNWDFSVDVQQLYAGLNEAGVDYM
EIGYKNSPKLLKGAE EAGPWRFLNDDFLRKVIPQKGNTKLSALVDVGRVDENDILPRS
ESMLDLIRVACYSKDVDKALALVQTFHDRGYETTLNIMALSNVMENELLEAFELIKES
AVDVVYIVDSYGS LDHNDVKYLVEKFKTHLPNKRLGVHTHNNMQLAFSNTLVAAELGV
ELLDASVYGMGRAAGNCPTELLVAHLKGTKYNLRPVLGVLEQLMVPLREKEEWGYILP
YMITGALDEHPRSAMAIRSSEDKDKVDFYDKLTTPEVNFDK"

CDS complement(3986043..3987356)

/locus_tag="EFAGFIKM_03419"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRNRPVATTTGLIAMLAVLMAGIYLFPIFTLASFYAMEHLPYTL
FILVVLVGWLGQFIQH KIPGFSEKSTLIRGLAALVIGFLFALVVGMSLILPLPDIITL
VLCGVISAYTGLTFQPVFHSVLLWRLQIMGVISAIVLMIASNSLEFMQPIRTYTLWIY
IAGVISFAFWLVGRYMLQLDQAILNDGKRRLVLRDFARANHQRFMWMFIVIVAIGAFP
SLAAWLGPLRDRL LAWIRGWFGPISGEEPRLPMDNPNQPLNIPNDWREPPSEPSVFWN
ILGWVVMCAVAGAILWLLLRLGQKTINRLMDRFKGM LQPGEKKAEP RTEYIDVSETLD
APAKVRKNWFRKKEAPPAQDAERVRYYYRTWIERAAHRGVEIQGTHTPLEAAQTIIQN
GMKVEEDEL SARLPDTYNAVRYGEKAPDRSDMVEIDRIWRSYRSK"

CDS complement(3987353..3988327)

/locus_tag="EFAGFIKM_03420"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVETISNEKRVSPWLRLES MMPVSFVFRSGSGMDISQGEIYQN
HKSIFTLKPFRITRKHPFTCTQRGIYPLNTATMTGGDLFGVWRSTKPIPLQMSMIVY
PSLVNAEDLPAIQVWQGEVEVSRWIVEDPFLILGVRPYGAGDPMNRIHWKASARTGE"

LQVYKQGTADPQSWIVVNIQESADMWSVTRPEKIERALRYAATAAVDAIGRGLPAG
FAHNGYHVGGRDTRLIEPDYGTPLERLLEAMAETELKCMVPMEQFLNDEVRLNEEA
QQIRSYLLITSYVSAAMEHEIARLHEQGHRVTILPVEDVKGNTKAVSA"

CDS complement(3988473..3989438)

/locus_tag="EFAGFIKM_03421"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEIQGMERMNQQLMDHVGKVIVGKEHTIELVMTAIIASGHVLE

DVPGTGKTMLAKSVASSLDCTFQRIQFTPDLPSDLTGIIFFNQKEGDFEFRPGPLFA

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PEAQMDRFMMKIRMGYPSSSEESVEILRRTVASRSVDDL SAVISREELLKAQDTYKTVQ

INEDLLRYIIQLTEATRQHPELSLGVSPRGAQALLKASQAWAALHGRDFVLPDDIKVL

AEPVLAHRLVFRNRIRQQEGLAERIIQELLNQTEVPTENLATSGR"

CDS complement(3989560..3990666)

/gene="sasA_13"

/locus_tag="EFAGFIKM_03422"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"

/codon_start=1

/transl_table=11

/product="Adaptive-response sensory-kinase SasA"

/translation="MISEFQDTVPPQPTDGFPPVHLDNNKYENVLEHLD SGIMLFDSHG

VLTFINVQMAKLELPRSLLSGCTLMQMLHHPQMSRFKKKKILRIYRETIFHRKRYHE

LIDEYGRHWLVTVTYGDQMDGDFLFSVKDVS DYKQIEQTAYQNDKLAMLGRISASIAH

EIRNPLTAIRGFIQLLRPHLLQLGKDEYARIILTEIDRANDIIEFLNSSKPSAPQKT

VISVDSLLKEVLLTESEGLMKGCEIVLDEGDAPLNVSIDVKQIKQVILNMVKNAMDA

IEEVGEEHTGLIRISTATENKFVQISIADNGHGMDHNTLVRLFD PFFTTKESGTGLGL

SVSYRIIKNHGGTISVDSKKGEGTRFIIMLPLVY"

CDS complement(3991114..3991530)

/locus_tag="EFAGFIKM_03423"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSYCCGASMVGTKGTLKHYRTQVHNVPLLFCPVCHRVEVHYKVE
NEYEILAEYAHGDGASEIDFQDYVTEDEDAIFENCVNRESEDAMVIVQRQIDMALDLL
RLAKETKDEKWESELKRRLAVMSQRRLKIQHNKTGL"

CDS complement(3991887..3992426)

/gene="ahpC"
/locus_tag="EFAGFIKM_03424"
/EC_number="1.11.1.15"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P56876"
/codon_start=1
/transl_table=11
/product="Alkyl hydroperoxide reductase C"
/db_xref="COG:COG0450"
/translation="MAERLVGRPAPDFAMETVSGDGQDFGSVKLSDYRGKWLVEFFYP
LDFTFVCPTEITALSVASEQFKALDTEILGVSVDVSHKAWINTPVDSNGLGQLNFP
LASDITKQVAKDYGVLIEEEGVALRGLFIIDPEGELKYQVVNHNDVGRSVEETLRVLQ
ALQSGGLCAMNWKPGDTNL"

CDS complement(3992404..3992640)

/locus_tag="EFAGFIKM_03425"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSFLPRKILYNDYKKIMFIILTLGSPDDNILLVLVIKYQILI
TGKAYAFFLMMSNPQGCLHNPKGIFS YGRTFGR"

CDS complement(3992704..3993789)

/gene="leuB"

/locus_tag="EFAGFIKM_03426"
/EC_number="1.1.1.85"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P12010"
/codon_start=1
/transl_table=11
/product="3-isopropylmalate dehydrogenase"
/db_xref="COG:COG0473"
/translation="MADVKKIAVIAGDGIGPEVVAEAEKVLKRTEEVFGYRFETEHAL
FGGIAIDKGTPLPEETLSVCKSADAVLLGAVGGPKWDNNSKELRPETGLLGIRKALG
LFSNLRPAVVFDCCLKDASTLKPEVLEGTDLMMVRELTGGIYFGEKFRRESAQGEEAVD
TCAYNVTEVERIVRQAFEIAQGRRKKLASVDKANVLETSRLWREVVNRVAPDYPDVEL
EHVLVDNCAMQLLRPSSFDVIVTENMFGDILSDEAAMLTGSIGMLASASLGECSFGL
YEPVHGSAPDIAGQGLANPIATILSLALMFRTTFGYAEGADAIEAAVSDVLNAGHRTS
DIAVDKSTAISTTEMGDLIVAAIQKQA"

CDS 3994023..3995003

/gene="yajO_3"
/locus_tag="EFAGFIKM_03427"
/EC_number="1.1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P77735"
/codon_start=1
/transl_table=11
/product="1-deoxyxylulose-5-phosphate synthase YajO"
/db_xref="COG:COG0667"
/translation="MQYSYLGKSGLKVSRICLGTMMNFGPATDEKEAFRIMDAALDAGV
NFFDTANIYGWGENSGLTEEIIGRWFNQGGGRREKVVLATKVYGSMDHDDTDGPNNEAG
LSAYKIRRHLEGSLRRLQTDHIELYQMHVDPASWDELWGSFENAVQQGKIGYVGSS
NFAAWQIAIAQSEAKNRHFLGLVSEQHKYSLNCRLPELEVLPAAKELGLGVIPWSPLD
GGLLGRNALQKLEGTRSGGIAGRIEQQTQLEDFAALCRDLGEPQDTVALAWVAANPA
VTAPIIGPRTLEQFETALKCLDVTLDLDEAVLKRLEIFPGPGGHAPNAYAW"

CDS complement(3995266..3996807)

/gene="leuA_1"
/locus_tag="EFAGFIKM_03428"
/EC_number="2.3.3.13"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q71Y35"
/codon_start=1
/transl_table=11
/product="2-isopropylmalate synthase"
/translation="MRKIYVFDTTLRDGEQSPGVNLNTREKVEIAHQLERLGIDRMEA
GFPAASPGDLAAVNAVANAVKNVTVIGLSRSREQDIDAVKEALKGAQDPCIHVFLATS
PIHRQHKLRMDKAQVLDTARSAIRYAKKTFKIEFSLEDAGRTEYDFLVEMVNMAVEE
GAAVVNIPDTVGYLSPYEYGNIFKHLKENVHGIEKVQLSAHCHNDLGMATANTLAAIL
NGADQIEGTINGIGERAGNTAIEEIAMALETREQEFFQAKTSLQLSEIARTSRLVSRLT
GMVVPGNKAIVGANAFAHESGIHQDGMLEKKTTEIMTPESIGLKESKLVLGKHSGRH
AFRERLIDLGYELEEEALNRAFAQFKDLADKKKEVTDEDLLALIEEKLQDAPEVYKLE
SIFVTYGDESIPTAKVRIATLDGDTIEKQAEENGSDAIYNAIDQVSGEDVTLSDISI
KSVTHGKDALGEVHVLTQNQVSVQGRGVSTDILGASARAYVDGLNQLIEKRKTYTNR
VNVNL"

CDS complement(3996947..3997939)

/gene="ilvC"
/locus_tag="EFAGFIKM_03429"
/EC_number="1.1.1.382"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:K4LVZ1"
/codon_start=1
/transl_table=11
/product="Ketol-acid reductoisomerase (NAD(+))"
/translation="MPVTTYEQDAELNVLKGKTIAVIGYGSQGHAQAQNLRDSGLNV
VIGLREGKSFDKNDGFEVLSPAETSRAVDVQILLPDETQASVYKNEIEPNLKEGA
ALLFSHGFMVHFGQIVAPKNSDVLVAPKSPGHMVRRTYVEGFGVPGLIAIEQDATGK
AKEIGLAYAKGIGCTRAGVIETSFREETETDLFGEQAVLCGGVSALVKAGFETLTEAG
YAPEMAYFECLHELKLIVDMMYEGGLSSMRDSISNTAEYGDYVTGPRVVTEDTKKAMK"

EVLTDIQGKFARDFILENQSGRAFLTATRRNEAEHPIEVVGGQLREMMHWIKK"

CDS complement(3998201..3998683)

/gene="ilvH"

/locus_tag="EFAGFIKM_03430"

/EC_number="2.2.1.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WKJ3"

/codon_start=1

/transl_table=11

/product="Putative acetolactate synthase small subunit"

/db_xref="COG:COG0440"

/translation="MIRHTISILVNDQPGVLQRVSGLFGRRGFNIESITVGQSEEPGL

SRMVIVTIGDDKTLEQIEKQLYKIIDVIKVVDFSLKPMVARELALIKVKAEPSEPEREI

LGVVETFRASVVDVPGSLIVQVVGDTDKIDAMIELLKPYGIRELSRTGITALVRGNV

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CDS complement(3998680..4000431)

/gene="ilvB"

/locus_tag="EFAGFIKM_03431"

/EC_number="2.2.1.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37251"

/codon_start=1

/transl_table=11

/product="Acetolactate synthase large subunit"

/db_xref="COG:COG0028"

/translation="MGAQIPEVRSTDELREKWMKPEVISGSEILLRSLLEGVDCVFG

YPGGAVLYIYDAMYGFEDFKHVLTRHEQGAIHAADGYARASGKVGVCATSGPGATNL

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IIHEAFHIAN TGRKGPVLIDIPKDV SANKTLFEPSTEPVTLRGYNPRTVPNKLQVDRL

AQAIQEAERPMILAGGGVVYSGGHEELFEFVEKTGIPITTTLLGLGAFPSGHELWTGM

PGMHGTYTSNLAIQQSDLLINIGARFDDRVTGKLDGFAPHAKIVHIDIDPAEIGKNIA

TDIPIVGDVKTVLEIANKEVGRAERADAWRDQIKQWKQEKPSYTDSEVLKPQWVVE

CDS 4001033..4001479

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/inference="ab initio prediction:Prodigal:002006"
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/transl_table=11
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/translation="MVIRQRTSKLDDGAIMKLIDTQLVPLSHMSEKEINKIRKEIPLR
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ASRGCRRSKVMVDEGNTKGLQFYQKNGYSAIRYIMISRCYELEKTL"

CDS complement(4001486..4001875)

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/inference="ab initio prediction:Prodigal:002006"
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/transl_table=11
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/translation="MKQQVTRDEAMKLGKNIVAIAIKKDGRVTGKLLKVSGNKLVLKR

PGGPGGGYGPGPGFGPYGPGPRPPGFF"

CDS complement(4002137..4003099)

/locus_tag="EFAGFIKM_03434"

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/inference="similar to AA sequence:UniProtKB:O83324"
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RfuD''

/db_xref="COG:COG1079"

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IVINFLAAGSTLYLVKLLFEGSGDSPLVQGFNKFDPFLKDIPLLGEAFFKNVYPTTY
LAILFVFLTYIIMFKTPFGLRLRSVGEHPSAADTVGVKVLRYRYIGVMISGALAAIGG
AAITLTTTGTFSHNTVSGQGYIAAAMIFGKWNPIGAFGAAVFFGFSQAIRNYVQLFE
WSQSIPQEIIIFMLPYLLTIIVLVAAGVRSSAPSALGEAYDPGKR"

CDS complement(4003100..4004179)

/locus_tag="EFAGFIKM_03435"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNNVLKWFTRDSFILPVVAIIMGLILGGVVMLIGGYNPIEAYGA
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KFAGLPIYLHAPLALIAGALFGGLWAAIAGYLKAARGVNEVISSIMLNWIGLYLANLI
VRQFLLKGENRSVDISESASISLTWLSSELMGNSRVHMGTLIALVMAVLFYIYMWKT
QGYEIRAVGYNPNAAEYAGMHVNRNIVKAMFISGMLAGLGGAFFQVLGVFQYQTVMSG
PGTGFDDGIAVALIGLNHPFGVLLGAVLFGTLTYGSAGMSFAADVPEIIRIVIGSIIF
FIAAQGIVRWILKPFYSKRKKEKVL"

CDS complement(4004172..4005710)

/gene="mglA_1"

/locus_tag="EFAGFIKM_03436"

/EC_number="7.5.2.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P23924"

/codon_start=1

/transl_table=11

/product="Galactose/methyl galactoside import ATP-binding
protein MglA"

/db_xref="COG:COG1129"

/translation="MGAATPVVELKQITKRFPGIVANDAIQLRKGEIHALLGENGA
GKSTLMNIVFGLYQPDEGSIEVNGKPVIIIDSPNRAIDLIGMVHQQHFKLVQPFTVTEN"

IILGSEPTKGLNINYKKAEEVQRLSEQYGLKVNPHAKIHDSVGMQQRVEIVKTLR
GADILIFDEPTAVLTPQEIKELMIIMKKLVAEGKSILITHKLKEIMEISDTVTIIRR
GKVIDSVKTSETNPNELAEMVGRNVTFKVDKKPATPGANVLEVSKLTAKNKEGISVL
NQLNLNVRAGEIVGIAGVDGNGQSELIEALTGLRKVESGSILLEGKELSNHSPRHI
SGVAHIPEDRHKHGLVLDVSVSENVLESYYKAPYTRKGFLNFDAIKQQAQRLVEAFD
VRTPSIETKARSLSGGNQQAIIAREVDKNPELLIAAQPTRGLDVGAIEFVQKQLIAQ
RDQGKAVLLISFELDEINVSDRIAVIYEGQIVGEVLPEETNDRELGLMMAGSTQKRG
TAHE"

CDS complement(4006009..4007049)

/gene="tmpC_1"

/locus_tag="EFAGFIKM_03437"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29724"

/codon_start=1

/transl_table=11

/product="Membrane lipoprotein TmpC"

/db_xref="COG:COG1744"

/translation="MKKMLSLSLVMMLLAVSVMLAGCGSKPKEETNAGGDTGGTPTETK

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AGLTTKSNKIGFVGGMESPLIKKFEVGFREGVKAVNPDAQFISNYTGAFDKPDLGKAA

AATLYNEGVDIIFHASGATGNGVFNEASARKKQGQDVVWIGVDKDQSLEFGDEITLTS

MIKKVDEAVKRVNKEVVDGTFAGGSENLTLENGVGIADTSTANVSADTLAKVEEYKE

KIISGEIKVPTE"

CDS complement(4007629..4007988)

/gene="rplT"

/locus_tag="EFAGFIKM_03438"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P55873"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L20"

/db_xref="COG:COG0292"

/translation="MARVKGGFVRRRHKKVLKLARGYFGSKHRIFTANEQVMKSLV

YAYRDRRNTKRNFRRLWIVRINAAARMNGLSYNKLIHGLKLAGVDMNRKMLADLAVND

INAFNSLANVAKGKINA"

CDS complement(4008077..4008280)

/gene="rpml"

/locus_tag="EFAGFIKM_03439"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P55874"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L35"

/db_xref="COG:COG0291"

/translation="MPKMKTHSSLKGRFKITGSGKVLRYKAHKNHLLSHKSKRAKRVL

NGNPVMAAGDVRRLKQGLANLKG"

CDS complement(4008305..4008835)

/gene="infC_2"

/locus_tag="EFAGFIKM_03440"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P03000"

/codon_start=1

/transl_table=11

/product="Translation initiation factor IF-3"

/translation="MTWRWTIISKDHMINDEIRAKEVRLVGAEGEQIGITPIREALQM

AIDLNLDLNVAPQAKPPVCRIMDYGKFRYEQKKDKARKNQKIVDIKEVWFRSNIE

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PKLEGRSMIMILAPKA"

CDS complement(4009135..4010373)

/locus_tag="EFAGFIKM_03441"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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VLVAAHNEEQVIGALMENLKQLDYPEDLYDVFVICDNCTDGTAQIVREHGLNACVRTN
ADLRGKGYAIEWMLKYLWKLPRQYDAVVMFDADNLVDRNFLLEMNDLNNGSRVIQGY
IDTKNPEDSWITAAYGVSYWYINRLWQLSRHNLNMANFLGGTGMCFETNLLKEIGWGA
TSLVEDLEFTMRSVQRNVYPVFNYDAKVFDEKPLTFKASARQRLRWMQGHFTVARRYF
FPLLWQSIKERSLVKFDLAIYGANVYVLLTFLMTAVMWVDMCIFSGPHIANIYGYFP
LWVGFAIGLNILTFLLSMALEKVTFKVVLYLILFPIYLLSWYPITFYAFFTQNNKQ
WSHTQHTRVVRLEDEVQSKQG"

CDS 4011084..4011611

/locus_tag="EFAGFIKM_03442"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSRLFLKFQDYDRNVFMWINGRLHNRFMNFWLYYFTHLGGATSS
IAISLLIWLLAPAPWSTTGLQACIALAVSHIPVAIAKKLYPRIRPYLALPDTITFRNP
LTDHSFSPSGHTTAIFSVTVPFMTTDPILLILLPVALIVGFSRIYLGHLHYPDVLAGA
TIGTLVALATVAFWS"

CDS 4011662..4012813

/gene="ugtP_1"
/locus_tag="EFAGFIKM_03443"
/EC_number="2.4.1.315"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54166"
/codon_start=1
/transl_table=11
/product="Processive diacylglycerol
beta-glucosyltransferase"
/db_xref="COG:COG0707"
/translation="MEKKRVLLLSEFGTGHTQAAYALSSNLRKLSPDVQTKVLELGS
FLNPKVAPLIITAYKKTVTNQPKLFGYVYRHQYKKS LNRLTTLALHKLFYTHTRSVVR"

QLRPDAIVCTHPIPSAVISRLKRLGVQVPLCTVITDYDAHGTWINREVDLYLVSSDEV
KSKLMLRGVPAENIRVTGIPVHPNFWHEHPGREEIRSRFNLKNMPTVLVMGGGWGMLSD
KLVHPLLTRWHEDIQIIFCLGRNDKTRISMEQNPMYRKENIHIMGYTNEVDKLMESD
LLITKPGGMTCEGLAKGIPMLFHNPIPGQEEENVHYFTARGLGEPITSPDVVWNWMN
KLLHHYPDVVRKRKRHLAEIAKVHPMQSAQSIIDLLEDVRPSSAEEARL"

CDS complement(4012954..4014501)

/locus_tag="EFAGFIKM_03444"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRNKTIRHLSVLALMLFAGVLAACNNGSGGSTQGSEQGGTSGN

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VPSTWIEYVTEGIAYREDLREKYNLPKPESLETLEAYLEGIKANEPNMIPIADSNANH

THGIRQLTSKLVNTAGQLPYGLDIMYDTPSIVTSYWGSAQHLEDLKTYKRWMDKGFFP

KNVLNVKDTSNSLLQNGKAAVVLSENPKNFNADVIVQSTHPDWKLAYFPYPNAKGF

AQPVHPIHNGFAIPRSSKNPEKALAFYEKLVTDKRYNWLTEYGVGKNEVDNGYYKM

VGDAQTNGFPREGMNGWAWRNPEFMLYDKTFDDVLTMFEDLDKIKKPDYTGFAEDWT

PYQAEKAALEQVEKQYLYPLNVGLVADVEAGLNTFMEKAKQAGLEKIQAETKQWQEY

LKSTGIQ"

CDS complement(4014608..4015537)

/gene="araQ_22"

/locus_tag="EFAGFIKM_03445"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MNTPMNTHTRTNTRLRDSEFTFMFQLISYSFIILSIMCLLPFL

LILSGSFSSNESIVRDGYHLFPTDFSLEGYKMVFKFPTQVLKAYGVTVFTTVVGTTLG
LFLITMAGFVLQRKDFKYRNTFSFFIYFTTLFGGGLVPWYIMLANYFNLTDTYTVLIF
PGLMTPFLIILMKNFIRSAVPDELIESAKIDGANDFRIYFSIVLKLAMPGIATVGLFL
ALGYWNDWFTSSLFINNPDMYQLQFYLYNTMNTITFIDQMAIGTGITLSQDVPTSTK
MAMAIWVTGPILFLYPFVQRYFVKGLTIGAVKG"

CDS complement(4015568..4016473)

/gene="yteP_27"

/locus_tag="EFAGFIKM_03446"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system

permease YteP"

/db_xref="COG:COG4209"

/translation="MLKELNKNKIMFLMLLPTLIFFLINSYFPMVGIYYAFTRYDFEG

GLFGSPFVGLENFKFLWQSGMMLLKLTNTVGYNLAFIILGNGLAIFCAIMLSEIRGRL

FKKITQSVMFLPYFISFVLLSVIAYNMFNYESGFVNTVLKRFEAGPVDIYNTPWIVWF

LIIFYLWKNLGYSMVIYLAITGISDEYYEAAIDGANIFQRIWYITVPLKPTFVI

LLLFSLGSIMKGQFDLFYQLIGNNGVLYNATDIIDTYVYRSLKVTFDIGMATAAGLYQ

SLFGFILIMTVNYIIRKVNEDYALF"

CDS 4016881..4019133

/gene="rhaR_32"

/locus_tag="EFAGFIKM_03447"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MRKRSEDSQKVFTIRILIGIIISTVATLLVASSILYANYNRIALR

QVYRTDMNSLTQTSREVAKMTETAKSLSYQIYQDYTISSLLYSKPNIYEITSAMEQL

DNYRMSLPFIESIYVYNSKSNEFFISSDVRNGQQSISEIDDQGITSILQRFNDYKPFV

PIPRTYQVGSTEATEVNSYTYLCYDTINDNAKLNYAVIVNIKDDWLSPNMNAVDQPGK
TFIVNENGDLLSDFGDRALMKNLSSEAFMKPIMQDTEQSAYFTEKVDGEKSLITYTAP
DDLGWRYVRITPYDLITSDIRSMRHTVLFVCGLLFAGLLLSYLVSRKLYHPIDKVLV
RLRVMEAERRGSLHLLRQDFLRGALQGRETVTGGMLEERMKFYGSSIDVQRASRLVLL
RIDHFTFCETYRDETQLVKYAMMNICETETADLHYNAAEAVDMGGDLITLIFNEKAESH
ELGQPAHNRIEELLRMMQAAVMTHLKCSISCTIGTEEDSLEDASIYTRSAEASLHRL
FMGPGCLIYTADIMAYHAKEYAFPAGKERQLVDHLMTGKTREAKQVYADIVGETAAYP
FTVFQLALSHLTMTLNHVRNTLKKNQTLDSVSDGLMLPVKDAEDISEVHEHFYRMF
DELGSKVEEKRTLKHEELIRKINGIIERDYDTPNLCLTSIADELGMSPYVSRLYKQL
TLKGLTDVINETRIAKAQHLLVETENSVADIAERTGFTNSSYFYRMFKKFNGVTPNDY
RRKEFHSENF"

CDS complement(4019263..4020018)

/gene="trmB"

/locus_tag="EFAGFIKM_03448"

/EC_number="2.1.1.33"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34522"

/codon_start=1

/transl_table=11

/product="tRNA (guanine-N(7)-)-methyltransferase"

/db_xref="COG:COG0220"

/translation="MRLRGRKGIRENLEQQVDLVVLDPKQHKGKWSELFGNDHPIFVE

FGMGKGQFISQMSYKYPEFNFIGIDMYDELVRRASEKARNAWSQADVETPPNLKLALA

NIEQIEEVFEPEELERIYLNFSDPWPKAKHARRRLTHPRFLKKYTELLNPKGQIHFKT

DSETLDFDSLNAIADFGLQMTNISLNLHRDGLNEEHVMTEYEQKFMGKGMNIHRVEVI

VGEEALREYQQTRLDKYKVREASDESGEDQEQE"

CDS complement(4020171..4020371)

/locus_tag="EFAGFIKM_03449"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNSQVKNNELNHVSVELTAEELALTGVRFNGNPKVKAAARQKV

RDAFEKTFDFSHQDKVDYELLK"

CDS 4020690..4021643

/locus_tag="EFAGFIKM_03450"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNAPALQSPLLWGDKRFHTWNYEMRDQFNNKVKVMLDAGFTCP
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NTYAPVEELREYFEEILEQPGVVGLSIATRPDCLPDDVVDYLAELNERTYLWVEMGLQ
TIHDSTSTLINRAHDTKCYEEAVEKLRKRNIHVCTHIIYGLPQETHMMLDTGRAVAN
MDVQGIKIHLLHLMRKTPMVKQYEAGLLRFLDQDEYIKLIVDTLEMLPPEMIVHRLTG
DAPRDLLIGPMWSMNKWEVLNSIDRELRRERDSWQGYWRRRA"

CDS 4021644..4022228

/locus_tag="EFAGFIKM_03451"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGFLSVLSCAHQWIASRLQPGDLAIDATVGTGADTLFLAQQVGR
RGQVIGFDIQSEALTLAQARIRKQNDKLGSIKMLQLSHDRMAEAVPESWLGTVGAV
MFNLGYLPSESADSSIITETDSTIAALEAALALLRPRGIITVVLYPGHDGGAQEAQAV
LDWSSALPVEQAQVVMYRQLQRETSPFLIGIEKK"

CDS 4022418..4023395

/gene="manA_1"

/locus_tag="EFAGFIKM_03452"

/EC_number="5.3.1.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31646"

/codon_start=1

/transl_table=11

/product="Mannose-6-phosphate isomerase ManA"

/db_xref="COG:COG1482"

/translation="MSTPYPLQFQPEFKERVWGGRALQFGLTPPEGHIGEGWMIADH
PNGTTKVLNGALAGKGLDEVREQLGTEWLGTKGVSEKGRFPLLIKLLDCNDDLSVQV
HPTDEYEALPPGELGKTEMWYVLDAPGAHIIYGLNEGVDRTLKEALENGTVMDTLR
QVPVEAGDTFFIPAGTVHALCAGVVVAEIQQNSDTTYRIYDYNRPGLDGKPRELHVED
SLNVTAYEGAGASTMKTNNATPGEWLKLAECPYFVVEKGIVTERWELSTNPNSFTILV
VCEGEGTLEWAHAESDSIELKAGQCYLLPANLGSYTLNGNTTVLRSYLP"

CDS 4023437..4024417

/locus_tag="EFAGFIKM_03453"

/EC_number="3.1.1.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0QNZ7"

/codon_start=1

/transl_table=11

/product="Monoacylglycerol lipase"

/db_xref="COG:COG2267"

/translation="MQESTFALVASEGTRIHVYRWLPDRECNVKGVVQIAHGMSETAA
RYAEFADILTQNGYAVYANDHRGHGKTVENAKLLGNAGIDAFRWMASDMINLGEVAAK
ENPGVPLFLMGHSMGSFLVQHLMYAGHEQYHAFILSGTNGRRGLLRFGEKLAFLQCGI
QGATHPSMLLNAIVFGGFNRSFRPATTDFDWSRDSQEVQRFIDDPLCGAVCTAGFFR
DFFKLLLEVHLPHNMERIPKHKPVYLFSGEKDPVGLHGKGVNLVVSQYKKLHLENIEY
RLYPDGRHEMLHEINRTEVAQHVVNWLERNTPGSNTHPSPVSPPTETADSI"

CDS complement(4024552..4025823)

/gene="odhB"

/locus_tag="EFAGFIKM_03454"

/EC_number="2.3.1.61"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A5N4"

/codon_start=1

/transl_table=11

/product="Dihydrolipoyllysine-residue succinyltransferase

component of 2-oxoglutarate dehydrogenase complex"

/translation="MSEIKVPAMGESITEGTVSRWMVKEGDTVNQGDVLELETDKVN
IEISAEESGVLEKIIRQEGETVEIGETIGTLSAGSGGGSGSPASEPAEEKKAVTPAP
EAPTPPPAPVAAAPESSDSAKTASPSARKLARERGIELDQVQSKDPIGRVYQDDVKSH
NNQAPAPAAPPASKAPAAPSAPAAGSSTYTKPVERQMSRRRATIAKRLVEAQQTAA
LTTFNEVDMTAIMDVRKRRKDKFKEKHEINLGFMSFFTKAVVGALKKFPTINAEIDGE
DVWLKYYDIGIAVSAKEGLVVPVVRDADRLGFAEIEKSIADLASKARSNTLALSDLQ
GGTFTITNGGTFGSLLSTPILNTPQVGILGMHKIQLRPVAIDAERMENRPMMYIALSY
DHRIIDGSEAVRFLVTVKELLEDPESLLIEG"

CDS complement(4025829..4028702)

/gene="odhA"

/locus_tag="EFAGFIKM_03455"

/EC_number="1.2.4.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q99U74"

/codon_start=1

/transl_table=11

/product="2-oxoglutarate dehydrogenase E1 component"

/translation="MTIVEGNKKPWESYYGPNMGYVQEYELFTQDPGSVTPAYRELF
EQWGAPPMSGRDARTTLNSGNAQSASGSVDIQLLQKAVTAGKLVWNIRTYGHLAADID
PLGISEDTDTSLLPQHFELNEEDLKALPASLIWEGADGQTATGWDAIQRLRQIYTG
MAYEFSHVHEVQEREWLNRRAESRTSPAPLNPKERKALLERLVEVEQFEDYLHKTFVG
QKRFSIEGNDVLPMLDEAVRIMAEAGSSHILMGMAHRGRLNLVLAHVLGKPYSKIFSE
FHHAPNKDLVPSEGSTGINYGWTDGVKYHMGANRFVKDGETVQARLTLANNPSHLEYV
NPVVQGFARAAQDDRRDPGYPKQDVTKAATILMHGDAAFPGEGIVAETLNFKALPGYQ
NGGTIIHVVNRLGFTTDSSDSRSTYYASDLAKGYEIPVHVNADNPEACIAAIRMAA
EYRNRFKKDFLIDLIGYRRYGHNETDDPETTQPIVYDKVKNHPTVSHLYQDQLKEESI
IDDASITSIRDGVTNKLKEAYDQMKKNEVHEYYQRKISEPEAVTITPTAVPLENLRSI
NADLLKWPENFNVYPKLQRILQRRSTSLNEGEKVDWSLAETLAFATILADGKPIRISG
QDAERATFAHRNLVLHDSENGAKFCPLHHLPQARASFAIYNSPLSEESVVGFEYGYNV
YSPDTLVIWEAQFGDFANCAQVIFDQFVSAGRAKWSQKSSLVMLLPHANEGQGPEHTS
ARLERFLQLCAEDNMTVANLSSASQYFHLLRRQASLTETEDARPLVMMSPKSLIRNPR

VASPAVEFSEGKFELVLEQAGLTQPDRVERIILCSGKIAIDLEDAIEKDKADRSWLH
IIRVEQLYPFPAEEIKRVLARFSNVKELVWVQEEKNMGAWTYMEPRLREVAPEGTTV
RYEGRPEHASPSSGYQLVHSMEQQQIITSALKQTTKNNIPLGR"

CDS complement(4029337..4029771)

/gene="nudI"

/locus_tag="EFAGFIKM_03456"

/EC_number="3.6.1.12"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01846"

/codon_start=1

/transl_table=11

/product="Nucleoside triphosphatase NudI"

/translation="MNRHITHIGVYGLVAWEDQFLLIHKARGAYQGQWDLSSGRLEFGE

QPETALHREFEEETGLTHLQVMIRSAESIVLEWVYQGEPEELHHIGMLYDVVLTVASQ

PDHIKKEPDGEDSLGADWFTLEQVRDLSLTPFAEYMISQSTS"

CDS complement(4029772..4030269)

/gene="yvbK"

/locus_tag="EFAGFIKM_03457"

/EC_number="2.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32248"

/codon_start=1

/transl_table=11

/product="putative N-acetyltransferase YvbK"

/translation="MKLSFRILDWEEERPYELLLMADPSKAIVDEYLSRGVCFIAEYE

GEMVGEFVLLKTRPETAEIVNIAVQEELQGQGVGKHKMIKEAMEAARRLGCRILEIGTG

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ERKSP"

CDS complement(4030388..4030810)

/locus_tag="EFAGFIKM_03458"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MGIVFRDTLESIALEQLGGNFFDGWPNPPSTPTFLKLLEQSYAI
ELAVDEDTGNVVG FVQAISDGVLSAYIPLLEVVP EYKGRGIGTALVQRMFERLRNLYM
IDLLCDPELQAFYEKQGMANASGMIIRHYQNQSGAVCD"

CDS complement(4030913..4031278)

/locus_tag="EFAGFIKM_03459"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGYQHALQGYIAATNTHQFDEVSKWLSPQAVYWFTGTSCCTPNE
IRAYFENAWETVKEEVYRAEDVKWITTSKEQAVCIYTYHWKGIYQGEPAYGKGRATNV
FVAGLNGEWELIHEHLSLG"

CDS complement(4031306..4031989)

/locus_tag="EFAGFIKM_03460"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MYRCTGRPPFVCIYIIIDYTVRPVKIRMNQSGNKEGKHRLFP
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RKGFPGYIAPGGKVDF
PESIVDGAVREVLEETGLVVNEITYKGLDEFCDPEQGLRYMVFN
YLATSFEGQLLQDP
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FERSVIWEKSSGRTLQETFMVYSD
SVLEQSRTTR"

CDS complement(4032054..4032842)

/locus_tag="EFAGFIKM_03461"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIVYEREHDFVLTAQHEHGLVAGEMTSHWKNEL
LSDAAHRDELI"

LAKEHDRGWIELDSSPFWWDYSQSPYSFRDFPLRPRFVFYHKGIEEVRQKNLYAGLL
CSLMYTELFQKNLGANAQDDDDIRDYLQQEHERQLDWEKQLGGDAEALKQRLQSDVEI
MLFCDQLSLFLCMEEPGTPAARYDFFAEGLSCTFDACSRQPIQAEWLSNEKVGLSFFP
FDEDFTIVLPYKSVPKASIRKFGMQQAYRRAEWKERRVLITELN"

CDS 4033038..4033967

/gene="coaA"

/locus_tag="EFAGFIKM_03462"

/EC_number="2.7.1.33"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WPA7"

/codon_start=1

/transl_table=11

/product="Pantothenate kinase"

/db_xref="COG:COG1072"

/translation="MNLSPYIEFNKEWAELKQHQTTLPLTEAELEQLKGLNEEVS

QEVEDIYLP LTHFIDLYARVSRELNQLTASF MKKEALPTYIIGIGGSVAVGKSTAAR

LLQALLARGKN SPKVDLVTTDGLYPNAV LQEK GIMNRKGFPE SYDIKSLIQFMGDVK

SGKPEVKAPVYSHLAYDVIQGEEKQICQPDILIEGINVLQIKKETPLLVSDFDFSI

YIDAE EHIRHWYVERFKLLRNTAFQNTDSFFHQRFANIDEEETVRTANQIWQDINAK

NLHENILPTKGRARLILKKEADHSIGQIQLRKL"

CDS 4034032..4034394

/locus_tag="EFAGFIKM_03463"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39619"

/note="UPF0382 membrane protein YwdK"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQTLILGSIMMFLAVALGAFGAHALKRKLSADMIKIYETGVQY

HLIHGLGIILIGLLADRLESSSLVMLAGWLMFAGIILFSGSLYALSVTGVRKLGAITP

LGGVAFLAGWVMIIIAAL"

CDS complement(4034464..4035015)

/locus_tag="EFAGFIKM_03464"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQSIYLIRHAKATGQEPHAELTDEGIRQAEKLADLLAHHSITYI
VSSPWKRAVQTAMPLGIATLQHIHTDERLQERVLSSLDLPNWMDVLKRTYDDVDWVEE
GGESSRNAAARGLALLEELWSRPEQHGAVVTHGNLLSLLIREYEPSFGYEEWTKLSNP
DVYVLERQLPDAGLSTIRRIWTD"

CDS complement(4035040..4035822)

/gene="yrpC"
/locus_tag="EFAGFIKM_03465"
/EC_number="5.1.1.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O05412"
/codon_start=1
/transl_table=11
/product="Glutamate racemase 2"
/db_xref="COG:COG0796"
/translation="MNKKIAFFDSGIGGLTVLHKALKQFPEEKFLYYADTLHVPYGTK
SADEVRGHIFDCVEAIVQEDVQAIVACNTATSLAVKELRAKYDIPIGMEPAVKPAV
EMNRDSGKRVLVFATALTLSQTKYNELVSRVDDHHSVDSIALPELVEWCEQLDFDPGK
IADYFRFKLADLDLHGYGTVVLGCTHYPFYTSILRTVLPDHIQIIDGSTGTVNHLKQR
LGLVAQHGDRTGEQVTLSSSSGRPEEQEKMYNALQYLEMNSK"

CDS complement(4036070..4036456)

/locus_tag="EFAGFIKM_03466"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNRRLILGLLSVCTALTVAACSTRTEQALSATIESNLQQMVS
DPVLLTSSNPNDYIAGNREAYNDILNTGEAGLPFLLQQLESSPDNGLKEWIMAQASTE"

LLGEHNPVEAWHSGKEWLRQYKMSVE"

CDS complement(4036524..4036742)

/locus_tag="EFAGFIKM_03467"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIRTFVQKDLQYVIEAHIRIYRNEYNYDHSFAEFITNGARRLYQ

SVGFEVKGVRKQMLSGQELTEEQWELVL"

CDS complement(4036742..4037458)

/locus_tag="EFAGFIKM_03468"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVPKSNLSSMEMFKIQVSTLYTINEQQRLLSINEPGGGQAPAIF

IGLTSADSLIYYHEQLPPDLMNELGKDCELPDIPKLIRKVETFELVNRVWMGPAYAF

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NQGAEASLYTAPGYRGHGAAETVKCWQYYVKERGRVPIYSTSWDNFASQQVARKLGL

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CDS complement(4037676..4038560)

/locus_tag="EFAGFIKM_03469"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTDHVELEIDGVSFVLKESHSDWLQPLGTVFRVFDQQDSGNIS

FGIVQKDQKRLFFVKYAGAHTIHANHTGSPPEAIRNLKSSVSVYEDLAHDTLIRLTDF

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HIEVERRGYVAVDLYDGSLIYDFDKHAMKICDIDLYRKGSFTNTMGRMWGSSRFMSPE

EFELGAPIDAVTNVFNMGAMAFGLLGGEKERSYDRWDAGEALYQVVMRAVSDDRPERY

ASIAELGEAWKQAAVQGGQ"

CDS complement(4038557..4039135)
/gene="mshD_2"
/locus_tag="EFAGFIKM_03470"
/EC_number="2.3.1.189"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01698"
/codon_start=1
/transl_table=11
/product="Mycothiol acetyltransferase"
/translation="MNEDRKQETYIIRNIQRDEADIYWHLRLEALKTHPEAFGASFEL
SIQIPMNEVQERIHNEPDDYVLGAYTEEGTLAGMMGFKREHGLKLRHKGMIWGVYVAP
PYRGSGLASRLLREVLDGRHLEGIKQINLSVVTNSESARRLYERYGFVYGIERNAL
EVNGQGYDEAHMNYFYTEHSTLNEDISTGGVR"

CDS complement(4039132..4039590)
/gene="inhA_1"
/locus_tag="EFAGFIKM_03471"
/EC_number="4.2.1.103"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q8G9F9"
/codon_start=1
/transl_table=11
/product="Isonitrile hydratase"
/translation="MTDQVTDESGLTLKVDRVKPDSEYDLVFIPGGMGTRKLRIDES
FVGWLKQAESVPLKVSCTGSLLGAAGFLSGKKATTHPRAYNLLEPYVTEVIQKRIV
KDGNVITAGGVATSIDLGIYVVGLLAGQEAAANVKLQIDYPYEMQGVVEE"

CDS complement(4039612..4039713)
/locus_tag="EFAGFIKM_03472"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKMAFVLFDGLTFLDFAGFYDVINRLNFFEPTK"

CDS complement(4039927..4040847)

/gene="hcaB_3"

/locus_tag="EFAGFIKM_03473"

/EC_number="1.3.1.87"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01647"

/codon_start=1

/transl_table=11

/product="3-phenylpropionate-dihydrodiol/cinnamic acid-dihydrodiol dehydrogenase"

/translation="MTVEEHLTEAGQGRINTGSDVVKKKEGTNAPVALITGTSSGFG
MLTAITLAKQGYLVVATMRDLSRREELVKLAEQAGIAELLQYVQLDVTDAESVQKAVG
TVLHDHGRIDMLVNNAGFAVGGFIEEVSMEDWRRQMETNLFGLIAVTRSVLPVMREQE
QGLIINLSSVSGLSGFPGYAPYAASKFAVEGFTESLRHEMSSFGVRVVLVEPGSYRTP
IWNKGLGEIHRSEDSPIYKHKLDAVLRYSKHASETAPDPQEVADLIGRIARMRAPRLRY
ALGKGSRVLIIGKVLLPWKWLEWIIARGLK"

CDS complement(4040908..4042236)

/locus_tag="EFAGFIKM_03474"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSNTLRIVVHYALARGLRKWKTRERWQERRIIRHVHQIRAR
SSFYRKWWGSLNASDWRKFPLIDKSIMMQHFDTLNTVGITKDEALAFAGESEETRDFK
PSIQGVTVGLSSGTSNGRIFLVSDREQDAWTGTVLAKLLPGGLWEPAKIAFFLRANS
NLYESVQRGKLQFQYFDLLERVETLIKRLITYQPTVWVAPPSMLRLLADAYVAGYLTA
VPDKIISVAEVLDPDRKVLQVFGQTVHQVYQCTEGFLGATCCYGTLHLNEDIVHIE
KEFIDPATRRFVPIITDFSRTSQPIIRYRLNDILTGAAMPCACGSPFTAIERIEGRCD
DMLYFSQLHTGEAVPVFPDFVTRSVIAASPDIEHYRVVQQGDGTMEVSLRLGGSVM
QVETDVLWELMKLGERLECTLPEVRFVPYTFEPGITKLRRVERRHNGVTD"

CDS complement(4042233..4043093)

/gene="attM"

/locus_tag="EFAGFIKM_03475"
/EC_number="3.1.1.81"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q8VPD5"
/codon_start=1
/transl_table=11
/product="N-acyl homoserine lactonase AttM"
/translation="MLTTTPVELYLGAAGYCTHPEFLTLRGGR LSPVPFPAGFACIIH
PVHGPILLDTGYSSRFFEETAHLPNALYRHITPVVYREEDSAVHFLARIGLKASDIRY
IILSHFHGDHIAGVPDFPEAQFIYLPRAYDAVRSLGSIAAVKAGFLAGLLPADFMARS
LPVTCQPERWTRAGKEFPFDEFYDIFGDGSLLGVDVSGHAE GMMGLLLRTEEH DYFLC
ADAVWSSRAFREQRKPHVLAGIIMSDRKEYHRNFNKLVQLHQQFPHIRIVPSHCREVL
DAWGTGGQKR"

CDS complement(4043087..4044082)

/gene="oleD"
/locus_tag="EFAGFIKM_03476"
/EC_number="1.1.1.412"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q8EG63"
/codon_start=1
/transl_table=11
/product="2-alkyl-3-oxoalkanoate reductase"
/db_xref="COG:COG0451"
/translation="MNRALVTGATGCLGRHLAIRLAKDGWEVTGMGRQPKVGAELELA
GIRFLNGDIRDEAAVNEACTGQDVVFHCAALSSPWGRYRDFYSSNVEGTQNLVDGCLH
NEVQRFIHVSTPSIYFNYNPRYNVHENDPLPSKPANHYAATKLLAEQVVMEGHAKGLP
SIMIRPRAIFGPYDQTLFPRIVAANAKSGVPMIGGGQALIDLTCDNVVDAILLCRDA
SDEALGRAYNISNGDPRAFSELVSSLFGMLDMPLHRRNIPYRMAYGVAALLERVHGF
PALGEPVLTRYTVGSL SIPQTL DITDAQEQLGYIPRVSIEEGLQQFADWWRAESC"

CDS complement(4044079..4045371)

/locus_tag="EFAGFIKM_03477"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTTRSGETRHRTAASLRVLLTGGRAPVTLDLARMLHRAGHRVYV
AESAVRHLTRSSSAVEQCAVVPSPRHNTGAYLAELERLAQDWQIDLLIPMCEEV FYVA
QGADRLRAYCRVLVTTLLEQLHELHHKYDFIQLAGSLGLSVPDTRLINSRQEWMEAQSV
LETMGDWWVKPVYSRFAAKVRMPTLMTDDTGARTDQEGNVSQKSRRHIRNDPPEEGQL
SVASPWVAQAYIPGQMLCTYSIAHEGQLVAHATYDSRYRTGSVGASIFFEQVEHEDAL
AWVRQFVEATGFSGQIGFDFIEGPDGQVYAIECNPRATSGIHLFHPGDDLVRALTEPE
TLIKERKMITPARGSKAMLMLPMLGSGVQQIFGKGKLRWIAAWCGTRDVVYVGQDIQ
PLMEQFGVVLAAWRLARSQKCSLTEALTHDIEWNGEQQ"

CDS complement(4045361..4046362)

/gene="fabH_3"
/locus_tag="EFAGFIKM_03478"
/EC_number="2.3.1.180"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O67185"

/codon_start=1
/transl_table=11
/product="3-oxoacyl-[acyl-carrier-protein] synthase 3"
/db_xref="COG:COG0332"
/translation="MQLRRVRIAGTGKYLPEQEVTEELDRSLDVPAGWVSKATGVGV
RHYASGEETSSFMGARAAEAALADAGLQFSDIDCLVCTSGTKEQPLPSTAVFIQQAMG
QQDSGVPAFDMDATCLSFLNGLDVISYMVDAGRYQRVLLVATEIASAGLNWWDKESAA
LFGDGAAVIERSPGSSSQIVHASLQTYSRGARFSEIAGGGTRMHASNYKADQPEP
YLFHMDGQAIFRMASRLLPGFINDMLQATGNQMEDFQLVIPHQGSAMAMRLIRKKLGI
AEDRFMDITRNHGNTIAASIPMGLHEAIRQQRIQRGDRVLMIGTAAGLSLGGLIFDY"

CDS complement(4046747..4047637)

/locus_tag="EFAGFIKM_03479"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7A6Q5"
/codon_start=1

/transl_table=11

/product="Epimerase family protein"

/translation="MKKVVLGGTGFVGGQDFAQRFRKLGYEVLII SRQPGHIAWEDRA
GIIGALEEAEMLINLAGKSVNCRYTDENRKVILESRTTRTRILGEAVLACNHPPPELWI
NSSTATIYRHAEDRPMTEKEGEIGSGFSVDVAKAWEQVFFEFSLPSTRQIALRIAIVL
GEGGVMVPMTNLVRFG LGGSQGAGTQQFSWIHIEDLFRMVIYLQEHPHLNGVFNASSP
HPVTNRELMARLREQMGVRIGLPSPRWMLELGARFIQTETELVLKSRWWIPERMEREG
FTFTYGTLDAAALAKILNKKK"

CDS complement(4047754..4048275)

/locus_tag="EFAGFIKM_03480"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIITAYQLPALYEQKRVSMQAMEEIVRLLAQAPLLYDDGQGIQV
QDYMGGLEVELEHEVRRRAVTLEYELAVQACRVFADPLAYEQLQDALGLQAELWQEEVL
TLAKWMDWLKQISEGKRTLPEYNFTAMLGNLPDGFMIHDFYDELRYQLEQN PANAWAI
EKRDRLYATLGAK"

CDS 4048443..4048817

/gene="blaI"

/locus_tag="EFAGFIKM_03481"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P06555"

/codon_start=1

/transl_table=11

/product="Penicillinase repressor"

/db_xref="COG:COG3682"

/translation="MNQIQKLSETEMELMVVIWSCAPPVTSTELLDIFAEKGKAWKAQ
TMSTFLSRLVDKGALTVTRRGRTNDYEPLLPEDYKLQETQHVLDGLYQGSVKNLVSA
MYDGDKLSDDDISELKKWLSEK"

CDS 4048827..4050155

/locus_tag="EFAGFIKM_03482"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNIFFEILCSLIVAGSIVSVCILALRLIPVSVFPTKWLYRLGKL

AILFYLFVPVSLGLSWLLDMAFQTTSTIPGTENAAASGVLAGTFIPEQTISVTTAWFLL

CWWGIGVISFSAWQVYCYRRFLNELSRTPTVLCHSEPAIQLPLIKKALGLKRNITLA

HSTLVRSPILVGLFKPTIYLPPENTVKMDISMVIHHELVHLKHKDLWVKALTGVSAL

HWFNPLIHMIRREDIHTWSELACDEDVVKEMSHEERRRYGETILNVMAGTKKMPAQFCS

SLSGEGKQLKRRLMIMFNVKKLKKKHWMLSMGALLLITGVSTSTAVWASNHTVKVEAE

ASETVPFPSTDGSSEIVASPNKVGISEAVTAPSTSETPEIVALPEDEVSEAVPVPSAT

VPSTTLPSTTEPSEAKVETATVPFTGESPEIVALPGDKVSVTPVPSEK"

CDS complement(4050247..4050981)

/locus_tag="EFAGFIKM_03483"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIKKFLQKYGLIIDLVLLACFVAFLAFWGQGFVMMFFGMITIAF

IVLRRIDYQKHVILKRIILTGFVAVSFVIIIEALVFTQLGANDPDEADYVILGSGI

RGTELSLTLKQRLDASLDYIRSHPQTPVIVSGGQGPGESIPEALAMKNYLIEQGINPA

QVIMEDRSTSTQENLAFSKKIILESGLEHPEIMIVTSDYHMFERSKYIAAKNGYAAEYG

ISAPSPGYLKPVNMIREYFATIKTFI"

CDS complement(4051032..4051160)

/locus_tag="EFAGFIKM_03484"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLYEDPFIQTIIQHEQLMRDLRRVRSLHLPQSYIGAGYIRNY"

CDS complement(4051376..4052221)

/gene="rhaS_30"

/locus_tag="EFAGFIKM_03485"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MNWINALQVAIQYMEDHLLNMTMEQIAAQAHISPFHFQRTFAL
LTDVTVAEYIKRRRLTLAAHELLQSDHKIIDLAFKYGYDTPESFSKAFRRQHGIAPSE
ARKNSNVVQSYNRLVIQVSLKGAEPMKYKIVEHPEFTLVGVEQTFSYADGEHLQGIGK
MWQEAWTSGTEDRLFELNNGVIQGLLGVVVDQSEIQEKQMQYWIATTYDGEVPEGLSI
FTMPASKWSVFEEVGPMPESMQLLWKRIISEWFPSNPYEHAYMPELEVYPGPNQPPQI
WIPIK"

CDS 4052457..4052987

/locus_tag="EFAGFIKM_03486"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSSKKEMLLNVAEEFLYHGFHSIGLKRIITDAGIAIMTLYNHF
ESKDDLIVQVLLRREQRYLEQLRQYADNKAHPMFLNLAEGHAAWLKEHESRGCLFLRA
KEEFGGHADHIIVQTVNAHKRHMRTLQTLAPAASDRDLLQFSLLLEGSTALAETENV
NNVCRELIHMTHNSFK"

CDS 4053076..4054182

/locus_tag="EFAGFIKM_03487"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKIIFPGIALIAVCYAFGRFSYGLFMPEISEALQLNDAASGAI
NSGTIAYCLSLLTAPLLINRKGHYHVIQLAGISAVLGLTGIALAQNAWVLTFSIFLA
GLSTGWASPALGNTVNAELAPELQARGNSWINTGTSFGIVISGPLYWLTDFYWRPTYI
LFAVIGVVVLLWNRVIPPTKTLPTCKSIWTCMKPTRAGSALLMACLLTGVSIAIYWT

FARNFLTDEKGASDSEAVLFWIVMGVMGILGGCAGRIIERFEIGWSYRIGILLLAISL
GVILLPSMTASLISAIIFGSTYIFLTSVFIVWATRLFSPNVSIGISLAFLALGVGQFL
GSSMAGYTIEVFSNTTAFLAFAVLGLFGLLIRVK"

CDS complement(4054209..4054817)
/locus_tag="EFAGFIKM_03488"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTNLFEHCSGQTLNANLWLNPTDWSIEDGKVTITVSPISDFF
IDPGGEPVKASAPFLHTIVKGFSTTQVQVNMKEQYDSGCLMVRVDDTNWAKVCFEY
FEEQPSILSVVTRGNSDDCVSAPVDVNKPYLRVARAGNSFAFHYSQDGEKWKLVRVFG
LDCPEEIKVGIVAQSPIGQGTTVTFTDVQLQHGVGTGSVRRVK"

CDS complement(4054988..4056052)
/locus_tag="EFAGFIKM_03489"
/EC_number="1.8.3.7"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:D1A7C3"
/codon_start=1
/transl_table=11
/product="Formylglycine-generating enzyme"
/db_xref="COG:COG1262"
/translation="MHGQISKKENSACCSASRSGRMKVKIQSEDPELTASREMSAAY
GHASRHSVDLLTLAGDDRYIAGRNDKDRWIEGGRFLMGTNDPEAFASDGEGPVRETR
VDSFYLDCEVTNAQFGQFVRETGYRTEAERFGWSFVFHLFVSSQTSAHVRTVVQSTP
WWWVVEGADWSHPEGPDSDVHADRADHPAIIHISWINDANAYCGWAGKRLPTEAEWEYAAR
GGLIQKKYPWGDVLRPDGQHQCNIWQGTFTPTQNNAADGYAGTAPSRSPFANGYGLYNM
SGNVWEWCADNYVTDHEISILAKTVASPDEIRKVLKGGSYLCHRSYCNRYRVAARIPN
TPDTSTGHIGFRCASDVIPV"

CDS complement(4056077..4057975)
/gene="yesW_1"
/locus_tag="EFAGFIKM_03490"

/EC_number="4.2.2.23"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31526"
/codon_start=1
/transl_table=11
/product="Rhamnogalacturonan endolyase YesW"
/translation="MKTKSTVAKGTKVLFTLLLSGVIGWTGIVSSGGGVLQADAAEGS
APRLVENLGRGLTAVYLGGENKVYLSWRLLGTEPQQVTFDIYRRTGTEEVKLNDQPLTQ
GTNYTDTNVDVTQSHTYIVKSYVHGELQDASADVLAANPEIRNYFSIPLQNITSNPS
DYFVQHGWPGLDGDGEYEVVTRIPVNGGNKYVEAYSLTEGFLWRIDLGPYSVTID
TYNAPPASVSEFGVAGLGGWRDNDNITVFDLSDGKAEVLLRTFEGVTFADGQVVPAT
TERAQYVSVVDGWTGTEAARTTITNDYATDGPLSGHFGIAYLDGEHPSLITALKNRAL
SRNFQYVTSAYDYAGGALTERWRHAGADGEFFHQIRILDLDGDGKDEVSFGGWALDDN
GETLYSLPGVWHGDRFHITDIDPDRPGLEQFGIQQAENG NVNQFPWFYADAATGEIIR
TGEIPQDVARGTLADIDPTHNGLEMWSSSGNIYNVDGEVISSVQPSTNFRIWWGDV
GELLDKNFVEKWDWEQNTTTRLFTADDVRVNSRNAPVLYGDLLGDWREEILYETSDFT
ALRLYTTTIPSDVRIYTLPHNPAYRNGLA VKGYMQSLLTDYYLGEGMTTPTVPNILPV
VYNGDHES"

CDS complement(4058126..4059643)

/locus_tag="EFAGFIKM_03491"
/EC_number="3.1.6.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q0TUK6"
/codon_start=1
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/product="Arylsulfatase"
/db_xref="COG:COG3119"
/translation="MSQDKPNIIFLMTDQQRWDCIGTFNEHIHTPNLDKLA AEGITFR
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FGKTHWNHSEGVEEPSTRGFEVRSIGLSRQSGHYEQGATMMGDSHPEALEAYHQETKD
FGSGEENVNGYTGLTSQIPMNQHRDGWVAEQALQFLDEGVDPERPLFFYLSFLKPHAG
FNVPKAFEDLYRLEDISDIPQPPWEDEMQTHLAASDELNSNSRQSYLDKKKVWDQRSS

EERRRTTLRYWANCSWLDHYFGLALEKLENQGRLENALIVFVSDHGEMLGERQFRFTK
YNLYDSSVRVPLILSGTHIQEQKRGTTIDQGPAELVDLVPTLTRAAGLEANPMLPGVDL
LGDLRHRGTFCFHHGKGVTAHSAAPAYMWRTTEWKLILYLEGSVAESASRVHETKGEL
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CDS complement(4059686..4062103)

/gene="yesS_5"

/locus_tag="EFAGFIKM_03492"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31522"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator YesS"

/db_xref="COG:COG2207"

/translation="MIFKRTADPLPKGRYFRRSLMMILFIACIPGVITGVLLYGWVTV

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GKPMPLQDQALGGLQHAVREHMLNLEGNLSSFLMEYEGLTYSVQTGTFRRLGTDWTV

SAVPLNEIVAPIVSVPRIVLLVNGSGLLLALILSWVGSLLQLYKPFTKLLRIFTATGAP

IEAIAPEVSSSPKVLSSASIRSNPQVLDEVKHIEQRWIGVNRERESLQRRLEEQLPL

ARESLLIQLTLGHLLLSSDHEWKERLAQLGWVLRDEQFIILFAHIRPSGVLLYGAKER

NRSESQEWINFAAIDILNRQLEGLPFRAETINYHDMISIALLLAVPPEIEPETTKFRKE

LSRMGQHWLETVQSEWNVNRMVTSISKLTSDASHIPQLVRESRAVLRKRQFSSNATIID

MNEEAEPDVNDHGVYPLELEQAIIISALRSGEQDSALEQFSIFIGTYARSEVPEKHVRQ

ALFQLLARIQHTLLQLGEDPVELFGVGMYYEVLQLQDLDELFLWFRERIVHVCVEEFT

GKEEKQIQMAVHQMKEHAQQQYAEALSLDELADLHGIHSYTLSTRAFKQSFGQNFVDYL

TEVRLHRAKELLESTDVKISEIAEQVGYQPSYFNRLFKKSEGTTSPRYREDIHKHTGH

NRGNRSV"

CDS complement(4062147..4063019)

/gene="ngcG_6"

/locus_tag="EFAGFIKM_03493"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O50501"

/codon_start=1

/transl_table=11

/product="Diacetylchitobiose uptake system permease
protein NgcG"

/db_xref="COG:COG0395"

/translation="MHRMKWSERIGQSLNVVTLGLLAVVMFFPLYVVFVVSFTDPGEY
LQKKIVLFPERWSVEAYTYLLSTPAFARSLGNSAFLATVGTVC SLAVSSSLAYALSQK
RFHFRKILMFLIVLTILFSPGIIPNYLLVRELGLINNIWALILPALANGWTVLLMKNF
FDSLPAEISEAASIDGCSAIRTWYTIVLPLSMPALAAFGLFFAVGYWNQFFAALLYLN
DSAKWPIQVLLQNMLLNASNIDLVAPGQQVETPPTMLKMAAIIVAILPVLVVYPFIQ
KHFAKGALIGSVKG"

CDS complement(4063080..4064048)

/gene="yteP_28"

/locus_tag="EFAGFIKM_03494"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system
permease YteP"

/db_xref="COG:COG4209"

/translation="MSTHEQRISTVKGKQTSTKKKGLNLLSALRRDRSLYVLALPGIL
FFLIFKYIPMWGIIIAFQNYSPFRGIQGSEWVGLQHFTALFGNPDFALLFRNTLAISL
LNLILFFPFILISLGLNELRSVAYKRLIQTIIMPHFLSWVIIAGLTLFFFAGTGL
INELFTLWGWPRVDILTNPDSFWIMVTLQAMWKEAGWGTIVFLAAMASVDTQLYEAAR
MDGAGRRLRQIWHITLPAIRSVIIVLLILRLGDIMEVGFEQIFLMYNGAVSEVAEVFDT
YVYRTGIEQGDFSYSTAVGLFKSVIGLVVVVANRMVKRMGQEGVY"

CDS complement(4064072..4065649)

/gene="lipO_10"

/locus_tag="EFAGFIKM_03495"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37966"

/codon_start=1

/transl_table=11

/product="Lipoprotein LipO"

/db_xref="COG:COG1653"

/translation="MQKVGKRNTRNLAWIISVVMVMSVLSACGNKEERQVSGSSGNA
DDPLEVSIMTITPSAVPAADDNVIKRAIEEATNSKMNIQWVSNNIYGDKLNLTLASGD
IPDLIMINDPFGSTFTKMVKQGAFWDITPYIKDYSNLSGGIPDIAWDTTKAADGNNYG
IPRPRPVTGDSFFIIRKDWLDRLNLQVPETTDELFNVMEAFVEQDPDGNGTKDTTALA
AYISPDDLWGNGNLGPVLGAIESSFIGTNSSWKWDESQGKLVYRELLPEVKESLQYLT
KAYSRGMMPEDLLSLKLTQARELFKRNQAGIIVDKTGTMRKIYADDLKKVDPSPFKYTD
FYPLTNLNGYNPKGSGYNGILAIPASVPEEKMKRILQLVDTWMNPEVFEIQQFGIEGT
HYEVVDGKKVASSEKLTADNASDFNHIVNVIDLPWDTTGETDEETQANELFKKVEAER
DKTSVADLAAGLQSETGQKVLPELNKKIQDLKAKIILGREPIEAWDAFVETLRNDPNF
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CDS 4066113..4066379

/locus_tag="EFAGFIKM_03496"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFGVNVKKIEDQLVIRWQFSKIEIPAHITSVTLDDTYGGSEPS
AIRIGPVNGTSERILIRTVNQSYILFTSSVTLHTNIRAMLHPSN"

CDS complement(4066528..4067490)

/gene="manA_2"

/locus_tag="EFAGFIKM_03497"

/EC_number="3.2.1.78"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P49425"

/codon_start=1

/transl_table=11

/product="Mannan endo-1,4-beta-mannosidase"

/db_xref="COG:COG4124"
/translation="MTVREISRPVNKAATPEAKELMAFLVERYQKGMLSGQQDYSNL
NWINENTGRKPAVIGFDLMEYSPSRTERGAVSQEIRDAIDWHKQGGIVTLCWHWNAPT
DLIDEPGKEWWRGFYTDATTYDLSSALADTESEAFQLLIRDIEAIAVHLQELKDAGVP
VLFRLHEAEGGWFWWGAKGPEPAKQLYRLLYDRLVQEHLHNLIWVWNSEKPEWYPG
DDVVDIVSVDVYPEAGDHSPLAARYTNLRELVQNGKIIALAENGSIKDPKQMKQDVH
WSWFCTWTGGFLRDGTHNDVAFLKELYHSEEVITLDQLPKWSWL"

CDS complement(4067519..4068529)

/gene="araQ_23"
/locus_tag="EFAGFIKM_03498"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94530"
/codon_start=1
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/product="L-arabinose transport system permease protein
AraQ"
/db_xref="COG:COG0395"
/translation="MAASGTDRMVVVPKQNYHMRVRSKTSDLLYSIFRYALVIGISF
IILYPLFLKVSFAFKDKQDIYNPTIYMIPQHFTLDNIRLAAQVMDYLPLLANTLLFVT
ITLLTAISCALAGYGFARFSFPGSNVLFILVILTILVPTSTLMVPMYLHFRSFDFMG
IIQLFSGKNGINLLNTYWPSMITAATAGGLKAGLFIYIFRQFFKGMPEIEEALIDG
AGGFKTFARIMLPNAISPLITVILFSFWQYNDTFYSALFMSESPLISLKVASLPAQA
NQLIPQLMGFGSNSGIKADPNYVAMIVDTGILLAIAPLIILYLFVQRYFVESIERSGV
VG"

CDS complement(4068558..4069457)

/gene="lacF_7"
/locus_tag="EFAGFIKM_03499"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P29823"
/codon_start=1
/transl_table=11
/product="Lactose transport system permease protein LacF"

/translation="MRTIRLSLKSRRALLGLAFISPWLVGVFLFATPLLQSIRFSLS
NLSVAPGGYVLDFVGFKNFKDALLVDATFNRLVDSVGAMVLNVPMILFFSLFTATLL
NQKFRGRTMARAIFFLPVILASSAVAAAESAGLINLMGDASAVDASADGGTSFNVVSI
VRMLADVGLPMAYVDYIVEAIMRIYEIISSSGVQILIFLAALQSVPGSMYEVAKIEGA
TAYESFWKITFPMVSPLILTNNVIYTIIDSFAGSPVTQAIYQTAFKTQNFGLSSAMSWL
YTLVIGLVLVVGWVLSRRVHYN"

CDS complement(4069454..4072039)

/locus_tag="EFAGFIKM_03500"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKRQRLYTVLAGGAAVIMIAAGLLYINNRGIPAVEAAAYLDTT
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PKERAEDGLASAYEKEVLSSQLNVSFRDSMGTLENFPNFSSSISNKQFTVGQIDQGIR
VNYTLGDTSLGIDALPKLISKQRLEEKVLSKLDATVARYTSARYYPTKNNPDILERLD
GQISKQLVLNKMGLAFETAGYTVDDLAFDNQENGVEGGGVSDKPSFVISVEYRLEQGA
LVVTVPLSQIEESGQYRIRNIDLLAYFGAADTKGEGYMLVPDGSGLIHLNNGKTQEE
QYVQRVYGADPNDNSLRPQVSESAYMPVFGLKNGENAWFAVIEKGDGIASISADIGG
RQNSYNHVHATFSLRGEDELEMYTSQKIQEIQLLSEEPYRGDIQVRYHFLHGEDASYS
GMARLYQQQLIEQDVLKPLPEQTELPFYVDVLGAVDKKASFLSVPYRTTLAMTTYEQA
TEMAAKLQQDGVERVQMRYQGWFGGGISHHTPTQVKLDSEVGSRSELQALSTKLEQSG
GALFPDVAFQHIYHDDMRFPSSDAARFVTKETAELYPPYNPALNRMDQSRDSYYLLSA
AKLPYVVFSEFADKFNKLDLGGLSLRDLGQVLTSDYRDSRVIHRETAKKIVKEQLGKLE
QSYPNLMVSAANSYAWGSAQHVVNVPAGSSRFNITDEEVPFYAMVIHGYMNYAASPMN
TSGDQDLRKQLLRSELGAAPYFQWYEPSSRLKLTNYDSAYATEYGYWVDDAVALYK
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GGVNG"

CDS complement(4072054..4072674)

/locus_tag="EFAGFIKM_03501"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
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MILQKQYAGFLVNYIDPRINSIIIEIATVAVPFFLWCTANWAVTTLMEGEGKFREIVL
ATGYSLIPIILIYAPMIVISRFMVQEETAFFYLFNSIAFFWFVLLLFIGMMTVHQYTV
IRTMITMVLTLIVMGIIVFLGALVFSMLQQLYEFGYNIYRELIFRT"

CDS complement(4072655..4074121)

/locus_tag="EFAGFIKM_03502"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MARTVKRWLVLLAAVSLLLVNAVPAASPAPYESYNYNYWKEAV
PSPDAYLPERTISGRDLGISEFKDPGDVNVSPSGLIYVLD SGNSRIVVLDPGFKLLRI
IDGFMMEGTKETFNLPGGLFVDEEERIYIADTGNSRVVLDGEGTLIQTITKPESDIL
STQFQFQPLKLTVDHVGRVYVVAQGVYEGIMQFDESGKFIGYVGTNKVERDYGEYIWR
MLSTKAQRAQMVLFPTEFSNADIDHKG FVYATNIDPGSNEPIKRLNPSGEDVLKRFG
YYDVKGDIRFRNPNPGPSKLIDVKVLGNGMYSVLDATQNRVFTYDDEGHLLYIYGKGN
QVGT LKTPVAIEQSGEHLVLDRGKNNLVVYEPTRFGARVNEAVALHYRGEDTEAVNS
WREVLKLNANYDIAYIGIGKSLLMEKKNEEALGYFELGMDRKSYSVAFKRHRREMMKE
HFGTFLTAAIALIVILILTRVAVKWRRRRRQVDREAGFH"

CDS complement(4074133..4074996)

/gene="ngcG_7"
/locus_tag="EFAGFIKM_03503"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O50501"
/codon_start=1
/transl_table=11
/product="Diacetylchitobiose uptake system permease
protein NgcG"
/db_xref="COG:COG0395"
/translation="MAAIATGKKRVNRSLSGSLSFALLLVFGAFMVLPLIYAINNAF"

KPLDEIFTFPPTLFLVKNPTFSNFTDLLNLLSDSWVPFSRYIFNTVFITGIGIVGHVLL
ASAAAYPLAKHKFPGKVFMFQVVVLSLMFTPAVTAIPNYMIMSWLGWIDTYWAVIIPA
FAYSLGLYLMKQFMEQIPDALLEAAKIDGASEYRIFWSIVMPNVKPAWLTLIILLFQM
LWGSDGNGYIYSEQLKTLHYAAGQIIQGGISRAGAGAAVALILMSVPITLFIFSQSRI
IETMASSGMKD"

CDS complement(4074999..4075967)

/gene="araP_4"

/locus_tag="EFAGFIKM_03504"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94529"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraP"

/db_xref="COG:COG1175"

/translation="MPQISLRDQGNSPPEKASRMGMKSWWSWKLQEMKASKHSYVLLA

PYMLLFIMFTVIPVVISIILSFTYFNMLEFPRFIGWQNYTRLFLEDDVFLIAIKNTLL

FAITGPISYIACFVFAWIINELTPKWRAFMTLIFYAPSIGNVYFIWLMIFSGDRYG

IANGLLIKWGFLLEPIQWLKTEAYIMPILILVQLWLSLGTGFLAFIAGLQTVDRTRYE

AGAVDGIKNRWQELWYITLPSMRPQLMFGAVIQLTTSFAVADVSIAGFSPVNYAAE

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CDS complement(4075986..4078913)

/locus_tag="EFAGFIKM_03505"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAGILQRKTWILSTVIIVAAACIILYVTSGADVKSANIPPGSLP

AIEVDAVLQQTRQKKGYEQYRSGTDQATQPNVDITIEAGDYIKAEGEDVRKLTNYEGM

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TLTLKSSREPMVIRSIRLFNEKRAVPAETAGAQQSDSSGQPKDVLIRIEGEAAIAKS

SPTLYPTSERSSSAVSPYSASQVRINTIGGFNWRLPGQWIEWEVDVPESGLYHIGFTA
QQNFVKGIYSTRKLTIDGDVPFAEMAKAPFRYQSDYRIDVMGGKEAYKFQLDKGKHVL
RLENSLGDFAPLIRNVEDSLYNLNSMYRRILMITGTPDEFDRDYRVEKQIPNLLEVFS
GESKRLKDVAACLRLLSGQSSDQEALIKTMALQLDEMIDKPDTPRRLAAYKTNTGGL
GTWVQQAREQPLEIDALYVTSIDRDIPGTGMGPLAKLGHEAKIFYHSFFIDYNQIGNV
ATSEDQRTVTWIGSGRDQANTMKAMIDKTFTPDSGINVNLKLVNMGTLTPATLSGEG
PDVAMQIGNDLPVNFAMRNSAVDLTQFSDYSSVEKEFRESAIVPYAYDSGVYALPETQ
TFNMLFYRKDVLEELGLEVPQNWEDVEALLAILSKNHMEFGMPIVTQANMQGVNIPP
SQYATMLLQNGGAFYRNDKESDLDLRIGIETFKQWTEFYTDYKLEREYDFANRFRGT
QMPIGLTDYTMYNQLSVFAPEIRGLWGFVPVPGTVQADGTLNRDVPGGGSVMMLESA
QDQVAWEFMKWWTSTPVQAEFGREMEGLMGAAARYPTANIKALDPLPWAEDYANLR
AQFETVKGIPEVPGGYFTGRHLFNAFYKTVVGQVEARESIMDYTQYIQDEIRVKRNEF
GLP"

CDS complement(4079039..4080421)

/locus_tag="EFAGFIKM_03506"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMRRWNVLPLMLLAVMLFVSACSGGGTAQTGTEAEGTTNSGNST

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NINQEANLIAKFPAIAGNEYAFESPTSIGLGLHYNRDLFKKLSLPDPQELYNQGKWDW

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VPIPNGPQGSKEVTYANNAASAKFIPKGVEDPKIVYQIYEETFDIPQIEEYPGQDYLE

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QAAIDKLGKQ"

CDS 4080949..4081986

/gene="exuR_3"

/locus_tag="EFAGFIKM_03507"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9JMQ1"

/codon_start=1

/transl_table=11

/product="putative HTH-type transcriptional repressor

ExuR"

/db_xref="COG:COG1609"

/translation="MKTKVTIQEIAHFTGLSKFAVSRALSGKSGVSDQTRDVILKAAG
KLG YFKDNSMLSGELYNSHELQEPKNTRSSG TILILFPNVRYQNQDSVYWGPVFNGIS
SKLNQKGINILTLTEPSADQLFTLLNPDAIRGIITVGSISTPILLEIKRLSIPVVMVD
HLDPVFHSDSIFTDNFASMREIMLYLLRKGFKTFQFVGNIGDAHSFYERWIA YNSVLM
GHGMEIHQIPELSNQALDEF RQTFTSVISEDNLPEVFVCANDFYGLYTIEALES MGIR
VPDQC VVTGFDNLYDNIPLLATVNVNKELLGARAVDQMLWRIANPESNVEKKLILADV
IIREQFGRHSG"

CDS 4082291..4082611

/locus_tag="EFAGFIKM_03508"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAKKGQTFQTYTEEFKLN AVRSYVEGSSSYKVVAEREGIRNCSQ
LKVWVKKWKKG EAFDERKNSVPNPLKGRPRTAFGSVEEERDYLQAQVDY LKKRYPNLV
KEKR"

CDS 4082776..4083471

/locus_tag="EFAGFIKM_03509"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISBth8"

/codon_start=1

/transl_table=11

/product="IS3 family transposase ISBth8"

/translation="MMAIH FENREFGYPRMTTALWEAGLNVNHKKVWRIMRELSIQSV
IRKKRKKSSYTPSVIYPNRLKRQFHATAPQ QKMVTDITYISDGNSFVYLSVIQDLFNN
EIVAWQLSKRNDVQLVLDTVEQWTQKRDVSEAVLHSDQGFQYTSQAYNTRLEAFGVKG

SHSRKATCLDNACIESFFSHLKTEKLYLNQCNSEAEIRQAVEDYMYNRYRRFQAKLK
QRAPIEYRCALAA"

CDS complement(4083478..4084587)

/locus_tag="EFAGFIKM_03510"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRNCAIYSSQFDLDQLFEVVQSIYPEETIERKEDKTHIQVTQKK

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IETEEDISEEFFGELLRLADALDAVIFWGGGSLNAQGQLLLDVNGESEVEDYTVTAH

TSFLDGDSPQSESGIQRKARSEQLLTEQGIPYNAHLPARAGDEHTTIRSKEEVARRAV

ALCLAALKGECLGAGESADDTAALVQEVIDKYEADSFFSPVEKRFIDQYGAEQQEIIS

FSWGYEAYHVMLWALGYVKELGAPTELCNVGKDVGYLQKDSFTDFLSDASLRNKS

SKI
LDEADLIYRYNWVCVDSRVNDKTPPAWSYPCQVDR"

CDS complement(4084797..4086017)

/gene="rtcB_2"

/locus_tag="EFAGFIKM_03511"

/EC_number="6.5.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P46850"

/codon_start=1

/transl_table=11

/product="RNA-splicing ligase RtcB"

/db_xref="COG:COG1690"

/translation="MRIVDNIKVWGEPLENAVSQAVTCSQYGDVLGVALMADHHKGYS

QPIGGVVAYRNMISPSGVGYDIACGNKAVRTNLMWNDIRDQIATIMDNINSTISFGVG

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KVWIANHFGSRGFGHKVASGFLNLAAGRQFSGKAPGESMDQPPTLFDLNSEMGMYWD

AMTLAGRYAYAGRDYVIEQVLGILGASAEYAVHNHHNFAWKEQHMGEEVVVRKGATP

LAPGQLGFVGGSGMDISVIVEGIHSEENTESFRSTVHGAGRTMSRTQAAGKMNYKLRT

RMGGEISEAQMHAIIRAYGVELRGAGTDESPFVYKKLQDVLNAHANTLKINHVLRPVG

VAMAGGNEFDPYKD"

CDS complement(4086198..4086620)

/locus_tag="EFAGFIKM_03512"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFKKWANVFMVLSLVFAVCSPTSAAAAKTVKVTVTLSAELVEN

NSVGNEWAIGASVNGKDLEEGSSVTNLNKSTGTLKLEAIAEEQDKIPDYGDKSTNVKL

SSFSKSTNKTLSVVVTENRGRYSGNTATWEFKFKISKK"

CDS complement(4086729..4087163)

/locus_tag="EFAGFIKM_03513"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVTIKGIELEDLPALSQLYNELMGMPNEQQMKKMFHYIQQNGH

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CDS complement(4087204..4087629)

/locus_tag="EFAGFIKM_03514"

/EC_number="2.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7CXI0"

/codon_start=1

/transl_table=11

/product="Acetyltransferase"

/translation="MSQININPSTSEDSEYVRQQLIAFNAAHVSEELRHRYEELNFNI

KNETGEIVAGVLSTLCWNWLEVDILWVDSEQRHRGYGSQLLLEVERIAREKSCDFVML

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CDS complement(4087646..4088176)

/gene="pgsA_2"

/locus_tag="EFAGFIKM_03515"

/EC_number="2.7.8.5"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P63756"

/codon_start=1

/transl_table=11

/product="CDP-diacylglycerol--glycerol-3-phosphate

3-phosphatidyltransferase"

/translation="MNLANKITLARIALIPLFMICFLNQQSVMIALIIFAVAAGTDKL

DGYVARKYNQITNLGKLLDPLADKLLIAVALVMMVQENMISSWIAVIIIGREIVITAL

RMVATEQGIALAADRYGKIKMVLQVAIIAILLNNVPFSLTDIRVDVALLWVATGVT

LLSGMNYIIVNYKLLR"

CDS complement(4088176..4088799)

/locus_tag="EFAGFIKM_03516"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MELSRNDDR VHASDSCITV KRGERSNLPGVLYASKKELSETIRR

TYVLFEEVFNDIHN SDKDKWVEGV DKTPAQMIAYQLGWMNLVMEWERNEQLGHESHMP

APGYKWNQLGSLNESFYEKYSSYTL EELRSLFRETEQQWQNWIDSLSEEELFVQGIRQ

WTGTKPGWAMVKWIQINSVAPFKSFRTRLRKWKKGHLANMDEGRMDV"

CDS complement(4088921..4090846)

/gene="bceB"

/locus_tag="EFAGFIKM_03517"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34741"

/codon_start=1

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/product="Bacitracin export permease protein BceB"

/db_xref="COG:COG0577"

/translation="MSLNYIIFRNLRKNLKNYYLYVFALVFSVALYFSFVTLQYDPSM

DEVAASTKGAAAIGASSVLLIFIVGIFLLYANTIFIKRRSKEIGLFQLIGLTKGRIFG
ILSAENSILYFGSMAIGVLIGFLASKLVLMLFKILGVDAITKLYFSPMALMQTVIVF
TIMYLLIMLMNYIFIKRQSILSLFQVSATSEQVQKMSVGQMIIGVLGIGFIVYGYFL
SARLFSGEAMDMQQLMYTMILILFSVILGTYLFYKGAVSFIFNLIRKSKNGYLSIHEV
LSLSSIMFRMKSNALLTIITTVSALAIGMLSLSYISYSAEAQAKESLPEDFSFAQA
DVKNRFBTELEHKQIPYEENHRQPYYIEIDAHEVMDSEMPQYLFSSVLSDNMVDNID
LLPGEVFFMGYGNVIQRMISIQEKGPVLHGLKRTLDDQLIGTTQKGVLPGYSSGGTP
VAVVDETVYQQLRQDLDPQLKSEWADYYGVRILNEGQAEEAYAVYKELQLEAPSFSSQ
IEFRNNQRNNMGLIMFIVGFLGLTFLITSGCILYFKQMNESEEEKGNYTILRKLGFQT
GNLLHGIQIKQLFNFGIPLVVGLSHSYFAVKSGWFFFGTELATPTVIVMIVYTLTLYSI
FGLLSVWYYKRVKEAL"

CDS complement(4090843..4091598)

/gene="bceA_2"

/locus_tag="EFAGFIKM_03518"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34697"

/codon_start=1

/transl_table=11

/product="Bacitracin export ATP-binding protein BceA"

/db_xref="COG:COG1136"

/translation="MWILEAKKIHKVYGNKLNKQEVLLKGIDLGVSKEFGVIMGPSGS

GKTTLLNLSSIDRVSQGTIDIEGKEFTGMKEKQLAEFRKHHLGFIFQEYNLLDTLTV

KENVLLPLSITSIPKQEAHQKFEQIARELGIELKDKYPSEISGGQKQRTSAARAFVH

EPSIIFADEPTGALDSKSASDLLGKLSDMNSTRKATIIMVTHDPVAASYCSRIFIRD

GQIYTQLNKGDESRSFFNDIIKTQGVVGGVQQ"

CDS complement(4091715..4092719)

/gene="graS_3"

/locus_tag="EFAGFIKM_03519"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A6Z3"

/codon_start=1

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/product="Sensor histidine kinase GraS"
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NVVICLVFIWARYLKETRFYKKLSIWDHTYDLGELDIAESPYEQIVHEAVSSQTQRYR
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DQQLHQKRIPFMHNDLFIEETELEPVLNSEIRALKSWCISKGIGFDVSLMVSRLTDS
KWLGFILRQLLSNAVKYSDSSDILIESWEQDGHILMIQDHGRGIETQDLPRIFDKGF
TSTRGRMDGAATGMGLYLVRQVVETLHVNIHVESSLGEGTTVTLTFPRKNDMVLLAGV
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CDS complement(4092716..4093417)

/gene="graR_3"
/locus_tag="EFAGFIKM_03520"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q5HI09"
/codon_start=1
/transl_table=11
/product="Response regulator protein GraR"
/db_xref="COG:COG0745"
/translation="MVNLLFKIMLIEDDESLFSEIKERLSQWSYDVYGVQDFGKVLQE
YSVIQPQLVIIDIQLPQYDGFHWCRIIRSHSNVPIIFLSSRDHPADMVMSMHLGADDF
IQKPFHFDVLIAKIQATLRRVYNYNTEHIELRTWRGAAIEYVKNTLTCGDESVLLTKN
EMFILKVLVEHKNQIVTREDLIRSLWDHEHFVSDNTLTVNVNRLRKKLEPIGLERYIE
TKVGQGYMATEEAEA"

CDS complement(4093589..4094353)

/gene="yueD"
/locus_tag="EFAGFIKM_03521"
/EC_number="1.1.1.320"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q8RJB2"
/codon_start=1
/transl_table=11
/product="Benzil reductase ((S)-benzoin forming)"

/translation="MGTETGKRHFIITGTSKGIGLQLAELLAKGDYVYGISRGGSDL
LESSEEWSGRGRHVQYDLADLNGIDDLITRILDQIPSQEADFIGLINNAAMLEPLKPI
DQCSAAEISQSLNISLAAPMILSSSFIQQTNHLSARRKIVNLSSGSGSYPAVSMVYC
TSKAGMNMFTQCVSLEQTGQQNPVEIIAFDPGMVDTELQAVARGKSAEEFALAGMFNQ
VYEAGQLRSPRDVAMQLIERLDENSDASHVIHTIES"

CDS complement(4094403..4095122)

/gene="COQ3_4"

/locus_tag="EFAGFIKM_03522"

/EC_number="2.1.1.222"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00472"

/codon_start=1

/transl_table=11

/product="Ubiquinone biosynthesis O-methyltransferase,
mitochondrial"

/translation="MEKTIKSVQDLYDMLDADFRSAKQFWEPFYEDRNRPIPPFPNNP
DENLVAHVNEGVLSSGGKALELGC GPGRNALYLTRQGYQVDAYDLSETAIWAKERAAE
EQLDVHFECRSVFELSPEQEYDLVYDSGCLHHLLPHQRIPYIEMIHNALRPGGYFGMT
CFAPGFGDIGGPEIVMNDWQVYQEKSMRGGLAFTEEKLRMYLEDGFECVEFRAMKAME
QHEPYFGVPFLWATLWRKKNS"

CDS complement(4095340..4095723)

/locus_tag="EFAGFIKM_03523"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFSKVGQVMMLYVNNQDESLAFWTEVAGFHIVDEVNLDEGMRWIE
IAPTPNSQTSIILQNKEFVARMSAGVNMGTPSLMFFTENLDQLYADLSGKHVTVGEIV
EMPTGRVFNFADNEGNYFAVLERAK"

CDS complement(4095899..4096372)

/locus_tag="EFAGFIKM_03524"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTIRLFQAIDQPAVLKMMTDHDFQFPSFIRDQYPARWDLFLKMT
DERISAYYVMVDEADVIGHAGYIFHPTVNRYEIVGVVTCKSHLRQGVARTLITKICI
KIAEFGCSDVMLYTLDHKENEALVFYERMNFQKEGVDMNYYTSGFHRLSLVKTL"

CDS complement(4096377..4096985)

/gene="inhA_2"
/locus_tag="EFAGFIKM_03525"
/EC_number="4.2.1.103"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q8G9F9"

/codon_start=1
/transl_table=11
/product="Isonitrile hydratase"
/translation="MKMAFVLFDGMTSMDLAGFYEAVTWLAILKAKENVSWTFCADKE
EISDDRGLKMKSDAVLPHLGDFDLVFFPGGLSTRTLRFDEDFMRWVRTAENVYKISI
CTGALLLGAAGFLNGKRATTNSSAYDLLNPYCAEVISERVVRDGNTVTGAGVTASIDL
GLYLVEMLTSTEIVLQVQQKLEYPYEEAGNLKDVMHTKGRG"

CDS complement(4097179..4097694)

/locus_tag="EFAGFIKM_03526"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSVHIRLLNENDPVIISKAFQEQGWGRSPEQYLHYLAEEQQNGER
VTLVAELNGEFAGYVNVLWNSSYPSFREQGIPEINDFNVLMKFQRQGIGSRLMDRAEE
VILERTDVAGIGVGVFSDYGKAQVLYAHRGYIPDGHGVHKHDHYIQPGEETIMDDDVV
LYLTKKLKATQ"

CDS complement(4097727..4098251)

/gene="yfiT_2"
/locus_tag="EFAGFIKM_03527"

/EC_number="3.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31562"
/codon_start=1
/transl_table=11
/product="Putative metal-dependent hydrolase YfiT"
/translation="MDERFPIGPFVHTGEVTLAQREKWIQDIAELPERAREAVKGLSE
EQLSLPYREGGWMLKQVIHHMADSHMNSMIRFKLALTEDTPTIRPYEERWAELSDSR
DLDVEFSLQILDALHRRWVFLNALTADYAKQFYHPSSEETTRLDYNLGMYAWHGKH
HVAHITSLRDRLGI"

CDS complement(4098299..4098841)

/gene="aacA-aphD"
/locus_tag="EFAGFIKM_03528"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7ATH7"
/codon_start=1
/transl_table=11
/product="Bifunctional AAC/APH"
/translation="MMNVYESNEITVRFLDSEDEQHLVKWLSDPVQLQYYEGRDRPHD
LEQVREHFYNQKEGATRCIVEYGGHPIGYIQFYEEEEERTEYGYGDTDEIYGTDQF
IGEVEYWNKGIGTQLMQSMLAYLINEKQARKVVM DPQSWNLRAISCYEKCDFQKIKLL
EKHEQHEGQMRDCWLMEYAL"

CDS complement(4098847..4099386)

/locus_tag="EFAGFIKM_03529"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRKSTIFWITGVTIILLVTLIIYSYVIPSVSAQDVVMAGTIRQI
DTDVVEVELEITRKREDKDQHMVYPVPGWEGVTFTEEQDDAWYMPSSVGSSYLDQVI
LEKYLKAQGKSMKSADNLIGFAIPDEIGSYKLRLTLRSLDGTTQPLENPVYYVHNEH
LLGKDLSWVTSENLEINKE"

CDS complement(4099408..4099848)
/locus_tag="EFAGFIKM_03530"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNTEFSEQKYGETGVKTSFEQMANGEQKYKMITEGSSYYCRTVA
SFQGAWQNSHVHINLTFYVVQTGWIAASYGDDQMFSIRVMRAGEHIIVQPGIHHNI
YMSAHSIAHTIKHGLNTSSDWTASPELARLTQSLTEKELLRKYD"

CDS complement(4099855..4100532)
/gene="COQ5_4"
/locus_tag="EFAGFIKM_03531"
/EC_number="2.1.1.163"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01813"
/codon_start=1
/transl_table=11
/product="2-methoxy-6-polyprenyl-1,4-benzoquinol
methylase, mitochondrial"
/translation="MSMDWYDMIARRNGGYKGRALYTLLEGYSAEDIFEERLIKLLPQY
TSVLDAGCGHGFEFTLKMSEYTDHIIGFDNSEEMIKIARNSLHSSRITNVEFVCVSTKE
KMPFEDKQFGLIYDRRGPTSIIDHGRLLQKGGVMIGIHTDITKVRERLERNAFKEIKI
EEYNEALMIFSDEKEFAIFLSDIPGNPDYSQPEYREQLKVKLKENRVDGRTAVRECKY
IWQAIRR"

CDS 4100714..4101487
/gene="spo0M"
/locus_tag="EFAGFIKM_03532"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P71088"
/codon_start=1
/transl_table=11
/product="Sporulation-control protein spo0M"

/db_xref="COG:COG4326"

/translation="MSFFKKMLASVGVGAAKVNTTELHTPEVTPGGIISGVVYIEGGDV
EQNVDRYLSIKTHYIREHDDRKVKETAVIAKYLLTEGFTLQPGAKLEKEFSFDLPEN
LPITLHRAEVVWETGLDISSAVDPSDRDLHVVP SKDMNTVLDAIDILGFKLREVTND
YAPKLGGNLPFVQEFEFVPTNKFRGHLDELEVLFPYMGDSLELLLQIDRRARGLSGIF
SEAMGTDES FVRLHLYERHLARGAHSVAQGLEEIISKHI"

CDS complement(4101584..4101877)

/locus_tag="EFAGFIKM_03533"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTIMNKRLALESFLVTLLFIIGFVAWNIVQGMIMTMNYVPDLMN
TASSGTLLQSKVAFGSRVQWDTTSMIMAVAGFILLAAAYYGLRSGMQRWTQRS"

CDS complement(4101896..4102465)

/locus_tag="EFAGFIKM_03534"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKLQEELQELLPLDQLEEMSGEEVVGSIAMDLYRAEFATIRES
GSELPQVLRDIILIIDLDEL SMNGMTS FLENASGQYLGETITTMERIGNDADVILK
KIEQMLSKSGVTHGQLRDNVNGLSEDDITSLQTHGEQIHEVLQQIELEAANLSMQSD
NEESFDLLYQYVDENKERLKQEMQHVLSN"

CDS 4102858..4104015

/gene="mgtA"

/locus_tag="EFAGFIKM_03535"

/EC_number="2.4.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WMY5"

/codon_start=1

/transl_table=11

/product="GDP-mannose-dependent alpha-mannosyltransferase"
/db_xref="COG:COG0438"
/translation="MRLALFTDTYLPETNGVAGTLHRLSNHLNRRRIEHLFTPNSVI
EGSHETQVRSVANIPFFLYPECRIALPNRADTHKQLQTFQPDLLHIATPFNMGLLGLR
YALKHHLPHVVSYHTHFDRYLEYYRLKSMIPLYWKYIQWFHRACDATLTPSQETLNTL
QTQGIQRLKLWSRGIDCNLYSPDKRSSDIRERYHITAPLILLYVGRIAPEKDIALTT
TMQQLPQEMQSRVHWIIVGDGPSLPKMRLQSPPNVTFTGYMHGEELAVMYASADLFVF
PSSTETFGNVVLEAMASGLPVVAANAGGVKDLVSHHRNGVLFEPGQADALIREICLWG
NHVNQLRMMGLEGRELAEQRSWEHIFDTLIGDYEEAIERRNRQTKNRIITA"

CDS complement(4104316..4104987)

/locus_tag="EFAGFIKM_03536"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLKYRMERKKLRWINYLLITVLIAILPSSHVEAGSTITVKTKV
QYYKGQPYIHILTGGNKSVDKLNKTFKLHAVKVARLDKEEKKSNNKYFYITMASVKYN
AKEKLSVVYEDHVTGGAHGMDATKSYNYDLRTGKELKLSEYVKDDTQMEKVEKSISN
SLLAMYNAGVSIFEENIYDFQLDQTSEFFLYDKGIVIRFHPYEVAPYAKGFVDIKVPF
SKFNQ"

CDS complement(4104987..4105514)

/locus_tag="EFAGFIKM_03537"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEIRQMATAFLSNGSDMLMMKKAGSRLDFEFWGGIGGHLEQGE
LNTPMTASYREIEEETGFKQEDVEHFRLRYILLEVNGGEIWQQFVYFGETTHRHFVPS
DEGELFWIPLDEVLDLHSSILIKATLRHYLQHPGAEDIWVGNVQSGTDLKGTTPQVIWN
RMQETISFEPKGVNR"

CDS complement(4105798..4106460)

/gene="yjjG"

/locus_tag="EFAGFIKM_03538"

/EC_number="3.1.3.5"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A8Y1"

/codon_start=1

/transl_table=11

/product="Pyrimidine 5'-nucleotidase YjjG"

/db_xref="COG:COG1011"

/translation="MDHIKAVIFDLNLTILNRTMTFDGFTQRLIKAYFGHLESTEDIS
KRIIELDQDGYKDKPLLFNELLNELPWAEHPPHAELMEFYGREYVRSSVLMEQAREVV
QHLRGKYQTGLITNGQTHIQYGKIDQLGIREDYDHIIVSEEAGVKKPDPRIFQLALDH
FGLSPEQCIYIGDHPVNDIEGAASVGMSTIWMKVNQPWQDRITTSPLHTIEHLSLKK
LL"

CDS complement(4106447..4106908)

/locus_tag="EFAGFIKM_03539"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQIQEISVWNHDDLVA MLVESSEGFRHIERLIHEYETGINTFE
QEDEALFECRVHDKVVGICGLNRDPYSEVTD TGRIRRLVVMREFRRHGVGRRLMDAVI
QKAENHYARLVLYTDQPVAGSFYRDLGFREVTSM EKITHVLELGEKKDGSY"

CDS complement(4107003..4107173)

/locus_tag="EFAGFIKM_03540"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKVIVILSLVVLVGVSSSAY AHPGRLDKNGGHNCSAKSKQKG
LCTGYHYHKKKK"

CDS complement(4107283..4108059)

/locus_tag="EFAGFIKM_03541"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5XAQ1"

/codon_start=1

/transl_table=11

/product="Putative bifunctional

phosphatase/peptidyl-prolyl cis-trans isomerase"

/translation="MIRAVFFDVGDTLLSQIDRSLSPRTAESIRELIRKGVQVVLVTG

RPYNLCEEFRNLGIDTIISANGALIKAGDEVHKSVLQAQMVRAFSEFAELHGHSISY

FTESFETNGLCTADGRVTEALRDTLGLMNSPQKISTLEQDVYCICLYADEAETEFQS

RFPSLRFRVRFHPYVVNVLEASEVSKSIAAEKVL DYLKISREDTMAFGDGENDVDLLVY

AGIGIAMGNGGERIKQSADYVTLRASEDGVTHALKQFKIL"

CDS complement(4108142..4109704)

/locus_tag="EFAGFIKM_03542"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIDMKRRHHPLTMLWSLWKLVKNSFAIVLFLVFRQGSSEQWLFY

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TLFHRLFRVTSIRFETGIKGEDATFQLHV VSLSEAEQLEKIVAGHMAEEAETAGATEE

HDTLDAVQVMEEGEAQSELVITDEVMSLPAKEKQERVVHYHSTRKDIFKASFTSLSFL

VLIPVLATLYSWVKDFFPDEEVTESLLLTWLD SWWIAGLMILVLLIISIALGIVRTFV

KYGNFQITSDAKRIYISKGMMEQTSFSILKERVQA IKITQSSMKRLLGLAEVELTTAG

SLGESEQEVNSLYPFLPVKQAYTLIEEILPSYRVTQEMEKLPRISLWLRLLKPSWGW I

MITGLLWYFKPLVFGQKHAWWMISAILLVWIATCRVMDFFHTRYILHQNFIQLRTGAL

TSTLFVSKREKVIEVQITRNVLQRWFGVASIHTV NRAKPVLHHRADISLDTAKSFQS

WYMGRTQDVQTR"

CDS complement(4109701..4110198)

/locus_tag="EFAGFIKM_03543"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MSIQWNTPEQRLSPHAVNLWRISAIWNVIGFLILAVLLILDSI
YGWKTWIGWILWGVTAISVLYAVWDIFIQPSWLYKHWFYDVNEEFLLQKRGALTKVHQ
IIPMAKVQSVTTNQGPLMRKYGLYSVSVGTMGSSHEIPALPEEVALALRHQIASYARI
NEVDE"

CDS complement(4110331..4110891)
/locus_tag="EFAGFIKM_03544"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDDKITIEPLTRSDAEGAYRVFETTIPAAFEQEGIGSLLVDIQE
EIAHKKAMIHMALQAKENIKASVFFLVAKMGDVIVGTISYGPCGKEIRECTEGRNGI
GELGSLYVLSEVQGGVGSALILALVTELQRLGIQQFCLDSGYQIAQKKWQRKFGEPI
VVANNYWGEQTDHMMVWLCEVQNFIVK"

CDS complement(4110919..4111341)
/locus_tag="EFAGFIKM_03545"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVRVYGVLLVWVIATFIAGCSQPNESNAEEGLPVLITLTCNPNL
ASEPCQDVEFDRPDEIRIMMKAIHKAERMPIIDYGTQYKMSINNADGSVTRYDFSLG
TDPKMQGLLVNEEDHTGTYSIPLEDANQLRRLIQRRTD"

CDS complement(4111443..4112123)
/locus_tag="EFAGFIKM_03546"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MPLPMVHLNLIADSLQMQADRGSFYLGNIAPDSIHMREGTI
RDDKEYTHFNP KDYGDYVDELKIFYSSYMQQLTDEGWKWFVRGYFMHVLTDYYWFRSV

HPEFVERV NKVDQHTGISRSKEELSHLYYQETDQIDFNLYQGSSWSEEVWQVLNSSPG
YDMTGRLTADEIVRWRDHTFSFLNGEEPGITPEFITGERVQVFVEETIERLISMLSSW
DPELRNLI"

CDS complement(4112259..4113038)
/locus_tag="EFAGFIKM_03547"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MDAFLEQINELNELQKDLVSLHPLFAEHYPVVVAYEALLYIYDY
SSKTQQYEWVKTPDDLYIPDECLAAMPVHHMDGRMCAIVTDATAFKDLEQKVYLFHEY
VHCYVYEKYDERIVNRLKIKHKMDELKRVTWELDYEFYEDEVVVERINSLLSALKSK
DLTLVHTARKALFTSLNEEQAEYWSWLEWNEGYARYIENLIRAKFGQESNHFGDTAPF
NRLV FYECGSEYISLLVKEHPEYHTDLEQLFDRMQVERIQG"

CDS complement(4113146..4113289)
/locus_tag="EFAGFIKM_03548"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MITIFLMLINVLLYGLGVYALILFIKLARRGIQALDIYLYEKR
ERF"

CDS complement(4113470..4113799)
/locus_tag="EFAGFIKM_03549"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTEDFYCDEVLSGKTKVNIVWETNQVLAYHHTRPYEHHIVVIP
KIHISFISQEAENDELLEMMRVIKKIAADMVEQTGSSKIVTNLGSYQDSKHQHWH
IVSGERT"

CDS complement(4113842..4114432)

/locus_tag="EFAGFIKM_03550"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSESLQDQIQFLIEIDKLKTIERKTRIMHGERLENDAEHSWHLA

MMALVLQSHANKDVDILKVIKMLLVHDLVEIDAGDTFAYDTVGNTDKYDRELQAAHRL

FGMLPKEQAEELLQLWLEFEAKQTPEAQFASSLDRLQPLIHNHQNEGDTWQKYNITSD

QILNRNREIANGSETLWEYAQQLIQKSVDQGILTKS"

CDS complement(4114456..4115295)

/locus_tag="EFAGFIKM_03551"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MITEINKHDFHKVKHLTDSCKNIEVKAVASGLNPGRIYVDDAEN

ITAALIWVHGQSGFQLIGDSRSEPFLNELKEYMWERIEPELLDLHMHAVEIGVVDEAW

EDVLRHISGKRDISSDIQHVFKLNPNSISQQVPLDICASQDEKVKILRIDEVLLEEKs

YNNFPFLMDKISHFWTTIDDFLQHGCgyIAVHNDDIASVCLSAFIADQTHAVDIETVE

VYRRRNyGTMVAKAFVEECGRVGIHPYWDcSPDNAGSIRLAQGVGMSLDFNYRVYWyD

LSS"

CDS complement(4115349..4115801)

/locus_tag="EFAGFIKM_03552"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQIFDTRQKPDVLQEAVQYFWKQWGSESSFHYRDCIERSVDTE

SDVPRFYVMLDGDRIIGGYALLRSDLNSRQDLFPWFACLHVDPEYRGRNLGGQLQTHA

MNEVKAKGYDKLYLCTDLTDYYEKNNWAYIGKGYLLDDEETRIYeyKI"

CDS complement(4115842..4116735)

/gene="yddE_2"

/locus_tag="EFAGFIKM_03553"
/EC_number="5.1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37757"

/codon_start=1
/transl_table=11

/product="putative isomerase YddE"

/db_xref="COG:COG0384"

/translation="MGRITVYHYDAFSTVPGQGNPAGVVFDADHFSETEMQQIAYKVG
FNETVFLNSEVADVRLRYFTPGHEINLCGHATMASLYGLKTRGMLSDKELITIETNV
GTLPIRFECNADTIYMEMKQDQPQFIPFQGDIEKLVSAINLTLDVLDLSTPIVYGSTG
AWTLLIPIRELNSFMKMKPDSSLFPGILIDNPKASLHPFCFETRSDAMMHARHFSSP
YSGTTEDPVTGTASGVMGAYYLYVKPEIDEVQFVVEQGHEIGRDGKVQVSVIRDGED
MDVRMKGTAFFVRELNVELDI"

CDS complement(4116813..4117355)

/locus_tag="EFAGFIKM_03554"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11

/product="hypothetical protein"

/translation="MEFVGKEVRITTVTEQDLDFICQLECDTNIWSFEETVETDEEKV
REKYGSHFAVADEKPYAYDFVIRRLNDPEDTPIGIVQMWSYVDYRKSWELGYGVLQEY
AGNGYGSEATRLLLQFSFQELQAHKVVGMCNSQNVRSAALMKHVGMTREAVYQEELWW
NNQWTDQYFFSILDREFKSV"

CDS complement(4117362..4117829)

/locus_tag="EFAGFIKM_03555"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11

/product="hypothetical protein"

/translation="MIQSGRFRSNDLFYKGDVGMSQNKYVQAAINAVHYVETKKFVNP
VEAWSFATGELFGEGSWGQRKGCPRTAFLGLCEDGYVRVIPQGRYNHRENSLNKRYAI

NTVKLFYKNSSMVHEDSKRLWSAVTEGKVIKSNYQVDIVKGLWGKGMILTERR"

CDS complement(4117798..4118313)

/gene="tadA_3"

/locus_tag="EFAGFIKM_03556"

/EC_number="3.5.4.33"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00972"

/codon_start=1

/transl_table=11

/product="tRNA-specific adenosine deaminase"

/translation="MKLSDYEYLTALAEAEQSLIEGTYPIGAIIVDVDGIVVSKGRN

RVFSDCDPTAHAEVDAIRRAGKHLLDVEKKKFSKKKDLTYTTCEPCPMCSCTILMSG

IKKIVWAADDEEYGGRLRRFKEGPHFIHMFDTLSCVAAPYLDLENKQRALLAKWNIGRG

LLDTEWEIPKQ"

CDS complement(4118408..4118977)

/locus_tag="EFAGFIKM_03557"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDITFIRHGHGEHLMYPNQLNCLHPGLTELGKSQVIALRKQVW

FAPEDVILVSPTKRTIETALLTPNKNLAFFSLLVGPRMFPQNPEIVPFVCDQIYSKE

ELSHQYTDIRIVELGFDYWEESINQMDAHRFQILA EKLLWCRQQSGNTFIISHDGTI

SNYRILLGEKELTKSDFLGEAEQYTIRNF"

CDS complement(4118992..4119483)

/gene="rppH_1"

/locus_tag="EFAGFIKM_03558"

/EC_number="3.6.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00298"

/codon_start=1

/transl_table=11

/product="RNA pyrophosphohydrolase"
/translation="MTTADNNNVSYEQNNNKFNFVRVAGIVMDAGRVLLHTEQDDFWN
LPGGRVKLNETTEAAIVREMMEELGVHVEAQRLAYVSEDDFFEYDGLKYHEVGFYYLIT
LPEAHKLYSETFEKGLDNGKLTQWFSLDQLERMEVYPVFLKKELSNLLDAKGIKHF
IQK"

CDS complement(4119480..4119665)

/locus_tag="EFAGFIKM_03559"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTFYGVALIATTAILIIIGVRSKRKVILRWGIASLILLVLIIIP
SFIMGFMDGFADGWSAR"

CDS complement(4119704..4120585)

/locus_tag="EFAGFIKM_03560"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MELKILYNLKDDVMMAGRLILIEGLPGSGKSTVAKMVSEILIEQ
GKTVQLFQEGDLDPADYEGVSFYAGDFEALLKTHEEYREILESNAIAHDQGFLIPY
RKMKEQWGDLPVHIVKNIFSRDIYEIPFEQNVKLITEKWQDFTQNVLSTKDDCITIF
ECCFIQNPLTMGLVKCNQSKEQNVQYVLELGRIIHALNPLLIYIDQKDVSYTFNKAVS
ERPKEWSEGFINYTNQGLGHAQGHQGVKGTQVLQERKKLESEIYGLLQMDKWLDN
SDYDREVCRRHKLEKILQ"

CDS complement(4120610..4121119)

/locus_tag="EFAGFIKM_03561"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKLTVVSLFLLLVACQNQENTEDAQQSIDSSAQSVTAKETQQ"

DEEISTSHEKEDIPPEYLDETNYTGDKLEIVKLMNARMRYLYEKDEKAYMSLIDPESP
ISGMGRYKVLKVTSMSDITIQEQRKLYQALVIVNELNENDEEYSNTMVFWKKKEDGDN
AQWIFADID"

CDS complement(4121396..4121797)
/locus_tag="EFAGFIKM_03562"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGFGEERRDYCSRNGVNGMKGENTQHGGKKGAGLRTGIVVLVVL
LVILVMTNPNEEDFVAWLASEHDIHSSYDVNEGRFTFTQTIDGEEKTLHYKGGHILHMG
IFSTYSYLFSDNEEKEVQIEAVGIMNMLFDR"

CDS complement(4121850..4122140)
/locus_tag="EFAGFIKM_03563"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNEEELPSLHDNIILSYEVDLENKRIRMTRSSHAVPKNMDVLF
SGVMAHAFDTPHLHGSIIIDLDEWDIEHFIPYSRGRAMVGLSVMIPMTNCKSG"

CDS complement(4122156..4122566)
/locus_tag="EFAGFIKM_03564"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MITQLRHSFFQVFTIMTLWITLLATIFFGDLPIQMSYLWNIAGI
AFIAAVLFGMMYNILWNYFTLKPIWNIVISSTFNIAGGMAMIWLFSDMFQFIAPWFP
GMWLLSIVLHVIAFYFYARMDSRKKAEELNNILK"

CDS complement(4122563..4123009)
/locus_tag="EFAGFIKM_03565"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKVIFEEDTAVEKRLAKVITHPAEKSKWDRIQKAICESETQLTV
IHVKNNRNIQIQLSSVVAFESEDRMCCVRVISGERYLLHKRLKFVEEDLDDLHFVKIN
NQTIIINTRYITSFSATDHARIKVDLSDSSSYFVSRFYIKNFRGKLS"

CDS complement(4123180..4123680)

/locus_tag="EFAGFIKM_03566"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKAKLLPEDIYSKQLSWLCIEPMLVSVRGRDMAAKTEIYRQLHE
GQQALFLFYSHNHTKSLAEFYWFSAYNIIIEIKSWNGIENGMRFFHLDENVNVLEQIE
CLITDKNRVGEEWREVLATDLDKDPILLQRTEALYATYQTVAQAAIAHMNKIILQNQE
MYLEIE"

CDS complement(4123706..4124209)

/locus_tag="EFAGFIKM_03567"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MANIHKGRYSAQIEEEFVVFIIIGMRINRLWAIHKWLPVFKSMGP
MIKELYMNPETGFLSTEYFISWRGVTLLQYWRSYDELEKYARGGLHLEAWKKFNRSIG
TDGTVGIYHETYKAQTGSFETVYANMPKFGLAKASEHVPSTGKMETSRRRMGRKNDPA
VEAPENP"

CDS complement(4124416..4124598)

/locus_tag="EFAGFIKM_03568"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MKALPEFVLHRYREIDEIILAVNERNIAAQQLYLKLGFLDRGVR
KMGIHGQQILHNHNRIT"

CDS complement(4124582..4124899)

/locus_tag="EFAGFIKM_03569"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MENSIRLALYHEQYDQDLDDFALRGDQLQFTAMPADVIDEAIQN
PDKDPMVILHEEKPVGFFILHKNSEYVEDKDASQYHTDTRSIHFDGTTRKWWCEGSNE
GIA"

CDS complement(4125449..4126042)

/locus_tag="EFAGFIKM_03570"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQKRVEDPLNLVKNKNSEVSEKMEQRNAPEVRIELWDEGDLGLL
RQLNSPEMTVHFGGPETEEKILARHKRYEIAQNGTGKMFKILLPHLEVVGSGVGYWD
QTWKEESIYEIGWSVLSEYQGRGIATEATAKAIASIRSEKKKHKFIHAFPKTKNPASN
NICRKLGFYSYIGECDFEYPVGTTIRCNDWRLAVGENE"

CDS complement(4126234..4126869)

/locus_tag="EFAGFIKM_03571"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPWPMVHFIAISELISKPSPELLLGSLAPDSIHVRTNLRTEKEK
THLMPEAGRFTTDEELKDFETQKKLAYSDPKFMQYLCGYIAHIYTDRTWTFDIYPAY
EVHPNGRSMYTQDVTKLEFMILRNLRANDWLIELKVGRAFDLGGLLESEVYQYRGEK
LEFLANPDNELLGDLNLSMEVTEEFIQKTALALKQLYTKWDVYKDLRSTV"

CDS complement(4126918..4127463)

/locus_tag="EFAGFIKM_03572"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGYDELRLNESERVKGTNVGMPKHHFVIEKKSQVDGNIHTSYS
WDSQGRIHGSGLTTHENHATLEDEFSAYIYDSLCLWLTWNPSTCMRCSGLNNYGITVIK
EQDALLKFHQLIRAWIELFSHATDPIVLTGNYCVDGEEQKGCYEKLVYNKVELINELH
KLANMAKYAEVYGKCIHFHGI"

CDS complement(4127601..4130318)

/locus_tag="EFAGFIKM_03573"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNC AKKLVTLLITV MLFSSFN VVSGAAESSASDIEGNWAESQI
TKWIDKGFHGYEDGSFKPNNTITRAEFFSLVNRSYGFTETASVSFKDVTSSNWAYAE
VSKAVKAGYIKGYRDGTIGANKPISRQEVAVIIDLLDLSNEASIGNHFTDSNMIALW
AKNSVDAIVAKGILQGYDNNFNPNKPITRAEAVVALDRSVNARATDYSLAGTYGPEAG
TQTIDGDVLISTAGVTLKNMIIKGNLLFSEGIQEGDVHLTNVTIKGVTRVEGGGVSTI
YLKNTVTSTLIVDKKKGPVLIITEGSTTVGEVSIQSPATLQESDTTGNGFGKITLSER
LPAGSKVGLKGTFDSTIKSGVQVDIPEGRIKDVIVAVTATGTTLNLGTDATIVNLF
LDAVAKIIGTGIEKVTLSVAKGGTTFETTIRLLDKVINTVTPATPTAPVTSPSTGG
TDTIAPTLSNVTSGHIAGGNPVVGRSNENGYLYLVPSATPKTVTSLNQSVAGLFGKKQ
SVTANVDTTMSTAGLASGTIVLYAVDLANNISMASAEIVIGTNQLTVSAPVLSTEKMY
DGTSSATVIADSLTGVAAGDHVTVSAAATYNDAIIGTGKTITVVYTLGGADA AKYIAP
SNYTTQTGAITAAQLTIGEPMLTLDEINGDSSVVVSAGSLVGVPGEDVTVSADAVYD
TTSRPNSALVTVAYTIAGTDSGKYIAPANNTNYTVYVQFSED TGVIIDLITTSKVYDG
NFATTALAGSRNGSCAGIGKQGICPGDDVTVSASGVYDNENVGTNKKITISYTLGSG
AGNYLPPTSIEVNTGVITAKQLMITDPTLILSKVYDGT LAANVT PGVLTNVISGDDVQ
VNAVARYNNAVVGTSKVITIKYTLTGLDAGNYIAPETQMVG TGEITATP"

CDS complement(4130365..4130553)

/locus_tag="EFAGFIKM_03574"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDATMRCPFLLYFSSDFVREEQKKMYTVYIQIWALNSLTDWVLQ
PYFMVSILCILLIFVIS"

CDS complement(4130624..4131034)

/locus_tag="EFAGFIKM_03575"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFIIVATKGSLKWVSGVFQAEDVARQYMDLIPDELKVYHEFIQI
ENITYPFYIIERQHSPFRFLGKDEVISLFDKTDVSEDEDEVHFNIYTVDSDYRPMKPG
TDYMGMLRHDHVTNESIEMYREERTAFLIRRRIL"

CDS complement(4131059..4131580)

/locus_tag="EFAGFIKM_03576"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKMNVQITSILAEQKELFLNLFNLYLYDLSEFSGEDLIEEGKYD
PTNTYLYLERDELHPFLIQYEGKVIGFVLVCSPPYVPEGMDYTVQELFLVKKYRGQGL
AAKAVDLVFAQFEGTFKVEQLANNAAAVSFWKKYYEQHQIEYSEYNIEIDNIAGR
RILSQTFREREREK"

CDS complement(4131773..4132009)

/locus_tag="EFAGFIKM_03577"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNVLNVAFVLLISLAGVVFQGVQVKKKSPVMMYISVIFIVPIL

LFMDWLTLFLPFIAPAALASGYLVKNKDKTNNRTL"

CDS complement(4132042..4132536)

/locus_tag="EFAGFIKM_03578"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKVGLLIVDMQESIVRKKMDQTSASIEHACEYINHVANVLRSD

HVVVHVQDMEGMEEAPPEEYRIIPEVDVNEKDITVTKEASNAFWQTNLEQVLKSHGIE

LVIISGFAAECEVLFTYNGAMERGFRPVMLQNGILSTHPEAVTSTYRDSNVISYPVVD

YLIQ"

CDS complement(4132604..4133314)

/locus_tag="EFAGFIKM_03579"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYLRSEVLLSAKIENRNQYPFDIPAIRSLERLELTNNVTFFVGE

NGSGKSTLLEGIAHQCGFNTAGGGRNNTYETHASESSLGNYLRLAWLPKITNGFFMRS

ESFYQFASHVDEMPASLQYYGGRSLHEQSHGESFLSLFVNRFSSKGIYLLDEPEAALS

PARQLSLLRILHDLSGTSQFIIATHSPILLGYPGAELSFDSDSHIQEVAYEETDHYQI

TRSFLENRDRMLNELFKD"

CDS complement(4133404..4133730)

/locus_tag="EFAGFIKM_03580"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLDRVRKDLRYYLQEHQDRNNLILHYFAFLSAFVAWIFLFIDIK

VTLLALIHIALSWIGHFYEGNKPAAFRYPHIGFYAGFTWFFMKTMEIITRKDIIRP

WLDQSE"

CDS complement(4133858..4134871)
/locus_tag="EFAGFIKM_03581"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTILIPSYEPDVRLNLVLQLQTFKLGPIVIVDDGSGPGYRGIF
ETAEAYGCTVLTHPVNLGKGRALKTGTFQYIKEYGPQGGLVCADSDGQHLPDIIKRIFE
VLLAQTTGPVILGSRRFSGQIPARSRFGNTITRAVFSLTGTGVYDTQTGLRGFPYSM
LDWLNQIPGDRFEYEMNMLLTAHKEGYEITEEFIDTVYLDHNESSHFRPLVDSFRIYM
PILMFSTSSVLSALIDFGLLFVIQYFTHNLFLSVVAARLCSSIFNYTINRKVFSAGR
TSKVRQSLPKYFSLVLLVLLNYGLLYFYNEKLIIPLLAAKLLTEVSIFVFSYWAQRR
FVY"

CDS complement(4134868..4135881)
/locus_tag="EFAGFIKM_03582"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MMKIYEKPTRKDPHKRPISPRKRRWLIITLVIVLAVGGILYSLA
DRYLIRHVQVVADGNTGTPITGNTNDSSNTSTTATEV NATSDDWNYSSDDMKVNIEK
VQTGSSSDQITYYADVQLTDASSLRTALADNSFGTNITENTSEIAAANNAIFAINGD
YYGFRNDGVIIRNGTLYRDSPTRDALALFNDGTMKTYNENEITSSELLAEGATNTLSF
GPILIQDGEIVSDFSSVKIDNNFGNRSIQDANPRTAIGMIAPNHVVFVVVDGRQDDSR
GMTLAELADVMKGLGATEAYNLDGGGSSTMYFMGRVVNNPLGRNQERGVSDILYLTEG
QGS"

CDS complement(4136178..4137134)
/gene="moaA_1"
/locus_tag="EFAGFIKM_03583"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01225_B"
/codon_start=1

/transl_table=11

/product="GTP 3',8-cyclase"

/translation="MTTKNRYKSLELETPGVYELEGLEVGVTSNCNYKCDYCCAYNRD
DGACINSQEVIRIIRELPRLKRVRLSGGEVTLKFQDCLEIVTYCAAHGIDTQLNSNAS
LLTEERILALRDAGLSNIHISFNYTDAESYAAYYRVHPRMYERLEQNIRLCTEAGLET
VLETLLFEGNQANMRAISDKVYDLGVRIHEIQNSIKMPHTDWTQIVSKESLVRVSVTEL
IKHKKPDTTLYFTCMDRFAEHLNLREQPGVYFSNCVDGTKQLHLHGNGDILICELCHP
VVIGNIYTGTSCLKDIYAQQPPALTEFLEKRPCPAYDALFADA"

CDS complement(4137303..4137911)

/locus_tag="EFAGFIKM_03584"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLFMTFLSSSEVTYNRNAVSKPEPASQSTKIFTEDEFQFQIKSK
DITIKLGSTREVVEQQLGTHVDYYKHTNVYQYKDMIIHYKDGIVDGIMIDDPKFKTY
KTPSGIGYGSTVQEVFKQYGKTAFIDTKKGKVKSTYVMEKNKQGNVHVIPSFDHAIL
EGGYENMKVLSMAFDQKGRVSFIMLASHEFAYNPEFNMDDIQ"

CDS complement(4137969..4138538)

/locus_tag="EFAGFIKM_03585"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISSpgl1"

/codon_start=1

/transl_table=11

/product="IS1595 family transposase ISSpgl1"

/translation="MKTIESFFEPFPVLETERTLLRPLTYDDLEDMYSYCVVPVSEF
TTWDAHQSKEDTKAFLDFVMSRYETDLIGPWGIEDKHTKRLIGSCNYLGCDSDNRRVE
LGYVLSQDFWNQGYMTEVVKRRIQFGFDEVGLERIQARCFVENTGSAKVMKAGMRFE
GLLRKYMKVKNELQDLKMYAIVKEDFYSC"

CDS complement(4138620..4139276)

/gene="pdxH"

/locus_tag="EFAGFIKM_03586"

/EC_number="1.4.3.5"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P21159"
/codon_start=1
/transl_table=11
/product="Pyridoxine/pyridoxamine 5'-phosphate oxidase"
/db_xref="COG:COG0259"
/translation="MSDKPIELLQRLKSLSGPFPTWDTGQLLERPGKLFLEWLRLAVE
NEVKEPHAMTISTVDQDGYPDARVLILKNVIDETFYFASSSESRLKGQQLKENPHVALT
FYWPSLGRQIRIRGIAEDRGDEAGADDFRKRSAGARAVAMIGHQSEVLDSEEVLDSSI
EAQKEKISHDPDVVTPHWRLYAVNAQEVEFWQGDSEKHHVRVQYVMQDGQWKSRLRLWP
"

CDS complement(4139315..4139929)

/gene="gpmA_2"
/locus_tag="EFAGFIKM_03587"
/EC_number="5.4.2.11"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01039"
/codon_start=1
/transl_table=11
/product="2,3-bisphosphoglycerate-dependent
phosphoglycerate mutase"
/translation="MKIYLVRHGMDEEGYRGGWSDRGLTEQGINQSRKLGEHLHHHAE
EYNIHTIISSDLPRAVQTTREIEKKLNMQASLMKDWREMNGDLAGMLHKDAEEHYPG
IYFNTLEMDSPFPGGESPRDFYNRISTAFESLFRGLEEKTVESNVLLITHGGVINILY
YLLEKKEWSNKSSFYPMDNTSVHTVEKGRHGWKLSSVNVLSHLG"

CDS complement(4140058..4140564)

/locus_tag="EFAGFIKM_03588"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MEPHIQEQKTDYRPLGVSGLGWLILVQIGLFLTLIFLALQLVL
YCLPMLTTETWELLTSKQSEYYHPLWGPVVIFETVYNALFLVFSIYTIIALYSKKSIF
PRLMIMFYSVSLAVSIIDYLLLLQIPMARELEDGSSLRDIGKSVLTCAIWIPYFIKSE
RVHNTFVR"

CDS 4140922..4141860

/locus_tag="EFAGFIKM_03589"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPIPKVKLLPFADISNYVEGFDIVSTQWGGDGLVYVLLMNQIPE
RERGMFVQSKLKQSYTYKVLIVTDQNIEEVVIWGQTFNYHYVQPLHDHLLLVGARCTN
YGNEQYDLNAKVCDLDGNTIREFLLGDGIQSVQVTEKGTIWTSYFDEGVFGNYGWSDP
IGSSGLLAWDEHGNKLYENREADIADCYALNVVNEKQIWIFYTDFELGCISGGTSEP
NVTFMNPNISGSSGFSTDGYHFLFDAGYRKHGTFVLKKMEKPGRLSKGQKIDLLNEDD
QPFKQARQDFRQHRLLLSEGNLLYRVTMEEITSVLD"

CDS complement(4141880..4142173)

/locus_tag="EFAGFIKM_03590"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MANDKGTLKTCEKGHLYYKSDCPTCPTCEAERKPTEGFLALLS
APARRALENEGITTLLQQLAEYTEKEILKLHGIGPSAMPKLRSALEEEGLSFKK"

CDS complement(4142252..4143199)

/gene="thrB_3"

/locus_tag="EFAGFIKM_03591"

/EC_number="2.7.1.39"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00301"

/codon_start=1

/transl_table=11

/product="Homoserine kinase"
/translation="MNDTQYNLNFELKCNELQLGELISSPKPISGGLHRMYAIETTQ
ANYAVKALNPQIMIRPTAVQNYIDSEKIASVAAEHIHAQPAKRLKGASMHNLNDNQFYL
IFDWIEGQRLEQDEVTINNSSLMGTLADIHKTD FRQLELDSSQATNSKKIDWMFYLN
KGRNENSEWIKILDSNMDKLYEWSMKAKNSSSMLASNNVISHRDLEPKNVMWRQDIPI
IIDWESAGYINPMHDLVETAVYWSVDSAGSINEEKFLAFISGYKKRVGSLTANWEVVL
DIGFAGKLDWLEYSKRS LWIECTDIEEQLVHHKS FGL"

CDS complement(4143242..4143835)

/locus_tag="EFAGFIKM_03592"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQELFKKIINTEVKPVFAKHGYSKKNLNFYKADGNLAYKFNIQR
AKYNTSRQVQFYVNCGVHSTELAE LHSVGLNGDILEFVSHFTCRIREIAPAAPAHYTL
TPDIDPDALSKELVSHLEEGMSFLHSLTGARDIVHYMDKTALHLSEVTFRFLKAGE
TEEAKHYLQQLYAKYGSEKRWTILEKKYAAVFAEYGM"

CDS complement(4143895..4144431)

/locus_tag="EFAGFIKM_03593"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSSLSAELFPALSTSIHWGIIAEFRLNEIVDETLVSNISIIPF
VGDQCWVFQLDNGDWELPGGTLEAGEHYMDGLKRELMEELGAEMRSYQIFGQFYCTSS
ALEPYRPHIPHPHFVRIIGYGDVELVGDPLNPEDGEQVVAVEVVEIDEAIRRFQEQNR
HDIAEMYKLAHMLREEAK"

CDS complement(4144595..4145272)

/gene="hrtA_1"
/locus_tag="EFAGFIKM_03594"
/EC_number="3.6.3.-"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A6QJK1"

/codon_start=1

/transl_table=11

/product="Putative hemin import ATP-binding protein HrtA"

/translation="MRNRLVLQGITQTFEDGGSKRTILDKLDLEVAEGELVAVMGPSG

SGKSTFLSIAGALLEPTEGQVLLDGASIMGKSKQDISDMRLQQLGFIQSANLIPYLK

VEEQLMVVAKLAGTDKNKAEKRVDELDTVGLTHRRKAYAEKLSGGERQRVAIARALM

NDPAVLLADEPTASLDAERGLDIVGMIARLVKEQGKSAVMVTHDERILPLCSRVLFE

NGKLVQD"

CDS complement(4145269..4146399)

/locus_tag="EFAGFIKM_03595"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WG17"

/codon_start=1

/transl_table=11

/product="putative ABC transporter permease"

/db_xref="COG:COG0577"

/translation="MYLAIREMRYAKGRYALIATIMVLVSFLVLFVTGLAQGLAYDNA

ASVKNMAATHFVLEQDSNHRFTRSQVDQDQLNQARSVVGQENAEP LGVKMTTVSPTGD

TKKIDVTLFMVNPEGWLAPT VTEGSPITDQTKGQVVVDQKLS ESGVTIGTVLVDQASG

TEWTVGGFVQNESFSHPVFLNEQEWLALQGSSRTSQGSTDTNANAPMYNAIAIKDG

GEQVDRLSTAMPNTEVITKSDAVSAIPGYKEEQGSLLMMIAFLYVISAFVLAVFFYVI

TIQKTSQFGILKAIGTRNGYLAGSVSLQVLVLSVGSLSISVLLVRLFESILPASMPFQ

LGLSTLALTCVLFILMSVAGSLFSVWKVTKIDALDAIGRTAA"

CDS complement(4146467..4147843)

/gene="hssS_2"

/locus_tag="EFAGFIKM_03596"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A6QJK4"

/codon_start=1

/transl_table=11

/product="Heme sensor protein HssS"
/translation="MRTLYVRVFLITIAVIMVSGMLGFLLSNIYYHTKLKDFNDEKLV
GIATHMKQFVEQQPGTMEQYLNNAAALGYEIVYTDGKGNDQFYGREFREKDLQAVE
LVLNGEVYHGVAQFPSKPFITGFFDNQLSNTVGVHLQLGNANYALFMRPDVILQFGEL
RIFFALIGALTIGISILIFLISTRYLVNPIERLSEATKRVAQGKYNLKLPTARRDEIG
QLAQHFMTMSRELERVDQARQQFVSNVSHEIQSPLTSIQGFAQLVADRDLPQEREHY
ASIIIEESRHLSLLSKQLLLLSSLEQGNEDLSKVKFSLRDQFRQAVQVLQWQLEEKEL
LLRISVPESIQLVGNEVLLMQVWMNLLGNAVNHLPPQGRSIEIHAEQTDNQCVIQIRDT
GDGIAAEHLPLFDRFYRVDRARERSSGRTGLGLAIVQKIIRIHDGTIEVSSSPEGTV
FIVTLPQM"

CDS complement(4147840..4148517)

/gene="hssR_3"
/locus_tag="EFAGFIKM_03597"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A6QJK3"
/codon_start=1
/transl_table=11
/product="Heme response regulator HssR"
/translation="MKHLLLADDDANIRALLRHVMTKEGYRVHEAQDGLEAVKLMQET
PIDLAILDVMMPGMDGLELCDFIRQHYDIPIMLLTARDQLSDKRNGYLKGTDEYVTKP
FEPEELVYRVKALFRRYHRTSSDIIRMNRIVIDRNNVEVTDGQSILFLPMKEFELLSQ
LAQFPGRLFSRDELIRLVWGADYEGDDRTVDVHIKRLRDRFADYTDDFIIQTVRGIGY
KMEVKAP"

CDS 4148811..4149794

/gene="czcD"
/locus_tag="EFAGFIKM_03598"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07084"
/codon_start=1
/transl_table=11
/product="Cadmium, cobalt and zinc/H(+)-K(+) antiporter"
/db_xref="COG:COG1230"

/translation="MSGHHHDQNHGHDHGHNNHANTTNNKKVLLFSFIITIYMIVEAV
GGFITNSLALISDAGHMLSDSIALGIALLAFTFGEKAVNTGKTYGYRRFEILAATLNG
ITLIAIALYIFYEAIGRFINPPEVATVGMLIISVIGLLINILVAWIMMRGSDTENNLN
MRGAYLHVISDMLGSGAIAAALLMMFFGWGWADPLASVIVAALVLRSGFYVTKSSLH
ILMEGTPANVDVNELVQTIKQVDGVKGVHDVHVWSITSNLNALTAHIVVDGTMDVYAS
EILVQKIEHMLEHKEIKHVTLQVESEKHLHDTSVLCTVKGDAPDAHAHHHH"

CDS complement(4149942..4150238)

/locus_tag="EFAGFIKM_03599"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKVLSIVSLIGFVLNFLIIVFIDGSQESA EVAAGLGILGVLYG

LLFSILALIISKRKKTTPVNVHEQLQLGDLKEKNIISEYEFDQKKEKLLSRYK"

CDS complement(4150302..4150685)

/locus_tag="EFAGFIKM_03600"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRSFRFTPYLSFIGFGLVLTLSVNVSFKLGIEKGLDEGALMLL

SVANAVLLVYPLAWGVFGVIEMVLLWKEKQRMKSKLERGKMNKEDFLDQIKKVKTSLR

INISYIVILLFQLGYVIINWDEV DV"

CDS complement(4150836..4151690)

/locus_tag="EFAGFIKM_03601"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLNQLSDSIYYMSNDNDRERPVLGLVCGEKHSLVIDGGNSVQHA

RDFIEEIRCLDVPPVQYVVITHAHWDHFLGMNEFGATIIVNRLTEQRLNEW RDYSFDD

QSLREYVDADIISAHCMEIIQAEIPRESFLLDKPGIVFKDSLQIDLG NKHCMLERIQ

STHTDDSTIVYIPDEKTIFLGDSPYGTCKNKLHFHKQSLNPMIQDIQMYDAEHFLG
HESICDREEMDVFWRELTSNRAVTSTFLEQAITSFEKEQLREPNGNELFFLKAFVND
QLLQAQKK"

CDS complement(4151842..4152225)

/locus_tag="EFAGFIKM_03602"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIVLTSAIVFTVLILIVIMFQVALGVGPWGEYAMGGKFPGKYP

VSMRFACIVQIAILAFMGIVVLSKAGLLWPQWSFFAETAIWFIVAYLVLGTILNLTR

SVWERRIWAPVTLLMLITSIIIAIT"

CDS complement(4152667..4153638)

/gene="iolS_3"

/locus_tag="EFAGFIKM_03603"

/EC_number="1.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P46336"

/codon_start=1

/transl_table=11

/product="Aldo-keto reductase IolS"

/db_xref="COG:COG0667"

/translation="MKQRELGNSDIVSSIGLGVMGMSPGMYGETNDEESIKTIHHAL

EIGVTLLDTADVYGNNGHNEELLGKALKGRRERAIATKFAYTPNYETLNGHPDYVKA

VEASLRRLDIDYIDLYYQHRVDPQVPIETVGAMADLVKEGKVRCLGLSEASASTLRR

AHAVHPISALQSEYSLWSRDIEDEILPTARELNITHIAYSPLSRGFITGEIRKFEDLD

VNDLRRYMMPRFQGDNFAKNIEVVDKIKEIAMEKSCTPAQLVLAWTMANNALPIPGTKR

IKYLEENANAATIELTPDDLARIEKVSPQHEVHGTRYMKEMMTQLNG"

CDS complement(4153664..4154080)

/locus_tag="EFAGFIKM_03604"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P44558"

/codon_start=1
/transl_table=11
/product="putative HTH-type transcriptional regulator"
/db_xref="COG:COG0789"
/translation="MAFSIKEASERLGCPAHKIRYYEKEGLLPYIQRDQHGNRMFEEE
HLDWMRLMSCFRATGMKVSTLKHMVSLALDGDSTIPQRKAILHEYKEELHRRQLEIAE
ALAAVNNKLTIIYEDIETGKLPSESKLLDQMESIGKD"

CDS complement(4154370..4154897)

/locus_tag="EFAGFIKM_03605"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDNKSSLNRLNAWTTSDVLHGDLLASKELIYDKCGFVCSQPYEE
AQNAEYGAYVFTINSLSIRFRVAKTMPKIGQFVTLWQRSEDGTTQPYDGSDPADVYV
ISTRAGSHFGQFVFPKNVLLQRDIISDQGGKRAIRVYPPWDKPASKQALKTQQWQL
DYFLEVPFTEPLNCD"

CDS complement(4154969..4155832)

/locus_tag="EFAGFIKM_03606"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLINPTINEINNLFKMHINEEITEIQSLSGTTAGRVYRLSTSL
NKHYILKSDEREQIHITQQFLDTYKNSPLLPEVLLTDSNTYFIYTYMEGTTHFNRGQ
KRDWLTRLVKELFNTYVRSTDTKSWGRIEFPQRTWKEFNQISIHEAKMNIGSVLTDD
YNLVQSKVDRLFHEEEEEKFLLHGDVGHNFFVYDRNELIGVIDPSPMVGPILYDFLYAF
SSSADDINTETLFATFELLEQVMDKSRLEEALVHLYCRIGLSNKHHPDDLPEYLKA
WHEWKQLCQEF"

CDS complement(4155917..4156390)

/gene="rppH_2"
/locus_tag="EFAGFIKM_03607"

/EC_number="3.6.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00298"

/codon_start=1

/transl_table=11

/product="RNA pyrophosphohydrolase"

/translation="MGMSDYKLNLRDKIGNELIFMPGVAGIIRNEHGEILFGRKHNES
TWGLIAGAIELGETPAQAMIREALEETGLVVEPEKIIGVYGGEARRLTYSNGHQVEYL
TIVFECRIKSGQLTPDNEEMKDLQFFPEDQLPPMANQYPDYIFSSNQEERAHFER"

CDS complement(4156515..4156955)

/gene="gmhB"

/locus_tag="EFAGFIKM_03608"

/EC_number="3.1.3.82"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9KTJ4"

/codon_start=1

/transl_table=11

/product="D-glycero-beta-D-manno-heptose-1,7-bisphosphate
7-phosphatase"

/db_xref="COG:COG0241"

/translation="MNPQVNVQAVFIDRDGTFGGTGHFIHPRDFRLYPNAQEAIMHLK
REGIMVLAFTNQYRISRGEASVEDFEEQFREYGFDSYICPHEQECSCRKPKPGMMLLQ
ASEELGLDLSKCIVIGDVGDTDMLAAHAVGATKIMLRTGWGNLH"

CDS complement(4156997..4157251)

/locus_tag="EFAGFIKM_03609"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTYYFDSKELDTIFEFIWTLVISIICLIVVLIFAAIVRYAIDSS
KTSKKLDVLIKEVHYLKTEIKKLQHHKQQDGSKHIIDEKV"

CDS complement(4157235..4157507)

/locus_tag="EFAGFIKM_03610"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEWTTSTFGYLSIPVFVVGIACYFFPDFLYKIFVLMRYRKIKPN
YEFEDNPPNSDIPKHIEILKVLGTIMVILGIWFWFSKEFYDLLF"

CDS complement(4157543..4158406)

/locus_tag="EFAGFIKM_03611"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKYLTKEWYELCQQTHLHFGLRVHNGAYESDENLFLRLYKRKEK
AHVKQERELYNLDPRFMLEHNGQVMTRVEKAFSGEEVTEEDQMVFHMPPEQRAHIEKL
IAEYDVRPPFDEKKCKEEYKESMEWNFQYKAENLPQEIVEQIADIRVFTLGYCTREVM
LQLNKQSAENRRKMERISKEFREVMMAQDISDEIHGRIQYHDCTVTELLTGDEVVIRF
DTRGGFTNINKLTLVAPEIIKQDGGIVGSYWLYQELYRIDNGYELHVLFEGENMPELI
VRCADILVEEE"

CDS complement(4158549..4158938)

/locus_tag="EFAGFIKM_03612"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLVIEAMFFRNIIYDENGIMKYFLIVILTFILGYIVFLLWRLLF
TKPSITLES DHVISMKHQRYDASQIECIYMNYRRIGIKLYGKRLVPMDLCFYFQRGQE
SAGVEAVHEWAARNNKEIKHKFFQTLG"

CDS complement(4158999..4159493)

/gene="rppH_3"
/locus_tag="EFAGFIKM_03613"
/EC_number="3.6.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00298"

/codon_start=1

/transl_table=11

/product="RNA pyrophosphohydrolase"

/translation="MDGTEHVKQVVPIRCEGVAVVLLKKS LDQYLVMLKRAGRMLHK

EWCYVGGGIEKGEKAWEAALREVHEETGITEVRLYSGNQFEQYYSPMGEYIYTAPV FV

GYVDESQVVRLNHEHTEYQWMTFDEAKENAALPGIDNILD FVEKHFARKAPSEWLRIN

EENN"

CDS complement(4159512..4159898)

/gene="ytcD_2"

/locus_tag="EFAGFIKM_03614"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34533"

/codon_start=1

/transl_table=11

/product="putative HTH-type transcriptional regulator

YtcD"

/db_xref="COG:COG1733"

/translation="MTEHGETSAPKKYKVGVEAALEVMGGKWKPLIIYHLM TGRKRTS

ELRR LIPDITQKMLTTQLRGLEKDEIIQRKVYSEVPPKVEYELTDYGWGLKPALDHLC

YWGE EHLDKIHGNKFKVLEDFDSQES"

CDS 4160143..4160730

/gene="kefF_1"

/locus_tag="EFAGFIKM_03615"

/EC_number="1.6.5.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01414"

/codon_start=1

/transl_table=11

/product="Glutathione-regulated potassium-efflux system

ancillary protein KefF"

/translation="MNVLVVVSHPRKDSLTFQVAQRFAQGLTDAGHGYEILDHLHGIGF
DPILREMDEPDYTQENQVFSPEVETEMKRLKKHDAVAFVFLWWWHLPA MLKGYVDRV
MNKGFAYGTNKLPHQQILWIALSGVTEEQMHKRNYGQSITNLLNVGIADYCGVSQSRV
EFLYDTLESKPEHYEALLKHAHHLGLNYANDIPTP"

CDS complement(4160860..4161501)

/locus_tag="EFAGFIKM_03616"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQTPFIQNHQFNVIQKQADFLKTLRSVDPKVLDTVRYTVSTN
AVGIFNDLTTEQKQLLEQLSTYEKTHELQTYLNQLESYLIPYPQVSAKQIQKLFPAK
KLKVPDLESIDYAHTTYLRWTDIATSRLFIVYPHEGRFLGIEGRITPTNKKGYCMFCH
RHQELGFFNVKTKAHSPDNFSSIAQYVCTDNTACNHSITDITMLEKFLLSTVK"

CDS 4161926..4163227

/locus_tag="EFAGFIKM_03617"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQAALLALNVIILLGIVALYLRKQNGNYLNELRTELEKTKEDVR
RLLVEQATQNRQEANVAAKLNREELAKSIGNMNQSLINNIGEVASQQKNLLDSFSKRL
SDMTAMNETKLERIRGTVEEKLVLQQLQDNNQKLEQMRATVDEKLHATLEQRLGDSFKL
VSERLELVHKGLGEMQTLANGVGDRLKVLTVNKTGTLGELQLENLLDQTLTVEQYDK
NVITKKGSNDRVEFAVKIPDKNNKNQIIHLPIDSKFPLEDYHRLLDAYEEGNSQAISE
NTKLLDTKIKNEAKSIRDKYIDPPNTTDFAIMFLPIEGLFAEVLKPKGLWESIQRREYR
VVIAGPTTLTAVLNSLQLGFQTLAIQTRSSEVWQVLSGVKTEFGKFGDILDKTQKKLQ
EASNHIDQASVRTRAIERKLRNVQELPSAESSQNLLLEAVIE"

CDS complement(4163352..4164149)

/locus_tag="EFAGFIKM_03618"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MRELALDQYHLVLPLLDSIQNKAVYVRSVIDHTQQGRVFNNEER
SPTSVLITSNGGFYGLAGDEEDELFIADVQFMNEESNHPGFFALGVFTTAWANKIDS
YHIRHGKKITRTYYSFNPCKFLKLYSGQDTIVQKPFEYLPLNAVIAQEYRQKFYPYYQ
LVWSSTEQFVEHGIGHFIKKNDQLVSVCTSPYVGGGYAEIDIITIEEFKRQGLASQLG
ILFIKDCLVKNLIPNWSCHSDNLASNELATKLGFEKIGEHPMYWYPE"

CDS complement(4164252..4165199)

/locus_tag="EFAGFIKM_03619"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKVSQVVIKIMKVLTDWFANPIISGAFITLCIFYLTEKEWILY
IYSLVYLICMVKELKGDVQKRKLIFVALFIILLFPSIIKIPILALILSVYIMFKFENL
MKRISYLLSDSKLSTSLINLYLQVAFFMIYLVFMIQIIAPTINIYYFGYLENYKTLI
DNYFTVYFVFLMSIFVGVWIIISLCFSLIKTALLIEAEKVKIQEIIMSYVGILLTFYIV
PDFMFSILYSYSYLLQSEVGIKEMFKFSFSLHHQIALSTALLKYQDAIMQNSLLSIV
EYTHVISNKIIEVTILSTIIISTFSDKVREYIKREHYKK"

CDS complement(4166187..4167059)

/gene="lacG_2"
/locus_tag="EFAGFIKM_03620"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P29824"
/codon_start=1
/transl_table=11
/product="Lactose transport system permease protein LacG"
/translation="MYHKTMPYRIFSIFNNVFLTILSLLCLLPLYHLLMVSLASAPA
NAGLVTFWPIGFTLEAYAKTFANTNFLSSLWVSVERTVLGTGLALIVNTIAAYALSKE
TRVFRARNIYLWYFVITMLFSGGLIPGYILILKGLMNTLLALILPGLVAVFNIILL
NFFRTVPKDLEEAFFIDGAGHFQTFIKIYLPVSPVIATVSLFMMVGHWNAYFDGIY
IRDAEKLPLATFMQTIIVQADMSKLDPEAVANLSQRTIRASQIFISALPILLVYPFLQ"

RYFVTGIVVGAVKE"

CDS complement(4167076..4168038)

/gene="yteP_29"

/locus_tag="EFAGFIKM_03621"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system

permease YteP"

/db_xref="COG:COG4209"

/translation="MEAKLEGKRFPQANVGNKLEKKRKKRYKQPWILHFMVLPAAIMV
FIFSYIPMSGILMAFQDYKPALGFFNSEWVGLKHFRYMWENDYFLQITWNTLFFACTK
IVMNLIIPFVFALLLNEVRKMALKRTIQTLYLPHFLSWVTLSGILIDILAQTGIVNQ
FLVSVFGIKPIFFLGDGSWFRFTIIASDVWKEFGFNTIIFLAALSGINPALYEAEEVD
GAGRWKQTMYTIPALIPIGIVATLALGNVLNANFDQIFNLYSPLIYQQGDIIDTFV
YREGLLSGQFSFATAVNLFKSVISLILIVISYRLAYRFAGYRIF"

CDS 4168208..4170019

/locus_tag="EFAGFIKM_03622"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHIWKRFMFFQGKTRSPFSLFAKINLLIVVLFIPILIMYTYSNN
VTYDVVSKELQISNTKQLTFLSSQIDSRINQMMDFSLILSRDPNVRAFNLNMWDDRY
DRMQTRYVIEKMMMLQTGVTDIWPTRYAVHSQQNKDVIANYNQTTGYDEAYLKKNMSG
RWTYGDQGAASQDELNSFYWFYTDLSLAQPGMLTGSNLVIEASFSYENIQNMLDTYKAG
GQGDPFLYHKGNSPILNRSADKQLSAELIQYLDTHSPEDTTQDVVELNGKNYLVSSVK
STYLDWHLVDVIPLYQILKPISLSQNLFYTCMILLVVGISASILYRNVQYPIKKLI
KGLRRVEQGDYSVRLYSKNQNEFSFLFRFNDMSHQIQDLIENVFHEKIRAREATLKQ
LQAQINPHFLYNCLGYIINMAQMKDEQAVVSMAHNLSAYRYTTRMERETSSLQEEIK
LLINYLDIQKLNRNGRIEYHIDIPEDMLGQSVPRMLQPMVENSVIHGVAKSYSSGEIR"

ITGERLNGFGRIYIDDDGPGLSPEQYEALNLKMQEPLQEEMGCGLWNTHQRITHLFGS

HSYLLFGPSPPLGGFRTEIIWEIPKEDTDSKGNLTDN"

CDS 4170250..4171860

/gene="rssB_8"

/locus_tag="EFAGFIKM_03623"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00958"

/codon_start=1

/transl_table=11

/product="Regulator of RpoS"

/translation="MQMMIVDDEAHWVDNLSMTKPWHTLGIEHVHKAYSAHEALQMID

THPIDIVISDIQMPENTGIELIERIRIRDKKIKCILLSGYSEFDYAKKAIQFEAVDYL

LKPPTDEELMGAVQKAIDQLNNEWEMVSSLTRTQFTLRENLPHLQGRLLL GALQGQRI

AAAEWDRKLANYALPFHTGDAAIMLVRLEEEFGHYDSNDQTLIEYAIINMAEEIMGEF

MEVWGVKEEHGYLVLLQLKDRKGDIGKETILEKLSIQLQSKVKQFLKGSL SIVITEW

FTFPDQLYDRFRQASAYFRQIVGDEREFVMRVSDVETPAAQG PLDVLYTPPTFISLLE

SGQWDAAEEKIRAVCAELDEKWSEWEHCMEAGFLITASFTNIAHRNKLT LTLMGDD

VEGLQSGEVFATISKLRKWSLSVLGKLKEGTSNEIKDIRSEYVKKIQDFTDKNLHLDV

SLRVLADHVNHLPHTHLSKIYKIETGEGISDYISRLRMDRACHKLVT TTKKVEISMEI

GYMDPAYFIKVFKRQFGVTPQEYRDQHK"

CDS 4172210..4173889

/gene="lipO_11"

/locus_tag="EFAGFIKM_03624"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37966"

/codon_start=1

/transl_table=11

/product="Lipoprotein LipO"

/db_xref="COG:COG1653"

/translation="MIKFKKTWWSLLMVIALITITACGSGETSSDNGNNTPGTVGSAE

AEAAFAKGKYDPPIEFSSVLMPKKYVQGDTKENNVHDRWMLET LGMKHKDTWYPANDD

QYRQKLQLAIASGETLPDFVTVPNTAVLTNQLIDSGQFIAIDELFDKYASQTLKD HAT

AHPELWYPFTKDGGKYNMPIMEYTDNDDTLLWLREDWMEKLNLEAPKTIADLENIMDK
FKNENPDGLSPDKVFPLAISLKNNTNTWMGQLDWLFGAYGTIEEQWNKDANGNLEYGS
VNPGAKQALAKLAEWMEKGYIHTDSALWDEGKSAESWTAGKAGILPGANWVPDWPAPD
LLKNVPGSKYKAYPVPAGPDGKIGTKWQNSGVNASIMINKDAKHPEAIFLYNYLLDN
LANPAAGSEYEYGFAGYDWDIVDGKPTSDKEKIKDFSNEFPFLTGPARIPLDFMCTL
VKLADGEKPEPTYEKQMAEFRKPENWYAGKVMSQIDIRKQNYFTGAATPTMVSKWNL
LRQSEMETFNKIYGLPIDAFDQFVANWKSNGGDQITQEVNDWFKSVSAK"

CDS complement(4173990..4174313)

/locus_tag="EFAGFIKM_03625"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDFPPWMQRAIQARLDEVSAIEHDSSELSRVRGETDESFEAMFE

GEDVEQTPGYAEWENRYIVSKGIENERLYMQGLRDGIQLTVSLLGQSMPEENDTKAQS

NNANP"

CDS complement(4174356..4174538)

/locus_tag="EFAGFIKM_03626"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSRLLDLLEEERRKLNQLGEASLKQAIPLWDNPEVQEQSRRVDE

LVARISEMKARHNRVV"

CDS 4174703..4174948

/locus_tag="EFAGFIKM_03627"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKHRQEPPGDKNIIIGSRVVAIRKSKGIKQREFLARLQTLGLDIS

QTSLSRLEGQYRLVQDYEVVMIAALEVSVGYLLGEV"

CDS 4175613..4176212

/locus_tag="EFAGFIKM_03628"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTSLTFYSIPIIVFLFFILVDISNFKWVHLKLRRPSRRFLKGIP

FTPEYELSEVNSDFFRYRQYNLESLQNLEKEITLKSPRYVENNQMSNYILSLVTIFG

LTIASYAIISNSIKFDQNVVVAVTTSSIVVGVAAYFMADLAIKTLNVNLMDRHLIVIR

IVIQEKEKELQREESRKIEREQLRKIRLQKAKKSPLKEA"

CDS complement(4176209..4176460)

/locus_tag="EFAGFIKM_03629"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MELLVEFEFISGDQETRDFVGEDEQRLAKLLTESDWFNIDGRHI

NMRNVKAFRVVSQKQKAEKEEAEQAEHADHLNKILGLSY"

CDS complement(4177049..4178680)

/locus_tag="EFAGFIKM_03630"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNCPKCNKKLSLHTDFITEETCPQCGFYIYIGNTLRIMFIANLK

VNQNEDIYFSNVHQRIYNPFITSYTGEVKKGAIEIVNRYIEDFKALISGYAKEDLYFM

ALALREISTWNVFSDNVWDSSHLRNMSHVFTLIELTEEKYFGDYMITKEEDFISVLV

TCEELFKISDNIKLNDFSWNVTLLEMLKTKIENDRLEWFHDMFEFKELVKPEEIEFE

ENTKLNLYLQKRNLKEMKKLNEDIGKEIEKLYGDFENLDIFRNEIIEISTKHEQIHAI

SPSVDGHFMKCFIFENQFTEMSLPIKKVHNIINYFIYESKGNSKQRLSSPHMDYKFI

FKYENFIAMGLLDSANSITVFKNLAMSDHFVQEMFGSKATMPFKKAQEKISTLIAYKI

ALHFHDKYDYYVPYIEKDIPYVNVKMFQNGVRKKIVNELNQDLGDLDAIVINKLKKE

VIIFEIKYYKPASELTEILKKDKKIFDDIDKIQRRATWVKENMKDIIAAWNLQDCEYI

VKTYLVTARPNYFGKQIETENANINNYFTLDSILNS"

CDS complement(4179132..4179824)

/locus_tag="EFAGFIKM_03631"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSQGLLDKIRRGNSADNPTGYPLEQKVAYLLRENNWVVFSSVEY

IVPPDQQRELDILCYKIINRRRIELRISCKQSSDKHWIFFTEKNRYLKFGSDLKFTPV

QMDNHIYHILPKKLKNFLYQYDRHVTNFTAFSEKKQHEARLVIKDGLLSAINSVHHR

IFPAQLIHDERGTIYFFITLFNGLMFESYYDPESDNNIVQDIEYTQWKTDYESNARFE

EILKYDGTYP"

CDS complement(4179947..4180153)

/locus_tag="EFAGFIKM_03632"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIFHDCQVFYQNPWSDFEIPVKSQWIMRLKSFDLNASWIDETN

EYLLARVEAKRNELQRIHQIFDEY"

CDS complement(4180265..4180621)

/locus_tag="EFAGFIKM_03633"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNRAAQEKLEQFYKQDTPQLQLKSKNELSIQVRTVAVNYIREKK

KDRIIELYKRILSNKGKAGQANEGAINILWLNFEEDSLSVSKNDVYPCYSRPFKDIYQ

TGNFGIWQMPLYGKKGD"

CDS complement(4180797..4181039)

/locus_tag="EFAGFIKM_03634"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEKINELKNMIPeQFRSSIRKNKGDTRSHSIDRMLRVLESEHAS
SHEKKYAEKLLLEVILTIKKRSPEYFKKKLGFKSSTN"

CDS complement(4181250..4181837)

/locus_tag="EFAGFIKM_03635"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKSNYWENLLNPLTLKGNLIKTSMFITAFELLKDRVINHPKTLF
CDDFDSEGWIIENENYQIKILSRNKSPLYASLDWFAEMETISETDIEIFNKLKHYNKL
THEMTDIISQGIDEEYYKLFSDLISFFEKIDKWWILNFELAIDPDIEMEHVDENSVQ
SGSVLMLKVMLDIVFSDEEESWKYYNDFVKTYVNR"

CDS complement(4182044..4183123)

/locus_tag="EFAGFIKM_03636"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSYQKFSLIPGQIEIVTSKGESNYKEVLNDFDSADYIFVTTYNI
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ESIDAFFNFQNHskVILTNNIAYIGSANFSESSNNRETGFIIRDKNLVQVVIDNLVP
IILNESIRYYGNSFEEKLVFSLASRLSASIRIEEESYTYVGRFEEVKNNYWDpQ
LHQESLENVLELLEVEVEEIIYRVNELYETDEFADLIDSESIEQIKILFSQNDHISELA
NFSERNYASDLIAEWNVHNEDMDEAAQQASDQTAERKRELAEAAQEDIENFFLYISKI
QNSFESVITKLKELEEEQKMNI DNT"

CDS complement(4183379..4184227)

/locus_tag="EFAGFIKM_03637"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKDLFGVGKLREQGMETLKMVYPDLLQPSVKKVGVALENVIGLL
ETISLPIKLANVKASALFNNHMKKYQEKLESYNESEIVSISPDIALPIMDRLYLENE
EIGEMFINLLVNASHVERSSKSHPSYFNTLNNISVDEARILKYLHDNEFPSIPFVNYN
ADFDYTEHTMLNLRNVTFLLNQVEFISPERIFFYIANLIKLGILEETRVYSDPEEDE
DITTYNKLDYIYSKGAHEVAESRSNSLELGEYELECIIRGSYQITEYGHFFIEICNSIK
DQEESS"

CDS complement(4184345..4184578)

/gene="xerC_3"
/locus_tag="EFAGFIKM_03638"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01808"
/codon_start=1
/transl_table=11
/product="Tyrosine recombinase XerC"
/translation="MRIHALRHSFATHLLENGKDLLYIQVLLGYTTTQRYTHVSMKNI
HRIQNQLDHMDMEIEHPNNSPFFTKFFFANITV"

CDS 4184777..4185157

/locus_tag="EFAGFIKM_03639"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MINKKLIIVVTLICILLLGFLRWDNLESSADFHYYKYDRWAGQK
WVEFYPPLAASSNSMEFPLIYRDEINQNDIDKYLKGQALSGELVNKWIERTKLTDGYI
GLLLLNLVVIYSSIKIFILRDKK"

CDS complement(4185342..4187147)

/gene="yfeW_5"
/locus_tag="EFAGFIKM_03640"
/EC_number="3.4.16.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01034"

/codon_start=1

/transl_table=11

/product="Putative D-alanyl-D-alanine carboxypeptidase"

/translation="MQMNRGYHTVKNKVIACVLSFIFIIMAIAPAHAAEEKQVETTPSR

IPLSKLEETIDAYVASYEKYTAAVSVAIKDGETIVNKAYGYADIENQRKADTSTVFE

WASISKLLVYTSVMQLVEQGKLDLETDIRCYLPEGFFKKLRYDDPITLMNLMHHNAGW

EDQTAAEVFYSEDETLELGETLRKNEPKQIYKPNISIVGYSNYGVGLAGYIVEEMSGQ

PFYEVVDQHIFKPLHMNDTSIHPTGQDHPDLVQRRNEVEGYTKDLKLIPENRVYLTFY

PAGAAIGPAEDLGKFLAALMPVDDSNVLFKNRDTLNEMLSTSLYEGTSTPRFAHGFV

EMEYWVPTLMHEGNLKGFSKLVDPESKFGMVMTNQSFEIYYYGLTKEIFGANVN

SNRVTSEGGGYFQSARRAASKFTNLFTALDIKKFTKAELSSSYNVVEHNGVVEKISFT

PYIDYLPVSNLKVNLKISLIPVALAIIFSLIALIGYLIRMLINKLHKRGNPTTNFNK

YHLAINFAGVALLLNLFIMQTRLRFPNYPAYSSLRINLMFNLLYVVLAVAYLGLLMYK

LRKNSYSKKQKAMYIMSGISAVILAAFIVGWNLYV"

CDS complement(4187405..4187623)

/locus_tag="EFAGFIKM_03641"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGVRKKYKHKIIRSNRLFYWYVEPDIDDEGIIKLHIVSEDKKLI

VTYEVGQHSNKNKPPFMASLEKNSKAGR"

CDS complement(4187804..4187995)

/locus_tag="EFAGFIKM_03642"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLVNCSEETLHTLLKDLDLIAWDCNEGEGQGLFYEKHFPGDGI

GGGMGEEMLRKDYGFITNL"

CDS complement(4187992..4188180)
/locus_tag="EFAGFIKM_03643"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MERKKDENNQMGVIEHHSPVRHMLNEANGLPNSQFIDSFKKAL
DTPDAYVIMDDKSICLAL"

CDS complement(4188228..4188683)
/locus_tag="EFAGFIKM_03644"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKNQKRSMVLIFLLMILALTGCISSSVKTDKIVEDGLNINSISI
GLGGSEEDGEITVVITYHFNLWNRTNKSILKTVEPIISKEIQERLIDRDIKLDINEKI
DGNTSEALTGTFRLDTEGLDKKGIMKLNINIKEFNIVTEQVVGINEVNN"

CDS complement(4188680..4188943)
/locus_tag="EFAGFIKM_03645"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKTAYILFWTPEQGEDI FSLINNDTIKVEIDRYDHDIEPIIE
SKQLDNVYLKGLRKYSQIRLAIALELANMDLKNEEKKLKEFPN"

CDS complement(4189325..4189801)
/locus_tag="EFAGFIKM_03646"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MYSFIFIFNIGGGFISNDNKPAAFGVAALSILGTIVFLLLGRL"

IYNSNSYIGPSILIIVVTAILTLPVVDVTSNLIGTYQTYRAKPHVESYMNELRTGFVE
TIAPLEFDYNESKTETLRYWSNNGHDIWIKLRKKNETMTSEDLNNVINAYLQLSMK"

CDS complement(4190200..4190595)

/locus_tag="EFAGFIKM_03647"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAYFCLFGDEFDPNHVTSILRIEPTNTAYKGDIINKKKHRIKETS

WTLGTDYEESLDVNHQLIKVVDMIRNKAKEINSIRIEHQLRIKFFIVIRIEEGKTPAL

YFDSDFIEFVNMIHAEIDVDLYANPYNDE"

CDS complement(4190733..4191122)

/locus_tag="EFAGFIKM_03648"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MINSISIDERNGTTFNEEIVMNPTWADSLRFLRKLDGDKFTLVF

IEVSDTGSALVGGGPEYFVVSITMDEHIYTLMNDKQGNSEITLVIGGQLGNYCDNIYI

ELIPMLEVLKYFYETGKLHESHQWKQE"

CDS complement(4191152..4191640)

/locus_tag="EFAGFIKM_03649"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSESGTLHESNGRYVLRFERSFHQNAEDVFLVITKPSSFAQWYP

FATGEMDLRLGGKIAFDDGEGTTYEGTITELEKAYVYGFREVDDLNVNISKAEKGCGR

LIFTHTFNDDSWAVNTAAGWHRCCLDVLVQIINGKPIQWQDNSTELRKIYSEAFKVEDL

NQ"

CDS complement(4191662..4191970)

/locus_tag="EFAGFIKM_03650"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNNINSHNCNLNIRYDLPDEVWDKVSQVYERMPGWIGYKSGIPY
WFGTEGDDVFIEASVEPSGLSFYAQMNSDVWMSWIETFKLEASKVLGFDVGEPEDEGYV
"

CDS complement(4192056..4192280)
/locus_tag="EFAGFIKM_03651"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNEKAKGKLLKQLLFIVLFIFIIGIQLITNNLVNHPPVWTTALS
TFSFIIFCILGLVTYLDLKKQVYKDQEIQL"

CDS complement(4192378..4192626)
/locus_tag="EFAGFIKM_03652"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKWQEVRELFDPDQFVLVSIHYHEEDNKKIVDEVAPIRTVSEQD
ANKEFFRVEPGNVVYHTSNQDFVIHLRKDPLMRVRRNR"

CDS 4192912..4193745
/locus_tag="EFAGFIKM_03653"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKLFTSLLSCLLIVGILSVQVAGASGFSNTTSTTNESGTYVIP
TEDGSTLEVSIEETDKEYIVTSYVNGEKESQTIKNKETRDMMTIDNDGKVEYSNESDY
IEKIAPDPITSNKESFATNAASNWTFVDSAYNSNPVKQWGYLYKQEKITFGETYNLN"

YDSGTKVSIIVGVILGLLTVSSGGIITAILVALGSTIVADKITKAITGQVYGRFAAQD
LEVRNNGKIGLRSKRTIVDAKVINTKNGKVEWVPIRVEGEGRSNTDLCIIGAYNAWLL
N"

CDS 4193835..4194275

/locus_tag="EFAGFIKM_03654"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYRKLIIIASLIEMSFLIFLQYRYNNILDLFPFIGALVFFIVLS

YFLKVQLSKKRREIAFFLQTLFLIFIPIYAITTLPQYTYESAVDKVTQNLEEPYVWNK

QKNTLIEDESNEIKKGYMFSVEKNLEVNSYVFDPWTGNYHKVQD"

CDS complement(4194654..4196396)

/gene="rhaS_31"

/locus_tag="EFAGFIKM_03655"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MPLQEQTSLWSDTTIKMLDGYSGLTQTSSVLSETELTSNVLLLA

VGGEGELAMNGEVCHIGASFACHVAKGTSFTLTARSDELYIVIMYKASSMEGASHAL

PSYRKHPLQTSFIQNPVTQAEWIQNAEKIVAKWRRGEGLERFHANALLQGVICELIME

YERGQGAESDMVDVVVSYISSHYRHNLELKEAALAGCSVRQLQRRFKQEKQLGPME

YVIQLRMENASRMLLHTDASIGEIADKMGYRDMYYFSRAFKKYYGVPPLRYRLAAASE

LDENYAQALLRNRTASSYESAQGPVICHMRGEYQVFESPQRIAVLDVQYADHLLALGL

SPVGSVSGSAVVNFPQYIRAGLQGTEILGTYEYPDLLAVERLSPDLICTEVHDQHH

ERLSRIAPVIMFKRNESWQTILSLFGELTGKRAEAKRILADYHRRTALLSEELAPVLA

GKSVALIRPLDSLVRVHSAAHRTGAVLYRDLGLPVPLFVSDTADTAYHISVDRLPAVQ

ASHYFLLSNELMQDGISATEQRVWGMMLDTAERQQIHSVDAATWIGCYGPMGINGIVDQ

IEQALLGLACLQQR"

CDS complement(4196442..4197218)

/locus_tag="EFAGFIKM_03656"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNLYLSTDLWKETVEDHSILLGEPPEHSVRTIALSELHDEEACR
EYIRWFQNYIDAPDMKVAASMLAKRLGYLWTTPLVTAMTFHHQHLLTFQLENSFLYHPE
LSDHEGGTRFPFLAVNGLQAEELTGDRNVWREKAVQEMFAVQLTPLLKTLAAIAPLSM
SILWENIMVRIGRLFAPDEAETEQUESKIIREDFSYLTQVASGEVFGERKNPLTRFTDC
KDNVHVAKSERITCCFYQMSGHEYCLKCPKIDNEKESQLK"

CDS complement(4197220..4198260)

/gene="yfiY_5"
/locus_tag="EFAGFIKM_03657"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31567"
/codon_start=1
/transl_table=11
/product="putative siderophore-binding lipoprotein YfiY"
/db_xref="COG:COG0614"
/translation="MNHGKKGQVAGSKGYAAHKSRLLMGLMLALILVLTACGAATGTD
SGKKSAATPAETPANAETQTDGAFPVTIKGMKGDITLNEKPKRIAILDVKFLDQMLAI
GEKPAGSVIAGGNTDFPEYLGDPNGVEVLGTRDEPNLEAIVALDPDLIIMTDFQEKK
YESVSKIAPTLVLDIFYEDWRDTLATVAKITDKQDEAEKVRTAYEDKIAGLTKLSEKL
GDETVAIRPRKEGIRVHGIEHRIGGIMYNDLGLKMPAVVQEINEDGSVEISMEKVPE
IGADRYFVLSDELFAAEAEAMVSNPWWKSLDAVKNNRTYDVNSTLWIAYYGPLAINLI
VDQAAEALLGSN"

CDS complement(4198396..4198689)

/locus_tag="EFAGFIKM_03658"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="METKAMNPEDHIQHMLQVIIIEKTQSIIKDSNKQSFGSLEYFLGH
IVEYRDVKQYLTDDEWHIRTPRWLGEYGNTPEEEDLLSDIYRLQAYITETLKGG"

CDS 4198858..4199223

/locus_tag="EFAGFIKM_03659"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRPSMKYGIIVSAVIIVFVPIIIGFYMLNKVIDPDETMVTRTEV
SPELITIQGGFADSIISRYHGYLSHHNNSLYIQIGSKLPIGGSKDFTISFSNTYGNV
DEIYLLGPGNSKKKIWPDP"

CDS complement(4199266..4199850)

/locus_tag="EFAGFIKM_03660"

/EC_number="2.7.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WL55"

/codon_start=1

/transl_table=11

/product="Putative O-phosphotransferase"

/db_xref="COG:COG3896"

/translation="MERGLIIFLNGTSSSGKTSIAMEMKNQGDI PFHLSVDQFLHNY
DQFIDNTYPDMKPTREVEHHVMTDILFDPINSLYCATIKLFSEMGLNVIVDTVISNDK
WFNDFYELLSDYPILFVGVCQSKEELTRREQSRGDREIGLAHSQFDYIYSYDEYDLEV
NTEELSSAACAEKILSYMKSDQEYSAFKKLSRRD"

CDS complement(4199874..4200596)

/locus_tag="EFAGFIKM_03661"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFADLFNRRGITLPATIVEEELEVHLQKQKDYKFFLRMLMQRDEIV
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YIYCIMALTPQSHLDSLMKYIDDEDMYVQERACQIMGFHRYTPAREKLVEVSKKGMHN
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CDS complement(4200652..4201377)

/locus_tag="EFAGFIKM_03662"

/inference="ab initio prediction:Prodigal:002006"

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EVVYEALGDLLRSRKDYNEAIEILSEAYYSIACDYWWAYYLQWPRYQGLQEAENCLYP

YFELYCYGYNLHWTQTKLYIGKR"

CDS 4201519..4202124

/locus_tag="EFAGFIKM_03663"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS complement(4202177..4202656)

/locus_tag="EFAGFIKM_03664"

/inference="ab initio prediction:Prodigal:002006"

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/product="hypothetical protein"

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CDS 4202887..4203420

/locus_tag="EFAGFIKM_03665"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRKLISLFSVIIIILVGIYWYADRELIALKTGSTLPLQWDTPY

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PIESTSINVPLDKIKQR"

CDS complement(4203678..4204322)

/locus_tag="EFAGFIKM_03666"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDLKTYLAEHFPNLTLEPPLFYNNWDVAIRFELGNPLMFGMNTEH

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CDS complement(4204462..4204791)

/locus_tag="EFAGFIKM_03667"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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HNGMFWG"

CDS complement(4205098..4207140)

/locus_tag="EFAGFIKM_03668"

/inference="ab initio prediction:Prodigal:002006"
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PGTFRFEIGVQSTNDPTNELVKRRQNFTKLSRTVNVKASGKIDQHLDLIAGLPEEDY
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QLEDLFTRLHSFLESRNTPHMDIVLGLMKLDYFLGHKYKPRKIWWEDPLQKDQWAGYM
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GVASLTSGDATGSAADGAADMVNGNASRALPMTSAMTAQTVMGARAFADLGLGEKELQ
KHTVLDVLPFRLERVLAGASPLAAKGRTLLVVVYQQHEGQQAQYYTLPLGEEAAAM"

CDS complement(4207546..4209426)

/gene="recQ"
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/EC_number="3.6.4.12"
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/inference="similar to AA sequence:UniProtKB:P15043"
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/db_xref="COG:COG0514"
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LAVAPFVDSLPERPVVAAFTATATPEVMGDILRLLRLQDPQTYVTGLGRDNLAFSVLR
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VMQRVVRKTAATASGTNYGGRRGRDAMPASVNETVFEQLRLIRRDLAKEHVPSYIIF
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CDS complement(4209783..4210076)

/locus_tag="EFAGFIKM_03670"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNESGVKKVMDTLEFLSQDREARRLYEERQKYLHDEASMI EWAT

EKGIAKGIEKGLVEGEKRKAIEIAKNMLSFGIEVSVIAKTSGLTVSEVEALKD"

CDS complement(4210073..4212034)

/gene="msbA_2"

/locus_tag="EFAGFIKM_03671"

/EC_number="7.5.2.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9KQW9"

/codon_start=1

/transl_table=11

/product="Lipid A export ATP-binding/permease protein

MsbA"

/db_xref="COG:COG1132"

/translation="MSNKIEDAAYADDVEMKSSHEKSGAYEINENNENEKSEIEAHHQ

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MPYSWVRRQKSGDVMLRIKEDTKHGAEVVEAIAEGVTVFIIALSLGYLYRADAWVAV

IALVSAGAIWFTARLYDQRIVHLSDEVESREGESQEQIQYVEGIPVIQMYDASPWFL

ARFRTQQQSLNRVQAKLQMTLSMSDNMAMAVFGLAQLAALFLIALSAARGTLSPGMVV

ASSLLFELVWPVLGLSSQWSQM QASVGAFGRISAWLKLAENKKTDSNTKHEELAQG

ICNQDQGNTQKGAHEENEIAMLRQLQVTVTDEESGRKILDQLTLNLVPGELVAVVGAS
GAGKSTLCQVCAGLIEPTNGSVLLGDKHVADYIEMDDQSRLTYMPQTPTFFTGTIEDN
IRLSIDATLEKVKLAQAGLHEYIEAQEGQYAAMLHEKGANLSGGQQQRLSLARLFL
RSSDLYILDEPTSSLDIQTEQNVNMHLLNFMKGSIGLLVTHRMEVARQCSRILVMEYG
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CDS complement(4212027..4213847)

/locus_tag="EFAGFIKM_03672"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q99T13"

/codon_start=1

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/product="Putative multidrug export ATP-binding/permease
protein"

/db_xref="COG:COG1132"

/translation="MFADKRTYTTLGMLTRLWTLTGKYRMFIILLFAACVVSLEVG
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SWVNLPLSLAIIAFTLIYPLVTVGLGQRLQRRHDQLNASAASRDEILTEIIQAPVEIR
SYGLAGYVHHHFKDRMDQVFRHTMSVSVLQRLSEAAGRSTYGGMILILYLGGMQVLN
GHMDVGGLAFLVASSQLTRPIESLSGLWNDFIGSASHASRIFEVLDERKNRVANTG
TNTYVQSDTHLGQLEKQSKPAGINVQHVSRYAEQEEVLTDITFEAMKGKLTVITGPS
GCGKTTLLKLIAGLDRPVTGSIQVMNQKNSLKDMHEVQTGNVNQVYVPQQAFTGT
EENIIFGQEGVSADQVEAAHMTAHDAIMRQSLRYGTELQPQGGTMSGGELQRISLA
RALLRNPDIILLNEPTSSQDPWHEQRLNDLFARITADKGTTVIAVTHRLSLIERADQV
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CDS 4213962..4214855

/gene="rhaS_32"

/locus_tag="EFAGFIKM_03673"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

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/product="HTH-type transcriptional activator RhaS"
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GIEVPANQYAVFKFVCDFHPSLINIDHLDVWTFIDEYWQSHSGYEKSDPYYFERIDG
SLAQDHYGELDIYIPAKQISL"

KHVSQQLPGEYIRSRKLARSLEQLVNLNWKIIDISGHYAFEHEQSYIRAFKQAFGITP
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LQYRKQGAGNLEFTARMTSSMITTLPYGYIFKPMYVRKPAMKLIGQRSHIRYADNEEH
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GIEVPANQYAVFKFVCDFHPSLINIDHLDVWTFIDEYWQSHSGYEKSDPYFERIDG
SLAQDHYGELDIYIPAKQISL"

YEANSAGNDFFEKHFHSHIPNVLQPNVYIGFTNEINQDYSTYQPSVEVTSLDHIPEELD
GIEVPANQYAVFKFVCDHFHPSLINIDHLSVWTFIDEYWQSHSGYEKSDPYYFERIDG
SLAQDHYGELDIYIPAKQISL"

GIEVPANQYAVFKFVCDHFHPSLINIDHLDVWTFIDEYWQSHSGYEKSDPYYFERIDG
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DTTVKTIYRAEHHGNNHLEWESENTLRIENWNEYTNETMTLNIDDEIYDGWGWACKS
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DTTVKTIYRAEHHGNNHLEWESENTLRIENWNEYTNETMTLNIDDEIYDGWGWACKSL
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/codon_start=1

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/product="Protein P200"
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A E A E A E A E A E A E A E A E A E A E A E A E A E A E A E A E A E A E A E

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ADIAVTHRREAGHHSARNVRILRKWIAEEGVAQGRLLFYYAGECYDRQRYAAAARGYA
KLEQPSGYREDRLIACARLAECYERLGEPRKLGALLQSFQYDLPHTDFCCAIAACF
HERQEPVSAIYWYMQAVDVSSRDPGLRPVPMACRTWLP HARLSLCYAH LGNWEQALMH
NTKAREYLPNDPGLLANRQKLEVVRKEMKEREERGEVSPRK"

CDS complement(4217788..4218534)

/gene="COQ3_5"
/locus_tag="EFAGFIKM_03677"
/EC_number="2.1.1.222"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00472"
/codon_start=1
/transl_table=11
/product="Ubiquinone biosynthesis O-methyltransferase,
mitochondrial"
/translation="MANHDRVSEYYYGEINSEDSHEATRTRIHWMCREATGKRILDVG
CSQGITSILLAREGFRVTGIDLEESVRYAQAE LAKESRPVRNNVDFRMLDITQWKVR
TTFDTVLLGEVLEHFAHPETLLIQIHRLLQEDGTLVVTVPYGYHPFYD HKQTFYAGNL
AMTLM PYFEVLKLEVHHKYLCCVARKRRSTQLHMSPTLDQLMEWMELDHVHF AEVEQN
HLRVMKQRKKALDSAVEQVKRLRRQESGEV"

CDS complement(4218521..4219924)

/gene="wbpA_2"
/locus_tag="EFAGFIKM_03678"
/EC_number="1.1.1.136"
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/product="UDP-N-acetyl-D-glucosamine 6-dehydrogenase"
/db_xref="COG:COG0677"
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QANVIVICVPTPLTAEHQPDISYISAAVDGMTPLYLQEGSLVILESTTYPGTTEERVKQ
PIEAANGWRVGEQFYVCYSPERVDPGSVHYGVKNTPKIIGGSTPACLNKQFYGSFL
NEVVPVSSTTVAETAKLFENTFRSVNIALVNELTPACEQMGVNIWEVLNAAATKPGFY
MPFYPGPGIGGHCIPIDPIYLSWAANRQGSELQFIQLADSTNRQMPERVVKRAAELE
QNGVSVQGARVVLGAMAYKKDIDDLRESPALDVYRLLSAAGADVFTDPMVPVFRKDD
GTVLHSCPAVPELWTGADLVIITTDHSGFNYQEMADHAKLIFDTRNATAGCHGVNIV
LGQPVHRVKTGETYGES"

CDS complement(4220000..4220989)

/gene="pseB_2"
/locus_tag="EFAGFIKM_03679"
/EC_number="4.2.1.115"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O25511"
/codon_start=1
/transl_table=11
/product="UDP-N-acetylglucosamine 4,6-dehydratase
(inverting)"
/db_xref="COG:COG1086"
/translation="MIQQQTILITGGTGSWGQKLTEVLLEQDPAEIRLLSRNEYAQIA
MQREFNHDPRRLRFIIGDIRDYRAVEDACRGVDVLFHLAALKHVPVCEDQPDEAFKTNV
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IRGGNVLTSGSVVPLFRRQIDEGKSPTITDKGMTRFFLTRTEAIHLLLKAAEAAVGG
ETFVMKMKACKMTELASVMLEQAGRPSFDYKVTGIRPGEKLHEVLISPFAPRTYQYD
AQYYVILPEHKDKGLTDQYSNLPRVNFSEYRSDSMMNKPATRFLRAGGYID"

CDS complement(4221008..4221697)

/locus_tag="EFAGFIKM_03680"
/inference="ab initio prediction:Prodigal:002006"

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/product="hypothetical protein"
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EMAQVLRFM"

CDS 4222010..4222720

/locus_tag="EFAGFIKM_03681"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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REPYNLNIVTALPFDSYDHMQETLEWIQTNQDTFDVALFSCGVNAVILAERTAALAGK
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CDS complement(4222940..4223347)

/locus_tag="EFAGFIKM_03682"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MGVFLDMRTSMNSGTVGQPGISLGPSPEAFGTIGLQTQGVANPI
ITLNGTVGVTGELGDTFVVELVRGFLYDPFYIIYRAEGTVGQNGGAEFHSFTAQDLA
PPALESVYTSFISGVSTAVRTGPEMLYGIAATS"

CDS 4223537..4224685

/locus_tag="EFAGFIKM_03683"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
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NFLQLHLKSGRNAVK SILGRGQVSVDQKV VTKFNEALTPGQIVYIRKEGAVAAPSLTG
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TSGVMMFAKSEEVQKLQNNWKENVQDRVYVALVEGSAKEEGTISSWLKETKTLKMY
SSSRPNDGQHAITHYKRLKSNREFSLLEVRLETGRKNQIRVHMEDLGHPHPIAGDRKYGA
RTRDLGRLGLHARILSFIHPTTDELM SFETDIPKPFLYPFRAETPPAK"

CDS 4224757..4225323

/locus_tag="EFAGFIKM_03684"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P50838"
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CDS 4225481..4226296

/gene="speD"
/locus_tag="EFAGFIKM_03685"
/EC_number="4.1.1.50"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A7F6"
/codon_start=1
/transl_table=11
/product="S-adenosylmethionine decarboxylase proenzyme"
/db_xref="COG:COG1586"
/translation="MTITPEQRIQLHGFNNLT KSLSFNMYDICYTKTKDEREAYIEYI

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SFDTDIMTMDYRVRGFTTRDTSGRKLFDHEIGSIQNYIPDEIKSSFDMIDVNVYQENI
FHTKCKLREFDLNLYFGYTKDKLSNKEQQEITEWLKLEMDEIYYGKNINRPS"

CDS 4226479..4226889

/gene="flgB_2"

/locus_tag="EFAGFIKM_03686"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P24500"

/codon_start=1

/transl_table=11

/product="Flagellar basal body rod protein FlgB"

/db_xref="COG:COG1815"

/translation="MIETNTTTRRNESLLQALTAQHNAITNNIANADTPNYKKKTVEFQ

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CDS 4227040..4228140

/gene="rppH_4"

/locus_tag="EFAGFIKM_03687"

/EC_number="3.6.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00298"

/codon_start=1

/transl_table=11

/product="RNA pyrophosphohydrolase"

/translation="MAPRHLNGFLGSKVRLAAPCPEDCMRLSRFTDDYEYLRNMDTDI

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RDGMHYDLISMSILAEWSAQSGPLPSFRSTHTPQSGEMDAGGFSQRNGNEQAALSLS

ELSSVPKGESEISPRIGVGAVILNERGEVLLAWRNRQPEQHTWSIPGGKVDPYESLES

AVIREIKEEVNLDIAIDSLLCTAETIQPQQKEHWISVLYFTKVIGGHARNLEEGGAIG

EIGWFPLNDLPSPLACFAVPGLEAVKKLYNQN"

CDS 4228159..4229022

/gene="btr_4"

/locus_tag="EFAGFIKM_03688"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40408"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator Btr"

/db_xref="COG:COG0614"

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RGHFAVNNENYLLLNEGQEYSLHIDSSTSVESFCIFFPPGYVEEIGRNLITSDLQLLD

EPYSYSSSSKMEWVERTYAMDNRLLGAALNHLRNLYSQETLDFWAIAQQLHQLAVHMLD

LHRNVQQEIHELDMIRIRSTREELYRRVYIGHEYISAYYDQPLTLEQTASAAQLSVNHF

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CDS 4229092..4229619

/locus_tag="EFAGFIKM_03689"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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GYASHYGQAEVRLLEHGADVNALSHSKISFIPSENTALHAALAGERSPEVIGLLEH

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STASCLRAAITAHQQ"

CDS 4230020..4230535

/gene="sigV_3"

/locus_tag="EFAGFIKM_03690"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O05404"

/codon_start=1

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/db_xref="COG:COG1595"

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DQLETKGDVPS"

CDS 4230532..4231848

/locus_tag="EFAGFIKM_03691"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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KKLPVAFSYSSLNPASESGIYEDKIDISFIESLPPHELTVIFKERGKEPNKWKVTFP
VDHSLTKGMKRIIPVNQTMNVDGQLIHVKQAVLYPTRLVLDIEYDRNNTKKIFGIRDL
HLVDEQGRAWRTDSSSIGGSGSSVFFESMYFSTPKKLTQGSGLSAVDKGELVISIDP
SSGEIQGGPSSLKLLQSTVQGKNLILEFSIADSQNATSGLSFTNIEDSKGNPFDINEV
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CDS 4231959..4233002

/gene="mccF"

/locus_tag="EFAGFIKM_03692"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q47511"

/codon_start=1

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LGFDVLESPSLRHNIKCVSASKEERAEMNEFFRNPNIAIIPPWGGEFLMDILPLLD
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QTKYGGQITQSSSTHYQSAWKPESPGFNLDTPSQWKQLGHSEADTAVSFSGRLIGGC"

MDTISSLIGTPYAPVQSYLDQYCADEGTIWYLESCEMNAGDIYRHLWQMKQAGWFAGV
KGFMFGRPAGYSdTADFNFTDALSSALGDLDPVLYDVLGHVPPQLTFVNGALGKVA
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CDS 4233058..4233372

/locus_tag="EFAGFIKM_03693"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MCIMSESTSTPSTRVVYQANQPMLQSVQSVRNMLHHTARQHVGK
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CDS 4233557..4234369

/gene="yjjP"

/locus_tag="EFAGFIKM_03694"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ADD5"

/codon_start=1

/transl_table=11

/product="Inner membrane protein YjjP"

/db_xref="COG:COG2966"

/translation="MEYIRHDSSPVSAETGMIGSNPTEQSRVIAICLLAGKIMLQSG
GETYRVEDTMKRMAAALGLPHSHSYVPTGIFFSVDATEPAKLIRISERTTDLDKVSE
VNAVSRRIGQGELSAQEAHDLLIQIEGKPSSYSTAVQLTAAALSSGCFTIMFGGGWSD
FLPALICGGIGYAAVIAFHRLVRVKFFAELTASFVIGLLAFFLIYMGVGHERDKIIIG
SVMPLVPGLLITNAVRDL MAGHLVSGLSKGAEFLTAFAGTGIAVVFSLFM"

CDS 4234388..4234846

/locus_tag="EFAGFIKM_03695"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLHFIEQALTSFVASAAGFIIFNAPRRMLLHGGFVGMIGWIIYI
VLEYAADAVPATLAATIAVGVISQVFSRMFRAPVIIFSVAGIIPLVPGGLAYNAMRSF
VQNDYSAAMEMAAKALMLSGAIAVGLVLSEVLNQMIRRI PASLRAKSSSK"

CDS complement(4234965..4235510)

/locus_tag="EFAGFIKM_03696"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MNYKYRNSELDTSSLQPKNGIRPERPGISGLGGWLILIQIGLWV
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VLLYKKKRKFPRMMIILYIANVFIGVMTWIMIARIEIPREQHVLDPTSAFNLTIRSLL
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CDS complement(4235625..4237493)

/gene="pbpF"

/locus_tag="EFAGFIKM_03697"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P38050"

/codon_start=1

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/product="Penicillin-binding protein 1F"

/db_xref="COG:COG0744"

/translation="MLKHMGRWMMYYVFDAAVVVLMMLTLFYLYLITYGEGILNRNPE
AMQVASSTIITNAEGTEISRLHTQTKGYSEYADLNAMPDLLKMAFLATEDRRFYNH
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MALEKKYSKDEILEMYLNQIYMGRQQYGVKAAAWRYFGIKDMHQLKLWQIAT
LAGMPKGPISIYNPVDHPELSKQRRRAVILGLMHEQGLITRKQMLQARDVEFT
PPETVLNATTSPGLSEPAYVSAVDAVIQEASRLTGKSEAEIQSAGWVIQTGL
DEQAQLAMEETFADAARFPDDRQDEQVQASMVIIDQHNGEVKAMMGGRNPL
KGGINRAIMDARQPGSSFKPIIAYGPALESGKFKPESILPDKRMQYGSYQPS
NLGGRYSGSIAMSQALQRSINAPAVWLLHETGLNDAHQFAARLGIELGKEDLN
LSIALGGVHQGVSPMKMAQAYTVFANHGKLNHTAHLIREITDSQGRTIFAHK
SENKQVISSSTANAMTRMLQNVVSQGTGSRAQLGQHKVAGKTGTTQAALP"

SVGREANRDLWVFGYTSNWTAAVWMGFDHTDEEHYMWSGSGVAAELFATVMRRATQ"

CDS complement(4237598..4238227)

/locus_tag="EFAGFIKM_03698"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKSQFSTVRLRYIYIGGASALLSAALLFVVYHVLRFARNHVLDP

AAWITRMMNWGINHIGTKPLFIFIGGVFAIFFWIRSQKIAEDLSQLARGTAELALGH

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HLEEDKENTQSISIQVDLPKLTLYGIQSSLNEIIQGRCQDEVEVQHWV"

CDS complement(4238326..4239459)

/gene="rcsC_10"

/locus_tag="EFAGFIKM_03699"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00979"

/codon_start=1

/transl_table=11

/product="Sensor histidine kinase RcsC"

/translation="MNSKLINTVRWKFIYAFLLSGILTAVILYGSSQVGQTILEAQTY

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GELSHRIEVKTSDEFGVVAASINQMAEQLQLSLQEERNAVAANKNDLITGISHDLRTP

TSILGFLEYIEKDRYQDEIEMRYYSIAYEKSILTLRKLIDDLFEYTRVSGGSLPLSLQ

ALNLNSFLMQLAEEFAPMLEDAGMTYKIIGGQDPLWIQAAPGELVRAYENLFSNAIRY

GSQGKRMEIGLALEGEEAVVRISNYGEPIPAQDLPHLFDRLFYRVDKSRSRRETGGTGLG

LAIKSMIELHRGSIVAYSENGRTDFVTRFPVTAAPPSNCSEE"

CDS complement(4239515..4240219)

/gene="phoP_4"

/locus_tag="EFAGFIKM_03700"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P13792"

/codon_start=1
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/product="Alkaline phosphatase synthesis transcriptional
regulatory protein PhoP"
/db_xref="COG:COG0745"
/translation="MAQPATILLVDDEQEIIKLMEIYFGNEGYRILTANDGLEALEQL
KKESIDLIILDVMMPNMDGIEACMKIREEQKMPIIMLSAKSMDMDKITGLSIGADDYV
TKPFNPLELVARAKSQLRRYHTFNEGRENKEHEWVIDDLVINTDTHEVWVDEQPVRLT
PREFAVLELLARHQGSVLSMEQIYRQVWKEEFMESNNTVMVHIRKIREKIELDKHPK
FIQTVWGVGYKMIKPQ"

CDS complement(4240246..4241202)

/locus_tag="EFAGFIKM_03701"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQRHNTWNASMDNTLIDRLKQIPELDQATRIEPIMKGYSTDAKF
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SYIEGEDASERLPQLNEQQQWAVGFEGAQLQLIHQLPMEEQIESWYIRKSTKHQRYV
ERYKQCPIVMKEDHAILTFIADHLGWMKNRPDGFQHDDFHPSNLVVKQDKLAGVIDFN
RYDQGDPIHEFLKGLFASEISIPYSIGQIQGYFDGNEPDELFWRLYSLYTAMALVSS
VWVIQVQKPEDTLEIMAKIERVREDHDDFRSFIPRWYTLNRS"

CDS complement(4241310..4241768)

/locus_tag="EFAGFIKM_03702"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MIQSFAKHIDVAVTSLIDICDQLSEEDLALPIEGKRPVGELLA
HLSVICRADVYISEGASEEEMAQFYAENQVHSLGEIKQALIDNQMYLYQRYRQFNTEE
LLHVTDSYWGASYSRLEWLLEIMGHVYHHRGQLYTMLTLTGKEPESVLFK"

CDS complement(4241953..4242894)

/locus_tag="EFAGFIKM_03703"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIKPEQCERLTRKARKTLEEYGLGVAADLLLSSSRWGIRLDVST
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RGMLYFFIGTDESACPIEHRVIFEPSSHNLIRREPEGDTALDGAPFVAHSVTVLPNLE
FPTYAYIDAAALNELSPALLETDEAEAEVSLYDRYLEFESSWNHPSTLNWGGMFGYPD
GQHPDAEHRALLQIALGEEYDYNEKECEKKLTKEYYGDEDRTWQELSHTLLLLKIDTH
DAIGFQWRDCGELQFFIRKSDLEAGRFEQTYCSLYSS"

CDS complement(4243044..4244333)

/gene="nrgA_2"
/locus_tag="EFAGFIKM_03704"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q07429"
/codon_start=1
/transl_table=11
/product="Ammonium transporter"
/translation="MTLETSTGIDTVWVVLSAAMILLMEGGFALLEAGFVRYKNSVN
IIMKVFADITIGTLLFYAIGFGLMYGSDVGGFAGVTGFFLNGDLSHLDVPVSLETFWL
FQAAFTIAVISIVSGAVAERINFRAYLLYIILMTAIIYPIGGHWAWGGGWLSQLGMQD
FAGSAVIHALGGFSALAAIIIGPRKGKYTPLGVSAIALPSNLPLASVGAFLLWFGWF
GFNAGSTLSATDVRIGHIAIVTMLSAASGGAVTLLYTLFRFNRS DAPSVINGSLAGLV
GITAGCAFVGDVAAIFIGAI SGLLMMAATNWLD RRQIDDPVGAFPVHAASGMWG TIAV
GLFATDGGLFMGGGWRL LGVQALGLTALVIWGFAMTWIGLKLIGKIVPVRSTEEEEEDL
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CDS complement(4244330..4244749)

/locus_tag="EFAGFIKM_03705"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MLVIDEVYHHTALQISSDLLYLIERLKVKKENEIETLKKKIEQ
FEQKRRAEEIAYQSLSPVRKWFAGRPASHHQAVEYMVQVKERFRKMEQIRRRIRELDQ
IAERIKHSDSIERDEIELAPDTIRELRQLSETEDVQA"

CDS 4245036..4245527

/locus_tag="EFAGFIKM_03706"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MFTRNDDIRNQIWEAVSGLEEEQLNRKPSPQQWSIMQVLRHLNL
MENVIGKQARMALEKEQTVSVDKKPYELSLDRSRSEAPPHLQPPAAPEALADVRS
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DESHQTLNNFALDHPDLLRSKSFHPVFGEMDLTQWIDFTSYHEERHLGQIQEIKQQ
LGV"

CDS complement(4245655..4246158)

/gene="ywnH"
/locus_tag="EFAGFIKM_03707"
/EC_number="2.3.1.183"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P71043"
/codon_start=1
/transl_table=11
/product="Putative phosphinothricin acetyltransferase
YwnH"
/db_xref="COG:COG1247"
/translation="MKLEDVQIEYARLEDLPRIVEIYNSTIEGRMATADLEPVTVEQR
VPWFEEHSPDHRPLWVMKQAGQVVAWASISSFYGRPAYNGTVEVSVYVDQQCRGIGAG
GRLLETVFAACPALGITTILGFVFGHNEPSLGLLRKRGFEQWGYYPEVAVLDGVNRDL
AILGKKI"

CDS complement(4246266..4247366)

/locus_tag="EFAGFIKM_03708"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNREGHLKSEQNTHSKLQNKKGWKVLAITLGACVILSACGNSNS
ITSDQAEQQSAEQASNNEASENSNQEQQSSSEVS AVVTPDNFIDTLMNGSKDAIYNQF
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ENQIEGLSIQPLQAHEDTDAKFTKTEFQLPMKGEWYVFWGGNDVLSNYHYEHETQRYA
LDIVRTKEQSSYQGD AKENQNYAFGEPLYAAADGTVVDIKNDIPDNVPGVMNPKEPA
GNYVVIDHGNSEYSITGHIKEGSVSVKKGDKLKQGDPIGELGNSGNSSE AHLHFQVSD
GPD LFTSR SINIRWADQSQQLTRGNTIQGLAE"

CDS 4247587..4248348

/gene="regX3_2"
/locus_tag="EFAGFIKM_03709"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P9WGL9"
/codon_start=1
/transl_table=11
/product="Sensory transduction protein regX3"
/db_xref="COG:COG0745"
/translation="MDNVSLLLVDDEQAILHMLKTVLLKEQFLDIDTVTTGEAAIEAC
NNKTYHCIVLDIMLPKGSGLEICPFLRQVTDAPILFLTAKTTDYDKLTGFAVGGDDYV
AKPFNPLEVVARIKSLLKRYLSSKTAATSDHVPSNVNTSSPSTSEGVYDFGRFQVLEW
AGELRVEGESVSCPALVFQLLFFCKHPNRIFTKSDLYERVWGSE AISDDNTVMVHIH
RIRERIEADPSNPVFLVNV RGLGYKLIQPEYVSRP"

CDS 4248345..4250105

/gene="sasA_14"
/locus_tag="EFAGFIKM_03710"
/EC_number="2.7.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01837"
/codon_start=1
/transl_table=11

/product="Adaptive-response sensory-kinase SasA"
/translation="MSIRRLMTRFIGMLAGAVVLIILLGSVATYWWVQKVNEVNLVD
DFAANGLDQLINTAEIMPDDTIRYDPELLKQVDKNKGWLQVLDEQGYAIDAYHTPADV
PTHYKPGELIAYWESQKPFYQIVMLIREKNGKDFTLLYGERNPAKSLMNNIRSDLAF
TNGKLNLPNQQEALRTANAYLQILDPSGREISSFNKPSMGVPTEYTIQELVLQVRYP
SRSGLSVATWYDEQSETTWLISIPVDPVNSGQNPYNFILEPALVVLIVSIILLILL
AFWYANRFGSPMLHMLQWLQRLERGHYEPTGAFGVPRSQRNGKWKRKYNVYAEVLR
SMQALSHTLKQDEELRKQTDLSREEWIAGITHDLKTPLSSIQGYAHMLEADKYSWTAE
EVREFAGIMLDKSMYMDRLVNDLAMTYRLRSGGYQPLVEETDVNTLLRDLIQAERNP
AYGEGRILFQPSEVPVYGLVHIPSFERIVDNLNALLHNPPESILVSVHSGKQADE
FSIQFADNGRGMDSMVWKLFFERYRGTDTGTSDVGSGLGMAVTKGLIEAMNGRIEVQ
STPGEGTIIRLIWDGPSETN"

CDS 4250578..4252578

/gene="thrZ"
/locus_tag="EFAGFIKM_03711"
/EC_number="6.1.1.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P18256"
/codon_start=1
/transl_table=11
/product="Threonine--tRNA ligase 2"
/db_xref="COG:COG0441"
/translation="MSKQENSNSASNKSGNEINNQANDLQPSSHSIEVRLQGGAVRSY
EAGITVGAVASSISKSLGKQAIGGIVDGQNVLDLWVLKQDCELVIVTLESAEGLYR
HSSAHVLAQALKRIYGAEQVKLGIGPVIEDGFYYDVDLEHALSISDLAAIEQEMNKII
QENHKINRRVVSREEALRIFGEIQDPYKLELIQDLPEDAELSIYEQGEFFDLGRPHL
PSTGRIKAFKLLNVAGAYWRGNSDNKMLQRIYGTAFPNKAQLDEHLHMLEEAKKRDHR
KLGKELELFMFSEEAPGMPFYLPGMTVRTELEQFSRELQLQEGYQEVRTPLMMNNRL
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HRHEFSGALNGMMRVRTFCQDDAHLYVMPEQIEDEINQAISLIGRMYDIFGFYKIEL
STRPEDSMGSEELWDQAERALQNVLDRRGVEYRINEGDGAFYGPKIDFHILDALKRSW
QCGTIQLDFQMPEKFDLTYIGEDSLKHRPVVIHRAIYGSIDRFILTEHYAGAFPLW

LAPVQVKLLPVSDHYADYALQVQSQLRAVGIRVETDLHSEKLGYKIREAQMEKVPYSL
VLGENEKNASSASVRAYGQGDQGIQRIEAVIEMIQQAVKAKV"

CDS complement(4252626..4253489)

/gene="fabG_8"

/locus_tag="EFAGFIKM_03712"

/EC_number="1.1.1.100"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P73574"

/codon_start=1

/transl_table=11

/product="3-oxoacyl-[acyl-carrier-protein] reductase"

/translation="MSNQTAIVTGANSGMGLATTIELARQGYHVIMACRSEKRGQEAL
QEAVRQSGSSAIELMLCDLGSLESIRQFARTFRERHDRLDVLVNNAGVVMVKRKETSD
GFEQSIGINHLGHFLTLLIEPLKAAKQGRVNVSSGAYKAGKIHFEOPHLHKGYNP
IKSYAQSKLANVLFTRALARKLSGTSVTVNCLHPGAVGTSIGVDRNTGFGTRIMAFAG
KLPFFLSPEEGARTAVYLATSPEVVGITGRYFYQQKEQQLKKHAVDDASAERFWTWSE
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CDS 4253594..4254136

/locus_tag="EFAGFIKM_03713"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLTKEDFKLKKQAKLEIALLEQEYQEILQNVDSTLYEKYGILD
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NMEIIQAELSKEFIALESEKEHFAEALSLVFQTRNKLVDNFSFVSIVKDGSNEEETF
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CDS 4254193..4254924

/gene="gloB_2"

/locus_tag="EFAGFIKM_03714"

/EC_number="3.1.2.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01374"

/codon_start=1

/transl_table=11

/product="Hydroxyacylglutathione hydrolase"

/translation="MSYPLTSITVLNLQIPTSGNSPIFPVMLRDEDGVTLVDTGMIG

QFAELQSALEQEGVQLSDVKRVIITHQDIDHIGNLGALLDAIPDLEIWAHADEIPYLT

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GHTPGHICLYFGEQQFLAADELRVVDDELVGPAPQATPDMPEALRSLKKLTDLKLNK

VLCYHGGGEYMNDPAQRIATLAESAE"

CDS complement(4255699..4256910)

/locus_tag="EFAGFIKM_03715"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNNRVTVPPLYASLLSVALLTASCSSGEPSTGGTEQTSQQGGTGQ

GQTANGGNTGASGNESGAQGEAVIPYQASVLVEGLNAPWEIVSPDGRMFVTERPGAI

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VLRLKVNDGKAVIDQELGNIPGGTNHNGGRIKIGPDEFLYITTGERYEPELSQNEDS

LGGKILRIGLDGSIPADNPWPNSPVYSMGHRNAQGLAWNPNGYLYSTEHGQRNHDEI

NRIVAGENYGWPEVEGDNDNGAYQAPLAHSGKDTWAPSGVAFVEEGPWAGSLIAANL

RGEQLLKVTLSEDGTQGEKVEPIFEDEWGRIRNVSAGEDGKLYVLTNNRDGRGSPRDG

DDKLIVLTPE"

CDS 4257149..4258261

/locus_tag="EFAGFIKM_03716"

/EC_number="3.4.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A552"

/codon_start=1

/transl_table=11

/product="putative peptidase"

/translation="MERWTTTLMNQNPISRLEADLSGQGLDAMLITDPKHIYYLTGFA

SNPHERFLGLVLARGEPELLIVPALDAEAAVAASSVSNIATHTDNDNPYALFDYQGR
LGRVGLEKEYVTVARYEQLTAALGAASFEDVGPLLRTLRLVKKTPDEVARIRHAIYLIE
ETLRQGLSHVRTGVTEIELVAEMEYQMKKLGADGPSFDTMVLTPGKTGLPHGTPGERK
LQHGDLLMFDMGVYAGGYASDITRTFAFGDISPELKIYNTVLAANEAAIQVVKPGIT
CAEVDRAARQVTEEAGYGDRFMHRVGHGLGIDVHEYPSLHGENMDILNEGTVFTIEPG
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CDS complement(4258552..4258905)
/locus_tag="EFAGFIKM_03717"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MYSTLRYTLESNGTTYENDSINASLLVELITNLELQEYVVLKPS
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LPQLESWQDITHEFD"

CDS complement(4258990..4259685)
/locus_tag="EFAGFIKM_03718"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_02088"
/codon_start=1
/transl_table=11
/product="queuosine precursor transporter"
/translation="MYVFMFNLGWGAVFVLVTYGFLLCYRLF GKKGLYAWIGVATVI
ANIQVTKTIDIMGIVLT LGNTMYVSMYLTSDLLNEKYGPGEARKAVWFGFFTLMITTV
LMQMVLVYFDPAPTDF AQDSMKTLFGLLPRLALGSLTAYFISQFLDVRLYSWLRKVAPG
RNQLWIRTNGSSIISFVDTLVFCTIAFAFIYPWDVWLEIFLTYYIIKFVLTAVGTPF
LYAARSFKFKDEA"

CDS complement(4260049..4261446)
/gene="tcyP"
/locus_tag="EFAGFIKM_03719"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54596"

/codon_start=1
/transl_table=11
/product="L-cystine uptake protein TcyP"
/db_xref="COG:COG1823"
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GVILQLVYTSGSDVVTKSVDWFNLVSGGYVRLQMVVIPLIMVSIISAIMNLKGKQNL
GKMSVSIIAILLITTAIAAGVSIVTSLGFNLTSIEIQGGDRENAQIQKVEERLVDVKD
QTIPQQVLEFIPSNPFADMTGERRTSTLAVVIFSAFIGVAVLGLDRKKPQQAETFRGM
VNAVYAVVMRIVTLVLRPTYGILALITKVTTATNAEEILKLIKFVIASYIALAVMFI
IHLIIISLSGFNPVTYLKKVLPTLVFAFTSRSSAAAIPLNVETQTKKLGVSDGIANLS
ASFGATIGQNGCAGIYPAMLAVMIAPTVGIDPLSWDFIVTLILVVMISSFGVAGVGGG
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TFNDQSRELDSAAQA"

CDS 4261799..4263499

/locus_tag="EFAGFIKM_03720"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MFRNRTVAGKIRGTLFLVLLVASLLFSISFYAVSMNIIQSYVLP
QFDKVLNTSIQDIYKNTSASKILQVQSGGAGSEGAAMTVESYLADKAKEHNLDAAVW
AIQDGSAAKVVANSSSGMKAQDEISVEPAMNAAIENKEMVISEVYSDSFGVHKAAPF
IAGSNMIMAVSMDAQFIQDKITQIFWLCLGITALVFVLGWLSTSMIKRVTKPIIKLV
QHASKQISQGDLTAELEIKGKDEIAQLAASFQTMTHNLKEMISRALSTSNEVVSGSNDL
LQRVESMSGMVRNSSRSAEDAEKGSISIASSASENARAMEEITQGIMHIASSSAEVSD
QIGEAANEAVNGNRLAQNAIEQMERYGQTASESLRYVETMNERVAIGTIVASIFEIT
KQINMLSLNASIEAARAGEHGRGFAVVAGEVRKLAEQSKTATEEISDYLGTIREDAER
SVDAMNRVTQEIGSGTTVVQQAGSAFQQLNELIQNVNLTIQTVSASTQQVSAGAEVVS
ASVEETAQITTKSRESMLQIASTADLQLSEMDSHSNTVRHLHEQAVELQSAMKNFKIN
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CDS complement(4263626..4265206)

/gene="cobQ"

/locus_tag="EFAGFIKM_03721"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WP95"

/codon_start=1

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/product="Cobyric acid synthase"

/db_xref="COG:COG1492"

/translation="MEDRPSQPAAVLMLQGTASDVGKSVITTALCRIFKQDGFKPAPF
KSQNMALNSYVTEDEGKEIGRAQGAQAEACGIEATDMNPILIKPVRDMHSQIVVHGVP
FAQMSASDYRQHFLPEAKHTVMDALNRLRETYDIVLMEGAGSPAEINLKDRDIVNMNL
AGWADAPVILISDIDRGGVFASIVGTLELLEPHEVARVKGFIINKFRGDLSELLQPGLD
WLEERTDIPVLGVLPIYRDIQIEAEDSVVLDSMRHGKSGKTELDLAVIRYPRISNFTD
FDALSREPDVNVRYVTSPEELGSPDAILLPGTKDTIGDLAYLRESGLEQAIASQTERE
HVQLVGICGGYQMLGRHLKDPFAVEANQIQEAKGLGWLPLSTTFLQEKQTVRASGRVQ
PDHPIRLYRERDVTASLPVNGYEIHMGVTECHEPERVTALFEISHPGGQPFQEGWGS
EDGSVWGTYLHGLFESDLFRRSWLNGLRAGKGLAPLHETYSVHERKEMEFDRAESLR
SALDMKRVEIMGVQAPE"

CDS complement(4265297..4266187)

/gene="cobS"

/locus_tag="EFAGFIKM_03722"

/EC_number="2.7.8.26"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P36561"

/codon_start=1

/transl_table=11

/product="Adenosylcobinamide-GDP ribazoletransferase"

/db_xref="COG:COG0368"

/translation="MKDGTAPAPQRKHAAAAAFQFLSRFPVKMQIDFVPPLLRESVVFY
PLVGAAIGLCVWLALGALSGAVLPALPAAVLTTLWWLTGGLHLDGWMDTADGLLSYR
SRERMLEIMKDSRVGAMGVIACVLLLMMKAALIADFIARGHWVYGALLILPMIWSRWF
MVYAMSAWPNARGDDGLAVLFKGLGERKEVQRRSSAVGLTLIAGAVTFAAVWLFPKD
MGIADAMVSGLGLTPWWLYPVTAVIILPVACYIIGRFVAARISERLGGLTGDTYGAMN

ELLEAALLTVLSVLQGLFWL"

CDS complement(4266184..4266744)

/gene="cobP"

/locus_tag="EFAGFIKM_03723"

/EC_number="2.7.1.156"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29931"

/codon_start=1

/transl_table=11

/product="Bifunctional adenosylcobalamin biosynthesis
protein CobP"

/translation="MSVLVTGGARSGKSSFAERLCMQRSSEAWYVATAQAYDDEMRER
ISMHQHQREASGYLWHTMEEPIHLPALISRMGEGHTGTSAPTILVDCLTLWLTNVLLA
HEYDEKQVLQAHLDALVEAIRTPGLLVLTNEVGDIVPEYALGRKYRDLAIGILNQR
IAAICGEVFLVTVGIAIELKSKEYRL"

CDS complement(4266741..4267862)

/gene="cobT"

/locus_tag="EFAGFIKM_03724"

/EC_number="2.4.2.21"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7SIC7"

/codon_start=1

/transl_table=11

/product="Nicotinate-nucleotide--dimethylbenzimidazole
phosphoribosyltransferase"

/translation="MNNEQVLEHLISKITAPDQQVAAETSAHVDSLTKPPGSLGKLEE
LVIRLAGMTGNARPRFDHRAVIVMAADHGVVEEGISAFPAEVTPQMVLNFLAGGAAVN
VLARHAGAGVICVDIGVNADLEHPDLLSRKIRKGTANMARGAAMTRDEAVRAILAGAE
VVS AEVAKGTQLFVTGEMGIGNTTASAAVMSALTGVAPAAAVGRGTGIDDAGLQRKAA
VVS RALSVNAPNPEDALDVLCVGGLEIAGLTGVILAAAAHRCPPVVDGFISTAAALV
ARQLAPLSTAYMIASHTSHENGHGALLRELDLKAMLDLDMRLGEGTGGVLSLHLIDAA
CLILNEMATFASAGVSDGASHASDSAASVDSSLQGESSR"

CDS complement(4267908..4268720)

/gene="fepC_2"

/locus_tag="EFAGFIKM_03725"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P23878"

/codon_start=1

/transl_table=11

/product="Ferric enterobactin transport ATP-binding protein FepC"

/db_xref="COG:COG1120"

/translation="MNSSTISNSTSLISIKGAGKSYGNHQALRSVDWHVGECDWWGV
GPNGSGKSTLIQLIAGTEQLNEGQIRIDGRDIGSYSRKDLSRMIAVLQQDGLPSISYP
VRDVVEMGRYPYQNWLGREVG DGALVVDRLVLEDLGLTELADRPLDALSGGQRQRVALA
KVMAQEPRLLLLDEPTTFLDIKYQLQFMELLSAWRQRNNITIVAVLHDLNLAALFCDH
ILALREGMAVGKGTPTHTLINDENIQDIFRVKPAIVSHPDHAIPQLLLRRDID"

CDS complement(4268717..4269763)

/gene="hmuU"

/locus_tag="EFAGFIKM_03726"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q56992"

/codon_start=1

/transl_table=11

/product="Hemin transport system permease protein HmuU"

/db_xref="COG:COG0609"

/translation="MSKKLILFGTTGMVLLVLTVLICTGIGSVALPIRDIAGILIHKI
PWVGDWITPDWNKAAEQIWKVRFPRVLLAVLVGASLAIAGTGFQGVLRNPLADPFTL
GVSSGASVGAAFLIFFGLQYALIGIWTLPVLAFLTGVITLWFMALAREGRKIPHTSL
ILAGVVMQSFLGAVVSFLSTMSKQTINEIYWTMGSLALRGWSYTAILFPYFLLGLVF
LWSRARS LNVLALGERQAAHIGIGVDRLKLSVLAVGTLLTAGAVSVSGVIGFVGLVIP
HMLRLLVGPDYRLVPLSAIGGAIFMVWADTIARSLLAPTEIPLGVVTA FVGAPFFAY
LLNRNKKLQKGMMP"

CDS complement(4269760..4270758)

/gene="btuF"
/locus_tag="EFAGFIKM_03727"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01000"
/codon_start=1
/transl_table=11
/product="Vitamin B12-binding protein"
/translation="MNFKNWKSVASLLSAAALALALAGCGNATTNEGTGTSQQPAQEQ
SQGQAQTDLKTQYPLTVTDATGESFTFEKAPAKIVSVSPAETESLFALGLDDQIVGVS
DYDDYPEAATTKAKMGGISKPNNEESIIAAEADIVFTGISMSEDAVKKLRELGITIFKT
DPKSIDVMSNIETFGKITDHQEKAQEITQMKQDVTDVTEAVKAVKPEEKKKVYVEF
SPGWTVGKGEFMDELITVAGGSNIASDKEGWYEINEENVIASNPDVILYANDVIDENS
KTLDQIIKARSGWDQITAVKNDVIGLDANLLSRPGPRVTQGLKEVAKAIYPDLFQ"

CDS complement(4271500..4272180)

/gene="cobC"
/locus_tag="EFAGFIKM_03728"
/EC_number="3.1.3.73"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P52086"
/codon_start=1
/transl_table=11
/product="Adenosylcobalamin/alpha-ribazole phosphatase"
/db_xref="COG:COG0406"
/translation="MVINAGNEVHTNQPEPLKRNILWVRHGTTLWNMEKRYLGHTDI
CLLPNAKEELAPLHEQLSGVSWNEVYCSDLLRCRQTLEQILPDAIGQVKFDSRLREND
FGQWEGLTQYDQLKDNVPVYRSWIDAPQEVTPPGGESWQEFTGRLLDSFLQEMLLEGRPSM
HVDEGRESTITVWTHGGVIRYALSRLIAGLGFWDTHVVPQGVIQVQLDQRGNEWFGST
VTFPPIGL"

CDS complement(4272171..4273199)

/gene="cobD_1"
/locus_tag="EFAGFIKM_03729"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WP93"

/codon_start=1

/transl_table=11

/product="Cobalamin biosynthesis protein CobD"

/db_xref="COG:COG1270"

/translation="MTFELEHLWTWPFWTGMAGAWIIILAYLLDRCIGDPRWIPHPVI

GMGKGISALERVIRSRVITDSGLKRAGLLFPMVIAGGSFAITWGFVYLLGLIHPVIAA

AAEVVLIATTIASKGLKDAGMEVYRHLKQQDWPAARRSLGMIVGRDTAHLDEPEVVRG

TVETVAENIVDAIVSPLFYALIGGAPLAMAYRAVNTLDSMVGKYKNDKYLHLGWASARL

DDVANWIPARLTAILLIVGAWVMKLDANGAARMVARDARLHPSPNGFPESAVAGALG

IRLGGHNVYHGVASFRAVMGEATRPMEAEDIVQTSRLMFWSAGAFVVL CVFITLGVWL

AGGTLLWS"

CDS complement(4273196..4274026)

/locus_tag="EFAGFIKM_03730"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTLPFYNYFTNGETDENEYASSFWPGLEISAHERHIKAQSPMAV

QALSSAVYGGGMFELDRIFNIYVDRDYRCDDPPRDIEQALNEWQEPRDQCAGLLTAVR

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LTIHPYVPGTINIMLWLNHMTTGAMVNAVQTAVEAKAAALADAGVLDSENGLPATGT

TTDAIVLAVRQAVEEPHPMITYAGTATTAGAAIGRLVYDTVTESLQAGLLWKERIRHK

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CDS complement(4274023..4275213)

/gene="cobD_2"

/locus_tag="EFAGFIKM_03731"

/EC_number="4.1.1.81"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P97084"

/codon_start=1

/transl_table=11

/product="Threonine-phosphate decarboxylase"
/db_xref="COG:COG0079"
/translation="MTGYIEVFGHGGDVETAASRFGREAADFLDFSANINPLGPPGGV
LEAIQQGLQSVIRYPDPAHRGFKALLSERLGVMQEQISVGNGAAESMALILLGLAPRK
VGTVEPGFSEYRSLARQFGAEVVHTEGREELAWRAEPEDIEQLMEKVDLLFLGQPNNP
NGVQYPLEVLQRLARKAEETGTVLVIDEAFMDFIPVDRRQSLAAQLNDYPNVIIIRSM
TKFYAIPGLRLGYALGRAEYIRAMTKKQVTWSVNGLALMAGEACLRSGEWYEQETISQ
ITRERGHLEGLKAYGCAVTPGEANFILARVPAPWTAASMQEALGRRGILIRSCAMYP
GLDKGHVRFVAVKDADANATLLEVLGSLVLETKGYPNADQTSIHESQEQTKDSESEQG
GKRQ"

CDS 4275403..4276407

/gene="lpJ"
/locus_tag="EFAGFIKM_03732"
/EC_number="6.3.1.20"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07608"
/codon_start=1
/transl_table=11
/product="Lipoate-protein ligase LpJ"
/db_xref="COG:COG0095"
/translation="MLFVDNQGITDPSVNLAIIEEYILKHLPMEDDSYLLFYINRPSII
IGKHQNTIEEINIEYVQDNGVQVVRRLSGGGAVYHDLGNLNFSEITADDGQSFHNFRK
FTQPVEALHELGVNAELTGRNDLQVGEKKISGNAQFSTRGRMFSGTLMFDLNLEHV
QASLNVNPEKFKSKSTKSRSRVANIRDLIDTNLTIEQFRDELLRHIFRMEPQDVPQY
KLTDKDWEKIKEISAERYNNWDWNYGLSPESNVKHTRKFPVGIIDLRMNIKDGRIEDI
KIFGDFFGVDVADIENMLRGKRYEETEVRTALEGLDVKHVYFGNLELEDFIGLVFLEE
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CDS 4276686..4277489

/gene="yidA"
/locus_tag="EFAGFIKM_03733"
/EC_number="3.1.3.23"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A8Y5"

/codon_start=1

/transl_table=11

/product="Sugar phosphatase YidA"

/db_xref="COG:COG0561"

/translation="MTYKLIADIDDTLINDNKEVTPATQTALEQAVAHGVTVTLATG

RAYASAQALARQTGLNVPIITYQGALVKNLLDEKVLERYVPQEASRKLYDYCLENNL

HLQTYIDDKLYAREENDKLRDYAKLNGTQYYIESDFIKVIEQKTPKLLIIDEPDYLDK

VAVDLRELLGSQVHITKSKPYFLEIMHNEGTKGHALTFLADHFGHQLSECIAGDSWN

DHEMLEVAGLGVMGNAIPALKELADYITASNNEDGVKEVIEKFVLNAE"

CDS complement(4277602..4277781)

/locus_tag="EFAGFIKM_03734"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRIILNFIASIIISIVFFIVLFFVDVPDTPNRVILSMAITISL

QLSLISALLLSKHKK"

CDS complement(4277817..4279343)

/locus_tag="EFAGFIKM_03735"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSDMKKAVVIGAGIAGLITARMLSDYYDEVCIIERDELPSEPAN

RQGV PQSFH PHRVLP RGGLILEHYFPGYNDELVALGAIP SHEEFMIANRYGTLVNKA

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GRNNREAMLAADMVIDAAGRSSKLIRWLEQIGLSVPEPEVLKVSLGYSTRYYKIPSSI

QNDWGT VITESDPVQGIRAGMLWRIENDIAGLLLFNAGRDEYPSTHPDEFQE QIKHLF

ASDEIVALADQLEPFQGPGRYRISESVLQHFELMENWPSGLLVLGDAFC SFDPIHGQG

MTVAAIEAETIAKCLDEQRMHPEPQFERQVLLRMQQAIEPAWWLSSVADLRWKGV EHV

GPSRMKGVAFAQKYINLFTKQAMKKASQENNKHLFFTQFLMNALILPPSEYFKGEILN

MILNDNGSEEMELRAELGVQDPELFQQRIDEIIPSFQLEFDGQIKKLLESFQHAMSK

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CDS 4279500..4280069

/locus_tag="EFAGFIKM_03736"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKMIDKKVDLRVTRTHKLLTMALLDLLCEKGQLFSNITINEICD

KAMVHRTTFYKHFKDKFALLSSTLTWVLRDYLHMNVENRLQQPLQSVSKILFGNVLET

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WIQHFEENVTAEQMDEYYYLLVNENIMSE"

CDS complement(4280134..4281072)

/gene="yedA"

/locus_tag="EFAGFIKM_03737"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AA70"

/codon_start=1

/transl_table=11

/product="putative inner membrane transporter YedA"

/translation="MVGIAFTVMCLIFGTTFLAIKIGVEAGMPPFLSAGLRFVIAGAL

MFAWMRMKGKVSWSLLFRKEMLLTGAGLTFGTATLYWAEQHVSSGVGAILSATGPLM

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SAGALYSKKVIHQFKEASPVAINAVQMMYGGLLLSLLSVGTESWNMSALDWVPAVSSV

IYLTVIGSMVGHSLFYWIMSRTNPLFPATWLYISPPIAVGLGAVVYGEHVS WVTWIGV

VLVVSGLLAMNEKVSGWLKKRSRARM TVQASESVLK"

CDS 4281193..4282614

/gene="dapL_4"

/locus_tag="EFAGFIKM_03738"

/EC_number="2.6.1.83"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01642"

/codon_start=1
/transl_table=11
/product="LL-diaminopimelate aminotransferase"
/translation="MGRTMMMTDNSLKLYEQVIHYLVVRIEAGEWAEHEKLPSVRSLS
ELLGVHRLTVFKAYQELKERGNVYVKDKSGYYVSPATPFSVTDQADDPVSAWLHWDS
LARVQSLEAEYQFSKSLIDPSLLPNRYWGELMRDLLDQYPRLLGYSTIQGDLELRSA
LASHLTKKERFYLSADEVLITSGAQQAIDVISRTLVPKPGDRVLMERPTYGPAMEIFRK
QGARLIFTDIHSDGYDLEQIEHLMKSEKPRLFYTTPTFHNPTGVNVPVEQRKQLPELA
EQYGCFLLEDDSTYDIYFKEKPPAPIFTYDTTGHTLYIRSYSKYVAPGLRIAAICRQ
RFMPGLQAVKSLTDNGSPLLNQKLFLRYFQSERMHQHLSKLRTAIQLRMEVMEQSLLE
TDWTWTRPEGGLNFWVELPEGVDTGRLLHRCMEQSVAFVPGTVFDSSDHSASRKLRLS
FSYAHEQQIREGMSRLITLAKEM"

CDS complement(4282671..4283252)

/gene="clpP_2"
/locus_tag="EFAGFIKM_03739"
/EC_number="3.4.21.92"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P80244"
/codon_start=1
/transl_table=11
/product="ATP-dependent Clp protease proteolytic subunit"
/db_xref="COG:COG0740"
/translation="MNVVPYVVEQTARGERSYDIYSRLKDRIMVSGEIEDQMANAI
VAQLLFLTAEDPEKDIQMYINSPGGSVTAGFSIYDTMQFVKPDISTICTGMAASFGTI
LLVGGTKGKRMALPNSEIMIHQPHGGTRGQASDMLIHANRIIQRQLNKLADHTGQ
TIERIEKDSDRDYFLTAAEAVEYGLVDKVISSS"

CDS complement(4283271..4284143)

/locus_tag="EFAGFIKM_03740"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MAFVKSVDCRINRPHDDGKQEKDFEFNGNDRKNQLNPSIHTVL
PDLMGSLYAYCLSLTKSVPDTEDLVQETCLKVLSSSVVGTYGMNKDINWEAYMIRIAR
NSWIDILRQRRERLAYKLDCLKPLHEMEEERQFEELESAVQLLVNTLPPWQRVIYVLR
ELMGYRAAETAEMLDTTEGAVKAALSRRARSAIAEVRHRLEQSDAELQYEEGAVEDNRE
ELRSYLLAFRNGDTARIIDLCLNRTDDPMAVAGTILQQTLSPSTQPMMYGYSTSGMN
SMSYGGGYTVNMVA"

CDS complement(4284262..4285068)

/gene="rbn_1"

/locus_tag="EFAGFIKM_03741"

/EC_number="3.1.26.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01818"

/codon_start=1

/transl_table=11

/product="Ribonuclease BN"

/translation="MDQLTFLGTGDAMGVPRVYCDCDVCTEARLTGENKRKRSSVLID
GGGDGEGEQFMIDCGPDWRSQMEDQGLRMVHTLLITHAHFDHIGGLPEWADACRWLEV
KGRLYAPREVIATIQGQFPWLGRHMDFLETDDGIELGGWKVHSWKVCHGHNGYSAYR
LDQGGYSWAYCSDAIDLKPSEKEPLHGLDLLVLGTSFVHELAEFSTRSVYDMREAQEL
LRELKPGHTYLTHMSHDVDVQQNYNLDQRITIALTGMKVPLGLTKLETNA"

CDS complement(4285354..4285809)

/locus_tag="EFAGFIKM_03742"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNWMSAEIKLSQSTAIRLEQARGKGMPEEEILKAIQAKDISAFD
AVSEEEYRYNEFFSYADEHGENLEVAVKDG YRITFNTRGGLGIWLEKAFKVQPERDFT
VGEGIVTGLQLKPEQAEVLAKRLASNWWITESKDVPAGQELTLKLRLV"

CDS complement(4285958..4287022)

/gene="sbpA"

/locus_tag="EFAGFIKM_03743"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P27366"

/codon_start=1

/transl_table=11

/product="Sulfate-binding protein"

/db_xref="COG:COG1613"

/translation="MQTRKKKAILLYVALMLLLVCMTAGCSKQEESSSEQNESSNDSS
NTLVIGAYSVAKDAVGELLPKFQEEWKAKTGQTINFQESYEASGTQARAIVGGFEADV
ALLAMESDIEKLVKADLVSSDWKQTPNEGMITRSIVVLGTRAGNPLGIRDFQDLTKPG
VKVLYPNPKTSGGAQWDINAIYGAGLKLSEEQEGKKDPAAAKAFLEQVHRNVESLDKS
GRSSMAAFEYGVGDVIVTYENELLARIAKGVDDYDIVIPKNTILIENPAVVVNKYADKH
GNRELAEAFVAYLRTPEAQRIFAKHGFRSVDPDVFAQTESTFPTPEGLFDINYLGWD
EVRSTLYSKRGVWYQVLAGL"

CDS complement(4287048..4288112)

/gene="cysA"

/locus_tag="EFAGFIKM_03744"

/EC_number="7.3.2.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P14788"

/codon_start=1

/transl_table=11

/product="Sulfate/thiosulfate import ATP-binding protein

CysA"

/db_xref="COG:COG1118"

/translation="MHVEVRDLNKHFGDFHAVKDVSFDAKGHLLGLPSGGGKTSI
LRMLAGLENPGSGEIRFHGKVVNHLPPQERGIGFVFQNYALFKHMTVFENIAFGLKVK
KTPKAQIRDRVMELVELTGLKGFEQRYPHQLSGGQRQRVAFARALAPEPQLLLLDEPF
AAIDAKIRQELRSWLRELIERVGITSIFVTHDQDEAIEVADEIMIISQGRLEQKGPW
DIYKNPQTPFVATFIGESTVVEDASQLKGFEHAVEGEGTRALIRPEYIEIGLKNEFTM
LSATEKGTVKHLHFRGSEWMVEVEVQGHKLITYRSLEKTTLEIGQQIRVLVHRAYLFN
DSNSWVVENRLKEDPMPVMI"

CDS complement(4288114..4288911)

/gene="cysW_1"
/locus_tag="EFAGFIKM_03745"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P27370"
/codon_start=1
/transl_table=11
/product="Sulfate transport system permease protein CysW"
/db_xref="COG:COG4208"
/translation="MRLLIGLTFVFIIVLLIPLGRIFIGAFEDGAGGFLKGLMRPE
ALHALMMTGLVVLVLTLLNTLFGIMMALYLVRAGWLSERIKGLLNSIVDLPYAVSPVI
GGLMIVLMLGPNSIMGAFFEGIGFNVVYAFPGMVIATLFVTFPLMVREVMPVLQELGS
QQEEAASTLGAYGWRTFWSVTWPSIRWAVVYGLVLTVARSLGEFGAVLVVSGNIMNKT
QTATTLVYQDVENFNAAAANGVALVLVTFVSVGLLLMMEWAKKRKEVH"

CDS complement(4288908..4289723)

/gene="cysT_1"
/locus_tag="EFAGFIKM_03746"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P27367"
/codon_start=1
/transl_table=11
/product="Sulfate transport system permease protein CysT"
/db_xref="COG:COG0555"
/translation="MNTVLRHKGWTWGFRSTVLLYFIVLIVLPIIGVYVNSFSEGWSN
FVQSIMDPIAWKAVLLTIRLAVIATLINVVLTGMIAWVLTRYRFVGRSFLNSLVDLPF
ALPTAVGGLMIMLLLGPVSAIGKLAESMGFEIVFHQPAIVIAMTFVTFPFVIRAVQPL
LEEIDPSEEEASYTMGASKARTFMQVILPSMAPGMISGGMLAFSRGLAEFGAVVLVAG
NIPGRTLTA SVFIYGEIESDNPTGAAAVSVLLLTLSFLILWLINLVQMRGRRR"

CDS 4290069..4290470

/locus_tag="EFAGFIKM_03747"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P9WFP9"
/note="UPF0047 protein Rv2556c"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLYTKNISTSTRDEMKDITWDVKQVVQSSGVQNGTVLIYCPHTT
AGIAINENADPDVKHDVLLRLDEVYPWEHPEYRHAEGNTASHLKSITTGPSQTVIIHE
GRLLLGRWQGIYFCEFDGPREREYFLKIMEG"

CDS complement(4290660..4291262)

/locus_tag="EFAGFIKM_03748"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MARRAVEQELSRERILEAARHLFITKGYRAISMRSIGQHLGYSH
GSLYYHFKEKAELFYAIVVEDFNHLGHLLQAMVRPVRDDVSKVEHIMMEFIRFGLEN
PYQYEIMFMIRDEELLSYCRTEQGRCFELFASIIRQYMNEANCTEEDIQRPRTLFLA
MHGFISYYIQDRLTFVEIESSALSHVKVLCRNLGQQPGDQ"

CDS complement(4291268..4291900)

/gene="yigZ"
/locus_tag="EFAGFIKM_03749"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P27862"
/codon_start=1
/transl_table=11
/product="IMPACT family member YigZ"
/db_xref="COG:COG1739"
/translation="MIERYRTVRGPGNLEIVIKKSRFIGHIMPVTTEEEAVAFIDEIK
KKHWNATHNCSAYMIGERDEIQKQSDDGEPSTAGKPILEVIKNQKLKNVAIVVTRYF
GGIMLGAGGLIRAYTDGAVVAIEAGEAITNVLHREVFVELDYTWLGKVENELRSREVR
TGETGFTDKVTLTCLPPDSETEAFIAWITDLTQGQSRITEGQRLYFIEGE"

CDS complement(4292077..4293432)

/gene="pgi"
/locus_tag="EFAGFIKM_03750"

/EC_number="5.3.1.9"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q81K75"
/codon_start=1
/transl_table=11
/product="Glucose-6-phosphate isomerase"
/db_xref="COG:COG0166"
/translation="MAKKVTFDYSTALQFVNQHEVDYFAEPIRLAHEQLHNGTGTGSD
YLGWIDLPTAYDKKEEFARIQAAAKIQSDSEVLIVIGIGGSYLGARAAIEMLTHSFYN
NLPKDKRKTPEIYFAGNNISSTYVTHLLDLVEGKDFSVNVISKSGTTTEPAIAFRIFR
AALEEKYGKEEARKRIYATTDKARGALKELANAEGYESFIIPDDVGGRYSVLTAVGLL
PIAAAGISIEEMMQGAADASKEYSNPNVAENEAYQYAAVRNALYRKKGKTEILVNYEP
SLHFVSEWWKQLFGESEGKDYKGIYPASVDFSTDLSMGQFIQEGSRNIFETVIQVTE
VAEHISIKSDPDDL DGLNFLEGKTMDFVNKKAFQGTLLAHTDGQVPNLIVNIPDMTPY
SFGYLVYFFEKACGISGYLLGVNPFDPQPGVEAYKKNMFALLGKPGFEEKALEARLS
E"

CDS complement(4293669..4293986)

/gene="ppnP"
/locus_tag="EFAGFIKM_03751"
/EC_number="2.4.2.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q6FF51"
/codon_start=1
/transl_table=11
/product="Pyrimidine/purine nucleoside phosphorylase"
/db_xref="COG:COG3123"
/translation="MSQFDQVSVVKEANIYYDGQVTSRTVILGDGSKVTLGIMLPGSY
EFGTDSREIMEILSGDLKVLLPGEEEWQEIQGQATFHVPAESKFKLEIRSVTDYVCSY
PAE"

CDS complement(4294285..4296327)

/gene="tkt"
/locus_tag="EFAGFIKM_03752"

/EC_number="2.2.1.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A0A0I9QGZ2"
/codon_start=1
/transl_table=11
/product="Transketolase"
/translation="MTDKNEAIQKEENTTIDNLSITTVRTLIDAIEKANSGHGPMMPM
GSAPMGYQLFAKTMTHNPDHPTWVNRDRFVLSAGHGSMMLLYSLLHLSGYDLPMEELKQ
FRQWGSKTPGHPEFGHTAGVDATTGPLGQGIAMAVGMAMAEALGATYNKDKFNVDH
YTYAICGDGDLMEGVSHESASLAGRLHLGKLIMLFDSNDITLDGKDLSSSESIKRF
EAYGWQVLRVEDGNDLPAIEKAIQEGQADTLRPTLIEVKTVIGYGSPNKQGKGGHGGT
HGSPLGADEAKLTKEYYKWVYEENFHVPAEVRDHFAQVKDRGISANKAWDEKFAEYKK
AFPELAAQFETAINGDLPEGWDRDLPKYAATDKALSTRVASGNALNGLAHNVPQLTGG
SADLESSTMTHLNNLENFTPEDYSGRNIYFGIREFGMAGAMNGMALHSGVKVFGGTFF
VFTDYLRPAVRLAALMGLPVTYVLTHDSIAVGEDGPTHEPIEQLASLRIIPNLTVIRP
ADGNETSAAWAYTLENKSNPVALVLTRQNLPILEGTVEGSRENVKRGAYVVSADKDGK
AVAQIIATGSEVQLAVKAQAALAEQGIQVRVISMPSWDLFEKQDKAYKESVLLPDVKA
RLAIEMAYPMGWKEYVGDQGDILGISTFGASAPGDRVIQEYGFVENVVSrvKALL"

CDS 4296725..4297201

/locus_tag="EFAGFIKM_03753"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MPDPAAHPSTSVKHSLPWISGILTGILSGVVLGFFLKLQAYTG
EQVYTLLLNIDFVPGLPPTLPEIIEFSLHLIVSVVIGIFYLLWVRHSGRPMIKGIPLG
AVSSLLFIPLSQLSSRPDLVDVSAILYWIVGHLLFGIVLGLCGKYVYTKKATPAS"

CDS complement(4297276..4298169)

/gene="purU"
/locus_tag="EFAGFIKM_03754"
/EC_number="3.5.1.10"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WHM3"

/codon_start=1

/transl_table=11

/product="Formyltetrahydrofolate deformylase"

/db_xref="COG:COG0788"

/translation="MEIHAKQVRPDSKNRADRARMILISCPDGPVAAVSHFLHQHGA
NIVQSDQYTM DPAGGMFFMRIEFDLSQLLVNLPKLEADFAEVASRFQMEWTL SAVSRK
KKLAIFVSKEDHCLVELLWQWQAGDL DADIALVVS NHLDMKDYVESFGIPYHHIPVTA
DTKKEAEQRQLDVIGNDVDVILARYMQIISPMFIEHYRNRIINIHHSFLPAFVGGKP
YAQAYNRGVKIIIGATAHYVTEELDGGPIIEQDVQRVSHGDDVTELKRIGRTIERVLA
RAVKWHVEDRVLVHENKTVVF"

CDS complement(4298212..4299318)

/gene="nfo_2"

/locus_tag="EFAGFIKM_03755"

/EC_number="3.1.21.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00152"

/codon_start=1

/transl_table=11

/product="endonuclease 4"

/translation="MLKIGSHVSFSDKGLLSATKEASSYGSSSFMIYTGAPQNTRRK
IESMYIEEGKVAMQEGGMEDI VWHAPYIVNLGSYKDNTFRLAVDFLQEEIRRTHAIGV
KNIVLHPGAFTDKDAHYGIGRIA EQLNEVLEGVKD TDVNIALETMAGKGTEMGRSFEE
IAQIIEKVTYNERLTVCMDTCHIH DAGYDIVNDFDGVLEQFDRTVGLDRIAVMHINDS
KNAVGAAHKDRHTPIGSGWIGFEAINRIVNHEKLQGRPFILETPWIGKEAKTQRPMYEV
EIALLRGDVAGRFGQDFLTEVEQLQHFFKGKEIESRSYILDVWTL LKNDAKAKKADPR
EPLERLYDMVTEAALFPHLNEEQ LNHRLIAWLAG"

CDS 4299489..4299956

/locus_tag="EFAGFIKM_03756"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MIFDSYAMILNSYSPSNWFMNTIAFWTFLLLGSMCIGGFFMMRK
FLKVLPKADGKSKLDWQNYWVEASRHLWTDEAKSFLDQLVEPVPGPFRDIAKHSIAAE
IGKIAVEDNATEVSRDHCIKGYIATPKRDNKFLVKFLEKNKIDYSPYQHLLIK"

CDS 4300116..4301027

/locus_tag="EFAGFIKM_03757"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7A6Q5"
/codon_start=1
/transl_table=11
/product="Epimerase family protein"
/translation="MKIAICGGTGFVGGALVDYWLQAGHHVKVITRKL PDLHNPSKNL
TYISWEQVEEHPHLLLEGMDALVNLAGETLNQRWTTKAKLEIVESRVTTVARVARLVES
LEQKPEVVVQASAMAIYGTSPNETFDESSPQKSMNFPSRVSEQWEVAADAIKNVRLVK
IRVSLVLGHRGAFPLMKLPYMLGVGGKIGSGKQWTSWIHIMDIVRLIDFSIQNKQVS
GPVNASSPNPVTNDEFGRTVGKVYHRPHWFPVPSFLIKTLVGELSVVVLQGQRVIPQK
ALDHGFQFTFPTLTQALEDLKHRLSD"

CDS complement(4301053..4302825)

/locus_tag="EFAGFIKM_03758"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MYGLTRDFIRNGGAFMVLEKEDGLRMEELSRVQMGM LSSNQIPR
LLPVHIREVDRNVTLQYDISGYKMLSQMLKSSIKLRVLYGLLFQLADACTECRQYML
EPRKLLIQEEYLFINGSFEQGELGMVYVPIMDTVEVDPTPQQFRELVIRLMAHVQELQ
GEGIQRVLQLCDNERWDIGQLRELLLELYADEQENGGA AFLSSRKSETVDDPRGDLH
SSISERDSRLATGTSWPYQPGAPVQNAAVGPQLNFRQPQKTSESEVEDIPVRSRTFPG
RRSPEQFPLESSNSMDQGRSNSYDSL ERVDMEEKPGSSKVTYIILGCMVAMALVWR
FIYMEQPGQTQMILCMVLSLGLFGVAGWTWK RKANPQNKAENKRSFSFNLGKNKGKQT
EDEEEQFQESWRWNTADRKEERINQMVASASEGGSEYSRFQNLHMTPEHSEPPFVQRH
VESVASTSELIRQDAVAEATVNLQNLSGGNVTGAGPVMASYLERRSGTGDQHERMDV

QGASFVIGRSADMVQWVDTATGVSRAHVELSRNKSGYVIKDLGSVNGTILQGNILAPY

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CDS complement(4302875..4303390)

/locus_tag="EFAGFIKM_03759"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEVEWFYIACGIYVIAAFITDIRSMKIPNRLTLPVTVAGVLAHI

IWGGWDGFLFSAAGFAAGFGMLFLMYAIGAVGAGDVKLFGGIGAWTGLAFGIHVVIYS

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FITVLVSGLFP"

CDS complement(4303402..4304466)

/locus_tag="EFAGFIKM_03760"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNDQDRFGGGIMDKQQHYEKESAQKQIRLTRIIRLQRLKSLKKQ

ICSPKKEQGSMVLEASLVLPVFLFFIMFLIFIVQMTLISTALQSTAGEAVKQLSTKIY

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QEIKTTVLETVLDPTVKPLLQPFIEPTLLNMERVHVNGISIPDLKNKTNPYFRLELSY

ELPVKVPFLSKPLRIQAAAAERVWIGDTGEGSDGSGGDGDTAGSATVLSKPDPAYIGN

NATIKVKVEPGATANLTIFYKSGESSAKHIGWATADENGIIENWNWVFGTRTTEGTWSF

VVETGEGAKTETTFTVASRK"

CDS complement(4304463..4306580)

/locus_tag="EFAGFIKM_03761"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFVAIFIDYARIAAFKVQTERMTHAAMRSVMSAYDTSREYGLF

GYGDSSGDAIMAKVLNDSVKPSAVKDGFPILDIQWDTTSLSMERELGRYDIFNRQIQE
DIKYRAPVDFTLEVINRFKPISDEMKEAAHTVDLLKKLQKLYDKREELLDEAIANQTE
SAEKLKLNLPKLIMDPPSQAIYEEMLEETPETAEEAAARYADYLNKKQADEGLPFREQQ
YILELARYRTGVGNVVTGISMIIQPALQAHQTKLEEAQSKIEEARKINEEMKRVIAEG
ENRSQNASYDNVGNNSNLPGTSPASAGSGSEAKSTRSLASELVRADSLFDQLKTRVVSQ
NSDFSNVRRDNMELNTQLRSVTAMSGVPIKPAVRQASQVTERYMDTYVRSGPANLILQ
SKQQLESGRGSDAQRKANDKESKGKLKEVKRILSQIQNGSSGSMDAFKQLEEYYNANI
SFNEASREEAKKAEIAGDPYDSGGDAMKGMDSLFGGMSGLLDSLGDSELFQNEYALAYF
NSMDFGQLFTWTEGGGDAGDVFKLENQELEYIVYGFHNPSGNIAAAYAEIFGMRLAIR
TAEGLIEHSKLGNPLLVLAAAILYGITNAIADMVKLAKEGSVELSKYIKVKLTYRDHL
RLFLLMHSNNERKMSRMLALIRLNTGVNPDEKQTYASGNMRSSIKLWFLPGVVRSIGA
VMGSADQVEDGRFFIERKADYSY"

CDS complement(4306672..4307346)

/locus_tag="EFAGFIKM_03762"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNSSNNKFKKEEGSFTVEASLIFPVVLFILVLLLFFTMYMYQKT

FLNQHAYAASERAAYSWDNSHKQAMTGEFVVGEHDNLYWRLTDDRMLGALFGWAGVDN

QVSVSIPAGEGGNLSEQKLAQAVQHMP SAMKGTIEYQNSLIQRKVTTKLEQVISLPLP

SFLFDSGNRVLTQGSSAVVEPVFIRTVDLIRYYAAKFKGKDGAATSTATEAGQVVQH

FGKSKK"

CDS complement(4307330..4307518)

/locus_tag="EFAGFIKM_03763"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMEVLKNKVNFAFWKEEDGLGTLELILIIIGVIIIIALIFKDQIKK

LVERLLTNVSNKSNEFFE"

CDS complement(4307530..4308399)

/locus_tag="EFAGFIKM_03764"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLLPVIVAGMLGAGWLVLDRTRGQTYRHLRRLDMEGLRLKKLHG
PFLFILDKFEIGRRPLVLMFRMQHAIQKMYGIQHSGEKTMLYCAEMLTYTWMLLVGC
LLSLVGDMGIGGMVGGLALGAALPFALYKDLNNTKVQRRDQDILMELPELLNRIVLLVG
AGETVQRAIVHCVTSQGERNHPLYNELRKTVGDWNNGYSFQQSFQFSRRRCGVQEVTI
FTTTVLLNFRRGGGDFVLALRDLSHVLWEKRAVSRAKGEQASSKLVFPMVLIFFTIV
VMIGAPAFMMMNM"

CDS complement(4308412..4309110)

/locus_tag="EFAGFIKM_03765"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVCMLISSLLFFGIGILFYHHWLAGAILAAGCIWVVPKHWTKVLL
ERKRMTLSLHFKQALYALSSALAAGKSVENGFKESVEDLRMLNPEADTDLIREFTILR
TRMEYGQPIEEALQDFSDRAQIEDITNFADV FITCKRTGGDLVEVVRRTSAVIGEKL
D
IQQDIMVAVSQKKFESKVMFAAPFIFLIFLNLTAKDFMEPLYSGMGYLISSGALLVLA
CCYLWINRIMDIKV"

CDS complement(4309196..4310500)

/locus_tag="EFAGFIKM_03766"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTDSSNRILDREEQFQMMRREVRAGDLTSSAGDDELWQGIERK
VLTPKLDLDTSGERHTLVQRLFDSFRGLDILQPLVDHPDITEIMINSHKEIFVEQEG
EVSQITLFEFESRERLEDIIQMIVSGVNRIVNESSPIVDARLKDGSRVNIVLPPIALKG
PTMTIRKFPSEPMKMSDLIEKGALHEEAAELLQQLVRSKYNI FIGGGTGSGKTTFLNA

LSQFIPADERIITIEDSAELQIVTPNLVSLETRNANTEGKGQISIRDLIKSSLRMRP
NRIVIGEVARGAEALDMLQAMNTGHDGSLSTGHANTISDMISRLETMVLSGADLPIAVV
RQQISSAIDIFVHLSRLRDRSRRVTEISEVIGMQDGEVMLNPLFRFQEQEEREKGIIG
GLVQVGKLNQVDKIQMAGLGKWLDEYIEQYSVESDSSYNNVN"

CDS complement(4310497..4311714)

/locus_tag="EFAGFIKM_03767"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIVLKVVLVSKDRDYISAWLDYVQGNSSGLHVRFTAFSQWDSFK

DHMNEQEGRELPDLIAEQEFLNDWLNNGGEVSGVPWLMLSEGMEEVDEAKRLMKYQP

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VLYLNLETLDSTLPFLEKGLTRSGQRHPDAETGLSRLLYDLKVGRKESGKQLQIQSKG

VDGYVVRHEALKSDVFWPLSNRKELLQMTREDTSNLLRYLTDCGQYDVLILDGDSGWD

GRSEGVLDAADAFVWLVEDDISAMHRWGQWLQHAERTKPDLYESMLERSRFVFNKYRD

NVVNALPRPDLHLDVLPYIPSWKQLSQEEVMLSSPIFQREVKRLCAMLVQDGEEELK

QTGRIQKQDWWAL"

CDS complement(4311876..4312259)

/locus_tag="EFAGFIKM_03768"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIEYAHIIHVSLAVRDLEIAKEFYSGLLGMQEIERPPFRSTGTW

YAIGSQQLHLLQHPEGHTLREAGIDTTDGHFAIWVTSYSGTIAWLEQQGIEYEAPDS

VAGFAQIFVLDPDCNIIIEFDSPYNS"

CDS complement(4312469..4313332)

/locus_tag="EFAGFIKM_03769"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MKKWTLFIGALLAVSLAACSNDTDNTATPPATNNETSNEGNTP
AEQETKIPTLDELITKTNAATKEMKSFTTEANIDQNLKLDAGEQSQDQQVKTSLKMDI
IKDPMMIYQEMKMEMSGQEAQNVKQYITSDKIYSQVGDQWVAIPEAQTKELIEQMKAS
MNPEGELEQFKKIEEDTEVTEEGDNYVINADVSGDNVKELAKAVMEQNGSDAQMQAML
DQMNITSMKMKYMINKETYLPASTDVTMVMEMEONGQKMTMDMKMNSTFSNHDQVEEI
KIPQEALDSAK"

CDS complement(4313400..4313822)

/locus_tag="EFAGFIKM_03770"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTANQTDVHQGHPIVLVDGVCHFCCGLTKWIIKRDPEGKYHFAS
LQSDVAKELLKKGNLSTDSMDTFVLIENGKYYTRSTAALRLAKGLKFPYPLLYVFIII
PKFIRNAVYNWVARNRWRWFGKDEACMLPTPEIKDRFL"

CDS complement(4313971..4314249)

/locus_tag="EFAGFIKM_03771"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSYRPRIADLELAYGNKEDGLYEFKMNLVDGKCRVFYTRSPEW
KMTNISRLQKTPCPCVRKDFICKCMDQWASDLHQQMIDDQWMEKAVTE"

CDS complement(4314349..4314594)

/locus_tag="EFAGFIKM_03772"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSIEEMIERRFVCTKCRGTDCNIKEVSMGAGLSKMFDIQHNHY
LFVACASCGYVEVFPDVLKGKKQGQVGTILDILFGG"

CDS complement(4314805..4315224)
/gene="ohrB"
/locus_tag="EFAGFIKM_03773"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P80242"
/codon_start=1
/transl_table=11
/product="Organic hydroperoxide resistance protein OhrB"
/db_xref="COG:COG1764"
/translation="MEALYTAVATVKGGRTGSVTSSDGVCLKHDLKMPKELGGSGGEGT
NPEQLFAAGYGACYESALANVARKAGVKLEDVVVTSNVSIGKDPADDGFQLSVRLDVS
MPGVDHSQAEELARKAHDFCPYSKATRGNIDVVLNVV"

CDS 4315568..4316920
/gene="mntH"
/locus_tag="EFAGFIKM_03774"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q99UZ7"
/codon_start=1
/transl_table=11
/product="Divalent metal cation transporter MntH"
/translation="MSKKNPFNAPSRESLSTVGMAPSLGEAHSSMKVPQNAAWWKKFL
AFVGPGYLVAVGYMDPGNWATDIAGGSQFGYTLLSVILLSNLMAVVLQSLAGKLGIVT
GRDLAQACRERFSMPVVMMLWILCELAIAATDLAEVIGSAIALKLLFNIPMLYGVII
AVDVLLILVLQNKGFRALETLVIVLMATIALCFGIDLFLAKPDMGGVLHGFVPNVEIL
QNPAMLYIAIGIIGATVMPHNLYLHSSIVQTRQIEQTPQGKKEAIRYSTMDSTIALTL
ALFINAAILIVSAAVFHSAGMTQVAEIADAYHLLTPLLGTTVASILFGVALLASGQNS
TLTGTLAGQIVMEGFLNIRIPAWLRRLVTRLIAIIPAVIVTAIAGEHGTEELLILSQV
VLSLQLPFAVIPLVMFTSDKKSMGAFANKLWLKISWWITAVIVMLNVYLIQTIRLF
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CDS complement(4317064..4317795)
/gene="gph_5"
/locus_tag="EFAGFIKM_03775"

/EC_number="3.1.3.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00495"

/codon_start=1

/transl_table=11

/product="Phosphoglycolate phosphatase"

/translation="MQDGESSFLCLQGIGVPDVGGLKWLFFDVGDTLVDEWEPVDDI
IGQFVREACALGYPTIEAVRELFASCYRKYEQWPMRVAIRTFIGDEKHQKQIQDKLK
FQKDLERPFPADSVLQQLSRHYRIGIIANQSPGTEERLESYGLRKYVDVLACSAEEG
VSKPDPELYAVALKQAGCEPEEAVMVGDRIDNDIIPARKLGMRTIRIMQGYGRFQPEL
SDDKRADWTVDSLDQLLPLIPYQD"

CDS complement(4317875..4318270)

/locus_tag="EFAGFIKM_03776"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDTEMILVTAPNEAGRKFILLMYKKMPFAVLNSAGEERRLR
IGVEHVIRMNTAAAQKWFLPQGSVGNVFIFENSLNLTCRYLQICRSWTSKSLCVITEQ
SHPKGIYRGMGADRIVYSLNGEVGFLNG"

CDS 4318936..4319415

/gene="gpx1_3"

/locus_tag="EFAGFIKM_03777"

/EC_number="1.11.1.22"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P74250"

/codon_start=1

/transl_table=11

/product="Hydroperoxy fatty acid reductase gpx1"

/translation="MTVYDYKVNTLRGQEVEMSDYRDKVLLIVNTASSCGLTPQFKGL
QELQDKFQDAPFEVLGFPSNQFAQKEGSSDDIAEFCQMNYGVSFPMFEKIDVNGSSAH
PLFQHLSTEAPGLLGSKAIKWNFTKFLVDQNGQVIKRYAPKTPDKIEEDIKNLLQK"

tRNA complement(4319560..4319645)
/locus_tag="EFAGFIKM_03778"
/product="tRNA-Leu"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Leu(gag)"

CDS 4320089..4320790
/gene="ureF_1"
/locus_tag="EFAGFIKM_03779"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01385"
/codon_start=1
/transl_table=11
/product="Urease accessory protein UreF"
/translation="MNRGNKLLDYVKLLDSSIHVGGFTHSFGMDIHIREGTIRNAEDL
ESFMRCQLHPSIVRLEGMAIKGIYTAADHKDTRIALIDKLVHVQRTPGDLREQAAAM
GKRLIRLARALHPWIEFSQLEQIFAKYDSVGCLSTVHAWINHHLDIPVEEAVLGYLHS
AMNACITEASKVIPLNNDTTKDLMVRLATDLENEWKTVSASAADGLAQPTSMMSKSFF
PSFHMLGAGLHAYRA"

CDS 4321287..4321922
/locus_tag="EFAGFIKM_03780"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRHVTSDLERLSFQSIRHQLIIVDDNWIIQSCNRAWQQGLGQCS
PNPDIHSSHRHYLHLTEAWAKRGKNANMALVAQNLKERGIPFNRNHTYDICVYTVYNE
KRWFRVELTPLSYANSILDTDLALIAHMDITEQRKTELQLKKALSEVRTLRGLLPICA
VCKQIKDEEEHWNSVESYLEKHTHAEFTHDICPECIRRLYPKYSNILDKRS"

CDS complement(4321951..4322646)
/gene="livF"
/locus_tag="EFAGFIKM_03781"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P22731"

/codon_start=1

/transl_table=11

/product="High-affinity branched-chain amino acid

transport ATP-binding protein LivF"

/db_xref="COG:COG0410"

/translation="MLSLQRIESGYGESNVLRSVNLDVQPGQVVCLMGRNGVGKTTLM

KTLMGLLKTRKGSIQWQNQELSTLD TAKRARAGIGYVPQGREIFPQLTVKENLLLGLE

TSAPGVKTFPEDVLAMFPVLAKMYGRQGDLSSGGQQQLAFARALASRPGLLLLDEPT

EGIQPSIVEDIRQVILQLKAKGNLSVLLVEQSIDFVRSAADYIYIMDKGTITLHGTPQ

ELDMSQFEHHLSV"

CDS complement(4322624..4323433)

/gene="glnQ_2"

/locus_tag="EFAGFIKM_03782"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34677"

/codon_start=1

/transl_table=11

/product="Glutamine transport ATP-binding protein GlnQ"

/db_xref="COG:COG1126"

/translation="MSKSLGKNLKSTEESAVLLAEDITVAFGGFVAVKGMNLKLHEHD

LHFLIGPNGAGKTTMLDVICGKTKPMMSGSVKMADGTELTRLKEHQIVRKGVGRKFQAP

SIFAGLTVQENLTAAETRRSPLQAIGIRRYGKMSVAMEHVTLQIGLQDRVDARAGAL

SHGEKQWLEIGMLLLQEPRVLLLDEPAAGMTDEETHKTGRLLQEIARERSVVVVEHDM

EFVREFAAKVTVMHEGKLLKEGTMAEVQADPKVAEVYLGKRRDDHAVAATN"

CDS complement(4323396..4324487)

/locus_tag="EFAGFIKM_03783"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSALLKTGSLKMRIIWAVVLIMMCLAPLISTEFRLSLLAKFLAL
AILAIGLDLIWGYGGVLSLGHGVFFGLGGYAMAMYLKLQASGATLPDFMGWSGLSGLP
WFWEPFRSFPVALLLGIALPALLAFALGWFTFRNRITGVYFTILTQALVLITVTLFVG
KQEWTTGGTNGITGYNSIFGFTLHSAGTTIALYITLAVLVIAVYLCRRMVNSRFGQVL
EAARDGENRVRFLGYDPAGYKTLAFAFSGALAGIAGMLFVLQVGIISPSMMGIVPSIE
MVLWVALGGRGTLIGAVIGAVVLNAAKTGISEAYPEGWLFVIGGLFVTVVLFPNGIV
GVYRHVVRLRKRRGESAHVQVTREKPKVY"

CDS complement(4324509..4325414)

/gene="livH"
/locus_tag="EFAGFIKM_03784"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AEX7"
/codon_start=1
/transl_table=11
/product="High-affinity branched-chain amino acid
transport system permease protein LivH"
/db_xref="COG:COG0559"
/translation="MDMFILQMFNGLSISSILLIALGLAVTFGLMNVINMAHGELIM
IGAYATYVTQNLFMSYAPAAWFGAYFVVALPIAFIVAALIGWLLEVVLIRHLYGRPLD
SLLATWGVGMMLQQLARTIFGAPNVGVSSPAWLNGGLAISDGIVFPYKRIFIILVAV
VLLCMYLYIRTSSGRRMRAVMQNRSMAGCLGISTRVDGMTFAIGSGIAGIAGCALT
LIGPIGPSLGTYYIVDAFMVVVLGGVGKLVGTVCGALGIGMFNTLFETYTSASIGKVL
VFVCIVAFLQWKPRGLVAMRTRSLD"

CDS complement(4325598..4326848)

/gene="amiC"
/locus_tag="EFAGFIKM_03785"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P27017"
/codon_start=1
/transl_table=11
/product="Aliphatic amidase expression-regulating protein"
/translation="MKKRSVKLWSILLGAVIVMTGCVGAAPPEASGSGGTGEPATSG"

EPIKVGILHSLSGTMAISEVSVKDAEMLAIEEINAAGGVLGKQIEPVEDGASDWPTF
AEKAGKLLQQDKVAAVFGGWTSASRKAMLPVFEQNKGLLFYPVQYEGLESSPNIFYTG
ATTNQQIVPSVTWLLENRGKTFYLLGSDYVFPKTANQVIKQLAAEGGEVVGEEYTPL
GHTDYSTIISKIKAAKPDIVYNTLNGDSNVAFFKQLKDAGISSDQMTTSLSVSVAEEEEI
RGIGADVLKGHLASWNYQTDTDPENATFVAKYKEYGADRVTADPIEAGYVAVYLWK
AAVEKAGSTDVEKVAAAAGLEFDAPEGKVTVDGENQHIYKTVRIGEVQEDGGQFKELW
NSGEPVKPDPYLKTYEWGASLSAK"

CDS 4327110..4327412

/gene="ureA"
/locus_tag="EFAGFIKM_03786"
/EC_number="3.5.1.5"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q07399"
/codon_start=1
/transl_table=11
/product="Urease subunit gamma"
/translation="MHWTEQEKEKLLITVAANLARERRARGLKLNVP EAIALLTSELM
ERARDGMSVAELMRYGGTILTRED CMDGV PDMIPEVQVEATFPDGTKLVTVHEPIR"

CDS 4327430..4327819

/gene="ureB"
/locus_tag="EFAGFIKM_03787"
/EC_number="3.5.1.5"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q07398"
/codon_start=1
/transl_table=11
/product="Urease subunit beta"
/translation="MIPGEYRLKPDDDIICH PDRLTLRLVLN RGD RPVQVGSHVHFY
EVNAALDFDRTSAFGHRLHIPAGTAVRFEPGEEKPVELTTFGGKRQIHGFNGLTEGSA
DQAPDPLKLEAFLKTFSPPIQDGGGEPS"

CDS 4327816..4329534

/gene="ureC"

/locus_tag="EFAGFIKM_03788"

/EC_number="3.5.1.5"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q07397"

/codon_start=1

/transl_table=11

/product="Urease subunit alpha"

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NPDTMDGVHPALVIGASTEIIAGEGMIVTAGGIDTHIHFCPQQIQTALSSGVTTMIG
GGTGPATGKTATTCTPGAWHIHRMLES AEAFPMNIGYLGKGNSSSTAPLIEQIEAGVI
GLKLHEDWGTTTPSAIDACLTAAAGEHDVQVAIHTDTLNETGFLENTLAAINGRTIHTYH
TEGAGGGHAPDIIRAAGESYVIPSSNTPRTPYTRNTVEEHLDMMLMVCHHLDPSIPEDV
AFADSRIRPETIAAEDILHDLGVFSIISSDSQAMGRVGEVIIRTWQTADKMKKQRGKL
ELNPNSPSDNDRIKRYVAKYTINPAIAHGIGHLVGSVEVGKLADLIWKPAYFGVKPE
IVIKGGMITFAQMGDPNASIPTQPVFGRPMFGAYGSAIASGSITFVSQAAADAGIKE
SLGLKKRVEPVKGC RSVSKKDMIHNDVTPVIEVDPETYEVRADGELLTCEPADEL PMA
QRYFMF"

CDS 4329569..4330264

/gene="ureF_2"

/locus_tag="EFAGFIKM_03789"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q79VJ2"

/codon_start=1

/transl_table=11

/product="Urease accessory protein UreF"

/db_xref="COG:COG0830"

/translation="MMNSGTQLLRVYQLLDSALPIGGFSHSFGLEAYTHDGTVRNTAQ
LEQFIRSQLHSSLVRLDGLAIKGVYQAIKQQDAALLALYDKRVHAQRSPRELRESGHK
MGKRLLKLARSYPWMDFLIDEAIREYGAYCGITTIHGYYNYQLEIELDEAVTGHL
TSVNAYVNSALRLLPIGQTEAQMLIQKLLDDIEAEWALIRDNDPEDMHSFGIAQEIYA
MRHETLPARLFMS"

CDS 4330298..4331017

/gene="ureG"

/locus_tag="EFAGFIKM_03790"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9RP19"

/codon_start=1

/transl_table=11

/product="Urease accessory protein UreG"

/translation="MCGGANHTHHPEWERKAFDRSRPMRIGIGGPVGSGKTALVEKLS

KALRTRYSLAVITNDIYTKEDAEILLRQNALAPERIIGVETGGCPHTAIREDA SMNFE

AVDELIERFPDLQLIFIESGGDNLSAAFSPELADVFIYIIDVAQGEKLPRKGGPGITR

SDLLINKTDLAPYVGASLEVMKNDTERVREGRPYVMSNLMSGEGVSEIVHWLEHQYM

DDDASAAHLHSHEHGTHSH"

CDS 4330959..4331894

/gene="ureD"

/locus_tag="EFAGFIKM_03791"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01384"

/codon_start=1

/transl_table=11

/product="Urease accessory protein UreD"

/translation="MLPLHICIHTAMNMALTRINSSSDPTGTEVNRNESAGASVTRRS

ELRATFAFQGDRTVMTDRYYTAPLRFSSFRPPGGGTCLCVYTSDVSPGVLNGDLYHS

EWELGEGTHVMLSSTSATRLHPTSPSSVNHFFRLGKGATLEYFPECVIPFKGSSSS

LAVTFELEEQAILAYADIWSAGRIHRREAFQFERYRSLTEIWQGEQLAVWDRFGLEPD

TDDPRHSASLLHYHTAALWMVAPGLGTVELEQVRSALPPDGRMLAGASLLASGGIGV

RLLGMAAWELQEQLQIWNTLRPHLLGKETLVFRK"

CDS complement(4332015..4332428)

/locus_tag="EFAGFIKM_03792"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MQSIYERIEHLIAERGMTKKAFCQQLKISTGNLGDWKRGSIPS
TNKLIEIASFFDVSLDWLMIGRPSKEAMVREKREDYFFDVLRLNCQESELSTVEQSF
ISEYIEFTRYRKSKEKSDAGDYRYQPENKSENDSE"

tRNA complement(4332596..4332681)
/locus_tag="EFAGFIKM_03793"
/product="tRNA-Leu"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Leu(gag)"

tRNA complement(4332698..4332773)
/locus_tag="EFAGFIKM_03794"
/product="tRNA-Lys"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Lys(ttt)"

tRNA complement(4332880..4332951)
/locus_tag="EFAGFIKM_03795"
/product="tRNA-Glu"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Glu(ttc)"

CDS 4333258..4334034
/gene="glcR_2"
/locus_tag="EFAGFIKM_03796"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94591"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional repressor GlcR"
/db_xref="COG:COG1349"
/translation="MFQEERMQLIVEHLRKHNRISSADDIVALFDVSRDTARRDLIKLE
EQDAIIRTRGGAILPPPPQEFRSYKDRLLDVSEEKRAIGKLAAAIVREGEIIILDSST
TVQACAENLNGKSCTVITNSIHSADLLSNHTAVQIRLLGGKVDKEQRYVYGTSVIETL
SHYYVDKAFIGGITMDGFSASEEEGKIKHQMMKAAKKVVVLADQSKFDRRYGYRFA

DWSLVDVLITDQWPTKEWLVLAEQQVEILPEPTDDKEL"

CDS 4334039..4334935

/gene="ywpJ_2"

/locus_tag="EFAGFIKM_03797"

/EC_number="3.1.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94592"

/codon_start=1

/transl_table=11

/product="Phosphatase YwpJ"

/db_xref="COG:COG0561"

/translation="MKLFATDLTGTLNIDSQISLENAAAIQKAQQSGMKVTIATGRV

YSDVVTISREGGIQTPIIGSNGATIHADGERLFHPLERDTAASVMQWLEDHDVYYE

ASTQQGIYAPRSSHETLLAEMERVLGSNPGEDIARMIRSIKKHYDKKDYHRVNSHLEI

PAEVIYNIMAFSMNPDVKVTGREYFASRSDVAMVVSFEHNFEMQHPDVSKGNALTKL

AAHLNISMEDTVAIGDNFNDVSMCLKMAGLGIAMGNGEPEIQALAKAITLTNVEHGVAH

AIECLLEGKPVSRPETIVGEGQ"

CDS complement(4335000..4335671)

/locus_tag="EFAGFIKM_03798"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEVEYLMRVLIAGICGVLIGYERKNRMKEAGIRTHFVAVGAAL

MMIVSKYGFQDQAGWDNLSLDPSRIAAQVVSGVGFAGMIFTQRHTVRGLTTAAGIW

ATAGMGLAVGSGLYWTGAGVTLLIVVAQMLLHRPTRWLVSARTETLTIHLQNEGEALK

TVLALLGQEKISVIGFKTEQQTSTDSMEETVLEFTLQLPGSYRGEQLIILLQDVPHVR

SAELK"

CDS complement(4335765..4336148)

/locus_tag="EFAGFIKM_03799"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MWKQVEALGRYTGVPVPEEKRKMGYEYCPNKFTVAGLTSECSV
QVAPDKIVECPLQIEAAVQYIRIPEHTPFMAIVEVKTLKVHAHTRLISGPNKINPEEW
HPLIYNFRHYFGLGKRQGENFRAEN"

CDS complement(4336212..4336424)

/locus_tag="EFAGFIKM_03800"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKITKQDFATEQLSASPAGIQHETINPSILYYGTPVVLLSTLN
EDGSTNLSPLSSSWALGDCLVLGLGT"

CDS 4336649..4337230

/locus_tag="EFAGFIKM_03801"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MASVTPQTASSHLAKLVEGGLLEVEQQGRHRYRLANKEIANLI
ESMASIAPPVQIRSLKQSDQLQQLSHARTCYGHLAGKLGISLCEALVQKGYLSEPEEA
HSKDYQVTEKGIQWFTTFGIELQVKPGSRRAIARKCLDWSERRHHLSGMLGEQLRHRL
AELDWIRQKTGSRSEVTEAGKKGLYEMLSISL"

tRNA complement(4337452..4337542)

/locus_tag="EFAGFIKM_03802"

/product="tRNA-Ser"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Ser(gct)"

tRNA complement(4337548..4337623)

/locus_tag="EFAGFIKM_03803"

/product="tRNA-Asn"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Asn(gtt)"

CDS complement(4337717..4338178)

/locus_tag="EFAGFIKM_03804"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00745"

/codon_start=1

/transl_table=11

/product="Protein SprT-like protein"

/translation="MENEELQQWIEQVSLDHFGVPFTHEALFNSRLTTTGGRYMLKSH

RIEINPHQLEAYGRDEVEKIIKHELCHYHLHIRGRGYQHRDPEFKALLQKVGGSRYCQ

SLPDGKGRKPLPYRYKLCKSCGTEYLRKRKIDPKRYRCGRCAGKLGLQNI"

CDS 4338298..4338654

/locus_tag="EFAGFIKM_03805"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPTMRYVILQQEQHLQFVEMPADYAYQLSALNLRHKEIDKLTA

ADVPLPWAIACDSDLNENLTIIGGLDYINALEESFAVLRESHYPLISLLTEIRA

LQAQLEQWYEEEMEAL"

CDS complement(4339161..4341383)

/gene="yhgF"

/locus_tag="EFAGFIKM_03806"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P46837"

/codon_start=1

/transl_table=11

/product="Protein YhgF"

/db_xref="COG:COG2183"

/translation="MSEQETVLEPNEETIKAERHERIIKQVAKELSLSLKQVRTTSEL

LDEGNTIPFIARYRKEMTGELDENQLRSIEERIVYLRNLEDRKLEVIRIIIEEQGKLGTG

ELKQSITQAVKLQEVEDLYRPYRQKRKTRASVAKEKGLEPLAVWIWGQPKQGDALQEA

AKYINAELGVEDAESALQGAKDILAENIADDAAIRAWIRRYTLDHGMLTSEAKDAQEE
SVYENYYDYRELAKKMPPHRILAINRGERESILKVGLDVQAEPABHRHMEGQIIRGASA
VQDILRDVIEDAYKRLIAPSIEREVRGELTEKGENQAISVFSANLRNLLLQPPIHGKR
VLGVDPAYRTGCKLAVVDDTGKLEAVTYTPPHNKKREAAEVFHRMIKQYDIGLIV
IGNGTGSRETEQFVAEIIQENGDESLVYLIVNEAGASVYSASKLAQEEFPDLDVAERS
AASIARRVQDPLAELVKIDPKAIGVGQYQHDVSQKILEESLKAVVESAVNHVGVDVNT
ASPSLLSYVAGVNATIKNIVKYREENGRFTNRRQLQKVPRLGAKTYEQCVGFMRIGE
GENPLDRTPIHPESYKVVDQLFKELQVALDKLGSKELSVLLSEQQPEQLAVKLDVGVP
TLRDILDSLQRPGRDPREEMPLPIFRDVLKIEDLVEGMELQGTVRNVIDFGAFVDIG
IKSDGLVHISQLSNGYVKHPMDVSVSGDNVTWVMNVDTKKGRVGLTMKKPASAQQSS
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CDS complement(4341660..4343849)

/gene="agaA_3"

/locus_tag="EFAGFIKM_03807"

/EC_number="3.2.1.22"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9ALJ4"

/codon_start=1

/transl_table=11

/product="Alpha-galactosidase AgaA"

/translation="MSIYINQEKLFHLQTREASYVFQVLPSTGYLVHLYYGKKLRD
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CDS complement(4344085..4344351)

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/EC_number="3.1.27.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P96622"

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/db_xref="COG:COG2337"

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CDS complement(4344439..4344711)

/gene="ndoAI"

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/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P96621"

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/product="Antitoxin EndoAI"

/db_xref="COG:COG0864"

/translation="MQNTKRIMISLPDYLLQEVDGIVALENSNRSELIRQAMKLYLTE
RKKRYIRETMQRGYMEMAKINLTMASEAFHAEEDADSTLDRLVSGV"

CDS complement(4344981..4346168)

/gene="alr2"

/locus_tag="EFAGFIKM_03810"

/EC_number="5.1.1.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94494"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0787"
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MLEGMFTHFARADEEDKTYTLEQYRRFQSVVHALRDQGCSIPIHTANSAAIDTPEL
SYDMVRVGISLYGLYPSAEVNHQVVKLSPVLTCLKAVLVKTLPPHWGISYGTRYFTQ
GYERIATLPLGYADGFSRMLTGKAQVLVRGRRVPVIGTICMDQCMVSLQSFAEEAEEI
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CDS complement(4346562..4347731)

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/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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PKQVEVSDSNANVVVDVKFDSFKFGAEFEKDAFDMQRNMTAATKEGGQTGTDSGVTPA
EQTGEGGKEPANPQTAPEPDGAVTDGQSGVGGDTEQQGTEGAATGQEGEEPTLAEPEG
ADSFQVIQPTYAPEGVQLKDDQILEEAGDYSVMLRYEGTYNYTIFEARPQDRAVSLAP
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CDS complement(4347922..4349805)

/gene="sgrR_3"
/locus_tag="EFAGFIKM_03812"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01449"
/codon_start=1
/transl_table=11
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/translation="MDVSEHYIQLRLNFPVHDEQEVHTTVGELADLLCCTMRNMNLI

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VTPVSDLSVETSLALAS
ALLRHSSYQG
QSLSLWVEEGEKMEAD
MVWFAERSKQIGLHIN
IMPGDPIHAVYQDGF
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LIQEALLPTYSFKEEHAH
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LRRLLWVKRSPGAAE
EDTSYPVYI
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CDS 4349929..4351179

/gene="mdrP_2"

/locus_tag="EFAGFIKM_03813"

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/inference="similar to AA sequence:UniProtKB:A0A1C7E424"

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/product="Na(+), Li(+), K(+)/H(+) antiporter"

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ESFRLLFSLVCLESLATLFI
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ILKTYWAVFQDKR

FMIFFTATVLAVSLEFQLDKYIAVRLKNEFT
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VAIPFSRWIGRFQSR
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RQVMLAGMIPDSDRAAYMAADGLSYNAAALLGSLGLTIGAF
LPSYAMAGLYILMGLGA

LVFFRMLLRRAEEQNQH
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CDS 4351354..4351563

/locus_tag="EFAGFIKM_03814"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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VVLALKIAHVFREPVEKIFELKGGD"

CDS 4351565..4352335

/locus_tag="EFAGFIKM_03815"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"

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AMILSGFSVILTFTWAALALSLYASNRTMPNSPELFNLLNFVASCISIIIVVVQTLTVKRYNRYYPERTLDLNSRNMKKDHFEKLDEGEKWIVYRAAYRSFQMMNVLLGVGMVSM
VLYSMLFTFAPFPIVMLSIVIWIANIGIYYRETYRASNQ"

CDS 4352386..4354593

/gene="yfeW_6"
/locus_tag="EFAGFIKM_03816"
/EC_number="3.4.16.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01034"
/codon_start=1
/transl_table=11

/product="Putative D-alanyl-D-alanine carboxypeptidase"
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TPMPQGGMLSTAEDIGKFMIAFLNDGVKDNKRIFKESTVKSMEQYRSSIHPLLPNTTYGFEAAFQLPGAGSSPKVITKGGDLTGFSYFLIPEQNTGVFLTYNQNGALRNLFYPA
FIQSFFPQYAEPVQFKDYTPQSAAELQRFTGLYADLRLSTIVSSLKGGGDKPGQLSINDVFLGQRNLIQVEDNLFKDELGTGQFTAFKKNADGTIYMKEPYLNPMGYEKKGQKPMGF

RDVRENSPYAEAIYAIQSLGGYENDANKSFQPKSAVTRAEFIENTLKLSGLKPSKTP
PAGTDWADHAAAGYIQLGYEMGMITGTDEQQFKPDQVIIRQEAMVMMWRIMQLQYPSE
LFNDVKLAGHTDAWAVPAIQMMAKLGIHGPEVKVMEDGSVDFLSRKPLIRQEEAAIMY
ALLTQPTDQIVAELMAAQPPQAEPAEGAEPADETSETAPVPVPAPVPSVTSAQ"

CDS complement(4354747..4355796)

/locus_tag="EFAGFIKM_03817"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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ISREKILELLEDFGRRFKSYGYSERSYWYRFRIFMDFGELEEAGRSYDRFRTMDRDF

MSDCEACEQDEIMRYFLLKGDDEKVLAAQPILKGRMSCAEIPHLTLSEILMPLYRLG

RTAEADKHQTKGYRLIKGQNDFVQSFAEQMDYLTRTNPAKGIDVLEETLVFAADHEDP

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CDS complement(4355796..4357631)

/gene="htpG_1"

/locus_tag="EFAGFIKM_03818"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00505"

/codon_start=1

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/product="Chaperone protein HtpG"

/translation="MTASNEYRFQVNLSGMIQILSNHLYSSPKVFLRELMQNATDAIT

ARTEAEPGYQGEVRVELTGTGEQLTMMVEDNGIGLTEADIHEFLAMIGQSSKRGQQAL

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PALARSRAEVLAFGERLLGEQFQDFIPLTTASGRTGGIAFVLPHAVNLNAKRSHRVY

LKRMLISEKAENILPEWAFFVKCLIWTDDELQPTASREHFYENEKLEEVRSSELGDSLRLK

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EGETLYFTSSVDEYRQIHVVASAQSMILINGGYIDSELMATLPMTVHNVHTERLQPD
QVSMFNDVPPAERNQYYDALRLADSALQRFRCRAEVKGFKPSDLPVLFTLSQESSTL
RALEKASEESTELFSSVLGSLSSGMSSAGYSTLYLNVSNPIIQRVLTSPDDQMTPIAI
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CDS 4358077..4358982

/gene="btuD_10"

/locus_tag="EFAGFIKM_03819"

/EC_number="7.6.2.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01005"

/codon_start=1

/transl_table=11

/product="Vitamin B12 import ATP-binding protein BtuD"

/translation="MIEVRNISKQFKVHQALHDVSFTIKQGSVTGLIGPNGSGKTTLI

RIMNGVLGASGGQVTINGLDAAREAIEKVLAMCGTLTEQSGLYENMSGRDNLTFFADV

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LDPDGIQMVLRIRWLNKEEKMTILVSSHVLSQLSAVCDHYIFMEKGRIVEEGTEQEI

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VYQARITGSDLESIYFAIREAHHHE"

CDS 4358975..4359808

/locus_tag="EFAGFIKM_03820"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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YGIIANILMYPMFGTLMFPNLNWILVWWWVPACSLMVILLNVLISAKVRGFQEAYQL

GGLIVLPLIALVAGQASGMLLIGPWLLVMIGAVLLLVVLLRLVTSWNSRQQLAESQ

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CDS 4359946..4360740

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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q45581"
/codon_start=1
/transl_table=11
/product="putative HTH-type transcriptional regulator
YbbH"
/db_xref="COG:COG1737"
/translation="MESKLLQKLKYASQLTAQEKHIVDYILSNPEVVFDSTAHELAQQ
TYTSSSTIVRLCKKLGTKGYPDFQLKLALLEYQQIPSAMQTQDHAIAEQGNVLAAIDSV
PYLYQQALDDTRRMLNAPVLVRIANWVKESVRIDVYGSDMNYYLAQQACAKWNELGIS
AIAHNSPNMHYLNTPNSLTLSFVISHTGENQSMIEAAKVLSNKQMKVIAITGNNHS
TLSRHCDETLAYGYNEQLRLSKMSSMVSVLYIFDMLYMGSISDTY"

CDS complement(4360744..4361733)

/gene="iolU_2"
/locus_tag="EFAGFIKM_03822"
/EC_number="1.1.1.371"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O05265"
/codon_start=1
/transl_table=11
/product="scyllo-inositol 2-dehydrogenase (NADP(+)) IolU"
/db_xref="COG:COG0673"
/translation="MMNIATIGTGSIVDAILSAINELDDVTCTAMYSRKRETAQELAI
KYGVGTIYTDLKSLFSDTNVDLVYIASPNSMHYEQAYQALQHKGKHVCEKPFTSTLQE
AETLIALAKEKNLLLFEAISNIHLPNIKVIEQLPKLGPikliQCNYSQYSRKYNDDL
AGETPNVFNPHFSGGALMDINIYNLHLMNLFSGPNTVSYTANKHANGIDTSGVVVLQ
YPEFIAECVGAKDTNSMNFVLIQGEKGYLQVVGANGCREIKLQIGNEPAEAYNAQTK
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CDS 4362003..4363289

/locus_tag="EFAGFIKM_03823"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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ESDGVLYKVSADGSNTTEVLIDFQGVDLLAAGSYLYYTQTASSTLLRVPNDGSSDAA
ETFATDVLSYYTDNGFIYYLDATGTIYRANGNSDASSVTKIADKADTDFPFLVAKGR
AYYNALVNGNTWIVSKTSNGSGAVQRIAAGAVEGRYFTNQAKNELQLMVNTDPYEEFY
STNAVVMYKVNNTGKATAVNPKAKLDVNAVYSGGWGNNLYVYNKGIVLDSNKDYNYA
KGKAFALTTSAKTLQLHNKSVREVSALVTDKVVLLIDADKKAYAKTVSGNKVTKSANLN
LNNVTYVANQLTNGTSTAAYISGNNGLYSVNTALKVTKLTGDEWDAFHIRDDVAGIFY
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CDS 4363486..4365117

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/inference="similar to AA sequence:UniProtKB:P40408"
/codon_start=1
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SENRLANHEKVDPALERSIMYMRRYMSEGISMQLAKIAGLTPSSYSRSFKKAKGMS
PTDYLNRRLRINEAKKQLTEESCILKDVAVSVGYGNEYFYSRKFKQTLGIAPSVYMKRD
QLRVATASIMGFHENLASLGLRPVAVLEGEVIDRETDEYEQERRLTRQFDQLRQAKP
DLIIGDFYHKPYDRLKNIAPTIILESTDDWKENHIRIAELVGREKQALLNFKELEFR
KLEASLNLQPYFGQKRLALMEVTNQFIRLQGTGEHPLNHLLYAEGLQPAQLVSPSS
RNEYVADSIPVLDTDYLLIHRASLQPVSEKVFRMKQTASWNRSPAVLYGNVHDISNW
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CDS complement(4365246..4365821)

/gene="opcR"
/locus_tag="EFAGFIKM_03825"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34709"
/codon_start=1
/transl_table=11
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CDS 4366323..4367552

/gene="opuAA"
/locus_tag="EFAGFIKM_03826"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P46920"
/codon_start=1
/transl_table=11
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OpuAA"
/db_xref="COG:COG4175"
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RRKTISMVFQKFALFPHRTVLDNVEYGLEIQKVDKEVRREKA KTSLELVGLKGWEDKM
PDELSGGMQQRVGLARALANDPEVLLMDEAFSALDPLIRDMQDELIELQDKMKKTI
FITHDLDEALRIGDRIALMKDGAVVQIGTPEEIMIQPANSYVARFVEDVDLSKVLTA
HVMRRPETITLDRGPRVAELMRESGVSNLFVIDRSKLLGVITAEDASRAMRENKVL
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CDS 4367518..4370106

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/inference="ab initio prediction:Prodigal:002006"
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DPGAGIMKSAKAIEDYKLTDWTLIEGSGAAMTATLDKAIKNEDPIITGWTPHWMFN
KYDLKYLEDEKSFSGDAEEIHTIARKGLKEDHPVAFEFLSRFQWTSDEMGMMTAIQD
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LGYKVNALQVEAGPMWTGVASGDVDASPAAWLPLTHADYWERYKDQVDDLGMNTGVR
TGLVVPKYMTEVNSIADLETGAASSTPSASANVGEEVNHQIVGIDPGAGLMKATANAI
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GDAEEVHTVGRKGKEDHPVAYEFFSRFNWTADQMSEIMVDIQKGVSPPEAAKTYAEK
HPDQIEEWTKGLTPVKGDNLRLGYVAWDSEIASTNLMKYVLETDLGYTVKALQVEAGP
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CDS complement(4370360..4370572)

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CDS complement(4371161..4372519)

/gene="ugpB"
/locus_tag="EFAGFIKM_03829"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AG80"
/codon_start=1
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/product="sn-glycerol-3-phosphate-binding periplasmic
protein UgpB"
/db_xref="COG:COG1653"
/translation="MKKRGTFALMLAALMFVISACGTKAETSSPASGAQAEAAAETT
QLTWWHSMGAGEKAINQLASDFNASHPDIQVKPIYQGKYDESLNKLKASMGSDSGPD
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PILYYNKDMFKAAGLDPENPPKTYEEFEQAAKALAKDGKPGASMAIYGWFMEQFFANQ
NADYVNNNGNRNEAATESLLNSEAGVKTLTWWRKMIDEKTLNLRSTDDTTAAFTAQ
QIGMTLDSTAGLRKIVEGSGGKFELGTGFLPRPADAKEGGVVVGASLYIMNNKSEAQ
QQAWEFIKYLATPEVQANWSVATGYFPITTAAYNEQVLKDNMAKYPQFQTAVDQLHA
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KK"

CDS complement(4372899..4373720)

/gene="araQ_24"
/locus_tag="EFAGFIKM_03830"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94530"
/codon_start=1
/transl_table=11
/product="L-arabinose transport system permease protein
AraQ"
/db_xref="COG:COG0395"
/translation="MSATWTKTLLYVLLTICAALVLPVMYTFFMAVMTPEDASAYPP
HIIPNSIDL SNFSEVFDIVPIGRFIGNTFLVAGLTTLGQLITASMAAYAFKMQFKGK
NVIFSMFVATMMIPWEVTMIPNYLTVRSWGWLDSYQGLTVPFLATAFGTFLLRQFFMQ
LPKELFEAARIDGCGHIRYFISHVLP LSRPALGT LAIYSFLSMYNSYLWPLLVTNTPE
MRTAQIGISMLEFQESTAWNLFAGTAMVILPSLLLLIFGLKQLVRGMAAGALKG"

CDS complement(4373717..4374679)

/gene="ugpA"
/locus_tag="EFAGFIKM_03831"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P10905"
/codon_start=1
/transl_table=11
/product="sn-glycerol-3-phosphate transport system
permease protein UgpA"
/db_xref="COG:COG1175"
/translation="MSELDNRISLPAAKRRVSGTSERRTASLRVQRMRENLLAYGFLA
PSLLLFVFLFYPMFKSVYLSLHSTDPTGQIAAYVGLDNFKAVFQSGLFMQGMKVTL
FVLFTVPTGMLAALILAALTHNRFKGMRFVQFVFSLPVVLSSGSSAVIWKFLFHPTLG
MLNYLLGKVGIDPIPWLTSPDWALISISIMTIWMNLGFNYIILSSGLAGIPDEIYESA
KIDGAGPLLTRKISMPLLSPTLFFVTVVSIIIGAFQSFGQINILTRGGPMDSTNVFVY
SIYQEAFFVNRFGTGSQAALILFVIMLLTLIQFKWVERKVHYQ"

CDS complement(4375023..4376840)

/gene="kimA"
/locus_tag="EFAGFIKM_03832"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P96589"
/codon_start=1
/transl_table=11
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/db_xref="COG:COG0531"
/translation="MLGKMKRILIGKPMKSAELDGEKLGKWKALAILSSDALSSVAYG
TEQILLVLVAAGFAALWYSVPISIAVLGLLVILIFSIRYQTFAYPTGGGAYIVAKDNL
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RGVTESASVLAIPYLFIFSIAVLIISGGIKFLAGGMEAAPEFGTSLSHVSMFLLLK
AFSSGCSALTGVEAVSNAIPNFKQPAEKNAAGTLLLMGCILGAMFIGITLLAYGYGVK
PDPKATVISQIAEATFGRGTMYFIIQGVTAIILFLAANTAYSAPLLSFMMMAKDKYMP
HAFMVRGDRLGFSNGIIFLSVMSALLVVGFKGNTESLIPLYAVGVFIPFTLSQLGMMI
RWIKVKPSGWQMKLLVNTVGMMLTSLITLIFTKFTQTWVIFILPLVVYVFMRIHR"

HYCNIADELRIDIQVDKPAKKGNTIVIPVAGITRVVMNTISYAQTMSDHVVALYIGFD
DEAIRKMEQKWEEWNPVRLVVIKSRYSIMGPLKKFIDTVEWKTAETDHITILIPQF
ITKHHWWQNVLHNQTSFMIRAYLINYKDVIVTTVPYHLNR"

CDS complement(4377119..4377964)

/gene="rhaD"

/locus_tag="EFAGFIKM_03833"

/EC_number="4.1.2.19"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P32169"

/codon_start=1

/transl_table=11

/product="Rhamnulose-1-phosphate aldolase"

/db_xref="COG:COG0235"

/translation="MNVTLTNETTQTAGFHIPFIREMAEITQHMWKNGWDERNGGNVS

YLLEEEVEAQYIDIHHVIRKIKPAFSVQELAGKYFIVTASGKYFKNVLADPESNLGLL

RVSQDQGQELELLWGLKSGANPTSELPTHFMShIERLKLDPNHRVVMHNNHATHVLAMTF

IHELDEAKFTKLWQMCTECVVVFPDGIGIIPWMIPGSNEIGRETAEKMKKEYHAVIWP

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GILGS"

CDS 4378401..4378751

/locus_tag="EFAGFIKM_03834"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAVLSTGPIENNLSGGSRPTQQVTIKMVNTDSINTSNVLEGYF

LNGTRTLYVLQSVNLTPGQVFSQTYANLDGYEYVFTTSGGAAALTEISVWGKDSTGQ

IVTAHRIVSNELAI"

CDS complement(4378856..4379377)

/locus_tag="EFAGFIKM_03835"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMNRTILFETERLECATWNEGDRALAFALWGDHEVAKWISSKGF

LSEDEVEARLTQEIQRQKEAGVQYWPLFEKESEVFGCCGLRPYSPEEEIYELGFHLT

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PTGKMHPSYVLRK"

CDS complement(4379819..4379977)

/locus_tag="EFAGFIKM_03836"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVPLGLYSLGKTITIIDIIMIILDLLILFRQFGLANLMVVVQSMN

CDLLVIVD"

CDS complement(4380000..4380443)

/locus_tag="EFAGFIKM_03837"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDKSLLDLVESTPSNSVTFTNGSTLVQYDNYIATDSNGEDELK

ITKVDDSKVKYENLQTGEVNIAIKKVRPVYEDLSYAPQALADDYVYKGKVENSTEIY

ATASAVAGILASFIGGPVSGKIAGILVSIGGYLSKDAPRAYWIT"

CDS complement(4380591..4380794)

/locus_tag="EFAGFIKM_03838"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKNRNITGIVVAIIYCVVLYAFLTDAPPGEAPNNPFWIYLLIPI

GAIVITSLFDYVIKFDFFRKKKK"

CDS complement(4381098..4381277)

/locus_tag="EFAGFIKM_03839"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MASVGHLVDGGLLFLWIYIDLKGYFEIIKVKNILAASYGGEAVG
ENVKFVGTTIAYVEG"

CDS complement(4381298..4381585)

/locus_tag="EFAGFIKM_03840"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAILLPQQFYNLPAVGKSYENLAGGTNASATVNNFGPFPVSL
VITRVNAPVVTYVVPVNSSLTISAGGVLVFALLANLGAASGTIQFAVADL"

CDS complement(4381766..4382254)

/locus_tag="EFAGFIKM_03841"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNGTLQIRDHLLNELETGVRTGASLIRLIRSEDWSYRPQENMRS
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KGLSEDDFLNRSTKAFYMEHGHLLQVQWQIETVTHVFHHRSQLYNYLKQQGHENFFML
YA"

CDS complement(4382282..4383217)

/locus_tag="EFAGFIKM_03842"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDHSLHPLFKPIQMNGTYPNSYYVEKLPAAGLMAYVACYWESGS"

LPNTHADVAKREGPERSMTTVPARVLPDGCTDMLITYDPVCSEHSYAYCGNYTQPFV
PEPSDDGSSAGDYTFGVRRFFPGGARVFHGMPLWFTDKRIALQECWPEKLNELQERMA
ETNHFAERVEVMNAYLSPLPVQASTSENDLMKNVLRIFIDGGRMSVQELALREVISE
RQLHRKFSEWIGISPKRFSEVVRFHRVLSDIHQGNTADWAMLAQDHGFFDQAHLRQF
RKFYGETPLTAAREHGRMLSDLYNRSAPSVILKS"

CDS complement(4383600..4384994)

/locus_tag="EFAGFIKM_03843"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGSVTKSMKRYAYVSIETYKNVDDKLLDQLLIKVIGEKNVRTIL

ENNVSALKSLKLTCTKLKVGQVDLKTISIEIGALLKENYALFNHGVNFLNDFYLGGIK

ERVEKNDHIDTAFLDVFTEMIESSRQNYQLVLLFCRHYKNGLHKELIKDVVDKWGDDC

ENIIIDETKKGLDGSTKLEKKIEDEQNLLLKESVEMMDDKTKLVAERIFSSDTITKYN

GFEEMLPLADQITEWMNSLSHLIKKNSKENLSREVTHEEKLREFEQLDKKMKDQEKEK

VGLHKQYKKQITSLINENNQLKKSNSQLQEKIEVQLKEHGKVTQMIGELRKEKETVIN

EKNVLERKNATNDKEVKLENIIRIGIKKEFDKELSHALQEKNNIERTLQKEFDDKTL

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ESLENLVNFNNQPY"

CDS complement(4384998..4386695)

/locus_tag="EFAGFIKM_03844"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAIFDRMPGEILEKLKGLGLGEPSESESEKFLVSQEEEEIELQAE

IFRQIEEEGEEDENLDIYDNKSVAGGNDGIVEVEYYGSIGYVDISFTSLNENISEVEY

QRILNAVETITFDTNEVKWKDSFNEIESFGERAVMILFRECRKFNLSDKQ TALVVQL

LNRLTNRSLKGRRTIKAILEQASIQQHVKLAILVSGTIRDKEVSQALITRLADPDYFT

LALQSLLKLAPKDLLPSILEVINKIDLRRNDLIEHAFIHANEFVRFQAVKLIFATY

ASLDIKQLHRVYIRAIQSFKEDAIPFLKEVFQETKDEKMMFIVCKTLGSLHIPHSTQI

LLEALDEHPEYKRAIRGLSFTDRDRAILPKVLKIMKETTDQGLRQECMTTIAFSGDRS
EQTKNEIRPYFQDRSTKDYLIALNSLVIMGDGEMMNYYIQMLVSGTEKEQYIIQKHIG
KLPSVQQLKLAEAMFHYPDEETLLIVMGLQKFNVLDLRIAGILERKLQETAHAALRIE
IYKLIGKHV NKQKELL PQKFLFEAKSNEKNPHILRELEQIISMNRFEGHISVQRGE"

CDS complement(4386712..4388496)

/gene="dnaK_2"

/locus_tag="EFAGFIKM_03845"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P99110"

/codon_start=1

/transl_table=11

/product="Chaperone protein DnaK"

/translation="MSKHIGVDLGTNSTISVAYLTVKGDIENTLEITQTNEQGTQL

VSDYTLPSILYMDPQGTPYVGKYAKRMNGFFPNSVIKSVKRSMGNDDIWTIDGREIRP

EEVSAWILSTLRSTASEYYMNEDVDSVITIPANFDFQQQQATKNAAVLSGFHPEKIH

MIPEPTAALIDFLNEEEKVDVDARRIDFSTGRKNLMVFDLGGGTCDVSILQVENNDQG

KLNIQEISISQYTELGVDVFDKAAMNTLLRMFAKQTGLKTKDIAEKYGRDVVSQLIAN

LYDIAENAKMKFSTTIDSRLRTEGKEYIEEKHKFDSIIFNEAIDSNLPDEFAANFRFT

KKEYDEMIHSLLYAESGSVKNIEVPILSALESSIVGKLKLEDIDAVFLVGGMTFYPTV

QERIYDIFNRRIKPIRSVNPMKSVSRGAAYHYRIHDISLKNSEYVAKDVAPSLTRD

QGLIGNTIPSNYVDVIGADPVILLEKGTMLPFERLIEDSFIVKGTEDHKEVLGMKLE

LFSAPFAKSIHVKKLKS AKINFKQPIKTGSKLVLVKVCNEEREVS VKAWLKEDETEML

DVNIGSHEFTKEEIEEWKENNKSLNKL R"

CDS complement(4388493..4389896)

/locus_tag="EFAGFIKM_03846"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDIKERLIDCILRHHGQTNEHLEEQLNVQFKEEEREAFKQIGIS

LQTRQSFYWRLYALTERVFIEQSDISDEEQLAAIVAQDWNESEDVPHLTSEVCRLFIQ

RSELKMSNKRKALESICRGDIESSKSFQGH SKFFTELLTRYVICHAKYKNELEVYELV

DEMTAWFFPENQRETAKVTMRNLGFLRAKKVLGRLKAYKKYVGVERLVFQAGITEILI
ENKGNQILSINVADFMNQLVVVEEIEPFNEQNNQRLIVEPYSTTAEKYSNLFLKRLLS
QSIGIITNLEEKQIHCVVEVKARTTAEVNLSNDTISLQSTLRIAEEEEIVRLKQTLQEQE
KLKTEEAKEKTLVKLITALAGSKARYLMSDLFEESLGIKPNNPVISTGRLINLFSTLD
LVIGLEPYTDGRELNQFTTIQRNELTKTFEVNAPIQSQEDEIAIKIYKWMLDNKVV
VSPLVAEIITKKEIESI"

CDS complement(4389905..4392247)

/gene="rnj"

/locus_tag="EFAGFIKM_03847"

/EC_number="3.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01491"

/codon_start=1

/transl_table=11

/product="Ribonuclease J"

/translation="MLERISNFYSRHNENFKAYLLAKLGIQQSGSLNVLLPLFLSNFK
KGKGRVEDLDELLNTHGIDYFVAENTQIANLYVASGEKDKAYAFLIQNAPRMDLLFIE
HPNEASSYISFYLLLTLEYEHENYNQARFHLRKLLYLESKLLTSLEMIMYWSIILDE
AEEWVKRSDFEDIYRLSGEGIEIRFYADMIQRKLKGSVIKAI RNQIYTSKELEHKR
SLCIRLINRVQKREDWLDGIEDDQQRYPHDLTMMLYGTYLEQNKPNESMPYAEMRYR
LHSDKVESIHSYWKQVREERSNKSFTLPSNTNLTFLGGGEKIGGMSILVTINGNSILL
DAGMHLRELTYHPDYTPMLEQGIGFKDIDALLITHAHL DHTGAVPYVYKQHPNLSMYA
TEATRRLMKILLDSLKDQENRANGFNEDVRMSVMGVAPVTEYLT FIVPSKKGQWKI
TFYPSGHILGACAIHVERDGV CILFTGDYSIDPQHSVGSLSLPPDLQVDVLITESTYG
FVPTNASIDRVKQEQMF IASLIETLKKGGNLLIPAFVGRSQEILMIIRDHFKGERFL
PFDLYIDGRVVEVCEVYEEIFASQSQDKTLLGEEVLVANKIYSNKR NSTFDNFYDD
YLLKGGNCIISSGMLRDFSSARYAERMIEQSQDAIAFTGYMDEESPGHHIMELDRG
VDDVSVKINGKTKTLRAKVDTFRLSAHASREQIMKVIMDTKPTSVFLVHGEHQKSYTG
IHTVVS GHVIYPTLLDLLQHLSKDINVT PVFNGQRY SIEF"

CDS 4393079..4393330

/locus_tag="EFAGFIKM_03848"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLYYPALHHSDRKRLNIAANRSVQATAERLHIHTNTLYLRLRKI
EEILGVDLNDSEGWMKVYLACHLSEVYSVAPTASGALKL"

CDS complement(4393336..4394178)

/gene="araC_5"
/locus_tag="EFAGFIKM_03849"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A9E0"
/codon_start=1
/transl_table=11
/product="Arabinose operon regulatory protein"
/translation="MYWMDTRIFFGKTEEAARLPIYMTTVGYWEHQYETERPEGFPDY
QIHQIIHGQGRLIIQEDEYIVGPGDVFFLYPDVPHRYMPISDRWELAWVSFQGREASQ
LLSYAGIPGSRVCRLRTATLLRGLKQLLVRGENGDTTDYADYDVECSKQLYALLLDLK
PLLIASANYNDELERLKPVLRVIAEHLDRSLSELADVAVVSPQYLCRLFQRALHTR
PVFYVNQERINRSKQLMFSERELRIYEVADRVGYENASYFCAMFKRHTGMSPERFRKL
HGLN"

CDS 4394296..4397415

/gene="cbgA_2"
/locus_tag="EFAGFIKM_03850"
/EC_number="3.2.1.23"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P24131"
/codon_start=1
/transl_table=11
/product="Beta-galactosidase"
/translation="MRKKLVHTPPANGYPEWNNNPETFQVNRLPAHASMVAFPSITEA
LSNDSSASPWYDSLNGQWKFAFAETPEQRITSFYENNYDASEWDEIAVPSNWQLQGYYD
YPHYTNMTYPWVEREPELKPPFAPTTYNPVGSYIRTFTVPVDWKDRPVLLHFEGVESA
FYVWVNGELVGYS EDTFTPAEFDITSYLTEGENKLAVEVYRWCDASWLENQDFWRLSG

IFRGVYLHSPSPVQIADFFVRTELDDAYQDAELLLDLKLFNHNAAQTPAGLSVQAQLY
DAQQQTVLKQPLTAAVTFQGEDELSFQLSAEVMKPLLWSAESPPLYTLVLSIQDES
TLEAVRSRIGFRKFELKDGLMQINGKRIVFKGVNRHEFSPDKGRAIGREDMIRDIELM
KSYNVNAVRTSHYPNQSLWYELCDEYGLYVIDETNLETHGTWDYGGQKEMNENNIPASK
PEWRDNVIDRCNSMFQRDKNHASVIIWSLGNESFGGDNFIAMYDYLKQVDPTRLVHYE
GTFHYRPSDSASDIESTMYISPQDVENYARMKGPKKPYIICEYSHAMGNSCGGLHLYW
DLFDKYDVLQGAFIWDWVDQSIRTTTADGVEYFAYGGDFGESPHDGNFCGNGLILADK
TVTPKLEEVKKCYQNVNRMETVDVKDGLLRKQFLFTDLSEYSLVWTVTHDGVSVENG
TLDIAVPPGESVEVRIPYTPSSDLFQEAVLTVSLVTKIATKWAGVDHEIAWDQFVVS
RLRPIQQVHQGGQNTQVKELQDELKVTGQVTLNPNPATGALTSYQINNQEQLLAPV
RPNFWRAMTDNDMGNRLNDRSAFWRDAHATSRLRFEHHADEQGILVTTDYTDWQHPG
CTLSITYRIDADGVLEISQNLIPGIGLPDLPEFGMLLQLNNRLDTISWYGRGPHDNYA
DRLTSARLGYTGAVRDQFVYLPKQECGNKTDVRFVTSADGQLGLHVEATIPFEI
NALPWTPEELEANDHVYKLPQSTQTIARINYKQMGVGGDDSWGARTHPEYTLPANRAY
HFTFTVKPV"

CDS 4397511..4398254

/locus_tag="EFAGFIKM_03851"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNEVQERFFPAITLLRGETLQYLFTTLFILGFFAFLIIVGMIL

SIRKGDRLPIRYIFLTACFAIALIGLFGMLTLSSNSTQSEIDQTPSSQIKLSGLHMT

TDEFKNKFNGAVGKYRLNGLSITRLNIQDSSEHGTGTFEYIFNDELHLVGAANADKSI

QEVRLYATGDTRKPTGGIFLTAIATLILTTDSEYSYNDAQDVIQDIGLLDREVDQSDF

DGATIRNGLEYRFSVQDSEHSTFEITVAK"

CDS complement(4398537..4398884)

/locus_tag="EFAGFIKM_03852"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLFKLPLILCTILLLSIVSACGADDRHLHGKSDNWDVSLQRSTG
SYSITYIGDEKRIKDFVFDLTSNNIKQQGKALEEQGVPFMSGTATEAEKTKDPITFK
MSWNNQSEIVTFE"

CDS complement(4399151..4399804)

/gene="czcO_1"

/locus_tag="EFAGFIKM_03853"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07085"

/codon_start=1

/transl_table=11

/product="putative oxidoreductase CzcO"

/db_xref="COG:COG2072"

/translation="MFLILRNHYPRVIQLHSSEYKNISQLLPETTWWVGGNSGAQIA
VELTSDDKQTVYISIRNITFRPLHIMKRSIFWYFEKLGILRASADRMVGKWLRNQPE
YVYGELKELMIQGVNMRPRAINAIDDRILYEDGSETAVDNIIWATGFKRNDGWIDI
NAAFDSQGTILHERGVSPVAGLYFVGLPWQTSRGSALLGWVKYDAQRIVSHIKGKSH"

CDS complement(4399743..4400198)

/gene="czcO_2"

/locus_tag="EFAGFIKM_03854"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07085"

/codon_start=1

/transl_table=11

/product="putative oxidoreductase CzcO"

/db_xref="COG:COG2072"

/translation="MYDVLVIGAGQAGLAAGYYLQQSGLTFLIVDAASSVGQSWRKRY
DSLRLFTPRMYDGLPGMPLSGNKNLSLPSKDEIADYFENYAKQMELPIKLNCEISRLSK
QDEVYYAETNDGMIEARNIIVATGPFQNKNVPHFAKSLSESNSASFIRI"

CDS 4400742..4402049

/locus_tag="EFAGFIKM_03855"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01212"

/codon_start=1

/transl_table=11

/product="Deoxyguanosinetriphosphate

triphosphohydrolase-like protein"

/translation="MNEINKLRAVRQFDESSTGRDSSDNRSPFERDYGRLIHSPTFRR

LQGKSQVFGAGSGDYRTRLTHSLEVAQIARSIARSITTTSANKEHPGLVIDPLVVEC

AALAHDFGHPPFGHKGEHDLNEKLKEYNLLFEGNAQNFRLLMFLEKRDSRYDGLNLSA

ATLLAINKYPYELTVDSSKGLYSSEWSYISEIRNKWDMPEKKATLEAQLMDLSDDIAY

SSHDIEDGIRAGKIQMNGSFLLNDRIDFVSIEVDKAYEKEPELWEGVQIKQEVKKVL

QEYLENWDEIHSKLQKNNSLTRKENKAFSVNNFVKQVGIIEDGEWFKVTFVDSNGMED

VDLKRKMIILKKLAWVTLRDLRVQRLQQRGENIINKLWDVFMKNTDSIIPTDWLDRF

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CDS complement(4402253..4402468)

/locus_tag="EFAGFIKM_03856"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGMASEAYNVNSKSPATIECKYQVIFTLRLIIIGNVPTIGVGFN

APTGEWIKIIEVDIAGGGMLDMGGM MY"

CDS complement(4402696..4403400)

/locus_tag="EFAGFIKM_03857"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MELRIYLVLLMVIIICGGVIWRVIKRLKWDVKFQRDQNNKLNEA

NYQLRDSIKSKESIKKMRLSALNLQNAINYKQPEDFNRHVFICNLNEGQQVVIIFDE

ELEYSQELQQKFIDRDRSPLKHSREIECVFVDGGKEQPLLMKHVFGGSNNAEIEDIN

CGKFTNRGIGTYILQNLFIVLKGMGIETVKASLSTVDYHKKDKLYNFYLEKNGFNLR

ELTEDKWGLVSKKLVN"

CDS complement(4403606..4405240)

/gene="groL"

/locus_tag="EFAGFIKM_03858"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q4MPR6"

/codon_start=1

/transl_table=11

/product="60 kDa chaperonin"

/db_xref="COG:COG0459"

/translation="MAKDIKFSEDARRSMLRGVDALANAVKVTLGPKGRNVVLEKKFG
SPLITNDGVTIAKEIELEDAFENMGAQLVKEVATKTNDVAGDGTATVLAQALITEG
LKNVTAGASPIGIRKGIDKAVKAAVAELQSISKPIDSKQSIAQVAAISAADEEVGELI
AEAMEKVGKDGVTVEESKGFATELEVVEGMQFDRGYISPYMITDTDKMEAVLDNPYI
LITDKKISSTQDILP LLEKIVQQGKPLVLI AEDIEGEALMLVVNKL RGT FNAVAVKA
PGFGDRRKAMLQDIAALTGGQLITEELGLDLKSAVVEQLGTARQIRVT KENTIIVDGA
GNKSDIDARVSQIRTQLEETTSEFDKEKLQERLAKLSGGVAVIKVGAATETELKERKL
RIEDALNATRAAVEEGIVSGGGTALMNVYSAAVAALSGDEQTGVNIVLRALEAPIRT
IAANAGEEGSVIVERLKKEQTGIGFNAATGEWVNMIEAGIVDPAKVTRYALQNAASVA
AMFLTTEAVIADKPEPAGAGGGMPDMGGMGGMGGMM"

CDS complement(4405314..4405595)

/gene="groS"

/locus_tag="EFAGFIKM_03859"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P28599"

/codon_start=1

/transl_table=11

/product="10 kDa chaperonin"

/db_xref="COG:COG0234"

/translation="MIRPLGERVLVEPLEQEQTTSFGIVLPDSAKEKPQEGRII AVGA
GVLKDGVRVALEVKEGDRVIFSKYAGTEIKFEGKEYLIMKESDIHAILD"

CDS complement(4405995..4406777)

/gene="tatC2"
/locus_tag="EFAGFIKM_03860"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O05523"
/codon_start=1
/transl_table=11
/product="Sec-independent protein translocase protein
TatCy"
/db_xref="COG:COG0805"
/translation="MTQQMEEMSITEHLSELRKRLIYVLSIFVLGLIAGFFVADPVYQ
YLTKSESAKGFVLHAFSFDGIGIYMKIAGLFSLIITLPFTVYQIWKVSPGLKPRER
KATLKYPYVFLFLTGMAFSYVIFPMALAFTTAITEKMGLVETYGMKQYFSFLFGI
VLPVSLLFELPLLIMFLTGLRILNPIRLRKMRVSYFVLIFIAVVITPPDFISDLLVM
IPLLLYEISVLLSAIVYRKQLAADEEIESRYVRSEDKKHAG"

CDS complement(4406856..4407104)

/gene="tatAd"
/locus_tag="EFAGFIKM_03861"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31467"
/codon_start=1
/transl_table=11
/product="Sec-independent protein translocase protein
TatAd"
/translation="MLSSIGPTGFILLAVIALLLFGPNKLPELGRAVGRTFREFKEGA
REIISEDSSNRKEQEAKPLAAESTPADKPADKRLPE"

CDS complement(4407313..4407798)

/gene="mog"
/locus_tag="EFAGFIKM_03862"
/EC_number="2.7.7.75"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9ZL45"
/codon_start=1

/transl_table=11
/product="Molybdopterin adenylyltransferase"
/db_xref="COG:COG0521"
/translation="MVWRTAILTASDKGARGEREDTSAQVIRELVEEELGGQIVEYRI
VPDEPDEIIAALIEMTDYFHADLVLTGGTELAIRDITPEATRRVIEREVPGMAEAMR
YSVMSKNRSAMLFRGVCGIRGRTLIVNLPGTPKGVHEHLAAIMDQLPEALLMVTGQFK
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CDS complement(4407836..4408339)

/gene="moaC"
/locus_tag="EFAGFIKM_03863"
/EC_number="4.6.1.17"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q5L3F4"
/codon_start=1
/transl_table=11
/product="Cyclic pyranopterin monophosphate synthase"
/db_xref="COG:COG0315"
/translation="MSSEANNGQASGGKLTHFNEQGRARMVDISGKEITVRTAVAVTK
VTMNPDTLEAIREGRIGKGDVLAVAQIAGIQGAKKTSDWIPMCHPLALTGVDIRFHDN
GVDELHIEVTVKTEGKTGVEMEALTAASAAALTVDYDMCKAMQKDMIIGPTMLNSKSGG
KNGDYSR"

CDS complement(4408355..4408993)

/locus_tag="EFAGFIKM_03864"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQDHAEKLSQLRSRLRQSRDLMDASMHQAMTKINTGVKRELER
LRQAKSKVVNRPLVIFSLSYGSEASTAFLFQEGWNHGDVMFAPKVLANPPRMELRRV
TGEQDLEPGIWGIPEPKDSCEVLTPDDWPGIDLILVPGLGYDLHGGRIGYGGGYDRF
AETLAATCAMTGKKPLMAAMVLPGQLQEEIPMDLLDLRIDLLITTEGILHIE"

CDS 4409273..4411231

/gene="yheS"
/locus_tag="EFAGFIKM_03865"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P63389"
/codon_start=1
/transl_table=11
/product="putative ABC transporter ATP-binding protein
YheS"
/db_xref="COG:COG0488"
/translation="MLLQVSGIIRFGVDPILDGVNLQILERERIGLVGVNGAGKSTL
LKIVAGEMSYDGGQIFKSKETTLGYLAQNSGLQSDRNIWEEMMNVFAHLTQAEADLRQ
MERDIADPAQMEDEKKYADLLERYAKRSDWFKDHGGYEMETRIRSVLHGMGFGFESPD
TPIATLSGGQKTRLALARILLQAPDLLMLDEPTNYLDIATLTWLEDYLRGYSGALLVV
SHDRYFLDRLVTTIVEIERHRSKKYTGNYSRYMELKAAEYETQMKQYEKQQGEISKME
DFVQKNIVRASTTKRAQSRRKALDKMERLDKPMGDLKKAHFSFETAVMSGKEVLRVDQ
LSVAYDEASPLFRNVSFDLRRGETVALIGNGIGKSTMLKCLTGSLRPVSGEIQWGTK
VQIGYYDQEQTGLNPSNTVLEELWSAYPGMEEARIRTVLGNFLFSGDDVLKKISSLSG
GEKARVSLSKMLKEANMLILDEPTNHLDLFAKEVLEAALMDYEGTLLFISHDRYFLN
KMAERIVELHPGGTEQYLGNYDDYVEKKQELEDIAREAAEARQASSKNSSKSDLNTAT
TEKSGAASFEEKQAKREERNRQRKQEALEQQIAVLETKITELEAQMALPEIYQDYMK
LQELQQQSEEHKAELTKAYEDWEELAME"

CDS complement(4411884..4413443)

/gene="leuA_2"
/locus_tag="EFAGFIKM_03866"
/EC_number="2.3.3.13"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q71Y35"
/codon_start=1
/transl_table=11
/product="2-isopropylmalate synthase"
/translation="MTTNNKRMIEIFDTTLRDGEQAPGASLQPEQKIELAHQLASLG
IDVIEPGFPISSPGEFAAVQAISRQLQNVEICGFARAVKGDIDAAVQATADAARRRIH

LFISSSDIHIEHQLRRPRSEVVATAREMVSARQFTDIVEFTAMDAARTKMDDLIEMV
EVAIEAGASIINLPDTVGYALPHEYGEMFRRVREGARGGDQVRYSACHNDLGLAVAN
SLAAIANGASQIEVTINGIGERTGNCAL EELIMALETRGDAIGATTNIKLNQLYETSR
QISRAMHFPIAYNKPVVGRNAFQHESGIHQDGLLKNRSTYEIMDPEALGIPRSMILG
KHSGRHALKDRVRKYGFEPDEQQMEQLYEVFKETADQQKVVSDQQLQMVSQTMNIPA
QDYELVELQVTAGSMTDRMAAVRIRTSAGEQSYSAVGGGPVDATIRAIGQSISDDIAF
VDMEMHALSGGEGASAEAVVTVRAGREFRGTATHNDIVMAAGLAYVAACNAAGLKAE
SSEHHEQEAHA"

CDS complement(4414627..4415682)

/gene="tsaD"

/locus_tag="EFAGFIKM_03867"

/EC_number="2.3.1.234"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O05518"

/codon_start=1

/transl_table=11

/product="tRNA N6-adenosine threonylcarbamoyltransferase"

/db_xref="COG:COG0533"

/translation="MNELNEKINSAPSYILAVETSCDETSVAVVKDGREVLSNLISSQ

IETHKAFFGGVVPEVASRKHVEVITLMLEQAIEQSGIRPRDL SIAVTQGPGLVGALLV

GIVAAKTMAMALGKPLIGHIAGHIYANRLTHELQYPAMALVVS GGHTLVHMESEG

KFKLIGRTRDDAVGEAYDKVARALGCPYPGGPHVDRMASEAEDVVPLPRVWLEAGSYD

FSLSGLKSAVLNVNLNQA KMRGETLEPSAVARGFQEAVVEVLVEKAVRAVREYGSRQLL

LCGGVAANRGLRSALQERCTKEGLELLIPPM EYCTDNAAMIGAAAYLKWQRGEIAEFD

AKADPGLSLEEWSVQSV"

CDS complement(4415679..4416200)

/locus_tag="EFAGFIKM_03868"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDNVANNKQEATLQFRFMTLADIPDVMEIEHEAFTLPWTEEAFQ

NELTHNHFAKYMVMELEGKAIGYAGMWTIMDEAHITNIAVRGAYRGRKLGEKLLDELM
STAAYLGMERMTLEVRVSNISIAQRLYQKKGFESAGLRKGYSDNGEDAMIMWANLP
SA
GRSGEEEGSVLDS"

CDS complement(4416218..4417072)

/gene="tsaB"

/locus_tag="EFAGFIKM_03869"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O05516"

/codon_start=1

/transl_table=11

/product="tRNA threonylcarbamoyladenosine biosynthesis
protein TsaB"

/db_xref="COG:COG1214"

/translation="MMMEDLQKEPRQRFLALDTSTAVMAAAMMEDHALLEERNEGAER
NHSVHVVPVMEQLLAASNTQPGQLDGIAGVGPGSYTGIRIAVTAAKTLAWAWDIPVA
GVSSLQAIWGGWHSGLAAKAEAAAEDAAAGAGGTPSADQGSGAAPVHWIVPLVDAR
RGQACTALFASAGSDAPRRRLAPDAIRKMDGWLEALAARMAEAAPEERPVAWVIVGETG
PHAAAAAELRCPAGTALQLVPYELEGRWVGRLGAAALLAGQRDDVHALVPNYTQLSEA
EANLLRKG"

CDS complement(4417069..4417551)

/gene="tsaE"

/locus_tag="EFAGFIKM_03870"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O05515"

/codon_start=1

/transl_table=11

/product="tRNA threonylcarbamoyladenosine biosynthesis
protein TsaE"

/db_xref="COG:COG0802"

/translation="MNQTHEQWVYQSHGIADTEALASALASQANAGMVIALDGDLAG
KTAFSQKFAWHLGVRDVSSPTFTLIKEYEGRPLYPHMDVYRISLEEDELGLDEYFY
GAGVSLVEWSSIIPELLPQEHLHVQIETTGLEDRITLDGYGETYAAMCRQFRQNGVK"

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CDS complement(4417819..4417998)
/gene="sspH"
/locus_tag="EFAGFIKM_03871"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00667"
/codon_start=1
/transl_table=11
/product="Small, acid-soluble spore protein H"
/translation="MMDAKRAKAIYDSKDTIAVTLEGDPVWIENVDEANGMATVQVGS
RPGNTQTVRVDRLEE"

CDS complement(4418000..4418296)
/locus_tag="EFAGFIKM_03872"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKNRRDEEEAHKHAFSPYPLAKAESAEFYTPATAVNWEAVTSE
ELPLDRESFMLDIDRMVNEGLGGGQVTEDNGYIGESTTDSMVRESHDDPEGEYE"

CDS 4418547..4419461
/gene="ku"
/locus_tag="EFAGFIKM_03873"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34859"
/codon_start=1
/transl_table=11
/product="Non-homologous end joining protein Ku"
/db_xref="COG:COG1273"
/translation="MHTVWKGAI S FGLVHVPVKMF SATEDKDISMRYIHKVCGSPLAY
VRQCPSCEVDVKWEEITKGYEYK GK FVLFEKDELEALNDSTNKTITILDFVDLTEID
PIYFQKTYYLSPDQAGGNAYQLLMNAMRDTGKIGIAKISIRSKSSLAAIRVLEDCLSM
ETIFYPDEIRPVSQV PNLPEVQNVNEKELTMAKLLIDQLSTPFEPGKYTDDYRSKLLD

LIQHKVAGEEIKIAPAKPEANVMDLMAALQASIEAVKPIPADPGTTAKPKKRAPRKT

PAQAVAGGESDTPAAPAKRKKATPKPKV"

CDS 4419780..4420649

/gene="catE"

/locus_tag="EFAGFIKM_03874"

/EC_number="1.13.11.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54721"

/codon_start=1

/transl_table=11

/product="Catechol-2,3-dioxygenase"

/db_xref="COG:COG2514"

/translation="MNTTYQIPATTHLGEVSLRIMNLDRSIEFYTEVVGLKLELSGK

VATLTADGKQSLLRLEELTDGITLPERSHAGLYHFAILLPDRKSLGLALRNLAASGID

IGQGDHLVSEAFYISDPDQNGIEIYADRARDTWKRSDNNYVMASDPVDVESLFAISE

NEPWQGLPTGTVIGHVHFHVRSLEEARNYYTGILGFDIVGNFANMSALFVSAGGYHHH

LGLNIWAGVNAPVNPDNATGIDYFTIVYATQEQLDQALEQLRQSGAVVTQVEGTWFTV

DPQNIRIRLTAN"

CDS 4420827..4421924

/gene="gerAB"

/locus_tag="EFAGFIKM_03875"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P07869"

/codon_start=1

/transl_table=11

/product="Spore germination protein A2"

/translation="MIEKGRLTVRQLASLLFLCTIGEQLVFPSMITSYAHQDAWLSA

LLGVAGGLGILFIMLIAYKLHPRLNLIQNALRTLGPWIGTLFGSFYLFYFLISTSTFI

REIGDFMSTQILPESPLLILHLVFMCALVWGLLSGLESIGKTAEVFLPLIVLFLILT

VCLIPHVRLANIQPVLAQGFLDPFKGFVAVLTPYCELCIFMMLFPYTKNEPHLEKDI

LLAGMIGGLLLTLTSMCLLMGPWMTQHWWFASFNLSQKINIGNFLQRIEAFIASVW

IIAVFFKAALFFYGFVLGVAHLFRLSSHRSLILPGAMLILAMSILISPNEFYLKVVI

PYWIDWDLTCGIALPLLLILVHHMKSRFQKI"

CDS 4421979..4422929

/gene="ligD"

/locus_tag="EFAGFIKM_03876"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WNV3"

/codon_start=1

/transl_table=11

/product="Multifunctional non-homologous end joining DNA
repair protein LigD"

/db_xref="COG:COG1793"

/translation="MFKPLIPFEPISRDTLPTGPQWIAQVKWDGVRMLAYEDGHELRL
VNRRLHDRTAQYPELVTPRNLCSGSSYILDGEVIALDPDTGKPSFYHVLRRDRMSRPE
GIAQAIHQIPVTYMFVDILFYEGKWVTDRLADRQRLLEVLNTAPHVQEVTNTLDAA
SLLTVMRQHQMEGIVCKDLTSSYGIQGKDQRWQKVIMHDVYAMIGGVTYRSGIVNAV
AVGVYDGNPFVYIGHVGTGKLNSNTWRELTHQVEPLIKQDRPFHNVPERSAETTWVEP
RIGVKVQYMELTTHHKTLRHPSIQTADVTRREDCLANQLLP"

CDS 4423001..4423891

/gene="ligd"

/locus_tag="EFAGFIKM_03877"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34398"

/codon_start=1

/transl_table=11

/product="Bifunctional non-homologous end joining protein
LigD"

/db_xref="COG:COG1793"

/translation="MAPKIQGTIIIEGTELTVTNPDKLLWPDAGVTKAIYLQKLAALA
PYLLTYTSNRLLTTIRYPHGAGGTTYQKNAPEPVPDYVHTEVHDGIRYVVMNGLPEL
LWLGNLAALEFHPSLHTVGSHLPSEWMIDLDPSEHEPRIMQAALIVGETLSLGLRS
IPKTSGATGVQIIVPIVQGVTFDELREIGYFVGKYVTQKHPDLFTLERLKKDRGDRIY
FDYLQHYGGKTLAAPYTPRAKSGATVSTPLTWDEVRSNVSQDYHLMNIIERLNKTGD"

LIAAVEPQPVELILKHLKKK"

CDS complement(4423947..4424858)

/locus_tag="EFAGFIKM_03878"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSNVTVKELTAKQADRGVKSSVFTLKLQ RIVMILIGAALMAVS

LEVFLVPNGVIDGGITGISIMVSELTNLPLGVFTLLNLPFLILGYKQIGKTFALSTL

LGIVVMSIGTSLLHHVPALTPGEPLLGA VFGGLILGVGVGLVIRSGGSLDGTEIVAIL

LSEKSPLSVGQIVLFINVFIFAGAGFVFGWPNALYSMIAYYIAMKMIDIVNEGLDQSK

SVWIISEKYRDIGSALTDRLGRGVTFLDGEGGFSGDEKKIIFVVITRLEEAKLKTIVE

DWDPQAFVAIGNIHDKGGRFKKKGIH"

CDS complement(4425206..4426645)

/gene="clsA_2"

/locus_tag="EFAGFIKM_03879"

/EC_number="2.7.8.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P71040"

/codon_start=1

/transl_table=11

/product="Major cardiolipin synthase CIsA"

/db_xref="COG:COG1502"

/translation="MFWLVIIILLVFIFQAATILLLEFRNPAKAVAWLFILFCVPLIGF

VVYYFVAQDYNKRKKLRKGGSRI F REMKETIWEQAHVIGDVEQMPGDRFSHQHRLFNL

LSHLSESPITGCNHSTVLTNGEEAFAAMLREMEKAKHHLHVEFYIFRDDVISTKFQDV

MIRKAQEGVKVRFICDGLGSHKMSWSFIRKLQDAGVEFHYPPLIATIDRRVNYRNH

RKIVVVDGQVGFGGINVGDDYLGQYPEVGFWRDTHVQIEGDAVYFLQSTFLNDWKLA

SGERITEPQLVELFPPHICSGEERI QILASGPDQDWD AIQEMCFGAISVACDRIYITT

PYFIPDPALYEALKTAAVSGVDVKIIPYQSDSKLVHLASLSYVEELLRAGVQFFQYR

KGFVHAKVMIVDELLATVGTANMDMRSFFCNFELTAVLFESSAIRRLITDFERDLGEC

SQIDVKVFQKR SRWQKGAEMLSRMLSPLL"

CDS 4427022..4428380

/locus_tag="EFAGFIKM_03880"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WFP3"

/note="UPF0053 protein Rv1842c"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MESERYALNLVLVAFLIGLSAFFVAVEFALVRVRPSRIDQMIAE

GNKRALAVKQAVANLDGYLSACQLGITITSLGLGWLGEPTVEKILHPVFESLQIPEAV

SSFLSFVIAFASITYLHVVVGELAPKTIAIRKAETVALLTSTPIIWFNRIMYPFIWLL

NGSANQLVKLFGIKPASEHEDAHSEEELQIIINESFESGKINQAEFGYVSRIFAFDEM

LAKEIMVPRTDMVCLYVNRTNEENLEIREEQYTRFPVNVESKDDIIGIINTKQFFLE

LYGNDEPVDLSSLIQPVSAVHETTPVKDLLKKMQKDGVHIAVLVDEYGGTSGIVTIED

VLEQIVGEIRDEFDADEVEDIQVINENYIMDGKVSLSKVNDMFMSSLDADEWDTIGG

WLYSHRPEMNEQEEYEFENLIFVLEKDKNRFYKVAVVPKEPLTMSDYTDEDEKESNW

SK"

CDS complement(4428506..4430095)

/gene="estD"

/locus_tag="EFAGFIKM_03881"

/EC_number="3.1.1.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9WYH1"

/codon_start=1

/transl_table=11

/product="Esterase EstD"

/db_xref="COG:COG1073"

/translation="MNNWKKLLLSLTFVGLILPVTSISEAAEKSAGSENLPVIREIAE

KNGAEVSWQQKTGQITIRKSELTIVVKVGEKQAMVNGQAI SLDPVQLTKGTTYMDGA

FLSETLNAAPEDIFISLISEGDGKEAAKYVHTSVSGVLSPTLLSQLWGALEGQNGKIT

SEAIAKHVENNTVHRNVYTFKTELRLNITVRMNHNGLVDDLHIAAATPDVYQKPSY

DDPSAYTEQDITVGQGD LALPGTLTPKGEGPFPVVLVHGSGPSNQDAAIGGAKPFR

DLAVGLASQGVAVLRYDKVYEHTYKVASQPKFTLKQESVDQVNDAVELLKKNAHIDS
TAIFVAGHSQGGFAMPLIAEDKQHDIAGSILLAAPSSSFVDVLTEQQDELVERMNQL
GLDTDVIQGGADFYKNVAAMVKDPKYSVDHLPEAFPLQPAYWWFEQRDYVPAELAKTQ
NTPMLVIQGENDVQVSMNQFQTWKSSLQGHSNVTYNSYPKVNHLSSYDGLSIGQEYA
EPSNVSKAIIDDIKWVLKSN"

CDS complement(4430154..4431254)

/locus_tag="EFAGFIKM_03882"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQLFSILPIILIFAPLALLSFAPYVTRETISFGVTVSQYNYT

PILRKLRSTFATVSLIGNGMILVCLYFLRSANEDSTAITGVSTMIFIVYWAALHIL

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SLPNVPIKYDLQGHVTSGVPKTYLSVLAINFVQLGIILMMLNVNWSIKSSKQQLTTS

NPGQFAAENIQFRRKWSLFTLVTLGLLLTILFAFIQINMFVPNLVLLTAISFSIPVLIV

LGAVWLSLTGRQGGGKIRNQQEDHERSKEQPVNDDHWWKLGFIFYFNANDPSLTIEKRY

GIGWTINFARPLSWVLLLFIIAIVVISIVLSQ"

CDS complement(4431279..4431674)

/gene="ytrA_1"

/locus_tag="EFAGFIKM_03883"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34712"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional repressor YtrA"

/db_xref="COG:COG1725"

/translation="MIIQLDMQSELPIYSQLVYQIIEGIASGELQLGEALPSVRNLAA

DIGVNLHTVNKAYTLLKQDGYILVHRQKGVVNPDPGMPGLTDDFLKRQQRELRPAAE

AICRGMTKEELSAVLDQMYDDVKMGHNKE"

CDS complement(4431880..4432953)

/gene="yhhT_2"

/locus_tag="EFAGFIKM_03884"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AGM0"
/codon_start=1
/transl_table=11
/product="Putative transport protein YhhT"
/db_xref="COG:COG0628"
/translation="MINNKFYRICTAIILLLLIVYLGEKVNFI FSPLTSLIHIIIPL
LIAGFFYYLLRPLVDYMERHKIKRALSVLIYVVIALILAGFSVLVWPSLREQLMNFV
ENAPALVTSLSDQLNALEKSNVVSRYLPDDSNLFSRLSDVLSQGITQVTNYVSGLFSV
VSNLVIILATFPIMLYYMLKEGSKFGTNLTLLLPRHYRKDGEETVHEIDEALSNIYVG
RVIVNVALGILMYIGFLILGLPYALLTVVSIILNFIPYVGALLAAIPVVIVAFIESP
TMAIWSLVIIVIAQQIQDNLISPYVYGKQLDIHPLTTVILLVGADLGNILGMIIVIP
LYMILKIIVRKIHYRIVEDKTEL"

CDS complement(4433253..4434044)

/locus_tag="EFAGFIKM_03885"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGSFGNLILNENMKIFRRPRTWIMLAILALISLLMPVLLREGMG
SNEVLYWEAAVTTIQITFFLNTIFCVVIAAESVAGEFTWGTIKLLLIRPWSRSKVLAS
KYLTVVGFSIVSTLLIIVMAMLTSYILFSHDAPGGSSSPATNALTLWGYLYVDLFI
TALAIFMVSSVFRSGALAIGLSLFIMFSQSIFSLIFNPVRYEWAKYVLFNNMDLSKYMTS
GADFALMGGPSAGMTLGFSIAVLAVYYVIFMVISWVVFVSKRDVAG"

CDS complement(4434037..4434945)

/gene="bcrA_1"
/locus_tag="EFAGFIKM_03886"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q5WNX0"
/codon_start=1
/transl_table=11

/product="Bacitracin transport ATP-binding protein BcrA"
/translation="MQQEPVVRIQGVSKIISRSLSVSDLTLDISPGQVFGFLGPNGAG
KTTTIRMMVGLMSISKGDILISGHSVKNEFEKAVAQVGAIVENPEMYKFLTGYQNLVH
FARMSPGVTKERIAETIERVGLTARIHDKVKTYSLGMRQRLGVAQAILHKPKLLVLDE
PTNGLDPQGIRELRDYLRLTQEEGITVFVSSHLLSEMELMCDTVAIQNGKLIDVRN
LRVEAGSDALIEVAFELNDADRAADLIQGAIVQGNVLVMRVSREQIPDINAKLVSEGF
QVYGIRNVTHLTLEEQLQVTGGGGIG"

CDS complement(4434978..4435229)

/locus_tag="EFAGFIKM_03887"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIETGRFYCVSCGMIVSVTRSSVEMKEEGNGGNHVFRTGFYRSE
MPLGCCEACVDEAKRQGKSQFAGQYTKDYDTLCSYEKRA"

CDS complement(4435481..4436002)

/locus_tag="EFAGFIKM_03888"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLRRRNARNALLRKIGFITIVLLLWLIARTIPYLFQADTSDEAA
AVAAEFYKYEQTGDFGSSWELFHPLMKERFPKSAYVQNRHIFMQHFGVETFELEMEQ
PEREFDVTVIDGVNPFSEAYRIRVTQKYSGTFGQFDMVQTCYLVEDGDQWTLWYYPN
QKNEDTSQVDNSD"

CDS complement(4436096..4436671)

/locus_tag="EFAGFIKM_03889"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKVVITILIEEGSRRRRRNHKRRRYGYLISVLLIISWILFIWSM"

SAQSYQQQTIQPWLHQWSEQIQWVLSLPDIQFTYGEHHYSLNARPYDFAEFIFRKSAH
VFVYAVLAVLVYCGMRYRRSGMKTCIGIALATVIVIASFDEYIQQFSPNRTASIRDVG
VDLIGGLCGVMLWIAGVAIYRKLRFSFSRYHR"

CDS complement(4436708..4438831)

/gene="xghA"

/locus_tag="EFAGFIKM_03890"

/EC_number="3.2.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q70DK5"

/codon_start=1

/transl_table=11

/product="Xyloglucanase Xgh74A"

/translation="MRMFRLPKFVLIVILMYTLMIPTSSNVVQSAESYQWDQIPIGGG

GYVTAVVVHPTPELDLVYARTDIGGVYRLDPINNRWIPLLDHIESGESNLYGIDGIALD

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PSNSNYLHVGTTRYDGLYTSSNGGDTWSQVREVPYGLSGQGIRSVVYGVNPAAKHEQVV

YVGVRGVGIFAKMKRSNGQMTWELIRNSPESTARMTVSKSGILYVTTDNRGILKYNGK

QWTNITPSSEYSSYYGISIDPSNDNHILAAVRTGGSNLPLYRSANSGQTWTSVNKTLN

DRPPWWSSNMFFSATSSVFDPHHPGRVYVSDWSGVFKTDDITQPMQWDAITDGHEE

VVALSATTPPQGAAFFSGVADQVGFRHSDIFNTPIQKLPLAGMQEVVSIDYHEADPNQ

IYLGSDWYGTITKLFVSTDNGLTTTSVNVPAQSGLGRIAYSASNPNIYFPQKGK

AVRSTDKGVTWQSMNGLPSNNTGGESIFTYNQTLAADRTNGNKFYAYYAGHLYRTNNG

GANWIKANIVALPRSEKIKVEAAPGMENVVWVSLGEAGLYASNSSGAAFTKIQNVQSS

ELFAFGKGKSGGVNPAVFIYGTVNQVKGFFRSDNMGLTWNNITPLTGIGLGNEPQVME

ADRQTYGKVYVGTNGRGLFTGYFAQ"

CDS complement(4438852..4439775)

/gene="tagU_3"

/locus_tag="EFAGFIKM_03891"

/EC_number="2.7.8.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q02115"

/codon_start=1

/transl_table=11
/product="Polyisoprenyl-teichoic acid--peptidoglycan
teichoic acid transferase TagU"
/db_xref="COG:COG1316"
/translation="MKLKLGIKISLTVLILMIAIVIGYAIYLYLHVKSAADNIYEPRE
PIKQVSIVDNRGGRFPIDMENQEPFTALILGVDERVNDRGRSDTMIVLSVNPTQKSVL
MFNIPRDTRTSIVGHGTEDKINHAYAFGGVNMSVQTVEQFLGVPMDYLLKVDMEGFAK
VIDLVGGVDVHNPF AFEYEGHRFEKGT LHLDGASALGF SRMRYDDPKGDLGRNDRQRE
IIKQVLKNTVQISTVFQLESLLGEVSEHVKT DVSFDEM KQMLS NYRNVLEHVESVEIK
GSGKKIDGVYYMVEQSEKNRIHQLIKEHSG"

CDS complement(4439790..4441121)

/gene="ywqF"
/locus_tag="EFAGFIKM_03892"
/EC_number="1.1.1.22"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P96718"
/codon_start=1
/transl_table=11
/product="UDP-glucose 6-dehydrogenase YwqF"
/db_xref="COG:COG1004"
/translation="MNITVIGTGYVGLVSGVCFSELGNNVICVDNNVEKVTMLTG GHV
PIYEPGLQEV MNSNMKAGRLSFTTNIQDAISRSDIIIIAVGTPSLPNGEANLSYIELV
AREIGSYMDNYKIIMTKSTVPVGTNDRIQEWISSLTSHPFDMASVPEFLREGTAVQDT
LYPDRIVIGTHSERAVATL KELHQPLTEQIIVTDIRSAEMIKYASNAFLATKISFINE
ISNICEKVGADVSRVAEGMGYDRRIGASFLKAGIGYGGSCFPKDTQALIQIAGNVDYD
FKLLKSVVEVNKDQRFNVIRKLEELDVL DGKQIAVWGLAFKPD TDDVRDAPAVEIIQ
RLLDQGATVKAYDPIATENFRKEVDSPAITWTSSAMEAAKGADALCVLTEWKEFMEVD
LTELAVHMQPILIDGRNIYEEDQIKDTAFQYYSVGRPGLTNIDGRKTAVL"

CDS complement(4441154..4442536)

/gene="algA"
/locus_tag="EFAGFIKM_03893"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P07874"

/codon_start=1

/transl_table=11

/product="Alginate biosynthesis protein AlgA"

/db_xref="COG:COG0662"

/translation="MRSILLSGGSGKRLWPLSNDERSKQFLKVLHGPEGEPESMVQRV
WRQLNCAGLASQALIATSLPQVEILTSQLGDDVKLVVEPERRDTFPAIALAASYLYSV
ESVSLSETVAVLPVDPFVEKEFFEVLATLPEMLDKSGADLALMGVVPTYPSEKYGYII
PQSLSSSKTSNEYVHVAKFQEKPCESDAVLMIEKAALWNCGVFAFKLEYLINLLIEME
LPIQYDEMLKQYGRQLQKISFDYQVVEKANQVIAIPYNGFWKDLGTWNTLTEEMGTSV
GKGWITDDSHDTHLINELNIPVAVLGLSGVWVAVSPDGILVSDKEASPRIKEIVKNED
QRPMYEERRWGCYRVLDYTRNEAGGEVLTKRICISAGKNLSYQYHLLRNEVWTVVSGT
GELILDGQRRMISEGDTVIIDRSM LHSVRVAVTELEIIEVQIGSQLIEEDIVRVTTTEWQ
DIVQTYMKHV"

CDS complement(4442533..4443561)

/gene="epsO"

/locus_tag="EFAGFIKM_03894"

/EC_number="2.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P71065"

/codon_start=1

/transl_table=11

/product="Putative pyruvyl transferase EpsO"

/db_xref="COG:COG5039"

/translation="MLGTNNIHPMEELKGHLLQILKVIPPRTDIYYLDYPVHSNGGDL
LIMKGTEAFFRDNHINVLARYSILDCPLSLKVPEGITIVLHGGGNFGDLYPAHQKLRE
RMIAQHPNHRIVLPQTMFYKSDIELKKTAQVFSRHKDVHFFVRDTLSYEIASKEFQQ
TNVYLSPDMAHQLWPLKSKSQPVAEMLYFFRKDIEKTQNQVQYESISGPKATFKDWET
LYNRVDRKIIRMISSRLKSGKGNALARWLWYKYSRDMVHTAVKEFNKYKTVTTSRLHG
HILACLLDQPNILLDNSYGKNTNYYTAWTRNNPVGRLEAGQTSTYNQSTKAGKSGSTV
VLSDGAAL"

CDS complement(4443548..4444921)

/locus_tag="EFAGFIKM_03895"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSQLALPKLLKGNSSLQTIVHTSGTNVIIMVFTTITSITSRMF
GVEGKGAFSAILFWPTFLIGLVSWGLPTSIIYNLKREAAEKSAEYLRLSFMVQIPISF
ILGAIAWIYMPSWMADYPPEVITIAFWFTVTIPVLILINLLSALSQSRDRFQVYNGI
RLYNPVLKVIVMISLWLLGAMSIGMASFVSIASSVIVVAWAAYTLRDSLKFRWFTKAI
DRKAAKNLFGYGSRVFGVELLGTLYTQFDKIIILALLTPRDFGLYSVVFALSRIYNAV
QNAISSVWFPKVTGLPQDQVIRTVGRAFRLSLIIMTIIVVPTMFVGNWLMGVLFGKEF
LEASQAFYILAFECIIGGGSWILASAFNALGRPGLVMIRQLIALSVTIGLFFVLTPLW
GLNGIAIALLIGSIVRMLVTVAAMKIAFKVKFSGMFFDKKDIAFLAERLNKKRRVTQG
GDGDAGH"

CDS complement(4444932..4445831)

/locus_tag="EFAGFIKM_03896"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKATVAICTYNRAYDLSESVLSVTRQHVEYDVEIIVIDNNSTDH
TAQLVQEIQDIEGVDNVKYVLEKKPGLSAARNRAIREARGEYILFLDDDAIASPLWIQ
HIVDVFESDSSIGCVGGKIEPLWESQKPDWIPSERLSLYTILDYADHVIEMPNSIPF
GANVAFRTQLFQDIAPFREDLGRVGKNLLSNEESELISRIRVQHKVFYTPFGSVQHKV
SKERTTKNWFLRRVFWQGVSDAVRKKDKGAIRTIKHAIRLGQGVIRALLCIYSPKRFT
RQLAQICYRNGLIIGILRYNSKE"

CDS complement(4445858..4446880)

/locus_tag="EFAGFIKM_03897"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MHEPVVYMLPKMIKTNKFNELLSQSIEDQGWDVKHFSKKDLKHV
RKNDVLHFHWPSFYKGNNAFSTFIKSILFILMIMYVRLKGAKLFWTVHNIWPHNSGR
TWHDYWMRRFLVRNCTKLIVMGKPLIRSVSETFHVPEKIEVIPHGHHYQGVYGRGTGQN
IRDLFNIPANDYVFAFFGQVSPYKGVDDLIKAFNHLDWKDAHLLIAGKKSADYDLEDS
IRHSDRIHTYFNFIQDGEYSDFEAIKSMILPYKNIATSGSAILALSFGKPVVAPRIG
LMEEYLPENCAVLYDPSDQEGLEEAMKKIRAKDDEFREGDGFQSMLEWVSGIAKRT
ISLYTI"

CDS complement(4446896..4447831)

/locus_tag="EFAGFIKM_03898"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEALVSCIITTHNRAELLKKAMASVLEQTYPFLEIIIVDDGSQD

HTEEVCRAWTKEDHRIQYIQVPAQGANHARNLGIQRANGKYIAFLDDDDQWLDPKIQ

SQTRALEENKGLFCFSKVLVYVDQDHKVTRRKVSVESRDLVFYADLLTYNWIGETSK

IMVQTQLARSVMFDEQLTSAQDYDFYLRILQRGHHAINIREPLVHIYIHQGPRISTSS

KKKFQGQRKVLIKYYKDMSEEQKRRQLHHYRMMEWSKNPKNVFLKNTLALYPWWKN

FTLFKRNIRITLVGYRLRKQFRSEALSKEEYKGTGTA"

CDS complement(4447853..4448920)

/gene="mshA_3"

/locus_tag="EFAGFIKM_03899"

/EC_number="2.4.1.250"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01695"

/codon_start=1

/transl_table=11

/product="D-inositol-3-phosphate glycosyltransferase"

/translation="MKPKVLVIGSSTKDMGGIVSVIVNIENSLIAEQYNLQRIETYIT

GSVLARLIIFIKGFLQLVLKLVTFKPDMIHMHMSYNGSFYRKALFILVGRKIFRVPVI

VHIHASSFDVFYNRHPLQQKLCKYVLNQVDKLIVLSYTWKSFFSKIVPESKIEVLYNG

VFIKEPPIREERQVPRCLFMGRLGKRKGVYDLLLAIQLLKQRGVEAVFTLAGDGEVNE

VRALVERYGITEYVEVPGWIRGEEKERLLHDADILVLP SYHEGLPMAILEAMNEGLPI
VSTRVGGIPEVITDELNGFLVEPGDVTALAHVLERLILDKELRVQMGLNNKKLVTSKF
NMNSLIENLSSYDKVHMKVS"

CDS complement(4448958..4449437)
/locus_tag="EFAGFIKM_03900"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIFVVLGTQRFQFNRLKAVDNLIHEGQMPSDVLVQSGYSEYKP
LHYQQKPFFNQEEMNEHIAKSEFVLSHAGVGVITSALQMNNKVIVMPRRKDHGEHVDN
HQL EIAKVFQDKGYISVAQNEDELHALIANIDKLDFQPYVKSNSQLLSSIKGYINSL"

CDS complement(4449434..4449892)
/locus_tag="EFAGFIKM_03901"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKVCLVSSTGGHLNQLLNLI PAVEDHDYFLVTEKSEASSKLNLS
NRTYFLSQQERKNILFLFIVLRNIIASL FILLKERPKVLITTGAGAVYPLCLLGKLMG
AKLVFVESYAKIYSPTLTGRMIYKFADEFYIQWETLQEAYPNAKYRGALF"

CDS complement(4449889..4451235)
/locus_tag="EFAGFIKM_03902"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQKTDYFASSRGNTLYIILSSLIIGMAVYLP IISIMALALLIL
FGIYMKHPSWVYMIVIGTFSLMDKIFRMQMMGFDASSFYKLLILFFILPIFLRYGLK
KQFIYPALAVGYLFIQSYFLSVMPGKMSPLDPFKAFLGLVVPFLLLMVNF PKEVSKRI
ISVLAWLPVFSLIGGLILQQFGMLSLSNLEGSGVSRLQGANIAAHLGMLCFISICVCL
MEIRYKNQVILNYALT LTHFIILIQTGTRGPLLALIPVCMYLFDHVRKFVKGRTSAL

LPVVLFLAAVSVMVVLQWDNYELRQESKGLSGRDSAWAFFIKKANEYPIFGQGLGSAL
VANDGSIFSGFTVPHNEYIRFYDGGVLGALLIFGALLFVYKKVYNKLNRLVKPYFVG
MIVGFSIYSFVDNTLSTIHLIAPFCVYLNALYQISDEKRVVPDNPQEFVHRKEIMQ"

CDS complement(4451270..4451968)

/gene="epsL"

/locus_tag="EFAGFIKM_03903"

/EC_number="2.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P71062"

/codon_start=1

/transl_table=11

/product="putative sugar transferase EpsL"

/db_xref="COG:COG2148"

/translation="MSPSPQTKEAEIVMDPSLGYNASTMSGQNADKVYLFMKRMLDLL

GSFIGLIILCPLFAVIGILIKIEAPQGSVFFRQVRVGQNGKEFHMYKFRSMVANAEDL

LEQLIDQNEVNGNMFKMKNDRITRIGKFIRKTSLELPQLWNVFRGEMSLVGPRPAL

PREVKNYTSYDRQRLQMIPGCTGLWQVSGRNSVGFEEMVELDLTYARERSMMVDIKII

FRTFKVLVGSKDAF"

CDS complement(4451965..4452921)

/gene="gtaB_2"

/locus_tag="EFAGFIKM_03904"

/EC_number="2.7.7.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q05852"

/codon_start=1

/transl_table=11

/product="UTP--glucose-1-phosphate uridylyltransferase"

/db_xref="COG:COG1210"

/translation="MPWFNFYQTKKKEDRVVFMKKVRKAIIPAAGLGTRFLPATKAMP

KEMLPIVDKPTIQYIVEEAIASGIEDIIIVTGKGKRAIEDHFDNAFEHNLLEKGKL

GLLEEVKSSNVDIHYIRQKEAKGLGHAVWCARNFIGDEPFAVLLGDDIVVSEVPCTK

QLIDQYDQVQHSIVGVQTVLAEQTDRYGIVDPLQSDGRLTEVLRFVEKPAQGTAPSNL

AIMGRYVLSPEIFEHLEQQEIGQGGEIQLTDAIQRLNETQGVYAYDFEGVRYDVGEKL
GFILTTIDFALQKQELRIPMLQALQQILEKESVEHVAGGEFE"

CDS complement(4453055..4453732)

/gene="ywqD"

/locus_tag="EFAGFIKM_03905"

/EC_number="2.7.10.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P96716"

/codon_start=1

/transl_table=11

/product="Tyrosine-protein kinase YwqD"

/db_xref="COG:COG0489"

/translation="MSRQTNENNSLVTYFNSKSQISEGYRKLRTNIQFSSIDSHIKKI

MVASAESGEGKTTTISNLAVTYAQEGKKVLLIDADLRNPSLHQVFSVPNHIGLSSVLS

NQYSVEDVLRRESYIDNLQLFTSGPIPPNPSEMIGSNRMKRLIEKLEDQYDVIMFDTPP

VLAVTDALIVSSLCDGVLLVNSGKVKKELVKKTKAALEHVNARILGAILNNIKNVAV

PVGYGEK"

CDS complement(4453713..4454462)

/gene="ywqC"

/locus_tag="EFAGFIKM_03906"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P96715"

/codon_start=1

/transl_table=11

/product="putative capsular polysaccharide biosynthesis
protein YwqC"

/db_xref="COG:COG3944"

/translation="MELKGYFRLLQKKLWLIVAIALVAGVGAGVKSIFFTQPIYEASS

KLIVNQTSNVQGQAMMDFSMIQTNIKLINSYREIIKSSAIMDKVATTYPDLGLTSAQL

MNSTSVSTASESQVMSITVQGTTYEKAAKTVNAISNVFQSQIPLIMKIDNVAILSEAK

VDSNASPINMKTTLSIIVSLFAGLVLAIALVFLMDYLD DTFKSETELEKELGPLVTV

ISKMKKDDLKNTKNYVSQQKVGDGKYVAANQ"

CDS complement(4454501..4455259)
/gene="ywqE"
/locus_tag="EFAGFIKM_03907"
/EC_number="3.1.3.48"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P96717"
/codon_start=1
/transl_table=11
/product="Tyrosine-protein phosphatase YwqE"
/db_xref="COG:COG4464"
/translation="MVEMHCHILSGLDDGPVRMEQSVAMAEKAAASGITSIIATPHHL
NGQYNNEPMVVNQAVNLLHAELRKRNIRLEIRPGQEIRVHDNLIGDLYAGKCCTLAGS
RYMLLELPFGHIPSQFPRILHELRIAGITPIIAHPERNRVILKKPKLLADYLSQGGLC
QLTAQSFTGLFGRKVRQWCFHFCKENGFFISSDAHDTCKRTFAISEGERAIERRFGA
EAVKRLAENASHILSNSCLVTERWKPRKWLLSIW"

CDS complement(4455415..4455819)
/locus_tag="EFAGFIKM_03908"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKLVNHMYIQEFHGKMVDRKRRPVLLLGMMDTQAITFLSDLNLPI
SSEMLIGLDVEDHHVCVRLHARLQWKQPFGEITMYHSNLHIQHEQELYITGQLNTMLT
EVQFPAVSRFQYEKATEQKALQEPYHYIDFTI"

CDS 4456198..4456566
/gene="xre"
/locus_tag="EFAGFIKM_03909"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P23789"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator Xre"

/db_xref="COG:COG1396"

/translation="MSYGNRIARELRQGLTQEELASSIHITRAALSHYEKNRRKPDF

EVLTRLADIFDVSIDYLIGRTKQSDVVMDEDVREFVDTLELSDKEVLERFDLMIDGKS

LTEEEARRFIAFVRMERSMD"

CDS complement(4456664..4456987)

/locus_tag="EFAGFIKM_03910"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVAIPAPYCSYLAFDKIRTPSKNVIAMRRQHRGTFSSIIRLVLE

GRESIKISEVSGMNMKHPNRDDRRPTGKQVEATQMDIMKVLLQCGIDPERWNHFVSSV

NNKRP"

CDS complement(4457050..4461648)

/gene="gltB_2"

/locus_tag="EFAGFIKM_03911"

/EC_number="1.4.7.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P55037"

/codon_start=1

/transl_table=11

/product="Ferredoxin-dependent glutamate synthase 1"

/translation="MRHIGLPPKQGLYDPQFEKDACGMGFVANIKGVPSHDIVSQALT

MLSNMEHRGGQGSEPNSGDGAGILIQIPHRFFAEEAKRLGFALPEQGFYGVGMLFLSQ

DPAIRSAHEESLKKIIEEGQTFLGFRDVPTFDEMLGRSALAAKPYVRQVFIGRSADV

KDELGFERKLYVIRRRALAIRYSADEAEGGSFYLPMSCKRIVYKGMLTTEQVGGFY

LDLQEELVESAIGLVHSRSTNTFPSWERAHPYRFMIHNGEINTMRGNVNMHARQSL

FESELFGNDAKVKPVINPDGSDTAMFDNTLEFLYLSGRSLPHVAMMMVPEPWSTDEG

MDPAKKAFYEYHSTMMEPWDGPAAMAFTDGLQIGATLDRNGLRPARYYVTKDDRILS

SEVGVLDAPEEILYKDRLRPGRMLLVDTQEGRIIADEEVKAIIAAENPYQDWLDEHL

MDLSELPEAPELPDPKHNDVTQLQLAYGYTFEELRKILEPMATTGMEATGSMGYDAPL

AVLSDRPQRLYNYFKQMFAQVTNPPIDAIREEIVTSTATTIGPERNLLNPEPESCRQI

RLDTPVLSNEDFAKIRHVRRPGFRSMTIPIFFTAEEGAEGLRKAMDLLFEADRVIDK
GHNILILSDRGVDAENAAIPALLAVAGLHHHLIRQGTRTKVSIMLESAEPRDIHHYAL
LLGYGVS AVNPYLA FETLDDMIQQGLLRGISHEKAVKNYIKAATKGVTKVLSKMGIST
IQSYRGAQIFEAVGLKSD FVD RYFTWTPSRIGGIGLEEVA AEAL THHNRAFTEKD GND
KVLDSGGDYQWRNDGEEHLFNPQTIHTLQH AVRTGDYKLYKKYSKLVQGENDQLLTIR
SMLKLKPVGASIPLEEVESVEDIMRRFKTGAMSFSGSISKEAHEDLAIAMNRVGGKSNT
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DHWKKKGVDLSVLLHVP EMPEGSARYRTQH QNHQLEETLDMQQLPLA QSAIESGQPV
EAVLPITNVNRAVG TILGSEITRKYGLAGLPEDTVKFKFVGSAGQSFGAFV PKGMTLT
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FAVRNSGAKVVVEGVGDHGC EYMTGGRVVVLGDTGRNFAAGMSGGIAYVYDPEG TFLK
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CDS complement(4462320..4464602)

/locus_tag="EFAGFIKM_03912"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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QGNQQLAAGAAELHGGQEQLLAGANQLVDGQKQLLAGAGQLSQGGAKLS DGLKQFSGK

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GLETHSVGLFYLFITITGLTFMLIVQALVTWLDLPGRYVVILLVFLAASAGTFPVE
LIPSWLQAFSPWLPMTHSIMGFKAVVSSGNLDMWHQAGILSIYAGVSILLTLAYFLW
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CDS complement(4464809..4465390)

/locus_tag="EFAGFIKM_03913"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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CDS 4465683..4466987

/gene="ugtP_2"

/locus_tag="EFAGFIKM_03914"

/EC_number="2.4.1.315"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01280"

/codon_start=1

/transl_table=11

/product="Processive diacylglycerol

beta-glucosyltransferase"

/translation="MYIHVVTHSIARINNEYLHFELKLMNKGELMRKPRVLLLSEFGF

TGHTQAAHALAHGIKKVSPHVHSRVIELGKFLNPTVAPLIFSAYRKTLQSVQPKLVSL

YRTQYNKSLNGFTKLALHRIFYTQTAQVVSQKPDVICTHPFPNAVISRQGLNI

PLYTVVTDYDVHGTWINPEVNKYLSTPQVKALLEIRGVDPSHIQITGIPVHPDFWEA

GDKVKLREEMGLQNMPTALLMGWWGLSFDEDHMKALTSWADRVQLVFCLGSNEKMIA

KMKEMPCFQHPNIRILGYTREVSKLMDVSDVLITKPGGMTCTEALAKGLPMLFIPPIA

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CDS complement(4467263..4468120)

/locus_tag="EFAGFIKM_03915"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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TIGHHTFYK"

CDS complement(4468251..4468853)

/gene="ytlP"

/locus_tag="EFAGFIKM_03916"

/EC_number="3.1.4.58"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34570"

/codon_start=1

/transl_table=11

/product="RNA 2',3'-cyclic phosphodiesterase"

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GVLPEHSTGVNSWTVEDIVLYVTRLGQSPMYEVVDFTFTFS"

CDS 4469061..4470017

/gene="ghrB_2"

/locus_tag="EFAGFIKM_03917"

/EC_number="1.1.1.79"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37666"

/codon_start=1
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/product="Glyoxylate/hydroxypyruvate reductase B"
/db_xref="COG:COG1052"
/translation="MGKIVCFPSLSEEQQQRIQNAAPEYTLKFGKAKELDPAELKEAE
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CDS complement(4470201..4471178)

/locus_tag="EFAGFIKM_03918"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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HRQKPQNYSTGFGITLARALVNIAVPRVENHRLDPCCGMGTVVIEALSMGIDVKGND
LNPLAVRGARINLPHYGYDSGRITLGDMMNELQDLYDAAILDMPYNLCSVLPDAEQRAM
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CDS complement(4471525..4473237)

/locus_tag="EFAGFIKM_03919"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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QESQGVVAELRTNVQETELGQEHVLTSGQLFRTINESVEGMVGVISTMTDGLAGMQEA
SGRMNDFSQQISAVSEQSAASVEEVSSASAEQVSSMETISGNIQSLKELSEDLLTSIE
KLKI"

CDS complement(4473523..4474539)

/locus_tag="EFAGFIKM_03920"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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/locus_tag="EFAGFIKM_03921"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01212"

/codon_start=1

/transl_table=11

/product="Deoxyguanosinetriphosphate

triphosphohydrolase-like protein"

/translation="MQWNDLREHRQYPELTKLDGSRAAYERDYSRLIHSPTFRRLQGK

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KYEHFEGNAHNFRIMHLEKREDIDGLNLSDAVLLGINKYPYPGTESKKGMYHHEWQY

IREIRDRWNVPAGKKTLEAQLMDLCDDIAYSSHDLEDGIKAGKIEVHEHFLQDPHVNR
LIVDKITTLEDLFWNGWTREAIQKQVEEVLASFLRIWNEKMPFCEHDYSRTRREVKEY
WVSFFVGSGLVIDDGDWKKVTFVREGAEDLDMLRTVSVLKSAFWVTMIRDLRVQRLQK
RSEWMIKRLWDAFLDPETSKSIIPSDWLQRYEKDQAKAQPIWTWEHMVIDYIAGMTDA
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CDS complement(4476653..4478533)

/gene="htpG_2"

/locus_tag="EFAGFIKM_03922"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WMJ7"

/codon_start=1

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/db_xref="COG:COG0326"

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VVYNAILFIPENTPFDYYTKEYEKGLELYSNGVLIMDKCGDLLPDYFGFVKGMVDS

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SDYGVNKDTLQDLLLFTSSKESKLVSLDEYVSRMPEDQKYIYYASGESISRIEKL

EGVLEKGYEVLYFTDDIDEFAIKMITNYKEKEFKSISSGDLGIEDSADKEETDAQDND

NKELFEAMQAQLAGKVKAVKASKRLRSHPVCLSTEGELTIEMEKILKAMPNSEN

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MV"

CDS complement(4479266..4480165)

/gene="gsiD_4"

/locus_tag="EFAGFIKM_03923"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P75799"

/codon_start=1

/transl_table=11
/product="Glutathione transport system permease protein
GsiD"
/db_xref="COG:COG1173"
/translation="MAKLSTNTGPSIDAASASTSGPWREAWRTFRRNRLALAGLIIV
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NALLAIAIVNIPTYGRLVRSRVLSLRQEEFITSARTLGAGNGRILFRHILPNSLTPLI
VQGTLGIGTAIEAAALGFLGMGAQPPDPEWKGMLSDSRQFIQKAPWTLIFPGVSIML
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CDS complement(4480396..4481400)

/gene="dppB"
/locus_tag="EFAGFIKM_03924"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AEF8"
/codon_start=1
/transl_table=11
/product="Dipeptide transport system permease protein
DppB"
/db_xref="COG:COG0601"
/translation="MNSYIVKRVLVLLPVLLGMTLIVFSIIHAIPGDPAETILGQKAT
EQSKQALRDQLGLDKPWFQQYFAYLGDLLKGD LGTSIRTKVPIAQEIVPYLTATLELT
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WLPSIGRMNARDPVEAITGLYVLDTMIAGQWNQLWTVTKHLILPSVALGTIPMAVIAR
MTRSSMLEVMSSDYIRTAKAKGLGPFFVVGHALKNAFIPVLTVIGIQTGSLLGGAVL
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CDS complement(4481609..4483243)

/gene="hbpA"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P33950"

/codon_start=1
/transl_table=11
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FVFKWKRNDSITLEKNADYWKEGLPKLNKIVRSIPDNTARFNAHQNGEIDVMEDLN
PDDLSELGNSSELQKIERPPFNVAYIGFNFKKKPFDDNVKVRQALNHAVNKQALIDAFF
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PYMPDGKKVAEAIQADFEKIGVTVTIESPEWATYLEDTKAGEKDDIYMLGWTGDNGDP
DNFLYTLLDKDAIPSNRYSYYNEELHVLTTDAQKETDQEKRAELYKQAQAIKEDAP
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CDS complement(4484195..4485142)

/locus_tag="EFAGFIKM_03926"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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PEPSNPTNPSNPNPPTVPPKGGEPMTAEKAAFDALKSQVDKLQARQQMEVPVWAKAA
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CDS complement(4485276..4485773)

/locus_tag="EFAGFIKM_03927"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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GDSKK"

CDS complement(4486258..4487403)

/locus_tag="EFAGFIKM_03928"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNEPKTPNLGLNKIDRSSPSTTYFDLDKYLDQNWEEKVDEGVATK
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DQVYVQLAIQTPGQSLILPNTFQSATSMWETRKL RIGNIEVDMTTGGNITYMVNNDTY
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CDS complement(4487404..4487949)

/locus_tag="EFAGFIKM_03929"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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CDS complement(4487946..4489004)

/locus_tag="EFAGFIKM_03930"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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KAKAFPLWDGPGTVKVALN
NNEMQTPADAVIKAVQEYIDPTQDGMGEGAAPIGPVTVVGAEVPIDVEVQ
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CDS complement(4488997..4489410)

/locus_tag="EFAGFIKM_03931"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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CDS complement(4489407..4489664)

/locus_tag="EFAGFIKM_03932"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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CDS complement(4489671..4490681)

/locus_tag="EFAGFIKM_03933"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQEQIRLDDKLANMKERLLDDKQGNPWDISEIAGDITYKTSRI"

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ICEALDRTLIYGGKNYIFYDDFGKLVLRDVEEMPYGFIGDNSLLTDYSYTRSIDDQT
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CDS complement(4490695..4491390)

/locus_tag="EFAGFIKM_03934"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS complement(4491391..4493376)

/locus_tag="EFAGFIKM_03935"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MYAMFARLYIMSNNMVQQFQNLPTVINSVFNPGNLSRIQLAGNL

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KAFEDGQKVAEDLLSDFSSTSNADSKEKGLPGNFGKDFTPEIPKTPSMPSIPTAPAPT
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CDS complement(4493578..4494000)

/gene="yqbN"

/locus_tag="EFAGFIKM_03936"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P45930"

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/transl_table=11

/product="putative protein YqbN"

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CDS complement(4494171..4494629)

/gene="xkdM_1"

/locus_tag="EFAGFIKM_03937"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54332"

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/product="Phage-like element PBSX protein XkdM"

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VKTLGRRGVQHKATGWSGSGSMTIFYTTSRFREMLQYMQNGVDYFDIEVTNEDPSS

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CDS complement(4494631..4495947)

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FTGEGALTATASPLTNGEDGTSTNQEHADFLSKLEVLDNFNTVGLISDDATLKSVYTA
YIKRLRDTEGKKVQLVLSDYPAADHEGIISVKNGVVLADGTVLTPKQTVAWTAGATAG
ANLNESLTFRAYDDAVDVNGRLTHSETEAALRNGEFVFTASSNRVVEQDVNTFRSVT
PDKARHFAKNRVVRVLDGIANDMKRIFESYYIGKVNNNEDGRSLFRSQCVTYLKQLQD
IGAIQNFDSKTDITVAQGNETDSILIEIQVQPVDSVEKVYMKVKVV"

CDS complement(4495947..4496156)

/locus_tag="EFAGFIKM_03939"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MFTKKEPDPKKTETQQKNNQKYSKAQFAESRQLSRIEKDILAAV

LLEQQTYTLQEAQQHIQQFMNGEAQ"

CDS complement(4496279..4496710)

/locus_tag="EFAGFIKM_03940"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MTTNQLTTAIAANTLTQHFPNIPIHPASVGGNSTPAEKGISYRLL

SAQLTRERSDRFVQSHAFEIRWLDPKNIPATLPDELFEALETIDVEGTPYRATMRWE

TENDTPRMLVYYTMRTTKVSESAATMQQLEHRPTALKATRE"

CDS complement(4497559..4498971)

/locus_tag="EFAGFIKM_03941"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPQETDRLKLPLPLGNENVTRESINGIFEKIDAGVATQADLDML

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MTGR LIMNQWGTISGSSNGSVLYGSNCFLDGSNFKYENDHTNLGARGIYMRYTGGAGP
EVMFDTGAVATTAGATFTPVLNIVNNGDSWQKHKLNDNGVTLNISNQNNLIVT
GFYAGENITNAPTTAVGAWWYIQVISMSGSHIKQIAMDLFGNTYQQR TNNGTAWTAW S
PDVFQSGVNAKQSVVDAINARGGSASTSDTWAQLAAKIQAFSTPTSLSLQESRGSITL
NVGQVIDYPLATIRAGTKYAMFATNATTVSFSYATTLYAYQNWRTALIIKDKAGVVVE
ITSATNNFTTYIKSVYIDFTNRSITYIADSTSATNTLISIPSNFDIGGTVVFAIRCSR
LYSGEDVRPAYNVGGRLLLA"

CDS complement(4498971..4499561)

/locus_tag="EFAGFIKM_03942"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSAPSIVDVGLTSEKGRELF SYLPRYYETSRVMQADMQAKGNEM

DL LYQALDETLEQFFVRTATWGLDFWEQELGIETDRLKPVEQRRAVVESKLRGAGKFS

GRLVANVAEAYAGGKVDVTFQPEAWSFTVSFVDTMGIPPNIDDLKRAIEELKPAHMSV

EYEYRYLIWDDLDKRQKTWDELDAASLTWNELEVWA"

CDS complement(4499699..4500838)

/locus_tag="EFAGFIKM_03943"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAEIPRYLEDQTEEEIMQRMLDRLPADLDKSEGSFLWD AEAPVA

FMLSEAALWAQELLRRGFASTAASSDPNFRSEELDRAGEHGITRRAGVAAQGA VRFT

GTPGKVVPAGTVVATLADEVSAEASLEYETVGRLELDAEGSGVVSVRALVAGKESNVP

VGTITVLSTPVSGVTSVTNVEVIKGGADIEADTALLERFYAKVRNQGTSGNKSQYVQW

ASEVPGVGATRVIPLWQGP GTVGLYLLDTEKRAAGTDLVA AVQKYVDPTQDGQGEGVA

PAGPVVAVMPAEVPMNIQVKLTLASDATLADVRALIERGV TAYLKQLAFADPLVRYT

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CDS complement(4500843..4501298)

/locus_tag="EFAGFIKM_03944"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPSLFPETGVVWGDEDDLGAASEEVRFGRSWRFDYDAGDFVLT

PSGKVAAAGAHEAWVQWCIAVKTPRYRHVIYSRNYGSELEDLVGQGDSRGVMESEIS

RMVTETLLADPRTDSVDQFTFDWNREQCMFSCRVASVQEEMFILESEVI"

CDS complement(4501291..4501701)

/locus_tag="EFAGFIKM_03945"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKDDPYGHFADVMRGAMSTHSRQAVSGLGAVLGMTSSGVKLD

DFKHEVQDYLVAELPGTLGLPEREAAGAISGIPDVANGGTTGTGRFLLQEEVEETVL

SLGKGLKAGDRVLAMRVNGGNDIVVLCKVWSAHA"

CDS complement(4501694..4502680)

/locus_tag="EFAGFIKM_03946"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTYKVIVDDKYDITKLVTITLKDSLQIAYQANIRLAVSASSG

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AKSGGDMYHPRMTPGGLQLFKVGSNAKVYELDRIDLTMRTLEGAVTKVKVMAASES

PSGKEVPSKVLAIEQDRVEELGTLQKLVEDDQVKSTTAAKKLAKSHLTGIQETFTISA

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CDS complement(4502677..4503345)

/locus_tag="EFAGFIKM_03947"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
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NMLEHGEFDFAQGEKVKEITFSSFFPKRYDPSYCMDEKYFLDPRVAMNVLNTFLISKK
PLRFISETGVNVPVFLVSLNSSFRGGETGDIYFDLTLRTWRDSKVEKVGSGAAASKS
GSRTDLKKSSKTYTVKAGDSLAKLELGNSSKWNEIYKLNTKIIGSDPNRIKPGQK
LVMP"

CDS complement(4503366..4505039)

/locus_tag="EFAGFIKM_03948"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAEMIVGLSKSNAEMRTTLRYLDQIQRSTDRLNRVRYQGLIKVN
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KVQFKVRHQISGVSVNVNSQPLMDALNTNTISILKLSAKLDSLNIAGGKEEKPKTFL
QKMKGMFDRGKSISSGVGKVFDAKNSGKKLWKEITTPATPGNKLKAFKVTGRGAKFV
NDFSSAGSDLIGGFDGLWGDVKGLFGGGGSGSGAGGSSSGSIISKLGGNLVKGAGKLF
APLRMYNNIKELASAPPEDRARAVGSVAGNAVGTAGTVLGSVIPVVGNNMLGGSIG
GWLGEKAGGWLGDKVGGFLKNNNAEDISKVAKFASEGASYVAEKTANLFNGVAGFFGFG
SKKEEQTAPAAAVITSPSTPVATQTPPPPIAPQMPPPYRPAVLSITGPEAYMNNRFG
SPTAAGLMGTSMMSQAVAMNNAGQPNEKASPLTVRISEEQMSSLAGYLKDFKTETT
QIAVNIAPGTVQVTVRENAIDYDAVSHQVGQRISDEFRRAMQNRKTIMA"

CDS complement(4505222..4505656)

/locus_tag="EFAGFIKM_03949"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSMNENMSEEQILDQLFEAAERLPEENVRIQRDLNLLTLRGLTS
SKVDHIRERCTIRKTTKGRTEEKVDTETFNALLISEATVKLKVRSLELSGWGDTRITG
RMKLSGGEQAVRRMLLAGELDAVGDKVLELSGFGVEIEDLKN"

CDS complement(4505831..4506238)
/gene="xkdM_2"
/locus_tag="EFAGFIKM_03950"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54332"
/codon_start=1
/transl_table=11
/product="Phage-like element PBSX protein XkdM"
/translation="MLDASRVILGTHGQLHIDGVWQTNINKLEASVEIEKRELNLVGN
DWKVHKNAGAKGTGTMTGYKVTSDMIQRGFTKFEISKLNDPESYGHESVLLRGCMVD
KIQLANWTAGEEVPEETGFTFEGFELLNPIVAN"

CDS complement(4506487..4507950)
/locus_tag="EFAGFIKM_03951"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
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/translation="MAGGNWEQTNRPVLPGLYMNFAQAAASSAIQAGTRGTVVVPVKAN
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DITAASLAKEINADEQNVWVTAQAIGDGTGVVATVAGAAFKGGVSGNDDLTNAEYIAV
QGALEGEQFDVLALDQAADAPLLASFAAWVKRVRSEGKPVVAVFGGSAADDTSATAAQ
KAAARSLTLNHEGVINVTGVRLGDAFYSSAETSAYVAGLIAGQRLNQSTTYAATPFD
DVTRRWTRAEQEQAVQNGVFIFFHDGRQVKALRGVNTLVTPAAGQNNAWKKIRSIRVL
DAINTDLQRSAEDTYIGKVNNTTEGRQALISAMKAYLALLAQSNVIEADGYDVILDPA
YYGAAPVLKPEADQVFLQWNVKLTDVMEQLFGTFYVQ"

CDS complement(4507950..4508150)
/locus_tag="EFAGFIKM_03952"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MASSVKKSKQTAPRYTRAELMNHAEALFAVKAEVLYGALYEAAQ
ETFSIEETQERINQFMKVKVKG"

CDS complement(4508552..4509475)

/locus_tag="EFAGFIKM_03953"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSMRNEISTAMSTSKMSKFIKKTLLKQLAVLVPDWNDRVLDVPA
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QVRLVDEAGEAFTCIYLGSSDSRVDAGSGMFTRSLRFGVYIPEDSGVWLAETGDAWL
AALQDWTQSELGSNWSVYGDVWPGGYEMPSVLWRLAGCSTSVAGTSALEVRQQWIGHV
LTDHSMLEHQTVTRLVRQLAVQSRLAITETGGEEHQGNTRYITVDEVTADLQTDAYLN
GQIRLTLQQRIRRPGTNPVFIHHSKGM"

CDS 4509908..4510252

/locus_tag="EFAGFIKM_03954"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKTFKITSLVILAFILGISCWAYFALLGNPLKKNDAAEQVTTY
LIEQKGYSPEQLIKVQGTYSKSSSEAPYGASVTFADLEAKYQYIIFNNGKIKQYSHT
SDDPKHEEPMVR"

CDS complement(4510257..4512107)

/locus_tag="EFAGFIKM_03955"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

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/translation="MKTVLYVPLDDRPANLDDVIVQGKAAGIHIVTPNLSDIKNRLDS
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GGGAYPEYDDETRLLDVIRVIKQKYPRKPVFVMDTIMRLATTSFADGLALDAYNESR"

ALMQQPRQTYTEFEDIIEGYNLSPDGVEYGTTTYFDKEQYYNTRQHKFKTNLYILDQL
ARTGYIDFLAVGVDDANTQGVQINEIKYVEARINEWLGGTNGQNPDRIVLPDADGLG
HALVARMANQLFRGGARTRYAVKYFGPHGNSIINTYEYMDVHENVVRHVDIVGGVLVA
DSAYPEPEVVTAGAGLENEQLVAVAADQVVPFDMTSELDRMTKGHPGNSGENTSIDI
EIIAITALDQVQAALERLTNSEQGLPSVLIDFVGKGPANVDVAEALLNSPYTGRVLG
YSAWNTPGNKIGIAVGMGQSRYALITTEKHEHKLRDAMNAHGSLLFKRFLKDYYYYKAV
AIADIRTYSRAHALYTNVATLSDQNMLLFNSEEDYVHLQTLLRDLMQTYTTALANKTA
FQTGNVAIKQICDEELSYATYSNALLEYGNPDFIWGRAFEITLNPQVTLN"

CDS complement(4513066..4514016)

/locus_tag="EFAGFIKM_03956"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDRRLLEEGLAIIVSSRERTGDLWHAHYGAGAIAYFWLRENRL

TALAAGSVTAEAKAMLRQHGISPGQTSPIGEMMPRENAEACITDALDRTIGELHWVGH

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SDGFPEIEDPVQLSRLILDELGAFQTIYHAEAHHDLIGHMLTYGHALNILEYELGYPAL

FHKGIPPFLTMVKALRLSRDVDIEQEMPTLQSPVDLLPLERAERSVALPHELEYWLTD

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CDS complement(4514318..4514953)

/locus_tag="EFAGFIKM_03957"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMIEELQLYTTRLEDLKHFYRDTLGMEVSNATDQAFNLEVGGTK

MIFKPCETGREPFYHVAWSIPTNRFKQAKQWAASRVVLSREGDRDETYSTNWNWSLSL

FEDPAGNIIELIAHHRIQNESDHDFSTQDILQVCEIGLVTDVLSVVNELQQIGLTRW

GEVSETFAPVGDVHGLFIVVKKDRTWFFSTQKAEIYPLEVSIHGVGKLRIG"

CDS complement(4514950..4515408)

/locus_tag="EFAGFIKM_03958"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MIK GIFETHLNVTDLERSHHFYETVLGLPHAYGQKERGNSFYWI
GGKGNAMLGLWQKEPSEVQRQHF AFHVSLEDMKHAVA HLENKG IKTQNFLNDDIGELY
VFGWMPAVSVYFNPDGHLLELIAMLPDEAKPELGMVPWSQWEEMQEKT V"

CDS complement(4515454..4516029)

/locus_tag="EFAGFIKM_03959"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNIVILAGSNRNNATSTRLGEYAVEIIRGQGHQASLFDLYQTPL
PFYAPDEKQADHEHLADLNTRMLAADAILSTPEYHGSISGV LKNALDHLSQAHFSGK
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SQDIEDRVQRVIGSFLNLAQTLTNARNSSMS"

CDS complement(4516217..4516951)

/gene="liaR_3"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32197"
/codon_start=1
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/product="Transcriptional regulatory protein LiaR"
/db_xref="COG:COG2197"
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LLKDIEPEDLAVAIRNVYAGQVELHPAAAGQLMHVMASSDWSINEHQPQHIQTDRSTD
SQFQELKQTKKSTEASLGGLDMLTRREQEVLGLIAQGLSNKEIAVQLVITEKTVKTHV
SHLLDKLGLADRTQAALHAVRNGWVI"

CDS complement(4516970..4518637)

/locus_tag="EFAGFIKM_03961"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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QIGSAVERMRLYRAEQRRADLYAKLGEFSTALGLAVNECSNSDAFCLKVVQLLGQHYD
WPFATIIQQKSGMFVLQAAYANDTVRTLSSSTPLSSEVTSHINHVINSHRVTSLSGTEI
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HPAAEAMKDIRALSQEALKEMRALIMQLRPAGLEAGLLHALQEYGTSSQGLQVVMNRTG
MRSLPRKIEEALWRIGQEALNNVRKHADVPSAEVTLKLSNHEVVFTVTDQGKGGANRP
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CDS complement(4518901..4519383)

/locus_tag="EFAGFIKM_03962"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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ERFHGATNVTGDSTARTAIYNVDVQRRARQAYCDTIDFVVSRLSEKERVLCERYLKDD
DVFDYKVYNHVFDPVSKDTYTKIRTRAFYKMALALSDRGLINMEPLSVSRKERQKLG
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CDS 4520219..4520659

/locus_tag="EFAGFIKM_03963"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MEHAFGPYMKQLREQQGYSINQLAEAAGISNSQISRIENGVRGV"

PKPATIRKISDALSVPYTEMMKQAGYIEPGSAAELQDVPGWATYKDRRDFKKMLEDDD

DLMFDGIPLDEEDKKRIKDVLTGLFWEAKQMNKRKKTDESDNRP"

CDS 4520702..4521118

/locus_tag="EFAGFIKM_03964"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDDIVTKLIRKHRTNCPFSIARAVGIQIRFTNLGKSTKGMFYCK

LRRRFIVIHNDLPPEWQRFVCAHELGHDRHLHKGINRFFLEEHSYFAPGKLERQANRFA

IQLLTSGVMPEPDESLEKFCLRTGLPREAQHFFYTL"

CDS 4521291..4523090

/locus_tag="EFAGFIKM_03965"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKIWKNYVSLLLTVCLLFGSVGIAAAATDTPGTGKHITILHTN

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VKIGIIALTTPETLYKTNPKNVEGLDITDPSAEAKVLVNEIRSKVDVVVLGHLGQDA

SSTDTSFKVVKEVPGIDVFIDGHSHTVLQDGLVSDNGTLIASAGEYTNVVGVIDLWVD

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LEVKGSDILAALVGVASYPEPSGGFPQVSGIKFKIDTSAAEGSLVHSVTVGDKALDP

EATYTLATNDFTAVGGDEYTMFAKYPTTGMYGALDEALINYMQLGAVDIKTDGRISE

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CDS complement(4523685..4525472)

/gene="proS_2"

/locus_tag="EFAGFIKM_03966"

/EC_number="6.1.1.15"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q831W7"

/codon_start=1

/transl_table=11

/product="Proline--tRNA ligase"

/db_xref="COG:COG0442"

/translation="MMRQSEMLVPTLREAPAEADAAGHRWLLRSGMIRQLAAGIYSYL
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REFALGPTHEEVVTALARDEVSSYRKLPTLYQIGTKFRDERRPRFGLLRGREFIMKD
AYSFASDWEELDRTYQAMNTAYSRLERCGLDIYRVEADAGTIGGQGETHEFMALADV
GEDTIVTCKHCGYAANLEKADYQTSGDIEKKEGSLEVPADSASADSALQTDEHSGAEK
VVRISTPGVRTIAELTVFVGKGAEHMIKTLlyVADGQLVAALVRGDHELNDIALKQVL
GAEELILADDAVIAAHPNLKVGFLGPIGLNLPVVADADVAVMKSAITGANEVDVHVSG
VRPGIDFALERIRFAAEGDACPTCGSPLVFTKGIEVGHIFKLGTKYSDAMGASFL
DRNGRQCAPVMGCYGIGVSRMLMAAIAEQYAGDDGIRWPAAVAPYDVHLITVSWKDEQQ
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CDS complement(4525838..4527784)

/locus_tag="EFAGFIKM_03967"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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PDIDLLMNAKELVPLTEQSTGDHTTITGMSITKEDGTTVQISTRSIIDATQDADIAAA
AGVPYSIGRQDIGDGKSKMVSTLVFKLSGVTDEVWQKFRERDGTGVDKMSAWGYGDAR
KYESSNPQH IKIRSLNIGRQNDTILINTMQIFGVDPLDPISVKKGLEIGRKEAPLIV
EFLKKNYDEFAGLQYAGTANELYVRESRHIYGEYRLTLADV MENRDHWD AIGYGSYDI
DIQSTSVGNPGTIMLSPIQYGV PFRSLVPLKVDGLLVVGRAASFDTIPHGSARVVPMG
MAEGEAAGAAVKLAYIHKESFRELSTSEERASELRKMLENQGM DLKVHRFEQPDYMEH

KDYRGLLAAASMYMTSGNYNNDGWELDKGMNPERFLSKLKRMQAMFPEAYTGSADQAL
ANMENAVTLPLTLDQAAYMLCLAMGSSETETSLEQALAQLQTQNFISDDTLAGIADKN
NLTNGDAFMLIRDVVEYYSGDVFD"

CDS 4528220..4528891

/gene="polC_3"

/locus_tag="EFAGFIKM_03968"

/EC_number="2.7.7.7"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00356"

/codon_start=1

/transl_table=11

/product="DNA polymerase III PolC-type"

/translation="MPYIIYDLEFTVSRNTRYSSSEIIDIGAVKVTESADGLVVTDTFH

TYVRPSNKSVLSTDTIQFTGITQKDIDAAPLFPAALNQFIAWMGSDPYYMCSWGPDDR

SKLISHCRTHQLDVAWITNHNDLQQQWSRTVRKEGKFRQLGLAQALEICGIEFDGTQH

RALDDAINTAKVFMHQFDRFTLENNCAADDEGITSKVYSSSTEDEEKESPFGNLASL

FKTKE"

CDS complement(4528959..4529930)

/locus_tag="EFAGFIKM_03969"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTDRLIRLMRIITLVQAKPGILARELAQRCETTERTIYRDMEAL

SAMHIPIANMGHGQGYMFISQFAMYPLNWSDEEAQAFMHLEVMENIRPLLKPAFESA

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EGEYLSQGKKGIVRIDPYCLIPREYRFELLYCHLSEKLRIQVSRQLRIRILPRTR

KEDYLMQSHFRIPWAYEGSTEWTAFKIRFAPHAVERVMQEQLIRPILTIEPEGSLLF

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CDS complement(4530082..4530864)

/locus_tag="EFAGFIKM_03970"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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GGADPVYMMVEWRNGAPAKRLRKIAPKIVSRDLELLLKPEYGVQLKGIYGCRSKETDI
GWLLRLGDMYKGESQILLEFVMGPHVSGKAAVCSAYWSTRKLKQSQRVLLRREQLYI
QYTSHLGMLRQPEDPKVEKTIKLSETVPLIKQALRAYERGRVQVGSNMLRRHADALLI
EAARKQDLDYAEAEIVEKLRHYEITFTTGYHDREKKILGE"

CDS complement(4530994..4531161)

/locus_tag="EFAGFIKM_03971"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MYTADQNTSTKITMITVNGEPVGRKLVIDSVTYAPVNEADGAQY
LHKMGINHPTV"

CDS 4531492..4531947

/locus_tag="EFAGFIKM_03972"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MPKSIQGYFIRVLFTTCILFTVSIAS TVSAASANIFTDIYSGWE
RVSELPGEVNALQESYKQTIEQLNQSTQLGQAQANVEAFKTQNEQLLAQNQKLTEMV
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CDS 4531966..4532670

/locus_tag="EFAGFIKM_03973"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MNIHLNNAEAGGAGQVVTFSLIQDDRLHILHPQQIVAFRGPSGS"

RNDKFMNITGIYRKKKLIKSEITGPCQFVAALPPGFTMKEVELTEDSDLLYDFRHLFF
YSDGVTMHTKIQIKINMLITRDAVKMKFSGKGKIGLLTQGQVCQQLHPTAPLYVDAG
SIIAYPENAHLELTVYGNNLASQHMNYHWKMTGHGSLVFQAGRENRLEQDLNDEGLF
KRILKEVIPFGNVLIK"

CDS 4533041..4533724

/gene="queC"

/locus_tag="EFAGFIKM_03974"

/EC_number="6.3.4.20"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31675"

/codon_start=1

/transl_table=11

/product="7-cyano-7-deazaguanine synthase"

/db_xref="COG:COG0603"

/translation="MLNEEKAVVVFSGGQDSTCLFWAKQQFAEEVVTFDYGQRHKL
EIECAAEIARDLGVQQTILDMSELLNQLAPNALTRTDVEITHEEGELPSTFVDGRNLLF
LSFAAIMAKQK GARHLVTGVCETDFSGYPDCRDSFVKSMNVTLNLSMDYPFVIHTPLM
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CDS 4533721..4534212

/locus_tag="EFAGFIKM_03975"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MREPGTFRIVEHLQRIGEDILPTQLRYHRKRVLVSKEFTFDAAH

HLHCYEGKCKNLHGHTYKVIFGISGYPGETGLTVDFGHIKDIWKTQIEGYLDHQYLNE
TLPLMNTTAENMVVWLFEQMEQALQTEPYAGLTDGGRTFVRLFETPTSIAEARREWM
IDE"

CDS 4534205..4534978

/gene="queE"

/locus_tag="EFAGFIKM_03976"

/EC_number="4.3.99.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31677"
/codon_start=1
/transl_table=11
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/db_xref="COG:COG0602"
/translation="MSSVTQQVNETGSRKEARIPVMEIFGPTVQGEGMVIGQKTMFVR
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ASLGGLVALLQENGIRTAVETQGSRWQPWLTDIDEVTVSPKPPSSGMDTDWAVLDDLI
ERLAAGPVERSHSLKIVIFDETDLDYARRVHARYSGTDLFLQTGNPDVTS AETPDLAS
SLLARYEWLIDQVSASDDLNNVRVLPQLHTLVWGNKRGV"

CDS 4535127..4535618

/gene="queF"
/locus_tag="EFAGFIKM_03977"
/EC_number="1.7.1.13"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31678"
/codon_start=1
/transl_table=11
/product="NADPH-dependent 7-cyano-7-deazaguanine
reductase"
/db_xref="COG:COG0780"
/translation="MRQPDEMQDVTLLGNQNVKYTFEYDPGILESFDNKHPYRDYFVK
FNCPEFTSLCPITGQPDFATIYISYIPDVKMVESKSLKLYLFSFRNHGDFHEDCVNII
MNDLIKLMDPRIYEVWGKFTPRGGISIDPYTNYGKPGTKYEQMADHRMMNHDMYPETI
DNR"

CDS complement(4535948..4536160)

/locus_tag="EFAGFIKM_03978"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MKSLSPYESAKRELVMTILYMAVITFQAIYVAPASLSVAIVIFI
IFQSIGVLMLRHYIRKVKELKKDQST"

CDS 4536403..4537677

/gene="fsr_1"
/locus_tag="EFAGFIKM_03979"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P52067"
/codon_start=1
/transl_table=11
/product="Fosmidomycin resistance protein"
/translation="MSTQSTLTKDATARSKAPPGSDAQSTVYRILIAISLVHLFNDISI
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FTFTGMLLLAFADSYMAVLISVIFVGLGSAAFHPEGSRVSHMAAGQRRGLAQSIFQVG
GNAGQSLAPLLTRWIFIPFGLFGAIGFTGIAAMGIAVQIYIARWYGRMLQSGGYLRRQ
AAARRAPNPALRKKITAAITLLILLVFRSWYIASIGSFYAFNLKDTFGLSTEDAQIY
IFLFLAAGALGTFFGGPLADRFGRNLIFLSMAGAAPLALLPYANLFWTGVLLTIIG
FIMLSSFSVTVVYAQMLIPGKIGTVSGLITGLAFGMGGLGALVLGNWIDVFGVSPVMQ
MCSFLPLLGIPTFLLPSDKLLNIWAKENGSEE"

CDS complement(4537801..4538289)

/gene="proX"
/locus_tag="EFAGFIKM_03980"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9L4Q7"
/codon_start=1
/transl_table=11
/product="Prolyl-tRNA editing protein ProX"
/db_xref="COG:COG3760"
/translation="MLNKQGFYDLLDRNNIVYESIEHPAVYTMEEIFSYPHTERIV
KNLFLRDDKKRNYLVITAGTKSVDLRSLSEKIPSRKLSFASEKDLLEFLGLEKGHVN
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VE"

CDS complement(4538348..4539193)
/locus_tag="EFAGFIKM_03981"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDSRETLDKLEQILKWEKQQKDLFIWDKIGRLPFAMLDKVMPK
ALKQKIGDSLNDVGQYVQNGGKFLVQKKKVAKLLQEEAGRSGYSMMDDTTYRLEQEPEA
EGTAKIHSVENLPLQVLDRVADNITDSRTKFAAAQGAATGFGGIVTIAADIPMVMGLS
LKVLQEMALCYGYDPDEPLERIFIVKCLQFSSADIVGKKAIEELAAYDDPDKPIEV
SQMQGWREVFNSYSESFGWKKLFQLVPIAGMVFGSVSNKNTIRDVAEAGKMLYKKRLI
LQRLK"

CDS complement(4539389..4540369)
/locus_tag="EFAGFIKM_03982"
/EC_number="3.2.1.55"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q82P90"
/codon_start=1
/transl_table=11
/product="Extracellular
exo-alpha-(1->5)-L-arabinofuranosidase"
/db_xref="COG:COG3940"
/translation="MTDSITFTNPILQQRADPWVYRHTDGYYYFSASVPAFDRIERR
AETLEELRDAEPVTAWTKRDTGPMSANIWAPEIHFIDGKWYIHYAAAHTSETNEGLFD
HRMYVLENDSANPLEGEWVEKGQIHTRWESFALDATTFEHKGIRYLVWAQKDPDIVGN
SNLYIAEMENPWTLRGEQVMISTPEYDWEIIGFKVNEGAAVMHRNGRLFIGYSASATD
YNYCMGLLTADENADLLDPASWVKSPEPVFQTCEANGQYGP GHNSFTVSPDGKTDILI
YHARNYKDIEGDPLYDPNRHARAQVIRWREDGTPDFGVPAPDGSAVAEAK"

CDS complement(4541098..4542375)
/locus_tag="EFAGFIKM_03983"
/EC_number="3.2.1.99"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A5IKD4"

/codon_start=1

/transl_table=11

/product="Extracellular endo-alpha-(1->5)-L-arabinanase"

/db_xref="COG:COG3507"

/translation="MNNAHDPVIIKTDQGYVYSTDVRVAGEAKPGVMVRKSDDLHW

TWVGQALPGIPQEALDWTGAVNLWAPDVIQAGDTYRMYYSSASSFGSTQSAIGLQTSSS

PEGPWTDEGLVVKTSANEQDKLNAIDANPIVDAEGNSWMVYGSFFDGIYIAPLNPDGTG

KFKDEGYGTRIAARDRATEEGAVEGPYIVYNPEFKKYYLFVSYDSLFDYNVRVARAD

SITGPYTDINGNNMLDTHLPQYEIGTKILGGYRFTEGEGWVAPGHNSVLKDGDNYYI

VHHARGEIDKNWPYLVHRRMLWTKDGWPVVSPEYAGETAQDIPKSMIAGEWEGMALD

PSVDGQIQVVPYTLTSNGKIKSEKSGTWTFFDDKQTLTLKWKESPWGGASTEELKLLP

SWDWERSQPALVVTGFNDRGVAVWGKQISAAEE"

CDS complement(4542372..4542578)

/locus_tag="EFAGFIKM_03984"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTQRKKFRRWSNSGKGVVASMLLLLVGATGCSGEGAGETVSRP

VFPEAPQDTQLYDTSILDDEYAGR"

CDS complement(4542575..4543417)

/gene="araQ_25"

/locus_tag="EFAGFIKM_03985"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MSYSQKRKLNSIIFIVLAIGAIAAMIAPLIWMLSTSLKEKQDVF

ALPPVWIPEVFQFGKYKEIWEAGPLLSGIKNSLIVAVSVTVVGTFTSSIAAFFAKL
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FPHKNKLFLALLASMMIPYPTVMIPQFIMFAKLGWVDTLLPLIVPGLFGNVIMIFFLR
QYLLSVPDAIIEAAKIDGSSYFRLYSSITFPLIKPAIAAQLILWFMGIWNDYLAPIIY
LNSPEKQTLQLVIANFNATYAIQTDYPLIMAASIVALLPVLIIFLIFQKQIIESVAIS
GVKG"

CDS complement(4543444..4544343)

/gene="lacF_8"

/locus_tag="EFAGFIKM_03986"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29823"

/codon_start=1

/transl_table=11

/product="Lactose transport system permease protein LacF"

/translation="MNAVITKSSLYRKEMLYGYLFILPPILGLLIFVMFPFLYSLYGS

FTDWDGLGQMNFIFLANFKDLLTDDLFYKAMFNTFFLMLGIPIGLLLALLLAMGLNRK

IPGTTTFRVIYYIPVISSLAAVSIMWNWAYNGDYGLVNQFLDLFGIKGPNWLANKDTV

KPALIIMTVWKGLGYTMLLYLAALQSVSRYYEAAELDGANGFQIFRNITWPMVKPVT

FFLIVTNIIGGSQIFTEMNIMTPTGGPEYSSASIVFYIWQKAFSNLQMGYASAMAMIL

GIFIFVITLVQFKMNEKSAYDGD"

CDS complement(4544340..4544474)

/locus_tag="EFAGFIKM_03987"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPAACNHAAGIIRIGTYWIPYGHVAFVDRQSSIEECHMLILEQG

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CDS complement(4544491..4545831)

/gene="yesO_2"

/locus_tag="EFAGFIKM_03988"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31518"

/codon_start=1
/transl_table=11
/product="Putative ABC transporter substrate-binding
protein YesO"
/db_xref="COG:COG1653"
/translation="MVKKKSWVTFMLLMLVSALVLAGCGGGSSASGDKELTFMFRGGT
DEQKAYQAVVKKFEEDHPGVKVKIIVTAADQYATKLRAAITGNSLPDVFYINPGDVKA
YVNSNVLNLTYSIENNPDVDLDNIWKYGVLDLYRYDGQMAGQGDIYGMPKDLGPFALG
YNKTLFEKEGIPLPDKDKPYTWEEFIKVNQQATKDTNGDGKPDVYGTGFNVQWALQSF
VWSNGGDWLDETKTKVTIDDPKFAEALQFFADMQNVYKITPSIEEAQTLDTYQRWMKG
EMAFFPVGPWDMSTFEKLPFDYDLLPFPAGSTGKSATWIGSLGIGVSAKTKHPEEAAA
LVNYLTASKEGMQQLVDAKVQIPNLLDMADEWAKDTSTKPANKQEFIDIVEDYGRALP
GNYTYNAEWYDLFFTDIQPVLDGKITAADYVKQQQPKMQKLLDKAVEQEKKSQK"

CDS complement(4545964..4546941)

/gene="abnA"
/locus_tag="EFAGFIKM_03989"
/EC_number="3.2.1.99"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94522"

/codon_start=1
/transl_table=11
/product="Extracellular endo-alpha-(1->5)-L-arabinanase 1"
/db_xref="COG:COG3507"
/translation="MEKLSNVKRFKWKRLALPALLVMVLLLAGQSKALAAFWNLTGDT
AVHDPSIIKEGSSWYTFSTGPGIQVLKSDNGSSWYRVPQIFLSKPSWWASAVPGQSG
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DWWAPDVEQYNGKVVLYYSISTFGSNRSAIGLASANSIGAGQWKDEGLVLQTTANNY
NAIDPNLVIDASGNPWLAFGSFWGLKIVKLDKNTMKPTGSITSIAARPNNGGAIEGP
SIVYRGGYYLFFASIDSCCQGVNSTYKMYGRSTSITGPYVDKNGVNMLNGGGTILDT
GNVKWKGPGGQDVYNGNVIARHAYDAEDNGNPKLLINDLLWDSSGWPKY"

CDS 4547273..4548190

/locus_tag="EFAGFIKM_03990"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIYIKDLMSGVNIFKALSSEIRIQIIELLAKNQSLNLDLTKL
GLSNGAITMHIKKLEESGLIEINTAVGKHGIQKICYLNEEKLMVDLRSQEINNRYEVE
IQVGHYSYQAAPTCGLATRDSIVGEFDDPRYFADPLRIDAEMIWLAEGYLEYRIPNY
LKPQNQSFSEIQLSMELGSEAPGFCDNYPSEIYFYVNGIEIGCWTSPGDFGNTRGTFNP
EWWPPHLNQYGMKLIRITQEGSYIDGCRISDVTLDQIGLDYKSDIHFRIAVTDGPLN
KRGLTIFGKNFGNYGQNLLARVLYNVQEE"

CDS 4548365..4549282

/locus_tag="EFAGFIKM_03991"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKLERLISIIYKLLNHEVLSASTLAEEFQVSPRTIYRDIDVICA
AGFPVVSHQGLKGGYGMMMDGYKMDKSLLGSYDVDSLITVLSSLSTVFEDARAQGTIER
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VKLHYKYRNWYVYGFCQTRQDYREFRLSRMMNVQLTSEHFQPHLELPQEAVVSDPSWQ
DQVSDVVFRVSPEALAEAMDHFQQADKRFHEDGSMTMRISVHQPLQARWLWSFLLSLG
SGAEVLEPIELRGILKEQLRNALKLYEEV"

CDS 4549366..4549875

/locus_tag="EFAGFIKM_03992"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNHPEQMYNYHAWANQTILGRIKELPSSVLSQEVNSSFPTIAHA
LSHIYAVDKMWYAVLNGTGMPEALQACIPLNSEIHGSVDEYIQCFTYLSAQYSEWLRG
QADLEQTILLDNPFAGVRETSLSDIVHVVNHGTYHRGNVSTMLRQLGYASIMNDYSL
FWYQEPAQV"

CDS 4549929..4550456

/locus_tag="EFAGFIKM_03993"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRNWLQTHGKVEKSCWVMISIKPVPNTLLYLDVVEESLCFGWID
GVKKKISSETQLAQRLSPRSKRSSWTELNKERVRRLEKLGFMHDEGRKVLPMDPSTAFI
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KMYGQWHDNRRLLDY"

CDS complement(4550530..4551396)

/gene="rhaS_33"
/locus_tag="EFAGFIKM_03994"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P09377"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaS"
/translation="MSNAYLRWFTSDHQQFPFFIQYGGHVEDMELHNMDFTELIVL
NGHATHVVNTEEFFIKKGNAFVINGDTHHAYKDPHDFRICNIMFSPEMLASAGPDLRK
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RLTEMVVYLSRQYDTQEKGIEGNNLMHLANAISFIEDHYLEPLSLEDIAGKSNISIRH
LNRIFRSYYQMTPISYLQKLRLKACHLLKNGNLSITEISYECGFNDSNYFTRQFKKT
FGKSPKTYRQTH"

CDS 4551567..4553081

/locus_tag="EFAGFIKM_03995"
/EC_number="3.2.1.55"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A7LXU0"
/codon_start=1
/transl_table=11
/product="Non-reducing end alpha-L-arabinofuranosidase
BoGH43B"

/db_xref="COG:COG3507"

/translation="MKYTNPVIPGFYPDPSICRVDEDDYYLVTSTFEYFPGVPIFHSKD

LVNWRQIGHVLTTEQLPLANAGSSGGIFAPTLRYHDGWFYMTTNNVSGGGNFYVRSA
QPEGPWSAPIFVDQGGIDPSFLFDEDDGHVYFQTACNGGEGEGIYQCEIDITTGARLTD
SRLIWTGTGGAAPEAPHMYKINGLYYLMIAEGGTEYGHMETIARSTEPYGPFDPCPHN
PILSNRSIKSSIHATGHADLVQIQDGSWWAVSLGIRPAGYPMRHHLGRETFLAPVTWT
DTGWPMIGVDGHIEQEMTGPLLAEHPWSPEAIRDDFDEPLLGMNWIFLRNPDPGSWAL
TENPEQLILRGHSVSLDDGQNPAFVGRRLSHFLCKMAAELHYEPNTSGEEAGLTLFMN
DKYHYDLAVTQIDGQKKIVLRRTVGSLRTEQVLDCDTGPVVLQIKADRNHFTFLYQQG
SSDAIEVGSGETHLLSTEVASGFTGVMIAMYAYAPSGECTPASFDWFDYEPLDE"

CDS 4553397..4555697

/gene="rhaR_33"

/locus_tag="EFAGFIKM_03996"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MKWNHFKSKLLFKYTLISIFLIPLVILTIIYHNAVDTLRSE

IEQTNVNQLTQAKTVIDDRMKELQDIAFRIAYDEQLTRYWTHHPYYSRESISALVKYK
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PAEQVVQGTRIPNSMLAYLVPIAPNNTPAHGTVMYLIHESNLTGLIDSILSDYHGMY
IFDNFGQVLAANYKGEIIEQEVNALFALEPGTHSISLNQEPHSVSVKSDAGWTYVT
AMPSNQFFSRIVHIRTFFVLVFSFMVVMGTFLAIMLARRQYHPISDLMEFIRLKNDDP
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NRSHYFVMTMGWEIHAFPIGDNPEQPTVMQLMNDVELPELSAYAYGVLPQADQLALI
VGFD AEIEHEGSLNARMEPIVEKLQWMVTEHTGAAPAIGIGNRYTPKQLNQSYIEAS
TAEASMLHGQGSSTYFNNLSGSGVQDSSFVWPKDVLLKLVSQSLKQGSYDVAVQMVST
ALNTLKSEMPSPVLLRCICFDILNTMLKTASELGIHHVVDQLPRITSYDSLEDLEKKL
TGLAAEICAHVEAKSETEESSLMDEIVAYIDANFSDYDLSLGTISSKFTISSSYFSRS
FKEKIGMNFTQYIWQKRMDEVIRLLLHTTDPDKDIITRVGYLDTPNFIRKFKKETGYT
PGQYRKMHRPNGSADSPDDDDDEECIG"

CDS complement(4555848..4556900)
/gene="chiA1_1"
/locus_tag="EFAGFIKM_03997"
/EC_number="3.2.1.14"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P20533"
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/transl_table=11
/product="Chitinase A1"
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QYYVDGTEMAKVQQYLDYVQLMTYDMRGGFQVLTGHHTNLYTPTGDLFRISTDASVTL
FVRAGVPKEKIVIGAAFYSRIWTEVPDRNHGLHQMAGSTGGYGPSFAELEAKYINKNG
YTRYWDEEACAPFLFNGSSLISYDDEESIQCKCDYVKDQGLAGIMFWEYGCDPTHRL
GAVHQGLKDLSAGKIG"

CDS complement(4556906..4559539)
/locus_tag="EFAGFIKM_03998"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTSQTLVFSLDAQSLERIEQKFQEKVRFAEARKSELFHIFQQEL
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CEPEARLNQGWFSPPARRAMLINTRIYADYPGPEDITLSEKGYTEINLLENYAPTRNI
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LEEGAQTRSEYEDTFLSEEEAVSLAKKVGLPSVRVWDVLRKARGNSREIAAFLEERSN
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LVPYRGVFQNAFSADEAAAFRENPSALARMLEQQYEYDDL PNLKGKGNPTGTFSLMK

GDSQSLDILFVAVCRSLGIPARLHPSAQKPQYLSDKGWEDAVFSLASPLTQESTSWGM
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TTGIRLKDGTAKVRVFTVNAGDTTEVVMSYRENEVDIPVLGKLAPGSILTRLDGSE
VELEELLGSEGAIAAWIEPEREPTKHLIRELCELAEPLDKLGIPIVLMIGDMEWNAAF
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CDS complement(4559547..4560569)

/locus_tag="EFAGFIKM_03999"

/inference="ab initio prediction:Prodigal:002006"

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GKLWKE"

CDS complement(4560635..4561921)

/locus_tag="EFAGFIKM_04000"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS complement(4562031..4563626)

/locus_tag="EFAGFIKM_04001"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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GQQDEIPLTSVKLDDL RMFFF GFWGIYNEGIYSDKDSKVHYPYQEEGYKGYLTFMNRL
WKEDLLDHETFSQTGDQKKAKGESNKLALFN DYHPYFTLGGE PSTDHPLMTPVKSEVA
DSPVYGKHPGMSARGTFAITSSNPSPEATMRWIDYLYSYDGATLFNQGP EGV LWKFKD
KENHVKEWLPVPGGGDREEYRGKITPNFGILTPGINDPDVAKGLRTEFDEWIDQQNQE
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KKMGSDRIIELYQGAYDRWNTGQ"

CDS complement(4563668..4564576)

/gene="dasC_7"

/locus_tag="EFAGFIKM_04002"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9K489"

/codon_start=1

/transl_table=11

/product="Diacetylchitobiose uptake system permease
protein DasC"

/db_xref="COG:COG0395"

/translation="MSSAVKESRSDKLFLCNYYLTVALVIVLYPLLYIISASISDP
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RTFFQSTIPKELQEAAHIDGCTNTRLFIKIVLPLSMPIIAVMALFYGVGHWNSYFSAM
IYLNDS SKYPLQLFLRQILVLQEMAAQGGGAIDTSSATAMNTKAEIAALVKYAVIIVA

TLPVIAVYPFLQRYFVQGVMIGSVKG"

CDS complement(4564592..4565563)

/gene="yteP_30"

/locus_tag="EFAGFIKM_04003"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system

permease YteP"

/db_xref="COG:COG4209"

/translation="MQPDGKSALSQNLSVYTNPSSKKNKLWRRRTIRNWELYLFIAPAF

LYFLIFHYGPMYGIQIAFKNFIPTLGVTGSPWVGFDHFIRFFNSYYFWDLLWNTLSIS

LYELAIGFPLPIILALAFNEVKDSFFKRTVQTVTYAPHFISVVVMMSGMIITFLSPSSG

MIVNLVQALGFQAPQFLTDPAWFKTVYVLSGVWQSAGWGTTIYLAALSGVDPQLHEAA

VVDGASRFKRILHINIPAIPTITILLILNMGSILGVGFEEKILLQNPPLNMGSSDVIS

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CDS complement(4566388..4567311)

/locus_tag="EFAGFIKM_04004"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKHKKGLAATLALCVSLTAGGASVLAFSDVKDEGQKSVVDSLKS

KGIVNGVTADLFRPDALSEPQGVQLIVNAFGLKNEFAEASAQNKISPDTWYADAVQA

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AVQNLLNMNIIELDKDGNFRPDQSLRMEAASMIFNALEFVDKHGNGGSTAPPTNPG

EGQQAIVPEVTTTKVDDKTTKVKLSAEMPHPGYGLKIDDVKLEKDGRAIVLSIIQPD

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CDS 4567673..4569415

/gene="yhel_3"

/locus_tag="EFAGFIKM_04005"

/EC_number="3.6.3.-"
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/inference="similar to AA sequence:UniProtKB:O07550"
/codon_start=1
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ATP-binding/permease protein YheI"
/db_xref="COG:COG1132"
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SARARFGATVDEIKSKQLRLVRLSSLFQALLPLLGAISLVVSLLVGGIMTMQHSITLG
SFVALTYLRIIMGPLQQIGNVINTVQRSGASLERVNDLLSEVADVRELPEATSLQTV
QDITMENLTFSGSSSPALKNIQLHIRAGRTVGIVGKTGSGKSTLVKLLLRITYEPPE
GTIRINGTDIRQLSLESLRSRIAYVPQDGLFSTTIRDNIAFSDREVSLDTVEHSARQ
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TESGILRSLREIGKGKTTLIISHRISAVRHADDIIVLDEGRVAEQGTHAQLMAAKGLY
AATYRLQEEGLHHV"

CDS 4569408..4571225

/gene="yheH_2"
/locus_tag="EFAGFIKM_04006"
/EC_number="3.6.3.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07549"
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ATP-binding/permease protein YheH"
/db_xref="COG:COG1132"
/translation="MSNANPELHPDAEADQSKRTSFKAMMAYAKPHKWAFAGIFFCSL
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VGQNIVSRIRKDLFKHISKMSMSFFDRFHIGSLVTNVSSDTETISSFFTQVLLSLIRD
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AENLSGMFLIQAFHQEEEQKKRFSEQNALHLKANIAQARSNVIFNRTFDILGNAALVM
MVWLGGRAVLGESLQVGVLAFISYIRQFFQPINQITMQWNTFQSTTVSMDRIWNILN
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TTGAGKSTLISLLNRFYDVKGSIEIDGDIRHLPQAKLHRIVGLIQQEPFLFSGSII
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IVVFQPRVLILDEATANLDSHTEQLVQQALESVSQGRTTIVIAHRLSTVMHADRLVM
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CDS 4571330..4571830

/locus_tag="EFAGFIKM_04007"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQQPETPKRNHQIHYQRSTALCKGSLCFLLLCVSLLWIIVD

GQAERLETIYYISAAVLMWLIPLFFMFVSRLTRTPAVLLSWDDDALSTGKRKIPWS

KIRKVELASPARSKWLLSSSPMFVLYLKDGTRSHIQTDHLLSKKELNKAVALLQRTLQ

EQQQAR"

CDS complement(4571865..4572296)

/gene="lrpC_2"

/locus_tag="EFAGFIKM_04008"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P96582"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator LrpC"

/db_xref="COG:COG1522"

/translation="MNEMIDDDIRILQILIQDAKRSHKEIGEEVHLTGQAVGARVRK

LQDLGVIEGYTVKWNPELGLGLQAFVTVFLNSGDRHAAFRTFIAERKDIVEVHRVSG

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CDS 4572428..4573180

/locus_tag="EFAGFIKM_04009"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKIQLIRNATLWLEYGGLNILVDPMLMDAEVMPAFPNTPNELRN
PRVGLPETETDYLNPDLLIVTHTHVDHWDEAAAKQLGKDIPLICQPGDENIFLGAGFT
NVTAVDEKHEHQSVQFVRTSGHHGTGEIGERMGNVSGFVLEADGEPLTYIAGDTIWCE
EPAEAIRQYAPEVIVNAGGARFVEGDPITMDGPDVVAVKRHAPSAHVIAVHMDAINH
CMVSRTNLATYLTSEQLDGQVLIPRDGESFEF"

CDS complement(4573241..4573936)

/locus_tag="EFAGFIKM_04010"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:ISfinder:ISBth8"
/codon_start=1
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/product="IS3 family transposase ISBth8"
/translation="MMAIHFANREFGYPRMTTALWEAGLNVNHKKVWRIMRELSIQSV
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SHSRKATCLDNACIESFFSHLKTEKLYLNQCNSEAEIRQAVEDYMYNINYRRFQAKLK
QRAPIEYRCALAA"

CDS complement(4574101..4574445)

/locus_tag="EFAGFIKM_04011"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MILGGDIFMAKKGQTFQTYTEEFKLNAVRSYVEGSSSYKVVAER
EGIRNCSQLKVVVKKWKNGEAFDERKNSVPNPLKGRPRTAFGSVEEERDYLQAQVDYL
KKRYPNLVKEKR"

CDS complement(4574632..4576137)

/gene="abfA_2"
/locus_tag="EFAGFIKM_04012"
/EC_number="3.2.1.55"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9XBQ3"
/codon_start=1
/transl_table=11
/product="Intracellular
exo-alpha-(1->5)-L-arabinofuranosidase"

/translation="MEKAKMTVDKDFITGVVDKRLYGSFIEHLGRAVYGGIYEPGHPS
ANEQGFRTDVLEMVKELNVPIVRYPGGNFVSGYNWEDSVGPVSEKRRLELAWRTIET
NEFGFNEFVDWAKQANSEVMMAVNLGTRGTDAARNIVEYSNHPEGSYYSDLRIKHGYK
QPHAIKTWCLGNEMDGPWQIGHKTADEYGR LAVEAAKVMKWTDPTIELVACGSSNLNM
PSFPEWEATVLDHTYDHVEYLSLHQYYGNQE QDPTFLARSLEMDRFIDTVKATCDYI
KAKKRSKKTMYLSFDEWNVVYHSNENDSKMDPWQIAPPQLEDIYNHEDALLVGCMLIS
MLKHADRVKMACLAQLVNVIAPIMTDTGGGSRQTIFYPFMHTSLFGRGTALVPLIQS
PKYDTKQITDVPYLEAIAVHNEEQGEVTVFAVNRHLEESLPLEVDLRSFGKCTVIEHI
VLESDDLKASNTAAQPNRVAPHNRGGAVVSDTLITASLAKASWNVIRLKVQ"

CDS 4576317..4577225

/locus_tag="EFAGFIKM_04013"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MIRANTDAEWLPLYEALASEVRLQIIRLVAETPMNVKDLAASLG
LSSAIVTMHVRKLQDVGIIQSKMIRKDGGTHKMNSLAVDWIGISMPQESGTARKLHEV
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YILSGQQINAIELSLEIGSEAPSVNPNWPSDITFMLNGIRLGEWTSPGDSGNNGRMFT
PEWWSDSVNQYGMLKVLRLITNEGTFIDGQHLSDITLADIPVERNQWTLRLSVEEDAQH
VGGLTLYGEGFGNYNQDILFRLYYHD"

CDS complement(4577346..4578140)

/locus_tag="EFAGFIKM_04014"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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DALGIKLPADSRKQGDYVKAKGTVQTNWKNLKRGDLMYFMSYKGSSASSYSGVNKSSA
TITHGTGIYLGNGKVLHTYSNAGGGVTTSDISGKHWEYRFLFGGSAL"

CDS complement(4578666..4581941)

/locus_tag="EFAGFIKM_04015"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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VDLSKVKVRYFTKDSASDLSFWCDYAQIGSGNVEGHFVSIDPAKGTADTYLEIGFKA
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CDS complement(4582212..4585211)

/locus_tag="EFAGFIKM_04016"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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WTVGVNGTRVKYTPGGLAWLDQWGS LRYAANASFISFVYSDWVSDPVKKSRYQDFAVS
QMNYILGDNPRQSSYVVGYGQNAPQH PHHRTAHSSWLNNEDIPANHRHILYGAMVGGP
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TWA AVSGAESYTVKRSEVSGGPYTTVATGVNGLTYTNTGLTNGTAYYYV SAVNSAGE
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VATGLSVLTYD T TALNGTTYNYRIA AVNANGQTL SNVLALTPSAPPVTTGTLEVQYR
SGGSGNSSNAVTPQFNMKNTGTQAIDLSTVKIRYYFTKDGADQMTFWCDYAEMGTANV
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CDS complement(4585547..4587283)

/locus_tag="EFAGFIKM_04017"

/inference="ab initio prediction:Prodigal:002006"

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TDLVQLIQKDTDHAVQAVKVNSSETEAGIEMVTAAGQAFEQISDAVNKVAGEIQEVSA
GSEEMSASTTEVVGYSQISNIAGEAAGGVHNVSAATQQQLASMEEIASSAGSLSKMA
EELQEQINKFKV"

CDS complement(4587492..4587977)

/gene="bcrC"
/locus_tag="EFAGFIKM_04018"
/EC_number="3.6.1.27"
/inference="ab initio prediction:Prodigal:002006"
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/codon_start=1
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CDS 4588228..4589223

/gene="tagU_4"
/locus_tag="EFAGFIKM_04019"
/EC_number="2.7.8.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01140"

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teichoic acid transferase TagU"
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LVDAVGGEIDVEKDMYYTSKADKHMIDIDLKKGLQHMDGKTALQYVFRHDATSDFT
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CDS 4589363..4590616

/gene="wecH"
/locus_tag="EFAGFIKM_04020"
/EC_number="2.3.1.-"
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/inference="protein motif:HAMAP:MF_01949"
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RIFTPAFWLTGIPDFRSLIRELFVPQTGYHLWVIMVFQFYILFPLFWTGAKAIQRRI
QNTSRFTPMQVIIGLIVLAAAFYGLLMKWSYYNMGSWTESMSEPWSTLLQYRSYSWVM
YWFYFLLGAVCAWSVDSWRSWTTKVLPWTICLFIGMYIWLGYDVLRGSGDVVNINIST
YLKPTTFLTIMAQMFMMYGFVLVLRGKDTQFQRLLSWIGRYSFGGYLVHALVIYAAY
VTRPLQLSGWHLPTLLSFLVTVGIALAISWALSKLPGSRFTVGLMRKPRSIPNSSVN
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CDS complement(4590653..4591390)

/locus_tag="EFAGFIKM_04021"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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SSGKPAKPCMQAGHGLFMIGETADLLGIGLRDLKEQMELGKTLSQIAKERKGLSEEQL
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SMVDKGEIARFIGVTPAQLHEQLQGGKSLAEIAQAKGISEQLVDKLKEQLTGDLKRF
VNQKGNMHPAPGPQEPVGRSTSSEVK"

CDS 4591802..4592749

/locus_tag="EFAGFIKM_04022"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRKDWLDPFRSDLEVVFASAEQLVREYPEPLSGHALEQLRSVNP
LLRDSGHSYIGYIPLWMQHSDKLPPEKAHQLSTACLIHMLYFLNQDDVMDEQPENAT
LKLSLGNLYYMDALQSYSVLFNPSSTFWVYFRQYVVDWAVSVTGEHSIDYFQQNPLLI
AQKAAPLLIGATGALLLNQSDRIIPVCSAINITLMTLQMTDDFTDTQQDAVHGNYS
YLSHISAALNHNYPVHPLSDRIHDNVYNTQLMNSYVDIAYHYNRTLSSNLGISHLEA
FNSYLCSTLVQAVQDITQRKKQLLQGGFHHWISEQQLGF"

CDS 4592804..4593046

/locus_tag="EFAGFIKM_04023"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MMVSEKTLHEDIIEKAWTDEHFRQQLHSNPKQALREAFGIVPE
HIQVRTVEEQQNDYVLVIPPNPSPVNYDVNCGPWRS"

CDS complement(4593124..4595022)

/gene="rcsC_11"
/locus_tag="EFAGFIKM_04024"
/EC_number="2.7.13.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00979"

/codon_start=1
/transl_table=11
/product="Sensor histidine kinase RcsC"
/translation="MKNVPKAIVILWMSVLIILGMPHGIVFATTGAVQQPVSITGWEV
KWGNVDDQGFISEVKGADIEWEKQGS DKLEYSNTDRSNSLWTRLTIPELSEESSAIRF
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TVQVGOPYAALQEKYIHNGLIDVILGATFVFTAITMLSCTFFLGKFHKGLWISLCIVMG
SIGTMIITYSQFLYTFYQVYGDLYSVVFDLAML LGMPALCYFFEQIIGPGLHGIFTKL
RKILFIYSVIAVFSLFYVTSGGQWEILYNLLVQRVVGIVLVILLTILLVGTIKALQ
RNREAMLLATGFGTFALISVAELLWYYQRS GTYHLLWWKWSMVAFVISLIAILGSRFA
EKHTKVLEYSKELELFNNELQRSEKMEIISELAASVAHEVRNPLQVTRGFLQLMTEQE
DNKNKGYVRIALEELDRASGIITDFTFAKPEFDHIISLNISDEFNHIEGILVPMANL
EGGKITTDIPPDLYIRGNSSKFKQAFINI IKN SIEALQGQGQIDIWAYKQDGMIVHV
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VSFAEFVD"

CDS complement(4595176..4595457)

/locus_tag="EFAGFIKM_04025"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDWYTLGNMITRIRIGQKASTPGFSRTVIRRPDGLFWVGGIWSG
QVVQLRDFLFSDIWTIYDDEETEQLWLEFRSQVEQKEREMIVNQFEDLRD"

CDS 4595602..4595763

/locus_tag="EFAGFIKM_04026"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNEPHRTVEVEHKDVQHKSDSSMVASTFIKYAAYIIIFGFLYF
LVKYVFPKF"

CDS 4595886..4596257

/locus_tag="EFAGFIKM_04027"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSDKPISNEESDRYYDRYQRSRDIPPETEVPEGDMDTFDEVSGR
RIVTEDSDLAPVAATAVDEPELDSRLAETPLESVPDADLLQPNSPVDPAAPDPDALHG
TDLLNGAGADAKPENDIPPRH"

CDS 4596297..4596488

/locus_tag="EFAGFIKM_04028"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKEDRQKHVHEPDNLVTERDIDPDFGLFTEDSFPEALEDEDQRD
AVEHAIPKEKASRKPSDD"

CDS complement(4596591..4597805)

/gene="sbnD_3"

/locus_tag="EFAGFIKM_04029"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2G1N0"

/codon_start=1

/transl_table=11

/product="Staphyloferrin B transporter"

/translation="MNFSWKRNLVILWIGVFFCSTAYSISIPFLPLFLSADLGVRDHL
ELWSGLAFGITFLASALVSPFWGSLADKYGRKPMLIRSGYSLAVLYLINYFVQDPYSL
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MGICTFSVMILEPLLTVYVMEMGVQPDRASLSSGIIFSAVG VATVIMAPRWGKIGSRI
GYGKVLIIGLVGGAVGNLLQFFTTGYIAFGILRFVYGLFFAAVFPAINAMIVQATASN
FRGRAFSLNQSAAQIGTMAGPIIGGV LGGWLP IRWIFIINGVALIITAIVAKWSGLDH
KLPVASKVSPKR"

CDS 4598061..4598711
/locus_tag="EFAGFIKM_04030"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSLQWKKN TVSVL LAMLLIVISGCGRPSSGATETPAPVEPTGP
NPVATIEMADGQKIVIELYPEIAPNTVNNFISLANQGFYDGLIFHRVIPGFMVQSGDP
NGNGSGGPGYTIKGEFTSNGHKNHLNHTRGVISMARQDGNLDSAGSQFFIMLADADHL
DNAYASFGKVTEGIETVDNIAAQEIGENDKPVTDQVMKKVTV DTHGLEYPEPVKMP"

CDS complement(4598879..4599061)
/locus_tag="EFAGFIKM_04031"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKTGIKSYTITDTATIPWRKESLFVEVNRGLLKGLAWGVAFSCP
LWIAIIGWLRLMGWMY"

CDS 4599190..4599450
/locus_tag="EFAGFIKM_04032"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAKSKKRTPAPKAAAQDKPTTLKDLLSSDVLEKLKAQADEAKAA
EASLKEQERQQAEEARQAEQKRRDND FEYLLNNSAMDWKKHK"

CDS 4599659..4600453
/gene="lvr_3"
/locus_tag="EFAGFIKM_04033"
/EC_number="1.1.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9LBG2"

/codon_start=1
/transl_table=11
/product="Levodione reductase"
/translation="MTEQRLEGKVAIVTGGGSGIGQATAIRFAEHGAKVYMLDRTPEN
AEETKQTIEKAGGEAYVIECDISKPDNVQKAINQAAAEAGKLDIIFANAGINGTMAPI
ETMEIEDWDQTMEINMRGTFATVKYAIPHLKEHGGSIITSSINGNRVFSGIGFSAYA
SSKAGQTAFTKMAALELARYKIRVNAVCPGAIDTNIDDNTYPSDDLKEVQIPVEFPEG
HEHPLKGEPGTSKQVANLVFLASDEASHVTGTRIYVDGAESLLRG"

CDS complement(4600593..4601354)

/locus_tag="EFAGFIKM_04034"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAYPPWLNPHYDAEPFILFSTSHIVSISVITALIVLMFLLRHHLR
SWSERARRILRIVLACIMFACEIVLQLWYVYGGIWSLQTSLELCSLSLLLSALLLL
TRSRLLSALLFAGIAGAHMAILTPNLGYGYAHFRFIQFFVAHACIILALLYMTWVEQ
LRPSWRSVAGSMIFVNVAALIVYVVDVMLDANYMFLRHKPSTPSVLDMLGPYPMYILG
EEILALVLFSLMYILLFAIPDRLKHRVKKGKSSAV"

CDS 4601617..4602591

/gene="mhqA"
/locus_tag="EFAGFIKM_04035"
/EC_number="1.13.11.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34689"
/codon_start=1
/transl_table=11
/product="Putative ring-cleaving dioxygenase MhqA"
/db_xref="COG:COG0346"
/translation="MQIKGLHHVSALTAHADQNYRFYTNIMGLRLIKKTVNQDDVSVY
HLFYGDEKGNPGTELTFFEIPMAGQTREGVNSISGTSLRVPSDAALTYWQQRDFEFV
PHGEIVERGGRGTLSTDFEGQRLILVSDENNTGVAGGKPWDQSPVPAEYGIVGLGPI"

HLTVKDASLTSPVLTELLGFRAKGSYPAFTPGQPDVLVFESGEGSGSEVHVEERNDL
AQERPGRGSVHHVAFRVDNEEELKQWVERVRNFQFPNSGFVDRFYFRSLYFREANGIL
FELATDGPFGDTDEELEHLGESLALPPFLEGRRAEIEANLKPLDTVIR"

CDS complement(4602742..4603449)

/locus_tag="EFAGFIKM_04036"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKKVVLGLMVGTLTLGIGTGALAATGLEQIKAYLNSKITLKMN

GATVTAKDANGKTVLPITYNGTTYLPVRAVGSLLGTEITYDSATSSVLIGGTNGSAPV

TNGKVTLALGTSVLGSTAWHTKDPKDDTYKGKDYKDVYLHNDPTKQGDDIQINTGKK

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CDS complement(4603718..4604563)

/locus_tag="EFAGFIKM_04037"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKTWTGILLMIILAVATISTTSAARTMNESQKQLNIDDQSSQTE

VVEASNIDKLHDTAKTTQESIPVKEEYVSVAPENENVRLYPMKVEGSGYIYNGMILEV

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LEEMKMQSLDEIAKQHVKSKVTVRSDRVDVDVAVDGVQAEPLRIEEDTSGGVYNEELG

FGGVTYYSVEDDQLVVSAGSYGAALYAGDLTFAYEYQDGEWKAVDLKYSMEVYEEY

YETFD"

CDS complement(4604762..4606048)

/gene="mcpB_2"

/locus_tag="EFAGFIKM_04038"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39215"

/codon_start=1

/transl_table=11
/product="Methyl-accepting chemotaxis protein McpB"
/db_xref="COG:COG0840"
/translation="MCTMKWTLGAKTVAGLVLSIITYGTSGFFIFFVKDWWTLDIPN
WVYISIILIMGVCWNGILGWFAWRWLTRPIVHLSRAAQQVSAGDLTEIPQRRQTDEL
TVLYDAFRAMVSNLRSIVNDIADSTRTTSQNAQSLSEAITQAAEQIEMMSDAVDHIAV
GVVEEQKVTSHQSLITADEMLNDFQRMHSQSMDMTEMSGQMERSVDHTKQTFSSLMKGM
DELADSHNRSRDIMLLLEKEASDIEVITQSVKNIAEETGLLALNASIEAARAGEEGSG
FAVVAQQIRKLADESKESVHRINELISRVQERIRETAQLSHEQHGLVNESERTISVD
QTLHELTGTVEVFMKGAHDIGSKIAEQTGRVEQTHGHVKKIQGKAGSFSDEARRIMDA
AHEETAIMEEISSAEELRQLTDRLLDKTKAFRMQP"

CDS 4606374..4607807

/gene="aspA"
/locus_tag="EFAGFIKM_04039"
/EC_number="4.3.1.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AC38"
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/transl_table=11
/product="Aspartate ammonia-lyase"
/db_xref="COG:COG1027"
/translation="MSTMSTRTEKDFIGEKEIPAYAYYGIQTVRAVENFPITGVPVHR
ELITAAVKKAAAITNMELKMLPSKIGDVIVMAAEEMMKGHLDHFIVDSIQGGAGT
SMNMNMNEILANRGLELLTKSKGDYFHCNPNNHVNMSQSTNDVVPTALRIAAYQLSET
LLATMKRLQDAFRKKEVEFNDVVKVGRTHLQDAVPIRLGQEFGAYARVIGRDIERLEF
ANRRLLTINMGATAVGTGLNAKPEYIVKVTEHLSAVTGLPLQTAEDLV DATQNTDAYL
ELSAALKVCAVSLSKICNDIRLMASGPRAGFNELRLPPRQPGSSIMPGKVNPMVAEVI
NQVSFQVMGNDHTICMACEAGQFELNVMGPVIAFNLLQSLKIMNNGIDVFTRYAVEEM
EANRERCELIMNQSFMTALNPHLGYNVAASIVKEALKTGLSLQEII LERGLLTPEE
LEEILHPEQMTTPGIAGEHFLRNMERL"

CDS complement(4607928..4609232)

/gene="rpoN"

/locus_tag="EFAGFIKM_04040"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A171"
/codon_start=1
/transl_table=11
/product="RNA polymerase sigma-54 factor"
/db_xref="COG:COG1508"
/translation="MLGVQLVQEQRIRLSITPEMKQSFQLLIMSGQDLTRYLLDAAEE
NPVLELEEQAAPLARIPRRMDQRRYDSYDPLLQAKGAEPTLEQLLIAQIRVMTIPDEL
ENMAVYLAGCVNDDGYLTVELAEVQATLELPMSKIAAGLELLQSLDPAGVGARNLQEC
LLLQIRRDPSAALNAEWMVEAGMEALVPFHPGRTGRRLGMTSQAQIAYDYITRLDPK
PCRSIGCTERPHYIIPDAIVGLRNGEVHYSLHAAGNPRVSMNEVCFRWIREEAPDTIW
STRVAEARAIIRSVHLRRRTLVRVLAAVMEEQKHFLVKGPSALKPLNLAVIAEKIGMH
ESTVSRVKGKYIETPHGVYELRAFFASGISTTSGDKTSASAVKRRRLKEIIRTEQAQR
PYSDSHLATLLAEEGIVISRRTVAKYREELQILPSLERKQWA"

CDS complement(4609361..4610908)

/gene="rocA1"
/locus_tag="EFAGFIKM_04041"
/EC_number="1.2.1.88"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9K9B2"
/codon_start=1
/transl_table=11
/product="1-pyrroline-5-carboxylate dehydrogenase 1"
/db_xref="COG:COG1012"
/translation="MNIPFVNPFPTFAVQANQEAFEDALRQVEAELGQEYPIIIGGQ
KITSSRTLTSVNPAAKNQVVGTIHQADQELA EKAIQTAAETFWKHTDPNERARYLY
KAAAIMRRRKHEFSAWMVYEAGKTWPEADADTAE AIDFMEFYARDMQRLSEPQPLVRI
AGEDNELSYIPLGVGVVIPPWNFPLAIMAGMTSAALVSGNTVVLKPASTTPVIAAKFM
ELLAEVGLPDGVVNFPLPGPGSEVGDYLV DHALTRFISFTGSRDVGLRINERAALTAPG
QKWIKRVIAEMGGKDSIVVDS DSDLELAESITASAFGFSGQKCSACSRAIIHKDVYD
EVLQKVIERTQKLTMGSPLEVGSQVGPVIDDKAYAKITEYIEIGKGEGRLVHGGGTGN"

VEGYFIEPTIIADVDPKARIAQDEIFGPVLAFIKAESFQDALDIANNTDYGLTGAVIS
RNREHLEQARREYFAGNLYFNRKCTGALVGTHPFGGFNMSGTDSKAGGRDYLLLFTQA
KLVSEKY"

CDS 4611229..4612152

/gene="fadM"

/locus_tag="EFAGFIKM_04042"

/EC_number="1.5.5.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8RMG1"

/codon_start=1

/transl_table=11

/product="Proline dehydrogenase 1"

/translation="MSVGTEIYRKLLTVAGNKAIVENLSIRYGKKLAGKFIAGNTLEE

ALEEIHILNNKGIMATLDHLGEGITRLSEAALYRDEYVRLVEGIAREGVDSNVSLKPT

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TVLQAYLHRTEEDTRDMIREGIRLRLVKGAYKEPGSVAYQNTSEVIHQFKTMIRNHLD

QGVYTAVASHDDHIINWTKQYAKDRGISPDFAFEFQMLYGLRMSEQLAKEGYRIRCY

VPYGTMWYPYYTRRLAEKPANLWMVVKNMFR"

CDS complement(4612379..4613545)

/locus_tag="EFAGFIKM_04043"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAILSTGPIENKISGITGIRPTQSVTVKIDNRNATEMFTVLLRG

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GELVAAHRLVSQELLGETLSTTGVTGATGATGVTGVTGGTGTGSGTGTGVTGGTGT

GVTGATGVTGATGSGTGTGVTGATGSGTGTGATGVTGATGTTGVTGATGVTGVTGSG

ATGVTGSGTGTGVTGSGTGTGTTGVTGATGTAGQGLSSYAYIFNTSAQTVAIEADVIF

DSNANLTGITHAPNTAAIIIGNAGDYAVFFNVAGVQANQFTLYQNGAPVGGSVYGSGA

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CDS 4613802..4613981

/locus_tag="EFAGFIKM_04044"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKIQHRSPLCRQHVCFMSKNIYTPHLESYNMGNHHSPVISYVDY
LYVTRVKKSFPKVMF"

CDS 4613996..4615705

/gene="norR"
/locus_tag="EFAGFIKM_04045"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01314"
/codon_start=1
/transl_table=11
/product="Anaerobic nitric oxide reductase transcription
regulator NorR"
/translation="MKHLLPELMSLLRTDMDILDLDLSTLTIPSSTSLVDAFCLFNTS
SYLFIQDDGPLLGYIAVSDVLHAMMHAHRLIEAYFETTLETAGSALTLINEAKVAYW
TTGAEHVFSISKDIIGQPAADFFPPDRLQSLKTYTGETVYRKQHQPDPDLFALINA
RPVQLDGHIVGAVAAEVDITTEIRLHQELLHMTSKVQHLEKAVARLRPELDPFARIKG
SGPVIKQCMETIRKISTTSATVLILGESGTGKELFAKAIHDLRESQTAPFIAINCGAI
PASLFESELFGEKGAFGADPKGKKGKIELAEGGTLFLDEIGEMPLELQVKLLRVLQ
EKSYFPVGGTRMKQANCRIIAATNQNLMSMIARNQFREDLYYRLNVINLVIPPLMRK
EDIYELTQTFLQEFSLLYNRHIELVPPEVFKLLFQYDWPGNVRELRNVIERLTILTTD
GEMKQEYLPDTLTLTMQESEQEQLTSGIHSCHANNEYQQRQDSAGAEQEPRTVANADE
SEPSDDSELVSGVIYQQKLDTYEAQLLIQYLKATGGNKRRTLAKQLGISRATLYNRMKR
LGL"

CDS complement(4615752..4617821)

/locus_tag="EFAGFIKM_04046"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MGNSSEAQYDNYVGDGKRFIGRTKELTTLERWFNHPEAPLTIFS
ITGMGGIGKSSLLSEMLSVRDQGATAIWM DGRSCGATPSV FMDYLSSTLGLETLDND
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ASAWRTHPRLHQR FVQMLQHFTFEEISEYISVAGSLNQGMAGTITRMTDGHPLGLAL
AVEAADQRRNLPHAEWAELSHMISARL LLELTIPRLHPMVEVLTLLGTANQELLSSVL
DMTVTQEEYHMLRQMSFIRSGPDGLALHDMGRVHLLRDLRQREPHRLQTM RIRIAKLL
KPLHEQAGSHERRQIARKMLLLCQESMLQFRKYADVSRDSLFSPLETMKQEDLPSLHR
LLQQWCEYSVAPDQAVFYGPFLDELAYRYPEGIVLMRDQLGEPIAMFITVLVHRESSG
LLLKYFPNEMNECF TPQELGNPDQSDTHFALLAAARD DVPGYTREELVGYMALDRLS
LLGDGARVILIATNPHLKLFLLSIGFQMRRTTRACDRYEDPADVLDL DLRSQGFGVW
VMSLLDPEWQDDRIQPGTTVRERTSWSEQEV RKMLGYLRSPGELHEYAGRVRGVKDGI
QLQLYVMDLLEGRVHGLSPQDQMLLYAAYWTHAGNPTAAAQTCSMSRATFYRHLRTAL
TRLARIL"

CDS complement(4618490..4620160)

/gene="pucR_5"
/locus_tag="EFAGFIKM_04047"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32138"
/codon_start=1
/transl_table=11
/product="Purine catabolism regulatory protein"
/db_xref="COG:COG2508"
/translation="MRNDRVFTIKDILARPVFGRARLAAGKDG VNRQVGWVHVLEITN
VSPFVSPHDLILSTGLWLQSEEGREEYLLQLIGSEAAGLCVEFGTSIYGIPEELIELA
DRHQFPLIVFEQPVR FVEITQDIHSLINHQHQLLKSLEAYS RQLQQR TLQSTDMSAV
LNLLHEYAAKPVVYISSMEPGSFVPELVP EMEQAIYTWYEQEVEHLDLNDSDTELWFH
MDEQKALLCHPVVCFGQVFSAVGMIVHHAAPVEYLKLLLDYAKAAAAL TLR SQFLEE
KMVRNQNELIQDLMNGNIHQEEQAQTRMGLRLLVKGQYWFAGGVIEIEHRLKGTGRER
MEANHQDVLVLLRSLLKKNLPSLIMLKNNQVYLCCAKEAVTAAARHQLLR LLEGIAQ
DVKRFASRNLKQVMIHVGF GKLRNRLTSLPESLQEAYQVIEVSRSDPMEHVHFYERM
GIYQMLKALPHSFLQPFVQDHLGMLIAHDQTHHLRLVETLDAYLQNF GSKRDAAAQLF

IHRQTLYNRLEKLEELMGPGYMDQGRRICLEMALLAHAMIENGQWQSS"

CDS 4620350..4621483

/gene="ald"

/locus_tag="EFAGFIKM_04048"

/EC_number="1.4.1.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q08352"

/codon_start=1

/transl_table=11

/product="Alanine dehydrogenase"

/db_xref="COG:COG0686"

/translation="MRIGIPKEIKNNENRVAMTPAGAADFIRAGHQVLIEQGAGIGSG
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LAKALIKSRVTAIAYETLEVNSALPLTPMSEVAGRMASQIGAQLLEKTEGGKGILLS
GVPGVSRGKVVIIGGGTVGTNAAKIAIGLGADVTLDLNLRQLDDIFGNQIHTLV
SSPSNIATAVAADLLICAVLIPGAKAPTLVSEQVVKTMAPGSVIVDVAIDQGGIVET
IDHITTHDEPTYVKHGVVHYAVANMPGAVPRTSTVALTNATMPYALQLANHGA AAAAIR
GSSSIRSAVNVLNGHITYEAVARDLG HAYVPAGQALENTAAVQ"

CDS complement(4621651..4622568)

/locus_tag="EFAGFIKM_04049"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAQYPQWSYSQSRASMFDECLRKYYYHYHGAHNGWKTD SADEM
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MDADQWRMNPKNRTMLSEIYYGDDTLNDRIATIKERASACVSNLYQTLTWEDLSRAST
DILEIEKWD TMMLHDTRVYVKMDLLYRRSNGNIVVDWKTGKEDDFSDQLMLYASYVR
EHYRIPLEQIELRVEYLLTGKHREFTATEEDIRKVEENVGRYIEEMRSCVEDEYYNRP
KDVTYFTAMP SHRSCRDCNFREVCSERAV"

CDS 4623093..4623776

/locus_tag="EFAGFIKM_04050"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNRPDWFQAEELQQIQVIGSDRNELVNIIGDVEGLNCIGTGTD
AAVFTYDGLPQYAFKMYSDHALDKLENEKQVYEQLKGLPYFPTYYGSGRNVLVISFEP
GDTLLECLEKGIPVPEQVMLDVDAAREAVRSRGLNPRDIHLKNVILQNGRGKVIDVSE
YIQEGNDNRWEHLVWAYHNIYPRIKGTPISPRMLQTIKWGYNQFDHANVKMDDLAKKA
NRLFSRFMK"

CDS complement(4624106..4625002)

/gene="rhaR_34"

/locus_tag="EFAGFIKM_04051"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MLDLKALHENTRIDHKSHPFQLFQNRCSMDKVEECILYLHWHEH
FELIIMRKGSALFHIDSKPYVVRAGEVHIIPGGTLHVGALDDGDVHYDSVVVNRALF
HDFTHDPVHEQYVAPYLEGRVRFVPKPAEENTACTGYYSLLNEAVEEMALQPPAYQLV
VKSKLHALFTLLARTFMPQQLPDKTVGSYFPNRERFKQLIAQIEADPTGKMSVTEAAS
HVGLNAYHFCKMFKKLTGRTFVEYVNGCRMSEAEQLLQGSSLTITEIARVGC DNANY
FTKLYKQYKGMTPSQGRGRKEG"

CDS 4625132..4626019

/locus_tag="EFAGFIKM_04052"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKSLRIGTLVGGQDAVRVIPQIMQHGFESFNLTFWQTTGDLDL
AETAKRVREIVDEQGIVISAVSIFGNPLTGAGDNADTLASWERVIDHAQLFGADIVSG
FTGRLTDLPINESIPRFKEVFGELARRAADRGVRIAFENCDMGGTWQTDWNIAHNPT

AWEMMFDAVPDDNVGLEWEPCHQMSSLIDPIPQLRKWAHKVFHVHGKDATIAWDIVKE
YGVHGPREFVWHRTPGFGDNNWADIITILRQNGYQGTIDIEGWHDVPYKDELEMTGQV
HALRYLKQCRGGDFVNPV"

CDS 4626156..4627211

/gene="afr_1"

/locus_tag="EFAGFIKM_04053"

/EC_number="1.1.1.292"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2I8V6"

/codon_start=1

/transl_table=11

/product="1,5-anhydro-D-fructose reductase"

/translation="MTHPYRVIIAGCGVMANTWADYALQRPDTEIVGLVDLYEQTAIA

FATRHGLTCPTFTDIREAIQTTGANIVFDVTIPASHYGIAMTALKEGCHVFGEKPLAE

SFSDCTDIVQTARSTGHIQAVMQNRRFDPRIRAYQHLISGGAIGQVGYAGADFFLGPH

FGGFRDLMDSPLLLDMAIHTFDQARYILGANPVSVYCHEFNPPGSWYQGNAMALCIFE

MSDGSVFNRYRGSWCAEGVRTSWEASWRVIGEKGTAIWDGHHDDIYAEVVTAQSLDADGK

PSFFQPSEIEAELPVMDKTGHHGCLEDMFAALESGRLPETDCSDNQFSMAMVLASLE

SARTGQKVFIADLLKNT"

CDS complement(4627525..4628844)

/locus_tag="EFAGFIKM_04054"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEQFRLPKIPMPQLELPQAVQDILTEADERLQHRPRLAQFRNC

FPNTLETTTKLLEDGTTFVITGDIPAMWLRDSVEQVMHYVPLAKGDEKLQRIIGGLIK

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ETELTDIFDERFKKVMENIVQLWETEQQHAERSSYRFMRRNCPAHDTLRNEGLGMPVN

YTGMIWSGFRPSDDACDFHYNIPANMFAAVTLRQMGEIAKWVFRDEQLVSRMARLEEE

IRHGIALYGTyrHPEYGGQIYAYETDGYGNFCLMDDAGTPGLMSIPYMEYASIEDTVYQ

NTRQFILSKENPFYYEGKVAKGIGSPHTPPGYIWHMALSMQGLTADNDEEMLATIELL

ENTDAGTGYMHEGFHADDPNTFTRPWFAWSNSLFSQLVYKAMKKGIL"

CDS 4628959..4630020

/gene="degA_6"

/locus_tag="EFAGFIKM_04055"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37947"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator DegA"

/db_xref="COG:COG1609"

/translation="MSRKVSIQTLADQLGLSKYAVSRALSGKTGVSEATRARVLELAR

ALGYRQSTPGASNSPATANHADPSDPPFVLICMNQLNRGEPHYWQRVLSGMISACNER

GWHHAIVSPSLGVTDENTSPEKAIAPHLDWERCAGIIVMGAFPHTVLQRLSQTGRPII

LVDHQEPLLNCDTISHDNLEAGITVARYLMSLNCRRIGLITDDGRAASFAQRKIGIEL

ALNHFHVDTSHTTSFREWNIPYENGWVNQLATAIQNIPDDKRPDAWIGVNDDIALQW

MHKLQEMGISTPKDCLVIGIDNVHSAVTSSPPLTTVNLCKEELGQRAVEALQRRIERP

GTPKETVMLSTTLIPRESA"

CDS complement(4630249..4631874)

/locus_tag="EFAGFIKM_04056"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKPISKDEDLWEHLYREEPDADFTLKV MQKLDGVSMESGEDQ

YPFVKKSMRANWMRRTGIAAAVVILAGGAWFAFDLTTEPSSPSVSAVDRPPLPNMPV

PEELKYSYFADDYKRLKPLGLVNP DININDQGYTLKIEDVLVDRSHMVM TMQQTTPD

GLGLSRLLSEMGRIVHTDEEGRQVATLARDTRTKGSVTERLLFQFHDEIPDQVVVRGE

LRNLNVGRYYDYEKKSYEDRDVTVDWSFQFNIDMTKAKSLAVENSMDNTYTTPEGLKL

DMTQLVRTPNGTRLDLNVSLDDELRAKV NEDWANYMSIIYHLEIPETNEYRIFNGIRP

DSRQAKFRLQDLSDLRNGGPLKLSETWDPAFVTVD AKNIRFVLDGYTLPVKEEKSVEV

DLEKLEKRRKDDTKFYTFVAFEQLGDKILIYDFEYEPVMESYDPPKIDVKKGYSVLVK

GS GTFRNAFMGDRWVAVDSDGKEYPVEVNGYPDQPNNNGEYVEDDLQLKIRGFNEEKG

TKFTLKRTVVNREYRDVNWEVDLPSYDSLWLK"

CDS complement(4631852..4632427)

/gene="sigW_4"

/locus_tag="EFAGFIKM_04057"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q45585"

/codon_start=1

/transl_table=11

/product="ECF RNA polymerase sigma factor SigW"

/db_xref="COG:COG1595"

/translation="MTQQIPEEELIQRIVAGDKQLFSVLVDTRYKNKVYGILRGMGASH
PDAQDLAQDTFIRIYRHLPSRREGSRFSSWVYTIAVNRMRFIREKKPAMSPVDQGIE
PVSNETPEKRVLHKEMQREIYRQLEQLPESYRLVLLLKYTNELSYEEIADITGMSSTK
VRNTLYRGKKTLRKQMERKGLATYEAYFKG"

CDS complement(4632569..4633084)

/gene="mug"

/locus_tag="EFAGFIKM_04058"

/EC_number="3.2.2.28"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A9H1"

/codon_start=1

/transl_table=11

/product="G/U mismatch-specific DNA glycosylase"

/db_xref="COG:COG3663"

/translation="MIPDHLDVGLSILFIGFNPSITSGETGHHYAYKGNRFWRILERS
GLTPRLYDTQEDGELLKLGYGFTNIVARPTRGMEDITKEEYAEGRQILRQKLEKYRPD
IACFVGKGVYTQYSKRAKVQWGFQDDPVVKEIQEFVAPSSSGLVRMSMDEIVAIYSQL
ADFVAEKNRED"

CDS 4633206..4634126

/locus_tag="EFAGFIKM_04059"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MIADIMLEVLPVFLLIAVGSWMQKVKLDLYTLAKINFYCITP
AAVFMSMYHSDMSGELLGTVTLFYTIYVLILYIVGSVFARSLRMNKGMKAAFNNSIML
DNAGNYGLPINALVFRGDPLASSIQALVMSLQALLTTYGVLSIQGAKLKGNRAVII
GFLKMPVPYALLLGILLHMWKVPLPTFLSMPLTYAQQSMVAVALTLGAQIVKYPIQL
YRLDVYISTFLRLLIGPAIGISIVLLLGLEGIAAQALIISGMPTGVNASILAEEDN
EPDFAAQTVLISTLLNIITITALISYAKTF"

CDS complement(4634187..4634438)

/locus_tag="EFAGFIKM_04060"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MASVILLVKQTEDDEKVIYRFGPNERKMGLIEMNKIKESVRELE
PVQVDGVSPSFFFNRAAQRLVRCLFREGGKFPERTTFET"

CDS 4634714..4635106

/gene="rutC_1"
/locus_tag="EFAGFIKM_04061"
/EC_number="1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00831"
/codon_start=1
/transl_table=11
/product="Putative aminoacrylate peracid reductase RutC"
/translation="MSQAQIYSHGVPWEEAFSVAQGYSINGTIYIAGQFSHDMQGTFI
GVDDIEAQVRQTLNLDRLVLAGFNVTKSNAIELEIFLVHPQEHLEPCVAVYKEYIGTH
RPAVTMVGTSGLAFPHQLIEIRAVAHTN"

CDS complement(4635241..4635870)

/locus_tag="EFAGFIKM_04062"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MRIKVISSLLAIFMIFATVASAHPGRTDSSGGHTCRTNCAKWGL
KQGEYHYHNGGSSSSSSKSSSSSSSSSGSTKKSNSSTATQKKATPKPEYIKSAVQVKV
NGSKVIFTESPIVMNNTNLVPLREMAKAMQAKTSWDSKTQTITVTKDKYKLIFTLGSK
KVKVNGKEVTLQAAPKEIKGTTYIPLRVLVEGLGASLTSSGNTLTVKVK"

CDS complement(4636032..4636835)

/locus_tag="EFAGFIKM_04063"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTYVHEEMKDTIRQQLKQIEQEEQVRIIYACESGSRAWGFPSQD
SDYDVRFLYVRPLEWYLSIEDKRDVIERPISDQLDINGWDLRKALKLFRKSNPPLLEW
LQSPIQYDEQYSVAQHIALSPLTFSPKSCMYHYLNMAKGNFRDYLQGEQVRIKKYFY
VLRPLLACGWIERYDAMPPMAFEELIQELVPATTPLYTEIHELLRRKKAGEELDLEPQ
LPAIQAFLAEKIEHFEQLAGQMENEQIIEFEELDRIFRFALQEVWGERG"

CDS complement(4636862..4638355)

/gene="rsr"
/locus_tag="EFAGFIKM_04064"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9RUW8"
/codon_start=1
/transl_table=11
/product="60 kDa SS-A/Ro ribonucleoprotein"
/translation="MSRAKQLFNQPQPPTTRNHGGYGAYERLVEEQYIQMLMTNTLNNT
FYADTQQLMDDAMVSHQEMA EVDAGFMARALVYARNEGLMRLQPLYGLALLSKVDVDH
FAKVFSQVVQTPADLADFLTILRGTRGQGGRVAVKRQVSQFLNGITEYWAIKYNGRGR
GYSLGDMIATAHPKPIDTKQALFRYLRGHEVDLTELPLQALEKCLKATPNPASRMHL
IEKGKLPYSVNSIMQPTRTVWEALMSQMPTFALLRHLNAMDRAGVFEKSKNIDYVTR
RLTDAEALRKSRI LPFRFASAYEMFAREELRDALRQAVELSIGNLPTLPGRTAIFLDR
SGSMQGDYLRIGSVLALALYKQTRGNALFWLFDH MVEDARPKMDESILSQAHRIRAQG

GTDTGRPVREL RDIGEKVDQIIITDEQQNEGSPLYAELERYRRMMNP ELKAFIVDIA

PYQQAMVPPRDGKTFYIYGWSETVLT YIAETVAGYDTLANRV RAMDI"

CDS 4638727..4640082

/locus_tag="EFAGFIKM_04065"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MARESFDKEIQFLRMLSLTSGAYNRKQYAERLGISVHTFDKTNR

RLKEIMQTVADQRSGAEAGREMA DLVRFQYGESAEPMLLFLFRAKSMKETEVQRLSVL

LHTLQHKALTAMELLDACCADLPEDLALPDEKTIRSDLKYLEEVGVIRKEPGGRPYQY

ALQQDVL TQLTVEEQLELYDFVDM MANTQVPSVQGYLLRDSLKKAITASFPQEEATEP

YIYKYHYYSRILDEAHLYTLLSAIRQRKRVQFLY YSPKKPSSYSSQNTNPRFEREAGG

RSNRIVPLEVIYDHQYGRWYVIGYQGRRGFVKFRMEGITQLEEQDSVEEQYMSELKQQ

WTDISRYSWLVDTGNTVTVQARFFHPERGQRNFILDRVRLQGQWGKIIPETDHTFLYE

IQVNGTTEIKPWLRSGSSCEIIPQRLRQEMIKEWKEIAEYEPVREDVQLPDDDTT

E"

CDS 4640030..4640914

/locus_tag="EFAGFIKM_04066"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNLFEKMFNYQMMTRLNETGLFTWTSQERAWLRMMLNHPAAREA

LSAVTLDKMYNMLNGEQDLNLQDYLTEKAKSEENS VSHPLLRLRLIILHHQGFRMTG

RVRNGRTSHDEFGFPYKLEYS MVKKEWYVLWYAPRFDKLMSTKLHSIVIVEAQPV EPD

TASGYTARIAAITEKRKTTITIEVLPQFNQELSRILYAFSCFEKQVEYLEAEQTYRIE

LTVPRNEMDYVLSKMRFLGKRVRIADHTMLRERMSETAAKALARYAETDSVMHPKHSN

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CDS complement(4641036..4641536)

/locus_tag="EFAGFIKM_04067"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MELYFRDNFFNAGYTEIMYPNQEAGHLDLKS VFGSSLDVSDNS
GLVCSGKFRMLTNRWDITAADGRHLGVLRARFSFFSKKYEYDAGSRGT YDVSAPAFSQ
EYDISGSGGRIVASFRR TSGWFSSGAFVLDNQSEQLDTYELIAVVMGVHAINKRRNSA
ASSGGT"

CDS complement(4641717..4642457)

/locus_tag="EFAGFIKM_04068"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MMTLLKYDFRRNWNTLLAGLVILIIAQVGLSLFVSEVTGIVLGI
MGYVGVGVAIYVKMIKTYTSNIRSYNRRLLPVTGLSHVLSPLIFGLLCGLGLVIFTT
HAYIYISMKL RMNMASNIDLSGLHVSDYISLLLFSAWVMIFMTVIIFLSISIAGSFRW
RTGPWIGIVAFFVLVNLIGWLENIITTGRFSPNEMFRYTEESTGIAITANGVLWSDGM
WGSIIFEVIVAVILVWATIYLNKKVEV"

CDS complement(4642454..4643152)

/gene="yxlF_2"
/locus_tag="EFAGFIKM_04069"
/EC_number="3.6.3.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94374"
/codon_start=1
/transl_table=11
/product="putative ABC transporter ATP-binding protein
YxlF"
/db_xref="COG:COG1131"

/translation="MSNILELNQINKTYGNKKALS NITLDIAPGRIVGLLGSNGSGKS
TLMKLVAGLLHPSSGTIQVTGKPVGLET KALVSFMPDRPLTEKW MRVRDAIAYYRDFY
ADFDEEKAREMLDFMNLVESDRVRHLSKGMNERLQLTLALS RKARLYLLDEPIGGVDP"

VARGKILDAIVKFYDEDSSLIISTHLVNDIERIFDEVVFIREGELVMREEVETLRLKY

GKSVDEMFKEVYAE"

CDS complement(4643145..4643531)

/gene="ytrA_2"

/locus_tag="EFAGFIKM_04070"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34712"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional repressor YtrA"

/db_xref="COG:COG1725"

/translation="MTIEFDNNLPILQIMQYIKRQIVTGTQAGDKIPSVRELAEL

QINPNTVQRTFQELEREEVVETKRGLGRYVTSEERKIMTIKKEMASELLERFLTGMQE

LGIEEQDILSIVADAVAEGKGGTTHE"

CDS complement(4643757..4644623)

/gene="yvgN_3"

/locus_tag="EFAGFIKM_04071"

/EC_number="1.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32210"

/codon_start=1

/transl_table=11

/product="Glyoxal reductase"

/db_xref="COG:COG0656"

/translation="MMHGNQTRTILLPDGTALPAIGQGTWNMGEKQSSQQEEVRALRS

GIEQGMTVIDTAEMYAEGGAEVITGKAISGHRDEVFLVSKVYPHHADRKQMITACERS

LKRLGTDRLDLYLLHWRGGVPLEETVEALEQLKQSGKILRWGVSNLDTRDMQELWSLP

EGSQCMVNQVLYHAASRGIEHDLLPWMRERSVPVMAYCPLAQGGRLRSELLEHPVIQK

IAQDRGVTTSQLALAWVIRDGDVLAIPKAVQLNHVADNAAVNIVLTQEELARLDEAF

PASKGKVPLDIV"

CDS complement(4644667..4645224)

/locus_tag="EFAGFIKM_04072"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTSYEQHVEYPNRKRMAWLTAGAALFVAAGFFLIFDSSSVTND

SILSDVIGLLSILFFGLCFYCYSLVKMIKKEPSFVIDEDGFVDASSYTAGGEVAWKDVE

NIFMYELMGQKMIGVKLRDEKAFLDRQNGMKRKLMTVNSNMVDATISVAQSSLTVPLD

QLYIMMMSHWRHVSDNMIYDSYNRR"

CDS 4645620..4647629

/gene="dpp5_2"

/locus_tag="EFAGFIKM_04073"

/EC_number="3.4.14.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:B2RIT0"

/codon_start=1

/transl_table=11

/product="Dipeptidyl-peptidase 5"

/db_xref="COG:COG1506"

/translation="MMSQRGITSEDLYQITWVNDPTPSPQGGQLVYVSRKTNEARDGY

CSHLRLLHLGSQKDRPFTSGEKDHSPA WSPDGSQLAFLREVDGKSQVWIIASDGGEAQ

QISHLKHGVSSLLWSPDGQTLLVKSSVDMMSGNEESEHTDPIDDKSKLLQEHVVDIRIM

KSDASGLWNGRRSHLFALAPIDAE AIPVTTGHYDVGDYAWSPDGTSAWIAQMPEEGE

DHNDYTLTNHVYLAKADGSDVQQLTPEGYTF SRLAFAPDGQSLALLASDRSYGNATLV

KLYTLQISGGELVCLSTNWDVQLNHSIVGDMRSHLTTTGPVFSRDGSSILCLATIHGS

VRIAKFARDGSSADYIRPDEREIYQFAE LENGQIVA AVADTLNPGDLIYEQPEDPEV

EPIQLTRSNPQLEDEIHLSTPETFWFNSSDGLRLQG WIMKPHGMVDGVKIPTILEIHG

GPHMMYGFSGFMHEFQILAAQGYAVVYINPRGGLGYGQQFVDACRGDYGGGDYRDLMES

VDYALSQYEFIDESRLGVTGGSYGGFMTNWIVGHTDRFKA AVTQRSISNWLSFYGVSD

IGYFFTEDQIGGNAWDDTEKLWKHSP LAYIGNVSTPLLIHGEQDLRCPIEQAEQLYV

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CDS complement(4647760..4648077)

/locus_tag="EFAGFIKM_04074"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKSKYLPADFPLPKDAKATSLIENIMDGNKKVVLTYTTKETLLT
VGTSYKDYYQTKNQSQNTQDIQTDGFSIVGREDGKYAVTITGSVSATNKDLNEITVWW
GEE"

CDS 4648213..4649406

/gene="patB_2"
/locus_tag="EFAGFIKM_04075"
/EC_number="4.4.1.13"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q08432"
/codon_start=1
/transl_table=11
/product="Cystathionine beta-lyase PatB"
/db_xref="COG:COG1168"
/translation="MNNNNSTFDQPINRISTGSEKWDALDIFGAADALPMWVADMDF
AAPPSVIQALQTRMEHGIFGYTVRTEAYHAAVAGWMERRHNWKINDDWIVFTPGIVPA
LSIAVQRFTQPGDAVVIQTPVYAPFYEVVRGQGRELITNPLVENNGHYTMDLEQLSS
LQTGRVKMLILCSPHNPVGRVWTHEELEGTLCLQYNVLMVSDEIHADLVHQRGHT
PLTLISDAVSDLSIICTAPSKTFNIPGLCTSNIIIPNAKLRESFAQGVKTMGLANIST
LGAVATEAAYNDAEEWLDECLAYIRGNMEYVQYVAEHMPQIKMHLPEATYLLWMDFR
ELNIPHAQLCNMLLHEAGLAFNDGSFFGTGTGFMRIINVACPRSTVEEAMRRLSVLLS
NVSGK"

CDS complement(4649598..4650203)

/gene="nikE_1"
/locus_tag="EFAGFIKM_04076"
/EC_number="7.2.2.11"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q2FYQ8"
/codon_start=1

/transl_table=11
/product="Nickel import system ATP-binding protein NikE"
/db_xref="COG:COG4608"
/translation="MSLEARDVSYRYDPKSWVFQQMNMQVKQGEVVGLWGPGSGCKTS
LGRILAGYAEPVAGQVLLDGKPLPRTGVCPLVLFQHPEKAVNPRWRMRRVLQEASVQ
DEQLLEALGIQQTWLDRRPSELSSGGELQRFVTRALGTATRYVIADEMTTMLDAITQA
QIWHTVMEVARQRDLGLLIISHDRDLLNRLCDRITPMSISM"

CDS complement(4650193..4651149)

/gene="oppD_2"
/locus_tag="EFAGFIKM_04077"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P24136"
/codon_start=1
/transl_table=11
/product="Oligopeptide transport ATP-binding protein OppD"
/db_xref="COG:COG0444"
/translation="MALLDIEGVSVSFRRARGWFGHEQTYVIQNLDLSINEGEIVAVV
GASGSGKSVLAQAIMGILPVNARLEGRISYSGEPLTPERQLHLRGDELMLIPQSVSYL
DPLMKVGRQVQPVTRDSGQKRGFITSRLKKTEQELTDYHLPQGTAGKYPFELSGGM
ARRVLMATATSGQPKLIIDEPTPGIHPEVLAETMKQFRELANQGVGILWITHDVTTA
LMVADRIAVFYAGTNVEAAQVDDFKGNGERLRHPYTKALWNALPQNGFQPLPGSQPLA
GQEITIGCSFAPRCVATVACTRERPELRKVRGGEVRCFHVT"

CDS complement(4651152..4652153)

/gene="dppC"
/locus_tag="EFAGFIKM_04078"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P26904"
/codon_start=1
/transl_table=11
/product="Dipeptide transport system permease protein
DppC"
/db_xref="COG:COG1173"

/translation="MKQTVECSSEQTETAKIQKLKTANQEVRYNINTESLQAGNGTG
TSRPSRKDYTAARDQNFRNPRQRAVIWGS LAVIWIWVWLTGRLLPAGSTLTSLMDRN
LAPTWAHPFGTDWLGRDMFMRTLKGLATSIQVGLLAACGGGLIALLLGLAAASSKAAD
RVISWIIDLFLSVPHLVSLVMLAFVFGGGLAGVAAAIALTHWPNLARIVRAEMIQLKS
AEYIQVSHKLGQSRLQIAMQHMLPHLVPQLFVGILLIFPHAILHEAAITFLGLGLSPQ
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CDS complement(4652150..4653145)

/gene="gsiC_4"

/locus_tag="EFAGFIKM_04079"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P75798"

/codon_start=1

/transl_table=11

/product="Glutathione transport system permease protein

GsiC"

/db_xref="COG:COG0601"

/translation="MTGRNGWARFVGFKMLRLVSLLVGVSVLSFILMQFSPVDPIEAY
IGGDMIRVSAEQRS LIEERWGLNESPVERLLTWGQTLIQGDLGTSMIYRQPVADIIQE
RFMNSVALMAVAWILSGIIGFTLG VVAAMRRDSKLDRLICWYCYLASTPVFWIALLL
LMVFSVWLGWLPVGLGVPAGMSADQVTWGD RVIHMILPALTL SLTGVASIALHTRQKL
TDVLES DYILFARARGERGFQLFRRHGF RHVVLPAILTQFASFSELF GGAVLAEQVFS
YPGLGQATVQAGVRGDVPLLLGLVMCSAIFVFTGNMVADILYRLIDPRMKEELMS"

CDS complement(4653188..4654846)

/gene="appA_2"

/locus_tag="EFAGFIKM_04080"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42061"

/codon_start=1

/transl_table=11

/product="Oligopeptide-binding protein AppA"

/translation="MGRFSWRWGKRKGRTGLGILLVCSIGLSGCAQSTAPIASSAENG
QSVPTSTKDELVLAVGTEPEGGFDP TTGWGQYGSPLFQSTLLKRDAKLQLVNDLATTY

SVSEDGLTWTVTLRNDVKFSDGEALTAEDVKFTFETAAKSGSVIDLTNMADV KAPDDS
TVVFTLKSPQSTFISLLTTLGIVPEHAYGADYAEHPVGSGPYKLVQWDKGQQAIVEAN
EEYYGNKSVFHKLTFLYLDEDAAYAAAQAGTVDIAAIPAAFSKQQVNGMTLEAVKTV D
NRGIMFPMQPAGAKSGDGLPAGNDVTSDLAIRQAVNVVIDRKALVEGVLEGYGRPAYS
VSDDL PWSNAEAVFTDANLEEAKQILAAGGWVDADGDGIVEKNGVKAEFNLLYFAGDL
TRQSLALAAADMVAQAGIKINVEGKSREETKKMAYSNV LFGWGSHDPLETYNLYSST
HKGEGYYNVGLYSNPVDSWMDKALQATSEEEALPFWQKA EWDGTTGFSYQGDAPWAW
LVNIDHLYLV TNGLNIGEQQIHPHGHGWPVTTNLEEWSWDNSTK"

CDS 4655272..4656459

/locus_tag="EFAGFIKM_04081"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKGKVKLFGLSLAASLMFSVTSSSLYAAPAPVEPKGLFFATT

EEISKNVVQSNIALEKPSSNLPNLNDYSSFAYEVKEVESNPELRSFLQKALQDGKKVY

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TLEDQDYKLFMLNYQNMDENGNEIPTDASIILKQIVNHEERVNQITPFATIVKSNAAD

IRTVGGLYGQDSGEMVTQWLLYKENNESDPKFDYFAVKDIIRINKLGGSTNSKKLTVT

HDILYAKDDLYSASPKTSSSGPYTVSFAYPWGIEWSFTYDGNPSIALTENTSTD TAKW

VITPGFLKNLQGS DTIELGSSWKANQAYTYTG VQISHATEWHS AVQKMFDLSNTFNVG

YNW"

CDS 4656459..4656596

/locus_tag="EFAGFIKM_04082"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKFQKIVSVLLVLIVLLCLNYFEIRYSNKLQNIIEHLYN HK

S"

CDS complement(4657519..4658058)

/gene="nikR"

/locus_tag="EFAGFIKM_04083"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00476"
/codon_start=1
/transl_table=11
/product="Nickel-responsive regulator"
/translation="MADKEDLTRFGVAFPTPLIEQFDQYIEEQGYKNRSEAFRDLVRK
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EVI AVRGNLGRRLRHLHQIQVQKGVLYAELSVTYVDELNKLAHAQSNGQDHNSDQSLD
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CDS complement(4658111..4659136)

/gene="aes_2"
/locus_tag="EFAGFIKM_04084"
/EC_number="3.1.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01958"
/codon_start=1
/transl_table=11
/product="Acetyl esterase"
/translation="MQSKLETKRTGAKGFKRKRYWIPSVVLILIIGFIGIGTQWTPKI
TVFLLKSLIETANTDTNSKDTMLSGGITRVVDVPYADEGRNDSTLDIYYPSVTSEPLP
VVLWVHGGGWVLGDKKDIADYAVQLAKQGYVVVSMNYALAPDTKYPIPIQTNQALTY
VKNHVSEYQGD PENIFLAGNSAGA QIASQTAAVVTNPSLAKLMNITPAAQPEELRGVL
LFCGPYNLSTVANTGFPLIRTLWSYTGKTFEDYPRLHEMSTVLQATAAYPPAFITS
GNDDPLTSQSI ELAQVLKRLDVEVETLFFSNSSEKLGHDYQFDLESDAGQQAIHSVR
FMQQYSR"

CDS complement(4659218..4660321)

/locus_tag="EFAGFIKM_04085"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MQTEAWKETINEQEAMECCSLLERTSLHNFIDHHGLIKGKKGRQ
NSEGIATEDITLMETSDILFPSPIAGSHSHMMEQSNVRRRQLPSLTHLIFGSRLIGL
VILFSAGTMYFASSVEAAGIDLGVTAQKAWD SVLNKADAQTKLTKQAYDKVGNWKTQ
EQAWEQKIKTLHAANTAQLERLRVEIRQIDDAKVAALAEKVKQTQARYEPLFALYSSV
NRQLDAAKAIKNKEWSAAIRTQAETLRPVVKLAREDIRIKKELAEARKRKS AEIKRL
RAMLAGADS AKKQIQ TAKKQASLAKERYSNALQQFKQNTKQGQTSRVLSSLNTLASAA
EKWAGTKQNIHTLEQKVSTMYVKVRQEIAKRPK"

CDS complement(4660610..4662664)

/locus_tag="EFAGFIKM_04086"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIFNRLFCNRGILIQNFRQHWIGILYLITLLFSLPLYIGTQYI

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VGMCIGQSILQGLTVFGLILIPVIFWGVYELHLQRYLLGFTYNNSSNFNMEKTSLLFR

MSSMGYYPPPEWGELGIYA AITCILFVLCYVLYARRHVESATQAITFRIVKPIFRFGFM

FTLVLLGGAYFTRIAPEGSGVWGIFGYLLGGVVG YIGAEMIIRKTWLIWSSRLLPRFA

VYGIVAGLILYIPVADWNGYANNVPSKENVQM VRLGGDHYIYVNDKSVKLDDSPFYSD

TPGYVDAVLALHQKIVHSDLPLLERVRNQNSGQNR SNDEYVLIDYQLNNGKTMTRYQ

IPEEEFRQELAEVKQWEDYKSTTYDTYALDEDVRSIGIRSSLNSERKVFISDPKLIRE

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GRLMEWLKQNNLYDQLTVSAEDMASAQFVKQEIDNPGKYRMVY PEPNFVDVNIDGNRQ

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NQ"

CDS complement(4662639..4663541)

/gene="ytrB_1"

/locus_tag="EFAGFIKM_04087"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34641"

/codon_start=1

/transl_table=11
/product="ABC transporter ATP-binding protein YtrB"
/db_xref="COG:COG1131"
/translation="MIELNQVVKA FEQEKA VDGMTMHIHKGSIYGLLSNGAGKTSLL
KMMAGIYRQDSGTVRIEDNEIYENMDLKGRITFMADSPYFFPQSSITQMAAFYRSVYP
RWNEERFKQLATVFKLDVKRKLHRMSKGMRRQAAVWLGLSCMPEVLLMDEPIDGLDPV
MRQQIKNLLFQEAAERQVTIVISSHNLREIEDLCDHVAIMHKGRIIVEKDLDLADT
HKIQVAFRHPDHAKAMDEQIDILHEEKRGSVSLYIVKGNRQQVTDQFRIHDPYLLDVL
PLTLEEIFIYEMEDAGYDIQPIVL"

CDS complement(4663534..4663923)

/gene="ytrA_3"
/locus_tag="EFAGFIKM_04088"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34712"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional repressor YtrA"
/db_xref="COG:COG1725"
/translation="MFELDVR SRKAIYEQLVDKVKEMIVYGILKPDEQLPSVRALSTQ
LTVNPNTIQKAYRELEREGYIYSLQGKGSFVSSSVEHPNEAMRDEIRESLVKLI AEAS
YSGLTKADMTLLFEEAMARIEKEEPHD"

CDS 4665117..4666022

/gene="mqnB"
/locus_tag="EFAGFIKM_04089"
/EC_number="3.2.2.26"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00991"
/codon_start=1
/transl_table=11
/product="Futalosine hydrolase"
/translation="MNEHRQDEDQNNKPNASFENSGHHGDSTGEINTSDISPVQANSS
QRVLIVTAVDAEKDAVLRGLGDTAAERFDVIAAGVGPASAAAGTAATLAYAVAAASTR"

ALAQGSTAPSPSDVAQASATSSKLGPLARTGSSPAYMLVISAGIGGGFPGRADVGS
LV
VADAMVAADLGSQTPDGFSLVDELGFGSSIVAADAELAARLRHELQRAGLAVSGGTAV
TVSTATGTAETAELLRRVPDAAAEGMEGFGVATAAQFGVPALELRAISNAVGPDR
DAWRIKDALDALQAASSILREVITS"

CDS 4666019..4666861

/gene="mqnD"

/locus_tag="EFAGFIKM_04090"

/EC_number="4.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5SI12"

/codon_start=1

/transl_table=11

/product="1,4-dihydroxy-6-naphtoate synthase"

/db_xref="COG:COG2107"

/translation="MKIAFSPCPNDTFIFHAWVHGLIPGAPKLDVRYADIDITNGLAA

NPDGPNTPEVMKISYAALPYVLSDYALLPAGGALGRGCGPLVLTANGTTDPAYLSGRR

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YQNYDLKLMTDLGNWWESDTGLPIPLGAIARRDMDAHALAGWARASVEYAWAHPDES

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LLRI"

CDS complement(4668102..4668725)

/gene="pcp"

/locus_tag="EFAGFIKM_04091"

/EC_number="3.4.19.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5XDD4"

/codon_start=1

/transl_table=11

/product="Pyrrolidone-carboxylate peptidase"

/translation="MVKILISGFEPFGGDAVNPTGALMDALANEVIEGAKLKIVLLPV

HFDECADLLIAEMEAYRPDVVIACGLAKGRSTSITPERIAVNVKDIPAGSYADNQQGRP

VDEPIVDGSPDGLFSTLPIRAMVKDMSAAGIPATVSNTAGTYICNNTMYRVLDHIRVG

QLPIRAGFVHFPASTEMAVLQPSVPSLPIPMMLDALRIMIRTAVVDS"

CDS complement(4668747..4669748)

/gene="iolU_3"

/locus_tag="EFAGFIKM_04092"

/EC_number="1.1.1.371"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O05265"

/codon_start=1

/transl_table=11

/product="scyllo-inositol 2-dehydrogenase (NADP(+)) IolU"

/db_xref="COG:COG0673"

/translation="MTEIAGRDKVRWVGIMGTGWIASQFARDLEHAGNAVKAAVGSRTA

GSAEKFAAEYGFARAYGSYDEMLQDPEVDIIYVATPHPVHKENVMACLEAGKAVLCEK

PFTMNARQLEQLVETARERNLFLMEGMWTRFLPPIAQARAWIAEGRIGEVRLQADFG

FRVGWEPEGRLLNPD LGGGALLDAGVYPISFASMIFGEQPQHVVSTANIGETGVDEQF

SVLLSYSEGRSASLSAAIRLNLSNEAVIYGTEGKIRLPLFLAGKEAFLHVNGQDEPEK

FTDDRTCIGYAFEAE EAGRCILEGRTESNTIKLDESLEIMKLMDTIRGQWGLRYKSE"

CDS 4670237..4671967

/gene="rhaS_34"

/locus_tag="EFAGFIKM_04093"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MTTIPGTAHSGMNPYTLHQQTSPNSEKESSIRADLDTFLNDTLI

ELRQAEHIITREKWRWSTTELAHHTFIYMHKFTGQLIMNGIKSHVIRKSACLSLPGTA

IELISDEDHDIELYIIHFDLYRATEKTKARRIYERELSSPVTGWIQGPFGIQRIAAQ

LTQLSNEGLETGLKAQLFTELLHMLWPQEDQTDVGAGQDEPEQWLRSTLQYMSENYM

HEIKLEKLAELADMHPYSYQLFKSRMQKNPIEYITHLRMNRAKELLTSDLRIRDVA

REVGYRDEFYFSRRFRNHAGYAPTSYSKQVHRNIVSLSYPYTDHMLTLGITPCAAQIQ

GHLPHMPKSLTLPFHAYEPWEQGRQAFLDVNPELILTKDNAATKAMEHIGDVAPIITI

PWNQTDVFGHLHQIATIVDRTQAATDWLDRHERKAERARKKIKEFVGDITVAVGTLTP
KGPRMYSHRNFGHVYRTLQLAAPQRIQTELAGKSPGVGFNWLPFTPGEWDGLEADVL
VLAINSMHEKATLLKEMASNPLWNSHPAVKNGRVHLIDWNSWVVYAPYSINIQLDEAL
SMLTNKPSLL"

CDS 4672067..4673140

/gene="feuB_3"

/locus_tag="EFAGFIKM_04094"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40410"

/codon_start=1

/transl_table=11

/product="Iron-uptake system permease protein FeuB"

/db_xref="COG:COG0609"

/translation="MKCVVGTKGVTRIQHPGLPHRPSNSRKSAVTVGLTFLSAIALL

LSMFVAISLGAKGLTLETVWAAIFQYNPALTPHQIIHELRLPRVLAAVIIGAFAVAG

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LLGMAAPGGLNSIRLTVAGAVIAAMLTSLSTGVAIYFDLSQDLAFWYAGGFGGIEWRH

LKLILPVLLVTLVIMPLARRVSLMSLGEEVAINLGINLRWTRFLALAAVVVLAVSV

SAVGSIGFVGLVIPHISRKLVGVDYRLIIPMSSLLGAILLVLADLGSRIVNPPEELAV

GIMVAFVGVPPFFLYLARKERRAL"

CDS 4673143..4674159

/gene="feuC_3"

/locus_tag="EFAGFIKM_04095"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40411"

/codon_start=1

/transl_table=11

/product="Iron-uptake system permease protein FeuC"

/db_xref="COG:COG0609"

/translation="MNFNTPSRGKRSIVVSITLLCIAIVIVISLNTGTIRLSPVAVL

QTLFGNGSSDDQIVLFDYRLPRILVTVLAGAGLGIAGAALQGITRNPLADPGILGLHA

GAAFGLMVFVLSFTMDGSVALLIPLFAFAGSVAAALIIMLLSYDRHNGVSPIKLILV

GIAVAAGFHALTLYLSRLDEDTYSFAARWLAGSVWGRDWVHVQALLPWVVLCSYIW
SRSKTLDAFNLGDAATSIGTPVRSQRIILLCAVALSAVSVSMAGGIGFIGLAAPHL
ARRLVGPMHRHLIPAAGLIGMVILVTADTIGRTIFQPNAIPAGVVAAIGAPYFLYLL
VRSK"

CDS 4674221..4674673

/locus_tag="EFAGFIKM_04096"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLKKNLMLVMSICLVLAACGTTNNSSSASGGSSTDTSTKNQD

NSANSGEQRIASMSIHLTNDLLSLGITPVGSGVIGGEAKGFLSHVADQLQNTTPLGPVK

DPDMEALLALKPDVIYLDEEFSGGDIKFEKIAPVHVFIWMTAHGATI"

CDS 4674691..4675167

/gene="feuA"

/locus_tag="EFAGFIKM_04097"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40409"

/codon_start=1

/transl_table=11

/product="Iron-uptake system-binding protein"

/db_xref="COG:COG0614"

/translation="MNREKEAEQYIQDYATETEEVKSLIHDTIGDGTVM AIRVTAKEL

RVFSTRRPMGPILYEDLGLTPAKGITDIDSTKPYQVVSREILPDYDADAIFVVVNSDD

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CDS 4675432..4675866

/locus_tag="EFAGFIKM_04098"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNPVQNDRMLGQLSELVKLKRYKVHEKLVNHPELYPGQPPLL FQ

LEREDGQSQKNLAEQLQRSPATVTVMLKRMESGGYVRREADPKDMRSLRVYLTQGRS

ALQELREVIQELEQQAQKDFTPEESEIMSELAQRMLQNLREA"

CDS 4675950..4677734

/locus_tag="EFAGFIKM_04099"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WQJ1"

/codon_start=1

/transl_table=11

/product="putative ABC transporter ATP-binding protein"

/db_xref="COG:COG1132"

/translation="MWTLKRFPTYKSAAIVAPLLMVLEVTMDLLQPKLMSSIVDDGV
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NLDTFQEGSLITRLTSDITQMQTFVQMLLRMFIRSPMLIIGSIIMAFITSVKLALILI
ATVPVLFILFILIKASYPLFASVQSKLDQVNAVLQENLAGIRVVKAFARARLEKKRF
KQSNEDYTTTAVKAWRIVTLNAPVLSLMLNATIVAVLWFGGFQVVGDDIAAGDLIAFI
NYVTVLSSLTSIGMMMSFSRAKVSAARINEVLHTQPDIQSGTDNSGNVQSHQSKRQ
QFPYQPSPLPSHTGGQVEFRDVSFRYDGDHALTDINLKARPGEKVALIGSTGSGKTS
VQLIPRLYDASQGEVLVNGVNVHRHWDLQDLRSRVSIVLQESILFSGSIRDNICFGRPG
ATDAELRAAAQAAAADDFIMKLKGDYDELGQRGVNLSSGGQKQRISIRALLMRPEVL
ILDDSTSAVDLRTEASIQKALQSLMKDSTTFLIAQRISSVKDADCIYVIDEGQIVARG
THDDLMAHSSHYQAIYYSQQRKEDVQFG"

CDS 4677727..4679559

/locus_tag="EFAGFIKM_04100"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9WYC4"

/codon_start=1

/transl_table=11

/product="putative ABC transporter ATP-binding protein"

/db_xref="COG:COG1132"

/translation="MAKPASSSIQQTVPPIGRPGPAGRGPVPKVRANKNARHALIRVW
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NVSTTLNQSVTQLMSSAILLVGSLSIMFALDVRLTLLSLVTVPLITIATRLIASRTRK
HFTAQQKLLGELNGYAQETIAGQKVVAAYNRQDQAHQHFENLNEKLRTSSTQAQTVSG
LVGPTMNMVNINIGFAILASVGGWMAYHEMTSIGLIVSFLAYSQRQIERPLNDLANQYNL
IQAAIAGAERVFHIMDTPGEYVEEQKKQLDQIQGKVVFDVDFGYSERDILKKVSFT
AKPGEMIALVGPTGAGKTTIINLLPRFYEITGGRITIDGCDITELEKDQLRRQLGIVL
QDAYLFSGTIRDNLAYGKPDATDEQIRQAAELANAHSFIRKLSQGYDTPIISGGSNLS
QGQRQLLTARAILADPAILILDEATSSIDTRTEMQIQEAMRTLMDRTSFVIAHRLS
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CDS complement(4680234..4681805)

/gene="sasA_15"

/locus_tag="EFAGFIKM_04101"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"

/codon_start=1

/transl_table=11

/product="Adaptive-response sensory-kinase SasA"

/translation="MLSYSYTMKMFVIFPLGCLLVILSSYVLRRLTPHMAIMSLSAILLVAS

IYGERRYPLVRKFQWIFLGIFHYFSELNWCNMLYMLIISMIQDKPRLAQTLPIISLLL

MLQYTLIRLSYVPVDYALLVSLFDLLTSVVIIFLYHTLINSEVEKRRRLREKNRFTL

HDPLTGLLNYEGYMEMLHKTVEEQRSFLLVLLNVNMFSGFKKDSFDPWCTVITGTGQM

ISNHFTEAYGISRYAGDRFAVVLPEIQDVEERMSSLLSVQLQGLQVSYSLYPEMSD

SLQHFMFTAEDRLQQRSKWLKNEEEVFRSERLRAVGELAAGMAHEIRNPLTAIRGF

LQLSRGQAFNIAPWYEVIMGEVTRVTDLTAEFLQFSKPHANHMKPEHLGHCLERVMSL

TESDAASRGHQITLEMTNEPVVIIMDRDKIVQVLINLIRNAFEAMTDPGEVHMDLLQD

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CDS 4682065..4682400

/locus_tag="EFAGFIKM_04102"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MTTQRKPLGLGTLSELLVLLMGLVFNFQWGKANFMISHYLFNLIN
IPIYSNGTQGLHIPFVVAALFWIPAFLIAKKNRSHYGTSVSYNVAGFMLLLCIIGPVI
PIIDWMVNG"

CDS complement(4682705..4683724)

/gene="mglC"
/locus_tag="EFAGFIKM_04103"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P23200"
/codon_start=1
/transl_table=11
/product="Galactoside transport system permease protein
MglC"
/db_xref="COG:COG4211"
/translation="MNTQMINQVKQYVTQRAIFIVLILLIIGIAIADPNFLAFSTLRD
ILQQSSTRAIIALGAAFILVTGGVDLSAGRVVGLTAVVSASMLQIDEYANRFFPDLPH
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QPIGGLREDFTVIGSGYIDLGGGYSIPYIVLIAIAVALICWVIFNKTRLGKNMYAIGG
NIQAAHVSGIHVARNLVALYAIAGALYGLGGVLEAARTGGATNNYGNMYELDAIAACV
VGGVSTAGGIGTVPGVMAGVLIFGVINYGLTFIGVSPYWQLIIKGLIIVAAVAFDIRK
YMAKK"

CDS complement(4683740..4685245)

/gene="mglA_2"
/locus_tag="EFAGFIKM_04104"
/EC_number="7.5.2.11"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AAG8"
/codon_start=1
/transl_table=11
/product="Galactose/methyl galactoside import ATP-binding
protein MglA"
/db_xref="COG:COG1129"

/translation="MESPYLLEMNGVSKAFPGVQALSQVNLKVKPGTVHALMGENGAG
KSTLMKCLFGMYRPDEGTIRIEGKDVDIPNSKAALQQGISMIHQELNPVPHRPVMENI
WLGRFPMRGILVDEKRMVDTLALFKDLNLDIDPKAQAGTLSVSKIQSMEIAKAVSFQ
SKVIVMDEPTSSLTGKEVDQLFTIINELRSRGVSIYISHKMEEILTISDEVTIMRDG
FVVGWDAADLTDLITRMVGRDLDERFPERTNVPGEVILKAEGLTSSQSKSFRDVS
FELRKGEVLGIGGLVGAQRTELIESLFGLRGLASGTISIHGRKVKINS PAAAKRH NIA
LLTEERRVTGIFPVL SVYENTIIASLG RYRNRVGLLDEKKGRE VAREQTQKFRTKTPS
VNTLIRNLSGGNQQKVLLARWLLTDPEILLLDEPTRGIDVGAKFEIYTIITELARQGK
SIIMISSEMPELLGMSDRIMVMSEGRLTGIVDGAEATEQDIMRLAAQQRMA"

CDS complement(4685320..4686381)

/gene="mglB"

/locus_tag="EFAGFIKM_04105"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P44883"

/codon_start=1

/transl_table=11

/product="D-galactose-binding periplasmic protein"

/db_xref="COG:COG1879"

/translation="MKKTWMTLLITACMVVAAGCSSGGDSAGGSTGTDGQTAAAGTE
TPKIGVAIYKFDDTFMTGVRNAMTAAEGIATLDIVDSQNAQPTQNEKVDFVSKKYN
AMAVNPVDRTAAGVIIDKAKAANIPVFLNREPVAEDMNKWDKVVYVGAKAEESGTIS
GQLIVDYWKAHPEADKNGDGKLQYVMLKGEPGHQDAELRTKYSVQAIQDAGIEVEALA
EDTAMWDRVKGQEKMQAFLASHGDKIEAVLANNDMALGAIEALKAAGYFKDGKSMPV
VGVDATAPAIQALQDGTMLGTVLNDAKNQGAATVALASVLAKGETPTKENTKYDITDG
KYVWIAYKKITKDNIADAQ"

CDS complement(4686554..4687732)

/locus_tag="EFAGFIKM_04106"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTDNKENRSDIHSHRVVGSYIRTFWKKVAASFPGIRKRLVTLT

AASCCLLICSACGLSSPDATAVPPRIALITPAGTGELAEAIRLGAEAAKENGAEELIT
VEAYPSDGDVYTPAILDSAGSQMQVKQANINSQTLRSAREQAQVAAAASALKQGASA
LLVDPLSEKALSDIIQEAQTNSNGTIVPVIVLNDEFVKGITSFISMDNVEAGRQAG
QAMAELEGKGHVALLGPDPLNSGLIQREQGVMEALVQYPNIQVEPKSICNTRDGCWQ
TAKQLLDQQEVDGFITLQEPASLGAADELNRRKSADKIRIVGFGSEQQLEQLQEGVF
DHLIVQNGYSAGYLGLNQAVARLNNQQVQARVLLETCLVSTDNMFWMNDNQKLLFPFVQ
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CDS complement(4687719..4689536)

/locus_tag="EFAGFIKM_04107"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKFLSRWVKSMGFQLRSRLRSSRVSSIRFIITWSFSVFIVLVT

IMAMLLHDKFTQAAERSAELTTRQIVDQVSYNLEDYVRSMHLYRAIEEHMLRDGTWE

GDLVDKQLDRTLSSREDIISITLLDSTGKLLKNRPTAELKTSAHVTQQGWFQSALRVP

DHLSFSLPHIQNMYTGPYKVVVSMKGITIRKNGQDRQVILLVDINFKQMDELSRRVS

LGQRGYVYIIDESAGNIVYHPQQQLMYMGLKSENIEQALVASGSYEDEADGQKRLNTV

KSVANIGWKIVGVAYLDEIMTTRQEVNGYLIRVLVVVLVLVLSLFLSSSLTRPIRR

MERKMKAVERGDFNVELPIEGPLEVERLSRRFNLMVKNKIRTLMDIIEHEQEQKRRELE

EALQAQINPHFLYNTLNSVVRMVGMSRNEEVITMITSLSSLFRISLSQGKTIITREE

LEHAQHLYTIQQMRFKRKFNFTIKADETLCDCLTLKLVLPQLIENAIHVGIEYHMDEG

CIEIDVYREDNKLVRITDNGVGMTEEQMSGLLSGRPVIKSGAGSGVAVRNVHDIRIL

YYGEGYGLEFASELEEGTTWIRIPIQSQQKEGEPDDRQ"

CDS complement(4689533..4691266)

/gene="rhaR_35"

/locus_tag="EFAGFIKM_04108"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MYRVLLVDDEEDVREGLVVEVDWEALDLRIVGLAENGREALEMA
ERVEPDIVMTDISMPFMNGLELAQRLRKRNPVKVILTGYDEFDYARQAISLSVDEY
LLKPFSAGHLTELLTRLRAQMASEVAEREDVQQLREHYHTSLPLLQADLMATLLHRQK
SSTYIHSKAKQCGLDLTGERYGVSVLTHMDGDVQKEKSEGVFSEPSQRHNKTSEAA
DQSEIFVPGGSLRQSEDAELKRFAALNIAAEVWAEHGAGHAFMHQETIVLLYVDRTGG
TDGAKRQQKALENVMRSINHYLRIPATVGSGQIVDTLADVN HAYEDALLALDYRLVPG
TDSIIYIADVERQTAGKLRFDELKQQTLTRCLKAGTQAELEEALAIIFREITVEHGRS
DIQLYLIEVLTTVWKAASGEAMEDIFGAGFQLYTDLFRLPGLTEAQKKVQEVCLLV
QHRIASGRQHVKYKDIVEQALVFTKEHYADPDL SIQKVCGLHISSGYFCGIFKKEVQL
TFLQYLMQIRMEAARELLRSTELKSFQIAEQVGFAEPNYFSFCFKKHIGVSPKEYRKQ
ASQAASEGSIR"

CDS complement(4691603..4692505)

/gene="xerD_2"

/locus_tag="EFAGFIKM_04109"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A2P6"

/codon_start=1

/transl_table=11

/product="Tyrosine recombinase XerD"

/db_xref="COG:COG4974"

/translation="MNQSSGISVQREATIEEFIHMLANEGELHPKTVKEYTSDLKHFI
EWYKESTMLSEEFSPRIEDVDTSTLVSYREDAHKVMLLKPATINRRRLITLKRFFKWAV
LESRLSHDPSKPLKFIPEDKVSPRRMTLEEEQAFLAAVEYGNSLRDQTILTMFHTGL
RTMEVCNLKPHDIELGRRSGHLTVRADKRN VQRKIPLNIQCVVMLNQYLSDLATDRAY
LFPSEKTNDRLTERALRH LIKKVMITAGLEGLSSHDLRHRFGYAMAEHTPLHRLAEIM
GHTNPDTTMIYFKALSTNHRKEQE"

CDS 4692674..4692874

/gene="cspB_1"

/locus_tag="EFAGFIKM_04110"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42016"

/codon_start=1

/transl_table=11

/product="Cold shock protein CspB"

/translation="MQTGTVKWFNADKGFGFIETEEGTDVVFVHFSAIQGEGYKSLDEG
QRVQFEVTQGNRGPQAENVTKL"

CDS 4692979..4693251

/gene="hupA"

/locus_tag="EFAGFIKM_04111"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P08821"

/codon_start=1

/transl_table=11

/product="DNA-binding protein HU 1"

/db_xref="COG:COG0776"

/translation="MDKEQLITEVAKAGGFSKKNAEKAVTVVLDSILEALKEGKEVQL
VGFGKFEVQKREARTGRSRKTGKEIQLPAGKVPVFTAGLSMKEALN"

CDS complement(4693583..4694227)

/gene="vatD"

/locus_tag="EFAGFIKM_04112"

/EC_number="2.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P50870"

/codon_start=1

/transl_table=11

/product="Streptogramin A acetyltransferase"

/translation="MAPDKTKLFPNENIRTVCIQNLPPRSNVDIGDYTYSDNTNPP
EQFYDRIQH HYDFIGDRLVIGNFCAIAEGVTFIMNGANHRMEG MTTYPFNIFGGGWER
VTPTLEQLPYKGDTV LGSDVWL GQNVTIMPGITIGDGAIVASNSTVVKDIEPYTIVGG
NPAKTVKKRFDEETIAL LLELKWWDQDEEWLDTHLERLVSTYDLQILRELLNSK"

CDS complement(4694263..4695951)

/locus_tag="EFAGFIKM_04113"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MRSMSIGTKISLIVISIFIVFSSAVAVSVILEMRQGITTFFATEK
AKRDLEMANSIITYKHPGDWAIKDGQLFKGDTALEGNFELVDEIGQASGDTVITFRGD
ERVATNVMVDGKRAVGTKVSDEVAQTVLQQGEKYFGEAVVVGQKYQTAYEPIKNASGE
IIGIFYVGASQSLIDVISSFLKTFLLVFLMLVAITLILLYVRRVRVRIERVSVAI
KRAGTGDFTPVVDNVQDEIGMLGMGYNEMRSNLQVIIQGGLQAAEKAHSTGLLLLKI
ADQTSKESAQIASSVEQVAQGAESQTISTEDNLQAMEEVAIAVQRMADNASSISDSAL
YSRKQAEKGGEAVQLTVQQMSTIESSVTTTDEVIRMLEGKSAKISQMVSIAIHEIANQT
NLLALNASIEAARAGEHGRGFAVVSTEVRLAEQAGDSSDRIEELVEAMEQDMQQSLS
AMSRVKDEVQEGLRLTRETEQNFSLIRDTNLRIATEIEDMAGTSEEMSAGVEQIVASV
HEIARHAQTASTNSQQAADSVHEQLKSVEQIKASAAILSDVSTELQTSLSPFKI"

CDS 4696307..4696804

/locus_tag="EFAGFIKM_04114"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MTTKDDFKKNDNLQELNNEEFSAVANYPISFSIFALARSHKGLA
AQLIRDTGLFPGQEIMLMQLYAQDHQSQNSLGRTRLRLDHSTVAKSVRRLEDAGLVTRS
RSKTDGRVTIVSLTEAGRALEDQVNNAWRQVEQITTAGLSDEEKNLLLSLSQKIAAQI
DSSLS"

CDS 4696834..4697775

/locus_tag="EFAGFIKM_04115"
/EC_number="1.3.1.103"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q59I44"
/codon_start=1
/transl_table=11

/product="2-haloacrylate reductase"
/translation="MHTSKMKAIQIHQYGGSDTLQFEQEVHKPQPAAGEVLVRIQYAG
AIPLDWKIRNGWLQDVFKELPYTPGTAMSGIVESVGEGVDTFKPGDRVFGNVNGSYA

EYGMAPAQDLVHMPDDLFSFEDAATIKGGAEAAWKALFTEGELEAGQTVLIHAAAGGVG
QFAVQLAKWKGAHVIVATASGANVDFVASLGADQVIDYKTALFEELVSNVDLVVEAVGG
EIEDRSWSVLKPGGKLVSLTQLPSAEKAAQYGVTAKFNSKFPTSEDLYTIAQLIANGS
LRSQIDSIFPLSEANQAHAKSEARHGRGRILLDVRVS"

CDS complement(4697868..4699865)

/locus_tag="EFAGFIKM_04116"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNILLRKVAVTALSLTMVTSSFGLIGSPNAAFAAENTATTTTSSAG

VTQAYESLFQTDNVINVSVTIDDAWKSMLSPDKDYKNVSVEVDGNKLDNVGFSTK

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LRSIGMDVPMNTNYVNLVYVNGELVGFYTGVEAVDDSYLERNYGEDYEEGVLYDTDEKSY

LQYEEGSDYSTITKDLGTDKDKAKLKTFTLQTLNEMPEGEKGDIESVLDVNSALQYIAG

NMVFNGYDSYNGDKGHNYMLYSDASGKFTVVPWDFNMSFNGYSGGGGRGTTTGSTTTN

TNATNVSVNEPVLGINMENVPMINLLAVPEYKEKYLsyvNELTDYMEGIQDRITGLA

DEIRPYVEADPTKFYTTEQFESNIAYSANADAAGGMGGGTPPAGFEGMTPPEGMEGMT

PPEGFEGMTPPDGTTPTQSGAATGNGTTDATTGTDNTQTRPGGNFGGGGMGSMAAGS

LTTFALNRLANLQEQLGREVTPLPETSEETGSNTSSGTNDKTITVTLDGKSITFPDQD

PLQQNGRVMVPVNAILEAMGAEVTWDKTAKSVTAVLNDQTLVLKIGSSTATVNGETLE

IDAPAIQNSRTLVPVRFISEGLGLTVDWDQTAAQVSLTSK"

CDS complement(4700094..4704419)

/gene="aes_3"

/locus_tag="EFAGFIKM_04117"

/EC_number="3.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01958"

/codon_start=1

/transl_table=11

/product="Acetyl esterase"

/translation="MKDLFKTWTKRAALVAISFILITGIAIPVHEVRAMEDDIPHSVI

NAAQEENIPEPEGPELEIYAENFDDPDNFGSTGGIALKAPWRQDGAGGSKAKTSSSTT
APSQPNMIKIDGTDALALPLDLTGYGNIRLSYYTRASSYISGSVIEWSKDGGISWST
LETFQLPPGNPDIKNKEGNTLKSRTLGAEANNNSTVNIRFRTGDVMQANMYIDNVAIY
GQAIPGITPAPSPVPPGEENTKFTPPQGVTLYEDVEIGMAGGRAMYSSIAVPETAAAE
PMPVMIYIHGGGWNHGDRKQALNSICNYVLKRGYIGVSLDYRLTPEAPFPAQIQDVKL
AIRYLRAHAAQYNLDPSRIGVWGSSAGGHLAALLGTTGDLVAGDPVLDTGVTVEVPN
LEGSGGWPEYSDKVQAVADWYGPADFTTTFANNYSSVTALLGGHRLDVPEQARLAMP
GTYASPDDPPFWIRHGDADATIPYDTSVTFAEQLQSAGVPMVDVKIVPGQGHTGTGA
SENANAEAWAFLDEHVKNRIVTEPIIFKSNPEDTSGDEEEEEETPLIEKVIASKLPS
DDAAIDSSKPDLNFNKATGSSTGLLSISSTSTKKYVYLKFDMTGNEPEGDRYRLRIA
AKKGTSNTDELSTLYGVDATDWNESLTSWVSNAPVQSLSEASLLGTLHVTADRNGSPAV
YEVDVTDYVKKRADVGQVAFLLGDAGATSVSVNVYTKEANGTSNPRPQLSVIALIEEG
SDTQLPEWEQGAELEIRNWGTDFAELRWPAASDDTAVSAYRIYRDGVLLSEQGKQSF
DSGLAADTPYTFQVRAIDEAGNISSALSTEMITLGVVPVSSLPVASVTASGSDGNLATN
TLDNNSYTRWSVAGEGQWITFDLGQAQPVGYVGIGFYKGDIRKTSFEMESSVDGEQWT
QIFNGESSGDTTEMQAFDIPDTSARYVRITGRGNSDGSITYSLSDVHLYAPFAGGGTP
VALIPYIVPHPPEGTMPFIAPGLTETDGTPHAVHAPHAVTGRIIDVRDYGADPADNTS
DDRPAIQAAMDEANVGDEVFLPDGVYNLLSWPDGSTNLMLKSGVNLRGESREGTVLKT
SLNQVTGSAVLKASQAHSILVSNMTITSAWSGSYTTDHQSNNPSAGGPDSMIHIANYG
EAPSYDITIDGVIVEKFKRMAIRIEHSRDVVVKHATFRNATDLGPGGSGYGISIQGTA
KTDRLGFDNDTLWNVEDSTFEGPYLRHGALIQFVAHNNVLRGNTFNGTKLDAIDLHG
ELEYLNEISGNVIMDVLTGAGIGLGNTGGSAPSNHSGKSGKGNYIHDNTITNSRIGISV
TMGTPDTLIEDNLIENTTVIAEAAGIKVLNGPGTVIRGNVIRNNTASGYWGVRLERDK
GDAGAGNVGEGDPENVWIENNIEGNTNGIGLFAGVGILMKANILNNVNEDYYKAAGV
TVTEL"

CDS complement(4704515..4706065)

/gene="lipO_12"

/locus_tag="EFAGFIKM_04118"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37966"

/codon_start=1

/transl_table=11

/product="Lipoprotein LipO"

/db_xref="COG:COG1653"

/translation="MKKWMVTGMALLLAATFMAGCSKSGAESGENGGDGKTRFSMSL
RTLAYTYVEKSPDINQDKWVKLEELTNSDLKIVLVPHEYEQKMQVQMFATNDIPDVV
QGDGGVNGKEMAGSVEAGVFQPLDELLQQYGQDLLKAVPKEAWDQVTHDGQIYAIPEY
LSNPSRRATWIRKDLLDQTGLPVPTTVEETLEVLRAFKKLGVENPYMGREDFKYADTF
FGAYDVQQFLSMMEQQGDQIVPKFMDNENMQQALTVEYKTMEEGLINKEFATINSTVF
KNTILSGKAGMWSMNANELIQWEKQIKASVPDAKIEIIPSPVGPDGKGGYYLYGPVTR
AYFINKDAADPASIIFFNWMVSDEAEKFFTYGTEGETYTEDNGVISYTAPTDAGVD
EERYRQSFLWFVQDTTYNKGSLSTEGRKLMNIYDTILAKEGRDGINFDPRLAEFVQ
NPEIAPNSDTPPQVLLTHMIKMVYGKEPISDWPKVVEEWKSKGGDQAIEEATEKFKKG
EGVSAPRR"

CDS complement(4706206..4708617)

/locus_tag="EFAGFIKM_04119"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MEVKRKLAEKSLYQPISGPFHVDYAPDEHTVLAENPPRFTWMAA
QQEDENAYLLQVSASPSFQEEETMTFAPIPNFFTPDRVFKPGDYWRYALLVDHPVQ
QQGSEYEAHVSQGKGSEAEGHASQKGKGEMSAWSEVRRFTVPVGLPETPLPSRAQRY
DSTDMSHPRLWLGERGLNELADGVASDSTYCGWDAFMANSVEPWANREPIREPQPYPE
NKRVAALWRQMYIDCQETLYAIRHLSIAGRVLRDELLDAAKTWLLHVAAWDTEGTS
RDYNDEAAFRVAAALAWGYDWLHDELNSEEQEVVRRSLLRREQVAQHVMVRSKIHV
PYDSHAVRSLSSVLVPCCMALLHEEQQAAEWLDYADYYACLYSPWGGSDGGWAEQPM
YWTTGMAYVTEAMNLLRNYAGIDFFRRPFFQRTGDFPFYVPPDARRASFGDQSTLGD
PVNLKTGYLVLRQLAGVTGNRSYQWYFERVRQSDPGTEGAFYNYGWWDFNDELVYRHD
YPQVEEESPVDIEPLKWFRDVGWVAMHHRMDDPDEHIMLLLKSSRYGSISHSHADQNS
FTLHAFGEPLAADTGYIIAHGSSFHREWRRQTRSKNNLLIGGAGQYAENNKVLNMAAT
GQIEEAYWRDGDGYVRVATDAYASTVPHVKRVVREIHFLQSAYFVVDHIDLEKPD
IQWLFHALHPLQLKGQSFRLNGTKAGLEGTFVYASSGELALSQTDQFAEVDPAEYEG
DRHYHLSAETRSATSHTIVTLLVPYKIEPKYVPYFIDDQDHGHIHYFTDNGVTKKIE

VSKTY"

CDS complement(4708653..4709420)

/gene="fabG_9"

/locus_tag="EFAGFIKM_04120"

/EC_number="1.1.1.100"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P99093"

/codon_start=1

/transl_table=11

/product="3-oxoacyl-[acyl-carrier-protein] reductase FabG"

/translation="MNINLQNKIALVTGSSGGIGAAIAGALARCGAKVAVNGLHNMER
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IETMSEELYSRIMDVNLKSTVFVSKAVIPGMKAAGGGRIINLTSVAAHN
GGGPGAAIY
AASKAAVMALTKGLAKELASGGITVNALSPGFIGQTAFHATFTSAEGRSSAVNSIPLG
REGTPDDVAGAALYLCSDLGSFITGETLEINGGMYMR"

CDS complement(4709452..4711290)

/locus_tag="EFAGFIKM_04121"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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IAQTMRNTVYQTDLYLQNYDRATYSILSNGSVKHFLDMNSED
SYAYYEYSRQIKRNVF
PPVFMLYPQIKFLYVIGGNRGRVIDDNQNSAGIPDIDAAQYKQLLAATPANGESTLL
TRSIRSGQANANVITIARRIRGVSSYTPNGVLAMEVNVLELDNIWGELDLGQGGYQYVM
DQNGNVIYTPGDDEEAQTMSSSTVNRLMHMEAGSLEQNTDGTKR
LFISELSAYSGWRF
VASVPLSELQRPIATIRSATLWVGAGTLLAALVVAYRIGASQVEPIRVL
MNGMRQTEK
GIWNVKEMKERRDEIGVLIRSYNLMVSRLSDMIESVYESELRRQKSEIELQ
QEALERH
RAEFQALQLQINPHFLYNTLETIKCYAVVQDSEEITQMVESMAHMLRYSIQ
TNLEEIT
VANELKHVLAYLSIMKHRMDRELEVEVIIAPDLLLEKMVRLTLQPLVENVLQ
HAFPRG
MEPGHFIRIDARRLDDRFLVIVQDNGMGMSNARLEKLRRRLELNRLAGEDTDDVYHRG
GIGLMNVHRRIQLVFGETYGLMMESEEGMGTITMALPADQHSKRI"

CDS complement(4711287..4712324)
/gene="rssB_9"
/locus_tag="EFAGFIKM_04122"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00958"
/codon_start=1
/transl_table=11
/product="Regulator of RpoS"
/translation="MFRILITDDEPMIRLGLAKMIEQAGLFDCEIRQAAHGEEALQVV
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AAWSNRYPAYALMPEQTAELFQELLELIVARMNARGNGTMSTSSKIIVSASSKECFEA
LGNEIQTLMNRIKEKRSGKRKHPVEEAKAYLEKHLRREVSLDEIAAKLGLNPSYFSQL
FKQTTGQTFIQYRIRSKMELAKRMLEQPGNRITDISYEVGYADHPHFTKTKKITGLT
PSEYRSKLGIE"

CDS complement(4712367..4713245)
/gene="araQ_26"
/locus_tag="EFAGFIKM_04123"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94530"
/codon_start=1
/transl_table=11
/product="L-arabinose transport system permease protein
AraQ"
/db_xref="COG:COG0395"
/translation="MRTPSVRYRIFRIGNLVFLTLLSLTMILPFINVLAQSLSSSEAI
MGGKVSFWPVAFTWINEYVFGDAAFWRAFAVSVGVTLVGTLVNLAATASLAYPVSRP
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FSQLPGELIDAARIDGCGEFGIWRIVIPLSKPAMASLGIFYAVGHWNAYSTALYYLN
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LQKH FVKGIMVGSVKS"

CDS complement(4713259..4714236)

/gene="yteP_31"
/locus_tag="EFAGFIKM_04124"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:C0SPB3"
/codon_start=1
/transl_table=11
/product="putative multiple-sugar transport system
permease YteP"
/db_xref="COG:COG4209"
/translation="MKPADIVPPSRGATGLHSSGLGARLGDAGRYLWRYRILYLLSLP
GILYFFLFKYVPLFGSVIAFQNYNIFKGITGSDWVGLEHFQKMFSHYDFLRILNNTLL
LGLYDLVIAFPVPILLAILLNEVRMIVFKRLLQTIVYMPHFLSWVVISGIFMGIFSMD
AGLVNKALGFLGMQPIYFLGEDSYIRSILIGSGIWRDSGYGTIIFLAAIAGINPDLYE
AAEVDGAGRLKQIWSITLPSLLPTIMILLLLHIGKFLDLGFERVFVFLNPLNLESGEI
LDTYIYKAGLLSQQYSYTTAIGLFKSVVGLMLILLGNFFSKKTTGESLY"

CDS complement(4714233..4714442)

/locus_tag="EFAGFIKM_04125"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MPEITIRLYEGRTDEQKQEIVEVFTRELSRIIDREPDYISIEFN
EIPWDENVDPNLRSAQTQKQGGEKT"

CDS 4714998..4716761

/gene="mcpB_3"
/locus_tag="EFAGFIKM_04126"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39215"
/codon_start=1
/transl_table=11
/product="Methyl-accepting chemotaxis protein McpB"
/db_xref="COG:COG0840"

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EQLHDQATVITQKWYDDLDTAKVAEAAKEKSYSGPVQLEMKAYLDSIHEFYPNIAQAY
IFGSELEEENGTSSIIAIPTNLLEPFEEGNLPAGAMYPLPQNNVVVLEQMKKDGKPAFS
DFYTDEYGTWTTLIYPINNADGSMYAALYFDVDASAVPKGLNKLTYGLMFLIGFLIL
FMVLQFILLKRTLLPIRNLMKGIEEVSTGNLDVTIDTGRDDLGVINEKFNAMIHRFNT
TIYKVQNASHHLSSESKQLLGISEKNNVNIQSISTNIREISTGLVSQDKATVENARAM
TEMSTVVQTIASSSADVADEALSMEQRSSTGNVVMQQVIEQMRLISGAVQNTSNSIQS
LENNNSNQISNIVNVITEIAGQTNLLALNASIEAARAGEEGRGFAVVAGEVRNLAEQSQ
ESAKQIRQLIEEIQRDIMQSSEAMQLGSKEVTKGLEVTQETGVFFENILTATNKVANQ
IQDISSSTEEISASTQEMSATADELSANVSKAASSSKQIEQSIDEQEASMAAIVSASD
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CDS complement(4717038..4717436)

/locus_tag="EFAGFIKM_04127"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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ETCWVLKSHYKHSNVDVGNALLSLSQIDNIIFEEDYMKDALRLFVEKGNVDIVDCYLS

AKSKTINMPVVTWDSDFTKLGCEYYKPNQL"

CDS complement(4717439..4717699)

/locus_tag="EFAGFIKM_04128"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSMYESGKVTSKGQVTIPVEVRKQLGIATGDKIIVIIQNGEAKL

EVRKQKKLTDLVGILKTGQEHLQEARKSAIDWVGNSYKKGE"

repeat_region 4717977..4719023

/note="CRISPR with 16 repeat units"

/rpt_family="CRISPR"

/rpt_type=direct

/rpt_unit_seq="atttcaatccacgcactccatacagagtgcgac"

CDS complement(4719217..4719507)

/gene="cas2"

/locus_tag="EFAGFIKM_04129"

/EC_number="3.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9KFX8"

/codon_start=1

/transl_table=11

/product="CRISPR-associated endonuclease Cas2"

/db_xref="COG:COG1343"

/translation="MLILITYDVSTIDSEGRRLSKVAKKCVDHGRVQNSVFECILD

AAQFRRLRFELEELIDKDTDSLRFYNLGDNYKSKVQHVGAKDSYDMGDPLIL"

CDS complement(4719517..4720548)

/gene="cas1"

/locus_tag="EFAGFIKM_04130"

/EC_number="3.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WPJ5"

/codon_start=1

/transl_table=11

/product="CRISPR-associated endonuclease Cas1"

/db_xref="COG:COG1518"

/translation="MKKLLNTLFTLPDTYLGLDGENIVVKQEEEILARYPLHNLEAV

CTFGYAGVSPALMGACASRNVSFTMTRTGRFLARVIGEDRGNVLRKEQYRISDDEV

RSARVARNMITGKLYNNKWILERATRDYALRIDTERIKKVTESLGETMKLLREVEQLD

ILRGLEGSAAVQYNSVFDDLILQQKESFYFYGRSRRPPLDKVNALLSFAYTLLANDMK

SALESVGLDAYVGFLHRDRPGRASLALDMMEEELRGVYADRFVLSLINKKVNDKGFYV

KENLAVIMDDETRKKVLKAWQDRKQEKIMHPYLNEKIPWGLVPYTQALLARYIRGDL

DEYPPFLWK"

CDS complement(4720545..4721204)

/locus_tag="EFAGFIKM_04131"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKDYNEEDYLLLSGIQHFNFCRRQWALIHIEQQWEDNVRTIEGD
HLHRKADQPALREKRGDKLVVRALPVQSRELGITGICDVVEFIRDPSGVPLAGEEGLY
LPYPVEYKRGKPKRNDSDHSQLVAQVICLEEMLVCDIPKAYFYYDEIKHRVEVIITAA
DRERVKASIQEMRHYFERNHTPKAKAGPHCLSCSLNNICVPDILNKRSVSSYIESRLN
E"

CDS complement(4721191..4722060)

/locus_tag="EFAGFIKM_04132"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTLDHKIDFAVLSVRNANPNGDPLNGNRPRQNYDGLGEISDV
CIKRKIRNRLQDMGESILVQSDEKRNDAAHRSIKDRVDANENVQEHAKGKKANKDMYAE
AACQSWIDVRSFGQVFAFSGTDVSVGIRGPVSIHTAVSLDRIDISSMQITKSVNSVTT
AKDPDKKGSDTMGMKHRVDFGVYVFYGSINTQLAEKTGFTYEDAEKIRESLRTLFE
ND
TSSARPDGSMEVHQLYWWEHSSKMGQYSSAKVHRSLQIELKPGVAEAKSYDDYNYTV
PLEGLAVQEYEGEGL"

CDS complement(4722061..4723989)

/locus_tag="EFAGFIKM_04133"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSWLANLSRTYDDHAKVVGQFEMKKNGKEYALIPISHTTQTAHI
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GEVKGTPYQDYLTQLKAWCESPFHSKVKQSILHYVSKGTLIADLVDRGILHADSRGKL
LEKWTAGPGDQEGEKPFIENVIAADQSGAFVRFAVDIPGEPESRLWRDASVQQSFIHF
YEMSLQDKDICFVTGDYLPVADKHASRIRHSGDKSKLISANDSSGFTYRGRFRTSRDA

AVVSYEASQKGHNAKWLIDRQGTIDGKVFLVWGSTSLDMPEPQEDAFSLWDEDDEE
AFAGGDTHKEFALQIRKAIGGYRYDGEYNSKHEVTLMTLDAATPGRMSIMYYRSLDQ
NEYLDRI LAWHESCYWLHRYRKNKNNDKPVSVFGAPATKDIAFAAYGPRASDKVVKGLM
ERMLPCIIDERPIPLDIVRSSIQRTSNPVG MENWEWEKTL SITCALV NKKEGYGVSLN
TETDRSYVFGRMLAIADVLERSALGKEEK RATNAIRYMNAFAQRPGRTWSIIQSNLQ
PYQARMGTGARYYNSLLDEVGDKLQLEDFTDKPLTGLYLLGFYSQRNDLYTSRKDKEA
AATLDKDDENQLNEQGDN"

CDS complement(4723986..4724711)

/gene="cas5d"

/locus_tag="EFAGFIKM_04134"

/EC_number="3.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q65TW5"

/codon_start=1

/transl_table=11

/product="CRISPR pre-crRNA endoribonuclease Cas5d"

/translation="MLRNQIEFEVSGKYALFTDPLTKLGGEKFSYQIPTYQALKGIVE

SIYWKPTLTWIVDEV RIMNPIQTESKGM RPIEYSGGNTLAYTYLRDVRYQVKAHFIF

NPHREDLIHDQNEHKHHNIAKRAVQVGRRDIFLGTRECQGYVEPCQFGEDDSFYDRI

GELDFGTMLHGISYPDETGSNEREVLWKAKMQHGVIQFIRPDECTLVRKVGEGTAKI

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CDS complement(4725391..4727847)

/locus_tag="EFAGFIKM_04135"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTYIAHICQKDGRITVQDHLVEVKQGAEQAGEKIGVKYLAGIA

GLLDHMGKNTDLFRNYIQEAVANPDAPPRKGSVDHSTAGGKLLHSLYHGRGTTLESKY

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MFKQAIEELQRYIKIIEHKLPPIAGALLIKYMFSC LIDADR TNTRRFEENETLAE EI

NYKSFFLQSYELLSQHLSKLEHSSIVDTPINRLRREMSRQCEQFAYRPSGVYTL SIPT

GGGKTLASMRALRHAIEHNKQRIIYIVPYTTIIEQNAAEIRNILKNDDMILEHHSNV
VDDKDDERHEGDEGETLDRKKNLKLARDHWDRPIIFTTMVQFLNTFYAKGTRNVRRRL
HQLSNAVIVFDEVQSVPVHCISLFNAALNFLHVIGRSSLLCTATQPALDFVKHKLHF
SKQPEIIQNLDEVGRSFKRVDLQDLTRESPSGWGAEVVSFVQEQMREVDSVLVILNT
KTAVRKLFEQLNEVEWLRESGVQVVHLSTNMCAAHRKEVLSGEYGVIPRLAKGERIIC
VSTQLIEAGVNISFDCVVRSLAGLDSIAQAAGRCNRHGKDKVRNVYIIRSSDEVLTNL
PEIQIGA EKTERVLQEFEDDPGSLGDDLLSSKAMSRYFEYYFNDIGDKMHYPIPKLEQ
NLFDLMDRNRYYVDAYKKKHDCRPEVVNHYAIAAEKYFEAISTNATPVIVPYGEEGK
ELILDNLGAIEPGEMSQLLRKAQQYTVNVYDHELRALEKNGDVRPLLHGHVLALREPA
YCDDFGVDSKGEAWENAIL"

CDS complement(4728352..4728465)
/locus_tag="EFAGFIKM_04136"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MMKKRNALNMVYSIVLATLAVLPESIMQLFNHGVGH"

CDS complement(4728462..4729253)
/locus_tag="EFAGFIKM_04137"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSRYDGYGLDSTVTLRIAYGLDNWREVVKLGETLYEESLRIY
NLQMLTKEQDIVEIHTQRAIVYYIGYSRLMQGIAYQKLLEFDKARECVLQYSDFQWIK
LTNQETLNEIEFYSDIAKINLMVLDLLEGNATKLDEYVAYIQKSKGEIMSGILTLEA
NRLNNLP IQEFEYLF EKHR LISDTTIMTDIDVSYYLKFSFELAMYYSRNGNDS DAIDI
LLNCLAISPKINQNKIKYVAFFEKIREQATHAQINTYKSILEGML"

CDS complement(4730190..4730546)
/locus_tag="EFAGFIKM_04138"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MRASEHLKLASIILGPFDDVQDFYIHQGYVMNESYIFFLDEGTL
WLRHVHKVAHVHDHLYINGDTGGIILAEHPQGNVKELIESIVDRLCGMDALTFLTDVLL
WTPERVDMNLKLD RFQ"

CDS 4730946..4731176

/locus_tag="EFAGFIKM_04139"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNE LLIRCLG DIMKERGLQNKD VVALTG VSRNTITSLAGNATK
RIDYDTLGALCNGLDVTPGDLLEYMPQSKKSR"

repeat_region 4731672..4732982

/note="CRISPR with 20 repeat units"
/rpt_family="CRISPR"
/rpt_type=direct
/rpt_unit_seq="atttcaatccacacactccgtacggagtgcgac"

CDS 4733360..4733929

/locus_tag="EFAGFIKM_04140"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRIIDRRQQVIDSAEKSFALFGYKATTMEQVARLANVGKGTIYT
FFENKEGLFDEILHSIITDMKQITEQTVKEENSFLDNVHLSMDSLLEYREEHELLIKL
FQEVNDFGTPQAKEGLQKVETAILEYLERQVQRAMELQQIREDDPKLVSVFLLKLYVT
LTSDWNKTHPTLHKDQIKTFVGLFLKSGL"

CDS 4734006..4736195

/locus_tag="EFAGFIKM_04141"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MMKSLTVFGQDLKSAFKKPKVFIPILVWLFIPVLYSGLFLNAFW
DPYGKMNELPVAVVNTDQGATYNDKSLEVGQNLVDELKKSNDFDWQFVTREQAEQGM
DDKYYMTIVIPEDFSKATTLMEDHPQPAELIYEPNEGYNFLAGQIGGTAVKQIKSKV
SAKVTESYTETLLDQVEKISSGLSDAGDGAGKINEGAALKDNGASTLKKNL SKLADGT
DKLETGMAPLKEGTATLAQGIGTLHAGASSLS DGLSQLAAAGTKLGNGALQAETGGKQ
LQAGIQSAQEGAALKDAGLEASEQGS AKLVAGLQTSVEGSSKVSEGA KAVAQGLAQLA
EASPELAANPAVQQLLAASQAVAAGSEQVYQGGQQLVDGSKSLQAAQQQLHQGSSQLV
QGEQQLLQGATQLSTGHKQLATGLQQFNTKLTEAAAGGAKLAEGSSQLNTGAGQLVTG
MNQLSDGITTIAEGSRKLDDGAGTLKEGTTKLTGSSSELSTKLNEAAAETSSVKKTDE
LVEMYAQPVQVDEHKHNEVPNYGTGFSPYFLSLGLFVGALIATLVVPTRGSTVTDTS
WNR FVSRTL AFTIMSAVQSLLASWLVL SVLGLEVQSIPLFFLFSFVTSLSFMYIIQAL
VTWLENPGRFLAILMLIFQLTTSAGTFPLELIPNWLKVFN PWLPMTYSVTGYKAVISS
GQFGVAWDQIGILCIFA VIGLGGTLTYFLMPRTTENADVSSEVALHL"

CDS complement(4736324..4736665)

/locus_tag="EFAGFIKM_04142"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDYRQNEVD RYSDTVPPPPYVVPKTNGKSITSLVLGILSVTIP
YVGILIGIVAILFASLAFKEIRVRMEQGRGLAIAGLVCGIIGTAIYVLLILLVLLFNF
AISISSEIYSTY"

repeat_region 4736896..4738278

/note="CRISPR with 21 repeat units"
/rpt_family="CRISPR"
/rpt_type=direct
/rpt_unit_seq="atttcaatccacgcactccgtacggagtgcgac"

CDS complement(4738504..4739259)

/gene="artM_3"
/locus_tag="EFAGFIKM_04143"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54537"

/codon_start=1

/transl_table=11

/product="Arginine transport ATP-binding protein ArtM"

/db_xref="COG:COG1126"

/translation="MTHIIEVNQLRKSFGLDVLKQVSFNVEPGEVIAVIGPSGSGKS
TMLRSLIHLEDISGGTIRIQDQTLVDNGRYAGAADIRKMTDRMGVMVFQHFNLFPHLTV
QDNLELAPKTLKKESSSVIRYRSLELLGKVGLSDKADVYPANLSGGQKQRVAIARALM
MQPDILLFDEPTSALDPELTGEVLRVIKQLAQENMTMMIVTHEMGFARDVADRVFFMD
NGEIAEAGPPEQIFGNPRLARTRTFLQRVKVEG"

CDS complement(4739293..4739952)

/gene="yecS_1"

/locus_tag="EFAGFIKM_04144"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AFT2"

/codon_start=1

/transl_table=11

/product="L-cystine transport system permease protein

YecS"

/db_xref="COG:COG0765"

/translation="MSWDYILTILKPMLEGAQTTIIMFLVAIVLSVPLGFAVTLAMRS
QFKPLAWIAHTYVYVMRGTPLLLQVFFFCFGLPLLPVIGEHLVFDRFVAAAIAFILNY
AAYFAEIFRGLLSIDKGQHEAAKVLGLTKWQTMTKVIIPQMVRVVLPATANESITLV
KDTALLYAVAVPELLSYAQGIVNRDAKLFPFFLAAIMYLLITLVLTLLFKALEKRFSY
E"

CDS complement(4740065..4740835)

/gene="fliY_1"

/locus_tag="EFAGFIKM_04145"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AEM9"

/codon_start=1

/transl_table=11
/product="L-cystine-binding protein FliY"
/db_xref="COG:COG0834"
/translation="MRKKAILLLFISICVLIVAGCSSSASKDDNTIVVGIDDKFAPMG
FRDEQNEIVGFDIDYARAAAEKMGKEITFQPIDWSSKESELNSGRIDMIWNGYTITDE
RKEKVLFTKPYLENSQVAITLADSPITKLDELGKNVGLQALSSAADALAASPLKDKV
KASEFKDNVLALTDLTKRLDAVIIDEVVARYYMSKEEGTFKLLDESLAPEQYGIGIK
KGNEELLNQLQKALDELNTDGTAAKISTQWLGEDKVLK"

CDS complement(4740968..4741525)

/locus_tag="EFAGFIKM_04146"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRIRNIWIITLVVLGIIGLVIVEGFVNPKEAKQARYEEEEQQNP
LTHYFAALAKYRSPYMGDNSNLSHLNQALPLRERLNGYQLYPETFTVQVNYSLDTRGM
DAEELERILVYNAVANFVMIDNLEQIVYQFENTSHTLRRESAQQWTGTTELKELQNPEL
WNSTVREKLVEPAQVKEAFSQIVDN"

CDS complement(4741522..4742217)

/locus_tag="EFAGFIKM_04147"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MRLEARITRNVNRLFAHAQDTLDNRELKEEIHNSLAARIDYIS
QGMSEEKAFQTAIQHIAGMDEVMSDHRRVQRPYWTALLQSALIYSLIAWIITIPMRV
LMQGSAINNLLMIVSLIVGGMYVLYLLINKTNSATSVKTTVIRIPALVQWNRRRIWWL
WAVLILVLWGTQAALRFGSNIWFNRPIQVDGPYQFAVIVIAFAIPLLSVIIPLVVHRA
YRIVSKYEVS DAL"

CDS complement(4742214..4742561)

/locus_tag="EFAGFIKM_04148"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MINSDLIRGNIDPIILSVLIPADNYGYSIIKEIYRKSGEQFELK
EPTLYSSLKRLEKSGYVESYWGGGETQGGRRKYYRITVQGLEAYREQVQAWQAAKALID
CMIVTGEKGDEDL"

CDS complement(4743026..4744531)

/gene="melA_2"
/locus_tag="EFAGFIKM_04149"
/EC_number="3.2.1.22"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34645"

/codon_start=1
/transl_table=11
/product="Alpha-galactosidase"
/db_xref="COG:COG1486"
/translation="MSFKVAFIGAGSIGFTRGLLRDLLTVPFNNIEIAFCDISQHNL
DMVTELCQRDIRENGLNIQIQPTTDRKEALKDAKYVLCTIRVGGLEAFATDVDIPLKY
GVDQCVGDTLCAGGIMYGQRGIAEMLDICKDIREHSAPDVLLLNYSNPMAMLTWACNK
YGGVRTIGLCHGVQHGHHQIAEAFGLKKSEVDIVCAGINHQTWYIQASHEGKDLTGDL
LEAFEKHPEYSRTEKVRIDMLRRFGYYSTESNGHLSEYVPWYRKRPEEINWIDLGNW
INGETGGYLRVCTEGRNWFETDFPNWMKDEPMQFIPEKRGEEHGSYIIEGLETGRVYR
GHFNTVNNGVISNLPDDAIIIEAPGYVDRNGISMPHVGDPLGPAAVCNVSISVQHLAV
EAAVNGDDKLLRQAFMMDPLVGAVCNPKIEWQMVDEMLVAQAQWLPQYGDAIAAAEAR
LAAGDLIPTKEYEGAARLKVKTVEEMKQDRDAANKNAGESDKGKDREKVQQ"

CDS complement(4744735..4745748)

/gene="rhaS_35"
/locus_tag="EFAGFIKM_04150"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1
/transl_table=11

/product="HTH-type transcriptional activator RhaS"
/translation="MSITKRWTGSLYQEALRTEDCGPRFYAYYYKQWDNYRMSYHNHD
STEIMYIISGMCRVDMQMSDGSSEQAVLKKGQFIMLDAGVPHRLLEDGVPCRMLNVE
FAFSNSPTGQLSIRQLALEEEEEVHTLLTNATPYLVLPDPEEVYHIMKSLVLELDQRGL
LEQGRANVPMKIIPPEERLHHREARNLSSPEQGILVRTLFIQLLVRVARLRGEMSRSA
PDQAELYVKRTIEFMHHNMDRNIQMKDIAASVNLHPGYLHRIFRQHTQRTPTDYLTML
RMEKAKMLLQQTNIPISEISDYVGVGSRQYFHMLFKKYTGRTPVFEFRSSMERHVSQYP
PNE"

CDS 4745929..4746555

/gene="gpmA_3"
/locus_tag="EFAGFIKM_04151"
/EC_number="5.4.2.11"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01039"
/codon_start=1
/transl_table=11
/product="2,3-bisphosphoglycerate-dependent
phosphoglycerate mutase"
/translation="MSTTFHLVRHGLKERRIGDVSLTAEGALQAEATALHFSKATFPV
TKILTSPLRRAQETANMIARHTSHITEDPRLRERANWGDCPDQSFEFIAMWDRCTS
DPDYIPPVGDSAKQAGERLASLLTELANEESSENSNIIVVAHGGLITDFMVQTFIEREL
NWWHSDFITMQNQLIPKCSITTLIYDQGNYTIEAFASTEHLNFNDVKE"

CDS complement(4746771..4749182)

/locus_tag="EFAGFIKM_04152"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MNSETTAPVHKGSVSGRQSGRRKARMPLAAKVLSSALSVALLVG
GTAGISGAEASNGNSATEASLQSQKGGSHVKEIQLEYLDRGLVAASTSEGVFLSWRL
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KRSASAKPWANGYVDIPLQKPADGVTPAGEAYTYSANDMSVGDVDGDGQYEFFVKWDP

SNAKDVSQKGYTGKTYIDAYTLDGQLLYRIDLGVNIRAGAHYTQMLVYDFDGDGKAEM
MFKTAPGTKIIKYNKKGKVTSEKYITLPKQDRKAGYSNEDDYRLSADGYYGHVDMFK
NWHKHDEVVKGNWPATLEEAFGIEKKYNYPLSQQDAESLADYFIDVYAVERSNRNELR
KFEGFIVDGPYVTVFEGKSGKELETIPYEPERHDDGLMWGDYAMARIEPGNRVDRFL
AGVAYLDGKKPSAIFARGYYTRSTMVAYNWDGKKLKEWKVDSGWTPMKNPFNDGPHG
VDGTDPPQYGSITTQGAHYFSVADVDGDGKQEIYGSATIDHDGSVLYSSTDLMPEASA
APGTIARLGHGDALHVADIDPDRPGLEIFMVHEGGPWAPYGYSLRDAKTGEVIYGGYT
GKDTGRGMVGDVDPTRRGLETWAVGLWTAKGEKISDQMPGTNMNIRWAGDMTTQIVDG
AIDVTPTIKDWNRGTLTATGTLTNNHTKGTPSLVADIFGDWREMLVRTDSSAIRI
YLSTEKTRKLYTLMHDAMYRVGIAGQNSGYNQPSYPSFYMASDMDWSKVTLPKFYTP
GKGGK"

CDS complement(4749790..4752234)

/locus_tag="EFAGFIKM_04153"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKTCLKTKSRGKKILRKGVKQMLAATLLAAGIFPGLSPGLTQAA

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QTYKTDYIDVLADIFADPKYQDIRIIAVIEPDSLPLNLTNLSTPACGQASSTGIYEAG

VKYALDKLHAIPNVYNYLDIGHSGWLGDNNRSAVALYTSVVQGTAAAGLSSADGFIT

NTANTTPLGEPNLSNPDNLNIGGQPIKSAKFYEWNPYFDETDFTAALYADFVQAGWPSS

TGFLIDTSRNGWGGVDRPASATGSNINDYVNSGRVDRREHRGNWCNASGAGIGEAPKA

APGPAHLDAYVWVKPPGESDGSSEIPNNEGKGFDRMCDPTFTTRDGVLTGALPNAPV

SGHWFHDQFVALVKNAFPVLPASNGGGNPPGGTTAPAAPAALTASAGNAQVSLTWTAS

TGATSYSVKRALSASGPFTTVAANVSGTSYSNTGLINGTTYVVVTTATNAVGESVNSA

TATATPVAGVTAPAAPTALTATAGNAQVSLTWTASTGATSYDVKRALSASGPFTTIAA

NVSGTSYTNALTNGTTYHYVVSAVNASGQSANSASVATPQSVVPTSDLVVQYRAG

DTNAQDSQIKPYFNIKNLGSTAVNLSDLKIRYYFSKEGSAAMDIAQVGGANIQR

TFTDSYVELSFTSGAGSIQAGGQTGDIQLRMYKTDWSNLDETNDYSFDPTKTSYQDWN

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CDS complement(4752805..4753881)
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/inference="ab initio prediction:Prodigal:002006"
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VEQLQSDLEKAQLENKMNQVTLDQANMSESLGVTEEERKKAFADREGKRLTNELNQKA
LVLKEKEIQKKQAVISKSVVYASASGIFQMNEEDSKTRAVTEGQLIGSVTNISKLFM
TIVGEEEMFRLKVGMPVKVRMTAQKDLQFTGKVSXVSKFARKSTDTDLKQASQFDVVI
DLKPDARMYGGVSLEGDIETMRKDKVTVVSSLAIMRDQTEPYVLLDKNGGQTEPLTIQ
AGMESGDKTEVVSGLKPGDIVVLP"

CDS complement(4753910..4755280)
/locus_tag="EFAGFIKM_04155"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRIRDVARMAWGQIIRKMTLLCMMGLSIGSAAMIIALSVGQS
VQTYSEKTLNDNYKMDEITITPNEGIRTGNGKNGQTSKFERGALTLEKIQIIQRLPH
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GAAFGLVDPKVTQKLFEQLNADPYNNELLEQFTEMSAKQDHLVQQLVQFRYEDYANAS
KTKMSGSIRVSGELTKPSNMDEMSEAQNDDKKVYLPLDTARALQDELGLQQADSSAAKHL
NSALVKVEDKRYVSQVEEQIKKLTNTQSNLFQKEAMAGQLAMYQKAALGIGGFIMLL
ASLSIIVAMIMSTHQRKQIGVMKVLGANLWQIRQMFITEAAMLGLMGGVAGVGIAFA
ALGGVNSLLASQMADQMNGPMTVVIQQSALPLGIVFAILVGIVSGIYPAISASRTNAL
TVIKSM"

CDS complement(4755299..4755982)
/gene="ytrE"
/locus_tag="EFAGFIKM_04156"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34392"

/codon_start=1

/transl_table=11

/product="ABC transporter ATP-binding protein YtrE"

/db_xref="COG:COG1136"

/translation="MLQVEQLSHSFRNGKGTVPVLQDINLTIGEGKMVALLGSSGSGK
STLLNLMAGLMKPDQGKILIAGQDIVRFSENRLAEFRRSHIGFIFQSYELLSNLTIRE
NVELPLVFMGISPSKRKAKALKLLEQVGLGEKANLFPSQLSGGQQQRVSIARSLITEP
SVIFADEPTGNLDTETEEIIAILQQLNRDMNTTFVIVTHEAEVAEQMQVWLTQHGI
LVEEAVREV"

CDS complement(4756197..4757360)

/locus_tag="EFAGFIKM_04157"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRHPGFWRKNRDRMLSLGLLIAFVSGIFGIGSLFSLGNLKPRTV
ILPSEQFNRLAPPPSSTIQIESATKIPNDFAIFDFEVLDRNTIIFNQPEFSYSGLKL
SLLHLDDKEVKNIAANTDYGVITSPDHKKIYSQYRAGQTQKTTYEYMIQSGERRKLP
YDNSYYRVFIGNDSYIGQDDLLFKQVDLSQGTSHVVYTYEELMSMFTGPKQGKGSSDT
FIVMDVLQVSEDHQQFYILVMLKDKYAIYRVSLDEHEVKAYAAMEDIQQYKLLKNGD
MLIQGTMNKVQGLYRYHAAEEQYDLLLQGSISFSDLDADESRIAYFFPMDSQNQKNEL
HVAYLNDSKISSDTVIYRNIDNFISLKWNDDELFAVSSSVDKSEMYRFSFRAW"

CDS complement(4757357..4758823)

/gene="sasA_16"

/locus_tag="EFAGFIKM_04158"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"

/codon_start=1

/transl_table=11

/product="Adaptive-response sensory-kinase SasA"

/translation="MKWTIQFKMVVLFVIVFIGFSVLLILSNKVAQENMYREVHEDM
VQSKRNLDIALNQYFLIHNRMSRDSLEAGSRELAEQIGSAVGGEIVYRPDASPYES
VGSEVNVAKRSDHPDVEEAVHSRIAYTTVVDKGRVTASLSFPLQMDQQLIGIVQMKKD
YTELFKRNLRFQNTIKFFAAVIFVFVFIASIFISRKITQPIRVLTKRSAEVAQGSLNA
DIQITTKDEIGELASSFTVMIDRVREQIDVIERERDEVKQVQARSKVFFDNVTHELKT
PLTTILGYAQILRDNGFTDQDFFDKGMNYIIKESQRLNTMVADILEVSVSSAVIQAYR
FERIDISDIIREACEDMSIKASKYNIGIHYLEEHQYLQGDRDKLKEVFLNILDNSVK
YSDVNSIIEVQSFRLGDSIAIVIRDQEGEGIGAEALQHVFEPFYQDKGINRAEKGSAGL
GLSIVKNIVERHGGTVEMKSIMREGTQVNISLPGEMNA"

CDS complement(4758820..4759533)

/gene="regX3_3"

/locus_tag="EFAGFIKM_04159"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9F868"

/codon_start=1

/transl_table=11

/product="Sensory transduction protein regX3"

/db_xref="COG:COG0745"

/translation="MRQKEILIEDEESIRDILSYSLRKEGFEIKEAATGKEGLDLLR
DSKPDILLLDLMLPDMSGFDVCRQLSVNSKIPVIMITAKSDMLDKVLGMELGADDYIT
KPFDIRVVARIRAIFRRIDLISETLENQSYEVVRLGKHIEIRKDEREVWKDGERAGL
TNKEYDLLLFLVTHHRKVHTRSELLDKVWGFDFA GDTRTVDIHVQRIRKKLD SGVQGI
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CDS 4759750..4760226

/gene="sigX"

/locus_tag="EFAGFIKM_04160"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P35165"

/codon_start=1

/transl_table=11

/product="ECF RNA polymerase sigma factor SigX"

/db_xref="COG:COG1595"

/translation="MNSTQINDAYVNYKSEITRYLSHIVKQPQDAEDLAQDCFIRLMN
VTVDIPEDRILYYLKRIARNLAMDSFRRRTRTLRRDSRLEVPTHHVDTSHLEISEGVH
DLVSHINNTEHRKILELRLIHGYSIKETAELVNRSEGMIKSSVFHAVNRIRAKVIS"

CDS 4760431..4763235

/locus_tag="EFAGFIKM_04161"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGKLTGMRGVFLKSLALSMALPLQIGLWNGDASVHAEGPTDPA
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PFTYDDLKEYNVFVIAEPQIPFKTSEQAALKQYVETGGSIFFVGDHYNADRKNRWDG
SEVINGYRRGAFEDPAKGMSTDERNSEAMQNITSSDWLSDNFGVRFRYNALGDINANI
VVPADQAFGITEGVSGVAMHAGSTLAITDPEKAKGIVYLPKTNAKWNNAVDQGVYNGG
GIEEGPYVAVSKLGAGKAAFIGDSSPVEDASPKYLREETGTRKTTYDGFKEVDDAVLL
VNTVNWLATQENYTSLTEVNGLELDTATALLPFEPPAASTEPQAEPWSAPAAGYKWYD
RSTFKAGSYGGPASSANAAYSFVKQDTLPNAEDFQIRVVVENMAPNTTVSGYSAGIYL
TGGTQVAMIQNESGTWPTSYGYSSTFSVTSDSQGRGIKDLNVRIKPGTTGAASLRLRL
NGSNLITNTVTVGNVPAEQLPEEEGPIAAITVAEARTKAAGTTVTIEGVVTEPGA
GGQAFYLQDETAGIYVFQHTSGFHAGDKVKVTAATTIYNSEFELTDIVAIEKTGTASV
PAPIEVTAITDANQGQLVQLKNVTIENIISATPVGSFEFDAAADGTSTHIRVDTRTG
VTETSFYPAAGDKIDITGVSAIFKDVYQLKPRSLNDFVPAEEQGGGEVPSTPAAGAPG
KPVLSNDNGYTTGLFEGTYNVSMNLWWGENGSEYKLYENGVLIDTQKLTAASPSAQSS
KTAITGKANGTYTYVAELTNDKGTTRSDVLTQVTNAAPGKANLSQNNWDGDGNYNVS
MNLWWGTNATEYRLYENDVLIDTQALNAATPASQSATTELSGRANGTYTYRAELINAA
GVTSSSETITVQVTKALPLAS"

CDS complement(4763333..4763593)

/locus_tag="EFAGFIKM_04162"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEIFYIWIWFIVLLLLYRMFFQKFKKHNIENIGLSAILIVFTG

RSYPYPHINWIFVISVIAVAVYAAVWNSILGWKKWNEPERLK"

CDS complement(4763911..4764717)

/locus_tag="EFAGFIKM_04163"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMKNETSRI RPKPRKNPLRWVIVLLLLILVYAWALAGVPFTGFKE

TAAQIMKAIVAGIFSPDWDFVYLPEGEDLLRGLLDTLAISVLGTVISAVLCIPFAFWS

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LYADEVENIDYGPSEALLASGANRMQQLWFALPQVMPGFLNYTLRFEINVRSATIL

GVIGAGGIGTPLIFALSTRNWQRVGIILLLGIIVMITIIDLISGYIRKKLV"

CDS complement(4764714..4765565)

/gene="phnE"

/locus_tag="EFAGFIKM_04164"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0QQ68"

/codon_start=1

/transl_table=11

/product="Phosphate-import permease protein PhnE"

/db_xref="COG:COG3639"

/translation="MKGQSNVPFQNSGGVGREPGSSPAQV VNRPKPPGRTKHLLTLVI

ILLLLWASAKQTDAGFTELFQGFPEMWKLLKDMFPPRWSYFDNIVQGMLETIRMALIG

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GILALAVFSIGLIAKLT YETLETIDQGP LEAMTAVGMNRIQLIVYG VVPQLAAQFTSY

VLYAFEINIRAAAILGLVGAGGIGLYYEATLGFLEYDKTSV IILFTLVIVLIIDYVST

KLREKLL"

CDS complement(4765562..4766359)

/gene="phnC"

/locus_tag="EFAGFIKM_04165"

/EC_number="7.3.2.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0QQ70"

/codon_start=1

/transl_table=11

/product="Phosphate-import ATP-binding protein PhnC"

/db_xref="COG:COG3638"

/translation="MIELHNVTKYANGTKGLDNINLKFEQGEFIAVVGLSGAGKSTL
LRSINRLHDISEGEILINGSSITKAQ GKRLRMIRRDIGMIFQS FNLVKRSSVLRNVLA
GRVGYHSTMRTIMGRFPNEDIELAFTALDRVNISEKAYS RADQLSGGQQQRVAIARVL
AQEAKIILADEPVASLDPLTTKQVMDDLKRINQDLGITTIVNLHFIDLAREYATRIVG
LRAGEVVF DGPVEEATDERFAEIYGRPILADELLDKQAVHEQGEVVV"

CDS complement(4766537..4767520)

/locus_tag="EFAGFIKM_04166"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKSALFLPLLILVLFLSACGSSSSTGSANGDNSSSNASGTST
AETEKVVEGYVPTELTVQFVPSQNADTLEAKAKPLEKLLGDKLGIPVKVSVSTDYNTI
IEAMASNKVDVGFLPPTAYVLAKEKGAAQVILQAQRFGVND ETGAPTEELADSYKSMF
IVKKDSPIQSIEDLKGGKVAYQNV TSSAGYVWPAGLLLD RGIDPLKDVTPVTLKGHDQ
GVIAVLNGD VDAAAIFQDARNTVAKDYPTVFEDTRVLAFT EPIPNDTIAVRTDMNADW
TAKIKQAFIDIGKDTEGHQIIKEIYTHEGYVESDDSKFEIVRQYGEKVKGE"

CDS 4767794..4769398

/gene="yfkN_1"

/locus_tag="EFAGFIKM_04167"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34313"

/codon_start=1

/transl_table=11

/product="Trifunctional nucleotide phosphoesterase protein

YfkN"

/db_xref="COG:COG0737"
/translation="MTSTNHTASFDILYTSDLHGAIPIHYNTNAYRPAGLALLASLI
RKERERSPELMLVDNGDLLQGSPSASYAASQVSKNEVHPFITVLNELGYDAAVMGNHE
FNYGQNLLRGAVEASNFPWLSANIVKDEQPDVPAFGPPYLIKTLSTGVKIALLGATTH
YIPNWEHPKNIEGLQFLDALETIRAWVSYIHEHEQPDVMVVSYPHGGFESDLETGEPT
RLTGENQGYAICRDIEGIDVLLTGHQHRQLTANIHGVTVIQPGFSGNGAGHVSQLEQ
SSGGKWQITDKQARLLLLDEHSEVEPDATVMKLTEELETAQAWLDQPIGEVAGDLSI
TNATALRLKAHPFIAFVHQVQMEATGAQLSNTAMLSEEARGFGSHITVRDVLSNFIYP
NTLTVLELSGQDIREALEQTARYFEVNASGEVAVNPAYMEPKPQHYNNDMWAGMEYEL
DISQPVGSRVVKLERKKGKPMMDMNGTYSVVMNSYRAAGGGDYAMYPGKKVLHEGATDMA
ALVEDYIRRHQPLTVEQADNWKVIGS"

CDS complement(4769501..4769836)

/locus_tag="EFAGFIKM_04168"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEFKFGNAALLFPPLHITIIIIIFILVRWSKQLETRRFTVFF
YFLISTFITPIYSQSTTKGVFELWIPAGFILVFFYLIRSERNHPSKMKASILGFSIAL
YQLILQYVG"

CDS complement(4770114..4771952)

/locus_tag="EFAGFIKM_04169"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9WYC4"
/codon_start=1
/transl_table=11
/product="putative ABC transporter ATP-binding protein"
/db_xref="COG:COG1132"
/translation="MFKAFIEPFRQPPPIDPETLRSGGGRKPKARAKNWSGTLGRIW
TYLARRKVKLSMVLLMVFASSALALLGPYMGVAVDDFIAGEAGASWTRFLIGLTAVY
VLFSLSWLQNIWMIEIAQETVFRMRYDLFSHLHKLPIFFGKRQQGEIMSRVTNDIE
NVSGTLNSSAIQIFSSVLTLLGTFGVMLWLSPLLTLTFIVVPLMAIGMRWITRRTGP"

LFKERQRNLGELNGYIEETLSGQRIIKAFSQEERVIRGFEERNTRIRISGFWAQTISG
FIPKLMNGLNNLSFAIVAGIGGILAIQGSVTVGVIIIFVEYARQFTRPLNDLANQWNT
LLSAIAGAERVFEVLDEDEEAKDEGA AISLDKVEGAVRFDKVSFGYDEGRNILHEISF
EAKPGEMIALVGPTGAGKTTLIQLLSRFYDPTGGTLTVDGRDMMTIRRENLRSHMAFV
LQDSFLFQGTIRENIRFGRLDATDEEVEAASRLANAHSFIVRMKDG YDKVLQADGSGI
SQGQKQLLA IARAILADPSILVLDEATSSIDTVTEIKIQEGLQRLMQGRTSFVIAHRL
NTIRQADRILVLKDGQLLEQGS HDALLEQGGFYSELYYSQLRKKAQ"

CDS complement(4771933..4773741)

/locus_tag="EFAGFIKM_04170"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WQJ1"

/codon_start=1

/transl_table=11

/product="putative ABC transporter ATP-binding protein"

/db_xref="COG:COG1132"

/translation="MIKLLYYLK KYRVAAIAALVMMLIELAVELAQPYLISKIIDNGI

QQGDLSVWWLWGGVLVGS AVVAFAAGIASSFFASHASLGFGYDLREKLYEKVQTF SYA

VFNR FATSSLITRLTGDVTQVQDTV FMSLRFMTRVPLVVIGSMIMALIVNPRLG LLLV

VMVPVLLIVVWVMIKKAALLFRNVQRRLDAVNGVIQENLTGIRLIRVFVRMGHEIERF

AGFSGKLMKGTISALRLTETTMPFLLMMNVCIIAVLWFGRVDIASGNATVGEVVAVI

NYLLRTIGAMSALSWILVTFSRASASAQRLNEVFNTEDTSETEQTKSLSTSAPSAGSM

KSSHFPQSVYPAKKQRAVQGAVEFRSVGFSYPNSEITVLDNITFTAKAGERIAIMGAT

GSGKSSLVQLIPRLYTEDQGKVRIDGADASELDLSMLRGAIGYVPQEVVLFTGSIREN

IAWGQEDATLDEIVEAAKRAQIHETIENLPNGYDTLLGQRGVNLSGGQKQRLSIARAL

VRRPRILILDDSTSALDVATEGRLLDALEELSCTTFIITQKISSTTSADLILLDDGQ

LIGQGKHEDLMESSELYRRIHESQYGEQAQHVQSIH"

CDS complement(4773987..4775039)

/gene="cotH"

/locus_tag="EFAGFIKM_04171"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q45535"

/codon_start=1

/transl_table=11
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/db_xref="COG:COG5337"
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LYLNGQLLGVYLRIEGVKSFFFRQRKIPVRSIFYAVNDHAGFTVNSDNSSTSTDLLSG
YSLIRGKNVDRTLRLNFIQQLNTKSKLELLRFLQSRVDTDNYLRLWLSGAVLTGNFDGF
HQNYTWYEKFKSGKYGILPWDYEGSWGRNCYGTRVDPNLVRIQGYNRLTGRLLAFRSI
REQYKKLLRQHLMNAFTEKRIMPLVNRLHNEIREDVYKDPYMKWPMDVFAGEPERIRE
YVVKRREHLSEKLRQL"

CDS 4775385..4776116

/locus_tag="EFAGFIKM_04172"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSMSGQGIRGLLGREIKINRGGPDSIQGTLDVRWDYMMANCKE
GIVYVNESHVKSITDTGRSGGNRNAAMGNPIPSNTFLGVMQALRFRRVQINRGGPEKV
EGILADANQNQLIMTLKNQEIVRIPMQHVKSVSLSVRGGNNNNNNNNSSNNTSQGNQAA
QGNQVAQGNQSRGNRSQGNQAAQGNQAQGNKSGGNKSRSNQGNRSQGQRVQGNQSQGN
KSGGNKSRGNQGSQSRGNKSGGKKK"

CDS 4776170..4776307

/locus_tag="EFAGFIKM_04173"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLIFVALVLIGVPFYWIVTPGRPTPSHEHLLQASSGLLPLGGES
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CDS 4776308..4777654

/gene="arsB_2"
/locus_tag="EFAGFIKM_04174"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AB93"

/codon_start=1

/transl_table=11

/product="Arsenical pump membrane protein"

/db_xref="COG:COG1055"

/translation="MPDYQLWLTFGVFIITVIFLMWRPGGLNESIPTSLGALLLILTG
VSSYAHIVGIFGIVSGAAITILSTIVMSIILDSIGFFRWIALNMIEKARGSGFRLFWL
ILLLCFLMTIFFNNDGSILITTPIIIRICSILRLKMHQQLPYLISGALIATASSAPIG
LSNLANLIALQMVG LNLNTYTQMMFVPSMLAIMVMTVLLFYYFRRSIPKVIHHFPVSL
QSSSGSGYHPLQTTESENKVDWWLFRVCIGIVVFIRAGYFLAEQVGIRMEVVAITGVI
LMLAVRWYRTRTGLKDVTQTPWHILLFAFSIYVIVDSLHRAGLTASIIQWMKPIIEG
GNASIIAVSGLMLTLLSNLFNNLPSVMIGTFAVTDLPLSESQLHLAYLANILGSDIGA
LLTPIGTLATLIWMIYILKTHHIRISWKQYMKVTFIVIPISLIVSLISLYIWTSILY"

CDS 4777668..4778330

/locus_tag="EFAGFIKM_04175"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MELVTHWLKGKFIIELESGCKLPIQGEIIDVGQDLIVVYGNQRFV
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GYITNIMNDYFMFYSPYHSIYVSINHLKYIIPSTNSTPYSLSKQHFPMPQSSMSLS
RTLDQQLHKMIGELVVLNLGCKPYRAGLLKNADNHLLALVEADGTSLIMHTDHIQTIH
LP"

CDS complement(4778394..4778960)

/locus_tag="EFAGFIKM_04176"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLDFSFEIIDETKINIYKYGSEFFNFNLYYANGEWTLHPFDGI

LIQNREMC SLIVSELLRNKDFHVMLAKEKIILSQLRTSVNLQSNEPDEWVADRRNADY
FRHDDDELMDYIGNHSFEDILQLEQEQIEARVQFFQQIIQRMFMEGLPEDADFIKVQA
VIRIYKETYDRLGDLNDDYRGDRGRRRW"

CDS complement(4779099..4780202)

/locus_tag="EFAGFIKM_04177"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MATEWAQLKQEDEQRINQEATQLIQKVSQSDPAHLDTLMDDIGK
LGVKTQERAGQTLKLLDRPVNELMSGNRAEVSNMILKLRDECESLQQSKNVSVFGKLL
RKSPKKNYVYRYQSVRTNIDAIINGLRDGKDNLEESIVNMRQLKRSSIQEIYNLQTKI
SFGNQLKALFETEIAKPENENRKAHLERGLRKVVTRTQSMTEMIMLYNQAIATDIIN
DNNDKLIDSVNNAIDKTANLITVSAMIAMALNDQEKVISAVEATNKTIEDQFKENARL
LKTTEKTNELLSKPAMSLEAVNQAMGDLMSALDLSEQSNRRRIESCNDYTNKMTTLN
AKMSDRLGLEGPKAAAIPEKNKPDSSALGSFLD"

CDS complement(4780214..4780969)

/locus_tag="EFAGFIKM_04178"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLRKTIGIGALVGYGLAAISSPFLPDVITWAIPALATVVGGLI
PSRSTPRTQVEGSSSAPVPITDIGRNEPSRLNGGQAPSAVPTGVNETSTAQPHSSSTP
AQHAGSEQAKPSRTEPDVPFDPVIEYLEVLEDMIISEGQKNELDNEIVEKSLALFARL
QRVIPSLQELNNGDINH TVRRILKDLNGFINPFLRLSGEAKRNNRRMLLNGLRDVDS
KISDIVSTIEHKDLMELQNKAELIHQRYNSSEL"

CDS complement(4781117..4782166)

/locus_tag="EFAGFIKM_04179"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MKKMKVYFNRWFSVTYHYMNAIRDNEDGMEFEIYGTHPDPGHMA
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VCSDTELLEQLMEKDRFYESVREKGIMEIPDYFTVSNAAQFQQAYEALRARGHDVCFK
PCNGEGGMGFRVINNERDPLQELFGYALNSISYEDALRAFSSAPSPNVMVMEVLEGY
EYSIDCLSDRNGKLITAIPRRKERGRLRLLEENEELLAARNVAEVYRIPYNFNIQMK
YRKDTPKLEINPRMSGGLHISCLSGVNFYPYLAVKSALGHDIGPLHPNFGILGSHIEQ
PFIIDVQKVSGVHHV"

CDS complement(4782167..4783018)

/locus_tag="EFAGFIKM_04180"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MMIYASDLQTLVYSRRALRIPEDTPGLVPAEWINGKLSAFMSA
YTLERLQSLPQDIVFMPVTRTVEQYRRIHIFQSQCIPKYAVTSNGGNIIVDGQVDDE
WNLHIRSLLRQQAAPPEEILDLFDDVLSPEWVINQRLCDELFFALLIERDKLPMERIA
DKIRVLETLGWESSIQGRKLYLVPSAVNKRAAVEHIRQRIGDVPVIASGDSLLDRCLL
DFAQHAIAPSHGELHVERQRVPEQVPYQFTEQFGAFAADEILDYVHRIHNDQQTQIDH
AEIRETV"

CDS complement(4783015..4784166)

/gene="stiP"
/locus_tag="EFAGFIKM_04181"
/EC_number="3.4.22.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q6FAX7"
/codon_start=1
/transl_table=11
/product="Cysteine protease StiP"
/translation="MNLTTLELIRQREIQSPEPMGSYAASDVVFLDKDISHVDLEKGT
GEREQAIQSGVHYSEMLPVEYQPTAEYIELFHQTLEQSAARIARHTAIVAEKIVERRG
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ETAIQFVDGWTGKGAIKVLKESCDQMERTYGISLDDDLAVLADPGQCSGTFGTREDY
LIPSACLNSTVSGLVSRVLRDDLIGPEDFHGAKWYREWSSADVSTQYVDTIAQHFPQ
MIDLAEIQTEDNATGTSEITWKGWQDIESIQQSFGITNINLIKPGIGETTRVLLRRVP
WKILVDRLDNPDLQHIMMLARDRNVPVEVYPGLTYSCCGIIQSLGGGGE"

CDS complement(4784163..4785458)

/locus_tag="EFAGFIKM_04182"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAARINKKRSFLVSRLLGKHIPVNPYTSLLSGAALAVLLYEHL

TEKTEETKVQIAEWKREMVEGLIDPQQARQVYNMLLQESLSFPETIRFVGFAETATAL

GHSMYEMFADQASYIHTTREYVPAMHPDIQFEEESHAMAHRCYALDHEAFAGEGPIV

LVDDEITTGKTTLNIRDIQARYPRKQYVIASLLDWRTEADENRFAELEAELGITITP

LSLLKGRIEVVGTPQLEATQQDEQLSHPAVTLQTSTVADAFTQLHATSEDGEGKRSTA

SYVQHTGRFGMQSRHNGVLRQEISRIAERLRSQRTGERTLVMGTGEFMYIPMRVAAEM

GEGVLYQSTTRSPIHTHPAPRYAVRSGAGYASPEDASVRNFIYNIAPGQYDEIFVLE

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CDS complement(4785526..4786899)

/locus_tag="EFAGFIKM_04183"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIGECGLREESNHSYLFNPSRLRRDWFLCPDSWNQLLQIGYCQ

RCEEETTLKYFNFLSLEEEDTLFFSSPVSFNHRTSKDLLAYAVGAALYMPATRTHIAD

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ARVRSPQQLERLIDTLGELVSMGTGVALPKFCVGNNGRAYFDQIRKYNQRKPDHYPVLY

GMPILETASIIYRETRWETLLGLRNILDENVEYVLNVRIGATDFSSLFGLRRSPELTI

YDIATIRDCISDIINLFGKMDKPYVISGPVWEYFSQRRVFKPQLRQTPFEETLGKSG

LHLRMKYITNTMDGLMREVMMDKENGIVGKTIHPSHIKPVQAMYVVTHEEYSDAQDI

IARNDGSLGVFKSNYYNKMNEIKPHLSWANRILRSQIYGVLEQQHFVGLLPKHEQQ

HNYVPNS"

CDS complement(4786862..4788118)

/locus_tag="EFAGFIKM_04184"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAISVVKGQKSDLTKTNPGLSRLTVGIGWEAASGVELDTSAFLI

GSDNKVAGDEDFIFYNPSTSFITYMDGGQVGGEKKQFAIDLGKIPARIEKIAFSLI

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NAIGSGFAGGLNALCANFGVDVDGGSDPAPTSTVPPTAVPTPPPPVPAPEPTPSPVN

SINFSKIELKKKGDTINLKKNAGGLGEILINLWNQQGSKGLFGRSKSVDLDLGCLFE

MKDGTTRDVIQALGQTFGSLNRFPIYALDGGDRTGSVKTGENLRINGARISEIERILVF

TYIYGGVANWSQVDGVVTIQKDGPDIIVRMNEYGSPLGMCGIAMLRNVNNETFSIER

IVQFYNGHQALDEAHDWGMQWVAGRK"

CDS complement(4788149..4788730)

/gene="yceD_1"

/locus_tag="EFAGFIKM_04185"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80875"

/codon_start=1

/transl_table=11

/product="General stress protein 16U"

/db_xref="COG:COG2310"

/translation="MTISLAKGQRIDLTNTNPGLTRVVVGLGWDTNKYSGGVDFDLDA

SAFLLYEDGKAKGTDDFVFYNNPSGGAGSVTHTGDNRTGEGDGDDEQVVVDFSKIPAH

IHRIGITVTIYDGDGRGQNFGQVSNAFVRVDAASDREVLRFDLGEDYSTETAVVFCE

FYRAGADWKFQAVGSGFTGGLSALCKNYGLDAQ"

CDS complement(4788824..4789399)

/gene="yceD_2"

/locus_tag="EFAGFIKM_04186"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80875"

/codon_start=1

/transl_table=11

/product="General stress protein 16U"

/db_xref="COG:COG2310"

/translation="MAINLSKGQKIDLTKTNPGLTKITVGLGWDTNKYDGGKDFDLDV

SVFCANANGKVEGEKNFIFFNNPQNEGWSVHTGDNRTGDGDGDDEQINIDLPNVPAN

VEKIAFSITIYEATERSQNFGQVSRAYVRIVNEANNEELIRFDLGEDFSIETGVVVG

LYRHNGEWWKFSAGSGYQDGLVGLTRDYGLQ"

CDS complement(4789490..4790083)

/gene="yceC"

/locus_tag="EFAGFIKM_04187"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P81100"

/codon_start=1

/transl_table=11

/product="Stress response protein SCP2"

/db_xref="COG:COG2310"

/translation="MASINLVKGQKIDLTGKNAGLTEVIAGLGWDPVTAKGFFGRKKQ

ADVDCDASAIMLNEEGKLVKDSNLVCFHNKQSACRSVIHSGDNLTGQGDGDDEQIKMD

LSRIPADVHKVLIVVNIYDCVNRKQDFGMIEKAYIRILDGKNSSSELVKFNLSENYTG

TALICGELYRHGGEWWKFSAGGESHAVHINELARRYS"

CDS complement(4790119..4790565)

/locus_tag="EFAGFIKM_04188"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSSFKGWLNSTKQGLEEQVKKFKNKDFMDAVVAGCALVAFADGS

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KPDVGRVIVGVCSAIGSADGNFDDQEKRVVAEICIVLGLNPSEFNL"

CDS complement(4790909..4792564)

/gene="lipO_13"
/locus_tag="EFAGFIKM_04189"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37966"
/codon_start=1
/transl_table=11
/product="Lipoprotein LipO"
/db_xref="COG:COG1653"
/translation="MALTMKAWMKSGLVGLIGLLAGCTGGNGSEQAEGEGSRGNIT
STIYDRGAVPSGMGTIEDNMWSKWINENGPANVKYTAVPRWESQSKLNVLFASGSAPD
IIFEFGTPIRNTLFNQKQLMPLDELIENSSVEYKALMEKYPQLKKAGIKSDGKLYEVG
RMNEVFPLTSFFIREDWLEKLNLEVPTNEEEMLAVAKAFTENDPDGNGAKDTYGIGGF
QFGDTAGLFRYMYNANWVNVEDGEMVVGPNMKEATAFKRALYEAGVVDKDLLTDKDG
AKAKQDFLNGKIGMYAAMTSDYTGFAAKELDTLMQNVPEAKLKVIALPTTSVGQHTMV
WNNPVQMTAAVNARAKNPEAVMQYIDFLTKIESGRTFKNGFENTHYTLNDQGCPRISD
QEKYQKEISWAGDYAMLYSRLEEGKCGYTEMLFSEEIPSQKEGLRLFKEAREVYMTDL
PVGEGVTHSEHMPQLPKELQVKLTNVTTAINDIFTRSIIGGSKYTVEQAATEAQKWE
QGGGPEIEAWYKDWWSKEKDNVLVWDDFYEIYEQQQADFEKAE"

CDS complement(4792625..4793494)

/locus_tag="EFAGFIKM_04190"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRKTKGEKV FYLINYVLLSLVAVSCILPLLNIVALSFSDARAVV
SGQVGLWPVDFTWFSYHSLITGTPILNAFWNSVEITLIGTGLSMAVTIMAAAYPLSRRH
FYHRRFFTAMVFTMIFNGGLIPTYLVVQNLGLVNSYGALWLPGLVSTYNMLIMRSYF
ENLPGEVDEAARIDGCGELGLLFRIVLPLSKPLLATIALFYGVGYWNSFMSVMIYIND
TSKYNMTVLVQNMIMSNLNVQDFTDPTMISNLTPEGIRAAAVIVMVIPLAVYPFLQK
YFVKGVMLGSIKG"

CDS complement(4793509..4794483)

/gene="yteP_32"

/locus_tag="EFAGFIKM_04191"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:C0SPB3"
/codon_start=1
/transl_table=11
/product="putative multiple-sugar transport system
permease YteP"
/db_xref="COG:COG4209"
/translation="MKGELTAGPPSGLQPPDSEMKHRIRQQRLRRFKMNIPLILMFVP
VIMFYLTFRYAPIGGLVMAFKDYNFYDGLWNSPWVGFQHFQTLFSDPRTVEIIRNTLF
LSLLSIIIGFPIIILAIMLNEVRNMAFKRTVQTVVYMPHFFSWVIIAMMIMTVFSLE
NGIVNRWVEAWTGAPYPFMYNKGSWVAVFVGSGIWKDMGFNAIIFLAALTTIDPSQYE
AAQMDGASKMRQIWHVTLPGIRSTIILLILSMGRVMEVGFDQVYMLQNSNVNEIADV
ISTYIYRTGLQGAQFSLTTAMGLFESLVAFILIFSANYIARRFNEGLW"

CDS complement(4794698..4795762)

/gene="cheB_11"
/locus_tag="EFAGFIKM_04192"
/EC_number="3.5.1.44"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00099"
/codon_start=1
/transl_table=11
/product="Protein-glutamate
methylesterase/protein-glutamine glutaminase"
/translation="MNGRMLVVDDEALFRQGLIHLVRNNPLGWEVVGEEADGEEAIQA
VHSCTPDLITDINMPVMDGLDLAERIHESGLDIMIIILTGYREFEYAQRAIRYGAIE
FLLKPFSLDEACQVLQKAHERYRRKQSDIRIREQYSQVDRTERLREELTSVLHHQFG
AIMNRIEILLEEVSGMSLSEGKAEIHMLMKVMTDLLVQQLQPQESGGMDPTAPDLLW
IHTIPEVIAWARCKSEEWVDMMLRLTQEQQDHVVTRVIQYIEMNYSSTCTLHAAHV
HVTPNYLSHLFKKETGQGFSQYVSKRRIDKAKLLHSTRQSMADIAELTGFDNSSYFT
TVFKQMTGVSPREYRKQVAK"

CDS complement(4795759..4797585)

/locus_tag="EFAGFIKM_04193"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MWWMNFCRFRFKTKLILFLSTATVLISGITGLITYRIHIDLFN
EEVSRQYSLTAEQILARLDSRVHDMYKVTDYITLNPVKNAIKAQTSGISSYDQMKLE
DELDDQLYQVRLEDAPEIMGLRIYDLKENIFNLGAFAGSFQQMDPSYLAEMVHRLEGTG
GEYGWNRRLGPDAFLQEEQSNWILAGRIMRSVDLETYGVMLILFNTSLFESYLKDLRLN
EEVAVYLFADAGELLYAFHNQDADPPPLTELSLGATEIRDEQGTTQLYTKQTSKAGF
TLVSKVSLAQIQNKGIIVKVAVFSAVASILCSWFIITVISGRLLRPLASLVNAMKRV
RDGQFDTRVRIETRDELGFIGERFNAMASRIDTLIHEVYERELSEKEAELKAIQAQLN
PHFLYNTLSMFFWKFYMLGDEKSARLVTALSEMLQYTLEPVQQLTTVQDEMKQIDHYL
QIQQARYQEALSIEIAVPAELLRCQVIRLLLQPIVENVFVHAFSDKRNNRHLEIRGSR
QNGHEGEPDLLIEISDNGCGMHASVIERIMTPVAHADEDRQHIGMRSVLRRIELIHG
EPYGVQIESTVGEGTLVRLRLPYQIGEDSCREIQVTERSRLC"

CDS complement(4797762..4798697)

/locus_tag="EFAGFIKM_04194"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVLRNIIHTIGEDYTMKWNYYTIKFTVMFGLAAILTACGGGAKET
SSSPESASGTEVASSETSSSNAAVTETAATGSNESEQTGSTTEESSSTDDGKIGKDST
LEELKQYQYADKLGYYIRIPLNDHPVRRVSEAGSKNINVANYSDAVVDMNAEVPPIHSDSQ
RLIDDAFPFFTTVQAPDESYITWEEATNLERAMVKTLFIAREGLLITEDAMKNKDYSS
TSFQDSKDFFRVTAKFESMAPVAQHPRDITLSTLYDKARTSWGKLAAMDPEQDEKAFA
EMYKTTRTDANNAMGLLNVLSTNEEERIKEIYGE"

CDS complement(4798921..4799652)

/locus_tag="EFAGFIKM_04195"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MFKKILSLFKTQPELANQITASASALPSTTTIPPRMVRSKRKKK
AEGDWTRQPEEPSTADQLIGLPSQYKVLNDLLVTNPKSRSGYSQIDHVVIGPRAIFVI
ETRNLTGGEIRGGRREANWSVSSSRVKMYNPLMQHRAHVEAIHAHLGDYKRVRLVSMV
TFTNRCRISVDPVRYVNSDELIYDHELVETIQRKTERLETEVPETVFQEKDIAIY
ALLSSVNSTDPQIRSEHMEKAKGIK"

CDS complement(4799931..4800824)

/gene="glxR"
/locus_tag="EFAGFIKM_04196"
/EC_number="1.1.1.60"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P77161"
/codon_start=1
/transl_table=11
/product="2-hydroxy-3-oxopropionate reductase"
/db_xref="COG:COG2084"
/translation="MTNTTKAPGETKVGFIGTGVMGKSMAGHIQQAGYPLHVYTRTAA
KAEALVKEGAVWHDTPGKLAATCDVIITMVGYPKDVEEIYLGEDGLVANAKPGSYLID
MTTSSPLLAARIFEAAEAKGLHALDAPVSGGDIGAQNAKLSIMVGSSEAFEAVRPLF
EQMGTNIVLQGKAGAGQHTKMCNQIAIASGMMGVCEALAYAKTSGLDAETVLKSIATG
AAGSWSLSNLGPRIAGDYEPGFYVKHFIKDMGIALESAKAMGMKTPGLALAESLYQE
IANNGLEEKGTQVLYTYYLQA"

CDS 4801020..4802141

/locus_tag="EFAGFIKM_04197"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSREKGQITIWLFSFSIILLSAGLVCHVLSIPGILEAAGRDGWLS
VVAAGPFFMLFLCMMYIIIRRVRGQRLTDWITREFGAVPSWIFRISASILLFTLGHTT
LYETTNWTVSTYLQFTPPYVLAGGGALVAAWAAAKGIRSIAMTSSLLLFPVILLGYFV

MSANMKYKDYSLLFPIMENGMGPVWRGMIYSLAGLMEIWILMLFQHEVKGKIRWWHVL
ILGVFMLSMAIGPTIGAIVEFGPEEAAKQRNSPYEQWKLVNIGKLLQHVDFLSIYQWL
SGSFARVAISMYLIVDLLNFRPPKKRYIAILTITVIMSFAMQWWRIDYVDYYVDHIQ
FPVMLAYVSIVTILTIAALIHKKDKEAPKRADLNPTQE"

CDS 4802113..4803615

/gene="gerXA_1"

/locus_tag="EFAGFIKM_04198"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9ZFB4"

/codon_start=1

/transl_table=11

/product="Spore germination protein XA"

/translation="MPISTQPKNNREVEPFRMNEHNLNTFFAGSDDVIINSHMFGPEP

MQLLMTYCSGMVDSEAIYDIILPELKRTYEDTHFILTSIEKCISLDWTRMDLQDPAF

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VNVALIRTRLRTNQLACNIELIGSRSATKVALMYIKNIANPELIEDVQDRLRKIETER

ILTANELEELLSPSKITLFPVTHYGRPDFAAECLLNGRFILIVDGNPSAIGPVNLF

LLLKSPEDASFPFLAVNVGRMLRFLGLMITVFLPGFYIALTSFHMDQIPFPLVATISV

GRMGLPMESGMEMFLIMLLMELFREAGVRLPSAIGQTLTVVGGLIIGDSAIRAGMVSP

LMIVIIAVTVVAGATIVNQVMTSSVLILRFLCFVLGASLGIYGFILSLILFLIYLTDL

KSFGIPYLTPLTLPHFKQAIASLFLKLPKGLGKRRPVYLETQEPRKKGNER"

CDS 4803612..4804775

/locus_tag="EFAGFIKM_04199"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRLLRRYMLGLLSLSMCVMTSGCWSAFEIQQVDYAKAFGIDYK

DGMHYHLYVQTLDFASVAKSESSTKSADTPPVWVGHAEGKTMSLALNELFRTAQLHMAW

GHVTAIVMAEGVLTSKHIKEVFDMLGRFPESRYTTWVYGTREPLEKILSATSIYNMSP

LDSILHNPLPTYMEESLYPPVLSFKLIATHNDPATTYLPSTIALNDTQWWENEKKHDL

FLVEGAFFEKTGFDFEYFPRSQLPGYHWLIKDMRRAPLLVQKDGTIYGALSVGLPKIK

IKPVIQGEDVTFNIDAQYLTALYEYLVPTS YEEMIQISEVKLREQIMQTYRHGLERGV

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CDS complement(4804910..4805485)

/locus_tag="EFAGFIKM_04200"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPKTSNRQRVAYVLFFVLVALFLIRSCGPQDIDTILSEEGIPPE

QVKLVTTIEPRTQLVLYKDLTTNNLTPALIQQKMWFSELARIGGGLQDNPVEPLSSHI

SGYEESKGMIIYIYGYLHDADITQVHIRYESNLATSRLAEIVESSSDQSSGRLWYA

VIQQPIHEMIWDIKGLNDEGHIIYSSLDSED"

CDS complement(4805744..4806106)

/locus_tag="EFAGFIKM_04201"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNLYTNNIWRWTINLLYPAIIFVFQSWGPILD SWMGPILFVALF

CFLWSDVKDMFLSTGLTWFIAPCWWYWIERPKPSFGAEHFVAHLWLIVLMYIVFVLI

PQTLILTTRLRVMHYYKK"

CDS 4806298..4806831

/locus_tag="EFAGFIKM_04202"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRLKSIIAVGAVLTCSTLLWGCNGTANNASQQQNDTFRSESWS

DPKRLEASHLEALERMEKDHIHRMVSLSASTDGDKVM TLERSSQKLEEMRPLAEMLQ

HEGHPALLQRIQDMSGDIQGSKS VIAEMKKLPQDGKIKIQSENSDSLHHISSFH DYHQ

YIQEKIQTLNKTNTDLH"

CDS complement(4807144..4807425)

/locus_tag="EFAGFIKM_04203"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTTSTGTVQEEGRLYDELRRALEEVEEGEQRQKVLNRMIRQLRF
AKWRKDRMRRVDAYCQRIKPATLWIILATGALTPVLLFSMFIWVSLWVE"

CDS 4807710..4808723

/locus_tag="EFAGFIKM_04204"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKLLIEEARPLYEAANRFKQQASWQWLSNSHTFGVQDPESGQIG
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EYKQLKALGYSYRGRNAWPTFHLYPEGYVPGPVRKAEDLRFFATCVEQAIEVASVVQS
DPDQLFSPDQRLFLTRVPELSSDGQALTWSSQWVEPQPIVVEETASILIDEFQQARLR
KLPCPPESFWEFGLSYLPTAIGDKERPYPQIIVVTEPASGMIIHSAVAEQKRSFQQC
AEELVDLLLQREYRPSRLILSRPELAQALLPLTSIDIEVYTAEQLPMVEDVLQEMSQ
FLH"

CDS complement(4808819..4810120)

/gene="galK_2"
/locus_tag="EFAGFIKM_04205"
/EC_number="2.7.1.6"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9R7D7"
/codon_start=1
/transl_table=11
/product="Galactokinase"
/db_xref="COG:COG0153"
/translation="MTTQPLNLIQSTEGQALLAQMYGQSQVDEQTARYTKLNATFEEY
FGAQEGSKLFSAAGRSEIGGNHTDHNHGKVLGASITLDTLAVAAPTAESVITFYSEGY

DKKYVIDLTDLTPNAEDDGTTALIRGMAAGFGEFGHQVGGFQAYISSNVFSASGLSSS
ASFEMLICTILNHFYNDGALDVVTLAKIGQYAENHYWNKPSGLLDQMACAYGGLIAID
FENPAQPVIEPVQWDFQQNGYSLVIVNTGGNHADLTEDYAAVPYEMRAVAQALGSEYV
REITADAIYANLKKVREAAGDRAVLRALHFLEENNRVDGQVQALRDGRFADFLKLITA
SGNSSWKWLQNVYQSGAVKEQEIGIALALTENYLQNLGDGACRIHGGGFAGVILTILP
NEKVEEYMSWMHDMMLDTPPIIVNVRAQGAVCLNALIANANK"

CDS 4810397..4811653

/gene="entS_2"

/locus_tag="EFAGFIKM_04206"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01436"

/codon_start=1

/transl_table=11

/product="Enterobactin exporter EntS"

/translation="MKIKTNYTKLFGAFSLTFLGDGLTAAVPWLISLTSDTLYASV

TMTALRLPWLLFSLPVGVLIDRYSRKHMLIGAGFTRMMLLLALTLCIWGGWVSIPILA

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LHIVFPFAIDAVTAVIALLLFLISLKGNFYPGDTETTKKEARPMKNWKREMWSGIQYVY

HDRFLRGLAILSVTITLMYSIILATQIFFVRDVLQLDAFAFGILISIATIGSIVGSQA

VAYMRKRWSTKQLIISSILCMGIIYGAVGLTTNAYMVGGLYFCAAFFIIVYNVTRSSI

LQRSVPNEMLGRVGSVFRFLSFGISAIGTLLGGLLVRVSETTFDRVFSLQLPYLLLSL

IYILSALMFTMKMKNHSESQQRNINA"

CDS 4811713..4812639

/locus_tag="EFAGFIKM_04207"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKITTLRSDQIYEEIIQAAPDEKLELYRERMMSPFMNKWNIQQI

PFRSQEPHGFVDVIMMNNFMNIAPADITPEINESLAASSEAFWQQCHEAVRTSLSTFT

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LAHECNHNVRYQYIQWNPQITLGEMVVSEGLAESFATSLYGEELLGPWWAKTDMETLN

KVIKPKMKDQLHVTGFDQINPYLYGDELAIMQNFTPVGMPYAAGYACGYHLIQYYLNK

TGTPITAATITPASVILAETKEFWNEDTLFHC"

CDS 4812614..4813390

/gene="mta_1"

/locus_tag="EFAGFIKM_04208"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P71039"

/codon_start=1

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/product="HTH-type transcriptional activator mta"

/db_xref="COG:COG0789"

/translation="MKTPYFTVKDIIQITGITKRALHYYDKTDLLKPSKVEDNGYRYY

DQEALGNLQMILLFKEMNFSKLDIAAMMQLSKDEQKDILREHRSTLVQRKQKLETIID

QLDEYVDGKDISHLHLFDDSSILSIQEQYESEAKFIYGDTEKYQFEANVSELSTEEQ

EKAYQQFSINMEQVFRELAKHQDLSPASGEVQALVREWKSCLEQFMSCDAEILRCIAE

AYTTDRRYAGYFDQFGDEGFLRFLYQAIMVYVEGVESDFV"

CDS complement(4813685..4817008)

/locus_tag="EFAGFIKM_04209"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIRKIITPLLSMVLILSSFLTIFMFRPGEANAIGVSRMYNDPVK

APNIYYFVGMVYFEVWKKADGTWTDNKKPGQSYRVDGFDYTFTFNSNRKIKDVKAEVF

NFKWDNAVNTFNASRTGELSQNPLDYYKNSASTQYSLNKGSWTGKGTNEAFIPLYVDP

GKLEAVLNPIDRKQEEIDKNNQVFHPNVEGYRYYFPTLFTIELEPTEGQAVIKHWTTT

GQSLDGMGFTDKEVKLEKDKEYNFAHTAPGEKYTYEGYKKSTVAAPSGGSRSSGDPG

KFTYNGKYPVYYVYFYKLNKNDGTPEIPNNVCTPPQPGRTLEGKYMDPVVTGIIKADQ

RGSEPFVDLKGIPTSSESLYGNVFSRDYLFQNNQFVQMTGTCTYTVNVEQTWTLTWTEES

TTDAEGNSQTVRTPKSDTEVPSQYQVVRPYAYWTIDELSVYNIQEATLINYAFNGE

QITITPEGYTPPEFQAEETGNLYPPPQPGTQQGPSRTKSGGNSRSPDQENLQDVAEA

AVPDVEVENDSLVFKGQTIMNKLRTAKEGPQPEQIPAPVQIGKDVLYSPYHYIPIGKT

NKKDTTSKGLINYILADGSIDAELEEYDIYGINVTVTHTPVVNYSLVSDDQPHNQK
TTPNMNRSALILERPFTVRIPTSGQHLDVNSYPGYGNRDYAKYYRIKQVRFPFDVYST
DRTQFYPRDTWIDIPVYVLDITFYLPVWVDEGDYQVEFRNIAENAPADFESMSRSNAQ
PDANTDLTYHLASDEVSVEVIGRLYDFQITDIADYNWELVFRRFKGSIAPTWISYWTG
TQDIDGDKRGNKPQFTVPIRPGSHPLQGYQNVAVKTGYHFKFDFKTKGNMFGPRDGIR
LTPTDFVSKDGKTRVPVDLYYSTNQRFIRIGSAEDQVKRFVILNDRLRQVPSEQLR
DTATYKYNRYGEIHPGMMSERSYQDYYREKYTKMKTPVGGYSLLLMPEQLRTFIGPKT
NIPTTASADVLRANAAIQQWYGEYSLPAEPYVQAGTNLAEYGRTHGGGLDAKSPIFLK
DGYIVVNFDESIREGNLAAPHLQYIHAPLMNQWLLEGFQRQVEDSYGNSFALRDGDV
VFYHADRSSRDDFSAQVPH"

CDS complement(4817022..4817966)

/locus_tag="EFAGFIKM_04210"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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FPDAKPFQDSQGSVMVPIRFVSEALGAKVTYAKTGKVSHVGIVGKDHKVDMTIGQTKA

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FKLKSLSDFKAYEKSNNYVFNNIKDEKFNGIKVIKESDLPLRLANGQVIYSLELVKRSA

GNYIEIRSSQRGTTIQLLVKNEFAKVRSHVENAFVNNNDQTGLNYYPENSSTDKFQNR

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CDS complement(4818122..4818397)

/locus_tag="EFAGFIKM_04211"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSGRILVELYDLMQAEKDLTHLMNLLKANKAHVQSIGESVGDWK

GQAAEEMRSKMDQFLTVMARRIAEFEHQVVDLARYNYRMEEADRAGN"

CDS complement(4818413..4819783)

/locus_tag="EFAGFIKM_04212"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPNYITEETYHFISKTVYINDLKLGDYEKIPDWKIVKPQTTLH

DSKTGFDAEVFRNENTNQIIIGYRGTEPGGRPIKEKLPDLETDLVDVVMGRAKQLENT

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RIADEG"

CDS 4819857..4820201

/locus_tag="EFAGFIKM_04213"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLKYTYITLVLIIVTIVSGCGGLSNKEEKVYYQKAIPIGQEYF

KKYYDAEIEFTDYQILLPMSSTIVLKG YVKDDPQTSVLSLYLPSLEIDSEGGPGEFI

QKRKSEEEVNSQ"

CDS 4820198..4820635

/locus_tag="EFAGFIKM_04214"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKFATQTLLQIRMINFLKLFHSVFLIITLVLIPTGCGGLSKNER

QAYYEKAIPVGQKYFHEHYDADVFTDYDINLPNSSTMFLYGYVKNDQAIKVSLSLDI

PSMEVRSGKGPEDFIKNERVRLRLTLNEAHNSNLSTNQDDSLT"

CDS complement(4820795..4823236)

/gene="uvrB_1"
/locus_tag="EFAGFIKM_04215"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00204"
/codon_start=1
/transl_table=11
/product="UvrABC system protein B"
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PHLKRAAERGAEVRMLAGDYLYITQPEGLRALCEVDSRIETRLWRSMGTSFHPKAYLF
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VNPDSIALYEEEEYRKYHQKNPEMIQRITEMEEAEFGTGLPEENDEETPVELSLAPIQP
RLAQLDALEALHGTMEEQYDKAMVVMATGLGKTYLAGFFAQRFKRVLFVAHREEILFQ
AKKSFQRIMPERSHGIYNGQYKDGAADCVYASIFTLSMQKHRDGFVDAFDLIVDEF
HHAAAKTYMSVIEHFQPKFLLGITATPDRLDGKDVYALCDGNVAYQMHFIEAIRRGWL
APFQYYGVFDDTDYSQVRWIGTKYDEEQLMAVQLQEEHVETIYAAWLRHKQTRTIGFC
SSIRQADYLAAYFRSQGVKVLHLSRTSEMSREEAIRQLDAGELEVVLTVDLFNEGTD
IPRVDTLFVRPTESLTVFTQQVGRGLRLAEGKSHCVIIDLIGNYRNADVKSLLDVR
GELEGTAKVRDSAVPEVPANCGIHLETRVVNLLQELSRKRLPRREKLHQDFLVLKREL
GRIPTYLELHLMGRSKSIGYRSEFGSYVGFLYWAELLSPTEGEVYVRHEDWLRDVEKT
LMNKSYKMILLLYMLERGEANWLDPITPGEMARFFHTYLTEKEYRKRKDFSDKGKLAL
WEWNEKTATRIEKLIIDMPMSMWSGAKGSMTRFEDGVFSLNVQVKDAEEKALLYRWTK
EICQYRLHAYFERGQ"

CDS complement(4823220..4823546)

/locus_tag="EFAGFIKM_04216"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MPTYNKLVRDKIPHIITSSGKECTRILDPEEYKQELRTLSEE
SEEYMSAGSDQEALDELADMLEVIRALAEVHGANAALDKLRADKAEARGGFQERVYL
IDVDEA"

CDS complement(4823774..4824271)

/locus_tag="EFAGFIKM_04217"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQSLEILIDFNKNNLDRFIKNDLNIQADQIKSSHFYDNRSEND

IEFQQIESLEEILSPKGTGNILLSQLNLGHTYNDVMIVFSFDEESGDIVMNFPEEELF

SGENSETTLKAQKLIEYILDIKNKYAIEKVRIGYEPAMDDDTCLVEIDKEMMDTNVIV

SKLLA"

CDS complement(4824312..4824779)

/locus_tag="EFAGFIKM_04218"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKSIYMKSKEEVLMPELMAYTLAKLSYEWNRTEMYPNPRIYE

KPAGFYFRFHNADQLYEELKHCIQHFKGNLEWMIYVSPLTKNQNYVIEPADVHHAKQT

EAYQVNLELEEVLQDSYKEICEQAIQDIPLLCNHIEQWFGLEHKQLHPPTIPN"

CDS complement(4824790..4825914)

/locus_tag="EFAGFIKM_04219"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTIKVTPEQLLYVSRQIEQGRQQLEGIRNDLTARIGFIQSQWA

GATQERFFYDFQQSRSVLDRALES MVKSSQDLFAIAERFEQADQEQVSLGAVAGQIAV

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PKQPVSSGGDIYDEQISAFKEGHH PVTGESIPAWQAAVSIGGLQTAKLVLAFTGTYNR

GYKVPKDGSVLSKSRLDGV RERTSSNKSPTPEHGTKLTKESTTVIGNSAVLNTMESKS

KFYKKELAYDCSEIADDLAHAAGGRGEIFTIKSRTELKDIQVKEYGEMKSYVYHTVYS

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CDS complement(4826075..4826347)

/locus_tag="EFAGFIKM_04220"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKRVIAIAFFILSILELVTILIGKSMMTGYMEPSTFSGIISFP
LGATYLSIWMFFSRQEFTGGRVAAQISFTAALLTACPLVCLLIIFY"

CDS complement(4826492..4827007)

/locus_tag="EFAGFIKM_04221"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MANNWSTIEAHCNHQVDFTPRSQDHDNSIQPKSTNTSVYHMLRT
TIMDYHQHAKYHLKLAAIMRNHNQFKACLILCDWALASTIRALYIKYHSVHPPKELT
MNEILPLVHTDTESGLDIALFIGTMQHLSSLEDHPHNQPLELNNIDMLLQRTEEILDE
LATRMKDDLSD"

CDS 4827152..4827505

/locus_tag="EFAGFIKM_04222"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEDRKILKLVGARIKVLRKDKGLSQEALGEKGGFHFTYIGQVER
GEKNVSLINLGKIAEAELEVNVSQLFAYVNDEIEFTETDIMIQEIVDMLRETSPSRIRL
SRTIIRELLNESRED"

CDS complement(4827558..4827962)

/locus_tag="EFAGFIKM_04223"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MLLLFSLVALILPDAVFSFLYLSFAETIDSNDFVNHANNNDVS
KMFFYYIKSFYYSFCLHFAVPIPTTEFYSNMQHAVMSYPHLKVLQFLHYTQNKLVLT
LFAVIAGHVSNALGLGTKNSKENINKTGENSL"

CDS complement(4828579..4831518)

/locus_tag="EFAGFIKM_04224"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLAQIRTCEIIASLKGTLGEEYNELQLDEQGEVLTHVYSKLN
SIRAVRDTKIVRPDTPISQSSLFTGAKSEPSMLLELQKEIVTADRIDWLVAFIKFSGL
RLLLEQLQLFTASGGKLRIITTTYMEATDLKAITELSKLPNTEIQISYDTKVTRLHAK
TYIFHRDTGFTTAYVGSSNLSNPALTSGMEWNLKVTEKDSLVDLRKIETTFESYWNR
EFTRYVAEDEVHEAQLKAALNRKKDQSNHFHLDIQPYDYQKEVLEQLHAERTLYGRTR
NLIVAATGVGKTVISAFDYKRFRASHAGAKLLFVAHREEILKQSRDTFRYILKDMNFG
ELHVGNYRAEALDHLFVSIQSLNSMKLTEITSPDYDYIIVDEFHHAAPSQKLLSQ
YEPKILLGLTATPERMDGKDITAYFDHTIAAEIRLTAIDRKLLSPFQYFGVTDTVDL
SQVKWSRKGYDLNELEKLYTHNKIRANQIIQSLNKYVTDLDDVKGLGFCVGVDDHAMYM
AKIFNEAGIPSMALHGGSSSEQERHSAKGQLVNGELRMIFVVDLYNEGVDIPEVNTILF
LRPTESLTVFLQQLGRGLRMAEGKECLTVLDFIGQAHQEYRFQDKFRALIGATKHSIS
YCVENGFSNLPRGTFIQLEKQAKKEYVMRNLKQMSRNRRAIQKLQTFQQDTGLPLTLT
HFVEHHGMTLYELYGGRTGKRYFRGMLAEAGLTAPIEGEHEEYIRRLPSVLTINSRSW
LTLIDYIEKGKETATADERRMLIMFYTFHRAAPEKLGLTSIEEGVQRVLSCEAFRA
ELVDIFKYNLAHLRFVDKSNSFPYTCPLDIHCLYSIDQVLAAGYWNAAEQSPAFREGV
KYFADEQTDIFFITLNKSDKDFSPSTLYEDYAINERLFHWQTQSRVSEHTATAQRYIH
HRETGNRIALFVLEYKEEHGYTSPFVFLGEADYVSYEGNKPMSFVWRLREEMPAKMVA
VANKCIV"

CDS complement(4831561..4831716)

/locus_tag="EFAGFIKM_04225"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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YLAAVTR"

CDS complement(4831905..4832567)

/locus_tag="EFAGFIKM_04226"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MILKKRFVMIGCCIGFVLLVLTYSFYKEKRMYEQYLTMNVRQD
LVDMKSAIINNDILFDRILKNEKITNEMVEDGEQASQLYYNFTNMTQIIDKYNLMNLN
FSEEANWLVKPASLFTNDLGQDDVMPPTLHRMRMTFERLDITSYPVTPELKARIEEYQ
QLNQRWLNIVGDFESKETNEKDWPQILNDLEQGTQTYFSEKKVDFVDDDWRDALNPR
YE"

CDS complement(4832721..4833206)

/locus_tag="EFAGFIKM_04227"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MSSVIILKKITNYSPEQTLENFKHAAQRANMYCFHLTVDLADN
KFQSAEGLSEVNEETLSNTDDEETIKYFTFNVNKVVEDSYDSFTWLTHSTDYFWAVD
IVNINHEYEFIYRFLVEYFQHKNEDYLWFDDAEWYYTADDILKLSQRPYNPKWCSEKI
V"

CDS complement(4833203..4833772)

/locus_tag="EFAGFIKM_04228"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MLTIHHESGGAVEDKKEKSEGNLSLHDGRLRTEGSKTTYTNSFG
NEISWTNQGPKDIDAIEKNLRSSKPGDILEGRVAETIRETGRLEGTGIELKLRNKLK

AGDIDILTASHIIEVKKSLSALDEKQLDKLINLSNKNYFNVDNREVIYYIEDVTVKNK

TQSDLVEKCLKDQNIKLISLEELKEVVS"

CDS complement(4833777..4834571)

/locus_tag="EFAGFIKM_04229"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:IS655"

/codon_start=1

/transl_table=11

/product="IS3 family transposase IS655"

/translation="MCNVLEIAKSTFYHEAKEKPNEDLTEAIVEIFHKNRKVYGRK

IKAKLQERGLIVSRRRIGRIMQEQLVSTYTVAQFKPHKTAYNEETVNELGREFNQT

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SQIQWFHTDRGSEFKNHAMDQLLGTFGIGRSLSKKGCYPDNAVAEATYKVMKTEFIYQ

MEFRNLRHLELELYDVNWFNRHRVHGSLGYLTPVQYRQEALKKV"

CDS complement(4834613..4834897)

/locus_tag="EFAGFIKM_04230"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISEfa8"

/codon_start=1

/transl_table=11

/product="IS3 family transposase ISEfa8"

/translation="MPKQQRRTFTTEFKQMVQLFENGKSRAAIVEEYDLTASALDRW

IKQSQATGSFKEKDNRSPREENELMAMRKELQRLRMENDILKQAALIMGRK"

CDS complement(4834914..4835618)

/locus_tag="EFAGFIKM_04231"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQRIEVHPDLLEEKARLVQKKQELERMVRELEKSIYMLQSDWS

GVTGERFFWDFMQVKEVFPTTLGLLDEIQKFTFIAMNFRITDGSGEVALYIPEELKP

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CDS complement(4835875..4836159)

/locus_tag="EFAGFIKM_04232"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPLVTPFQNSLRVFATIGDGTGTGATFAIAATAFTNDAGVAATA

FPGTYNNYNYINGLMQTADTSSTTTTTITIPGGDALNDGTPIVVQFVVS"

CDS complement(4836242..4837294)

/locus_tag="EFAGFIKM_04233"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKYLNKRTATLNKLRPSRSTSKCRNKHLGKRKKCHIIRRSYRRK

RCSLKRPLRSQKMARDKKVIALPRGGGPNVCCPEGPLAPLRQHELETVSLPGTQGV

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GPAGPQGEPGQLGVPGAQQPAGPQGEPGQSGVPGGQGPAGPQGEPGQPGVPGAQQGPAG

PQGEPPGQPGTPGVQGPTGPPGEQPPGTVPGIEIPTANRYFYFPDLDLSASVIIP

ATEFTNDGGSITEFAGVGLTSFNLYINGIVQPGNSYSVSAERLFFSSQSGVIFAGT

PITIEIIITNIING"

CDS complement(4837479..4838369)

/locus_tag="EFAGFIKM_04234"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEVIEQYLDQVLRFTFLTKREKSEWREEMAAHLYSSVDHLKRQG

LGETEAIERSIQQFGSISELRKTVTKETYGFNMKMIFGCALASLLLFIIVTLAGGLIAN

RYGVHNRYIELMPIFWITVCTLGACLVFTRKRVDRLCLLSVPLLFTLGYLQAYFQVMY

HYWGEGLTFNMFELFFSGVLHTSGGLESTLIASMFLGAQALIMFAISKNKYISIFPF
AFSIMYTFVHMLMFSLYYVFFASEQFSSAVTQGDSVFLNGNMQRVVEMGMSLTMAVAL
FVVFQGWSYWAEKRKLSSAS"

CDS complement(4838356..4838700)

/locus_tag="EFAGFIKM_04235"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLRNEMIKGYIDGIVLSVLNKQDAYGYEISRTVNDENGTNGQFDL

KEGTLYPALKRMEANGYIEGYWGEPISGPRRRYYRITPDGQTQLNLTLSWTENIKII

DIFLGDDLHGSH"

CDS complement(4839021..4839494)

/locus_tag="EFAGFIKM_04236"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRVLLTVLLVLIALPACEAKDRTVDSPVITKSFPEIIEPHNPE

QAEQSGDVVVLLLEGIRNEDKWNTFMKNVEKKHQDQVRVTMYTIEGGPIIQELIYDGTA

IQSTYDNSRDVYGSKQGMKTDTCKGIGTMKSEQGHTFYVLTGCEKGENPFWMPKL"

CDS 4839688..4841256

/locus_tag="EFAGFIKM_04237"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQSVNSSDHIAKEKRSTSRLNNRSKSNGKKTRRFTIAIATTLVA

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EWGNGNMPRQVPDITSAKNVRIGAFSTIALLDGTVLSWQNPPQAVALEQTRKLQTIS

GLKDIIQVESTGLHGALKKDGSVWTWNEPKPEPKAPSKPTKLKGLNNISSITGADAS

LLALDKKGKAWQLGLEGIVTPFHHELKVKKMDGNSGYTLLLTTSGEVYSYGRTVTGKE
GKVNHLSGITDVSAGYHHSLALSSEGTWVGWGSDDKYQEAGAPATSSGGMVYKPVQAKL
GTDVYLNSELFQSMYPAVETPQTVQLPIKAIAAAIGAEEFVHKGENSLSYTLKYNNR
TITITPNEAHYQITSIDLSSEQLIELSEPINNYSGATTFPFEVLRGLGLNVSWDPEKV
RLSIDDVDKKKSEL"

CDS complement(4841419..4844901)

/gene="lacZ_5"

/locus_tag="EFAGFIKM_04238"

/EC_number="3.2.1.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01687"

/codon_start=1

/transl_table=11

/product="Beta-galactosidase"

/translation="MNQKRLFNDGWQFAKSKLDVTEPAGLVYEPVELPHDWLIYNTLE
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ALVEGDNEIVVKVHQSNSRWYSAGAGIYRHVWLKTRDRNHIVTDGIYVSIKQQQGGW
QVEVDTELNLEQNQQAELVHTIWYEGKVVASSQANVTASVLENAAASADSQQIIVESP
NLWSTDAPHLYELVTELRLISDDQEHRVESVSQRIGFRDIKLDANEGFHLNGVKMKL
NGVCEHHDLGALGAAFNLTALRRRFVLLKEMGVNAIRTAHNMPAKEFMELADEMGMLV
VSEAFDMWERAKTPYDYARFFPEWVHTDVKSWVKRDRNHASLIMWSIGNEIYDTHADE
RGQEVTRMLMDYVLEFDPKGNAGVTIGSNYPWENAQKCADIVKLAGYNIAEKYYDKH
HEEHPDWIYGSETSSVQSRGIYHFPFEQPILADDDEQCSALGNSTTSWGAKEAEC
ILAERDTPYSLGQFLWTGFDYIGEPTPYHTKNSYFGQLDTATFPKDSYIYQAAWTDY
KKSPMVHLFPYWDFSPGQIIDVRVCSNAPKIELQLNGKTIGTYDIDHANGTQLSGWWK
VPYEEGELKAIAYDETGKIIATDVQRSYTDKIRLKAARGQLQANGTDLIFVEIDVE
DEAGNPVHNANNRVQVQVTGAGRLLGLDNGDSTDYDPYKGLSRRLFSGKLMALIGATN
EAGTVRIEVSSEGLEGAFAEFESLVAAELNDEKQVQPVFMNNEERPVLTGNAQEIPL
RKIEIISNAGQLLDPSNPELTVTAKLYPENTSYRDIEWAVVNDAGIESNIAKVEAVQA
ETGDNGEHQHAVKVSAIGDGEFRLRATSTNGTDKTKLISQLEFKADGLGTAYKDPYGF
ITGGLYDYTKGEVGNGNERGVATSRDGETHVGFNRNIDFGPYGSDTITIFIPTLSTEEY
FIQIWEGMPDEEGSTMIADVVDKESIWNVYQEETYQLSKRLSGITSICFVLKQKIHI

KGFSFERQSRAFEQNAAASCDHLYGDTFKIEADRVEGINNVSLFENMDFTAEGTSK
LVIYGHSPIDKNTIHIRFAGADGQSNQLVEFTQSGGYEERVFELEQVKG VQKVSFIFL
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CDS complement(4845158..4847005)

/locus_tag="EFAGFIKM_04239"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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PASAYEWFIKGERVAALRDRPFHPSSKAKVGFNAEDVTRYAAEFGKVISLRWVAIRLD

AVQQGCEDGLSILDVLDVQRGVVEAEFARKGITLNEYLPMPVHPWQVEHVILPRFTG

EIEAGSIIVLDIEVGDVQATSSLRSMAPSTESTLMLKLPVSVLSLGAARYLPVVKLLN

GLAGERMLRQAVACDKTLKDKVYMCEEQNWWGFMPESMGLFDDHPRHLAAQIRVYPTE

LLGEAYKVIPMAALGVNLEGHHLLTEILGDNLSSTDVLDVDFYTRIATTFYDIVMRLFKV

GVVPEIHGQNCCLVLKDNEVKGLLFRDHDSVRLHQPYLHKHGIEDPAYHIRPGYSNSL

YNETIQKLIFYVQSLGTQVNLAAMEALSEVYHIPDTKLWEITEQAWKEALQHVQLPE

ADRAALAHAFESNEWPVKLVVRPLLEADGVPGAMPSGKGIGWNPFYKG"

CDS complement(4846965..4848344)

/gene="sbnH"

/locus_tag="EFAGFIKM_04240"

/EC_number="4.1.1.117"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2G1M6"

/codon_start=1

/transl_table=11

/product="2-[(L-alanin-3-ylcarbamoyl)methyl]-2-

hydroxybutanedioate decarboxylase"

/db_xref="COG:COG0019"

/translation="MKPGVWHAIDELQRRMEDPVCAYVYDLAGIQEQVRQMLDSMPGN

TDLFYAIKANPDPRIIEALLPFVKGFENVASIGELLKVRTVSCEVPILFGGPGKKESEL
RLAMEHGVSYIHVESLLELRRIIVIAKERAMEQEQVQESRQKQEWENPEQRYTQAYG
EELMQEQKQKQKQAQEVRIILLRINLRSSSTLPRTKIVMGGGPPSPFGIDEEAVEEAIELI
RVEGAGVVRLSGFHFHSLSNMDARLHAEMIELYLQKVEQWQQQYDLPVEVVNAGGGF
GVTYDGGSPGFDWPLFTSLLEQSEARQRLASCGGELYFESGRLLVADHGYAAEVTDIK
TSHDQYFAVLRGGTHHNRLPASWGHNHFPQIMATDRWKHSFARPEVRDRRVHIVGELC
TPKDRMHSDAEVALLRVGDIVLFEKSGAYCWTISHHDFLGHPHPAFHYLTEDNNHVNT
DEAFQSASR"

CDS complement(4848341..4849117)

/gene="garL"

/locus_tag="EFAGFIKM_04241"

/EC_number="4.1.2.20"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P23522"

/codon_start=1

/transl_table=11

/product="5-keto-4-deoxy-D-glucarate aldolase"

/db_xref="COG:COG3836"

/translation="MRINTLKEKIARKQPVYGLFVSIPHPVIEEMIGHAEFDFVIIDL

EHAATSMESVEELIRAAELVGLTALVRISKVERAEILKVLDCAQGVIPHVEQLEQV

EEAVRYAYYHPVGMRLNSGRPGVFGKYPLTGYIEEANEQVMVPMIESVEGVQQSAQ

ILSHPQVSFVLEGAADLSQSLGVPWQTEHPDVRRALDELHATAQQCEVPYATVTRGVD

DMSLWAERGVHIYVLGDDRNTAFRAYAQKRNDYRNAGGQI"

CDS complement(4849114..4851114)

/gene="sbnF"

/locus_tag="EFAGFIKM_04242"

/EC_number="6.3.2.55"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2G1M8"

/codon_start=1

/transl_table=11

/product="2-[(L-alanin-3-ylcarbamoyl)methyl]-3-(2-

aminoethylcarbamoyl)-2-hydroxypropanoate synthase"

/db_xref="COG:COG4264"

/translation="MGVVGYRAEAGGRTEAVYVGVQERILRQTLEAMWFEGILDSHVS
GSEWRTEGLTSSGDSVAYTCEAERKFSFGRVKVKKGSIQREGALCTDLDFLEEIVLN
ALKGANVTAFIQELLEMAKDSQCRATLPLNIPNEDRYYDALESHMTDGHLYHPSYKS
RLGFSLKDNLAYGPEFNSEVSLVWVAVKKEFAQTAVSAGYSSEKLVGQHLLTAEDMQRF
QQILQQQGLTDMANVNAHATSADQLGSSAEVGETIQAKLHGGVREKGETVRSSGRED
GKVGIGIGSDVGARYVFIPVHPWQWEHQLETVYARQLMDGDIVYLGPPSSSPYRAQQSI
RSLSNRMNPEAPYIKLALSITNTSSTRILAQHTTQNAPLISDWLDELVREDELLQQAQ
FGILKEIMGLSFRYEQLPATQYGRAYGTLGAIWRENVSVHLKEGETAWPLNALMLVQP
DGVPFIQDAVDRHGVKEKWSEALVRTVTLPIIHLLYAHGIALESHAQNIILVLEDDLKP
RIIIKDLHDGVRYVPDQLLPERAPKLNPEPETHRKFNRYSFYAGDVSEVRDITYDA
FFICMTDIALALEKFGLSEAFWQLCAGVIVDYQREHPEYTDRAAFDLFAEDALIE
EMTKRRLYGDGELYFRKASNPLKVSKDALESKRTPELKGIVE"

CDS complement(4851089..4852885)

/gene="sbnE"

/locus_tag="EFAGFIKM_04243"

/EC_number="6.3.2.54"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2G1M9"

/codon_start=1

/transl_table=11

/product="L-2,3-diaminopropanoate--citrate ligase"

/db_xref="COG:COG4264"

/translation="MFEMENKLRSEAEQQAHEHSCKLLNLCYIRELALEKESDIRINP
NTLTYTVAFQASRVKVTGRLSYSAIGEHEYLSMESGGETVHYHDLVRWITSELGNG
EQGASSDQHGMMSVMEMKRSLELENVHPLGENMNRVELAYARDFKQVDNSVGNLTL
YIEQAAGLDIHDYRTSEQSLLYGHPFHPFKNSKGFSEQDVQKYSPELRTSFQLCYIA
VRQDVYMQEWVDDEAAMDLDLLWSHVEPILKEKSEMYGLLPVHPWQYAYISRLSEVQ
SYFRDEKLILLGSAGPTVYPTSSVRTVYVPEWNCNIKLSLNMQITNMIRTNSAEQMRR
TLDASKYVRQHDCFGTELNTHIAYETGVATCAFEEDEELTSFTIAYRPIEFDVENTYV
LSSLVEAPLPGMRSRLMTMLGGGRDIAERWLDRLACSLLPVRAAGEKGIHFEAHLQ

NTLVTLDGLPVDIVRDLEGVSVDEELISEQDRAASDLLFYSREKAWARTSYFIVN
HLGSLIHAMARDVNVPEEHFWKQVREVLVEELERTGNAYVRHLLTTDAFLAKQNLVSC
LRGISQTPAYVPVSNVMKRMGSEVRGSRGIQG"

CDS complement(4852854..4854287)

/gene="mdtD_2"

/locus_tag="EFAGFIKM_04244"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01577"

/codon_start=1

/transl_table=11

/product="Putative multidrug resistance protein MdtD"

/translation="MLKLSLMKRHAVLLAILIGAFSLVLTNSAFNLLLPYFVQYYQIS

TTAGGWIIALYMLAMTLTMPLASLIVDRLGRKQTYMLGISIYGLFSVAGALFYHSIEV

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QYGRLEMLFWLNVPLAIFSLIGCGRVIQTYIPARRKKWHPTSVMLLICAVGALS LGVQ

LYASPVVAVWVPWMLIALGVLLLIRFVQTENGRKEPLIRYQLLRRNAVFPLTVLISTI

QDCVMFGVIFTPLLFQDVFHLSPALSGALFIPLSICTSLFMWIGGSLLDRGRSIIHI

AWGTLLVSISILSFAVLPLGASIWIIGMLMACRGIGVGLSGMSISAIQLQALPDEDMH

EGSVLSTTIERLASSFAVMGLTLYYDMRWQWLAGAGTSMEMAKWGALKEICIGLGCAI

LLTLPLVLLITRKKVGIIVRDGKQAPV"

CDS complement(4854281..4855636)

/gene="dat_2"

/locus_tag="EFAGFIKM_04245"

/EC_number="2.6.1.76"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P44951"

/codon_start=1

/transl_table=11

/product="Diaminobutyrate--2-oxoglutarate

aminotransferase"

/db_xref="COG:COG0160"

/translation="MSVEVQTEYLKMQNEKESNARSYPHFPLVINKAHGVKITDTEG

RVFYDCLAGAGTLALGHNHDTVINAIRDVLDQQIPLHTLDLATPLKLSYMQELFSILP
AEMRDKAKIQFCGPTGADAVEAAIKLVKHATGGKSILAFQGGYHGSTQATMSMSGNLS
KKQHLQSLLPDVHFLPPFYEYRCPFGVGEGMTARLSAQYIENLLDDCESGIAAPCGVI
VETVQGEAGGAIADIEWLKELRRITAERSIPLIIDEVQTGIGRTGRMFSEHAGIIPD
VIICSAVGGSLPMSVVIYQEELDQWQPGAHTGTFRGNQLAMAAGLATLRYIREQDVL
HNVHLRSEQFMNQLNALKERYAEIGDVRGRGLMIGVEVVDPMGRKDRLGHYLPNGALA
ESIQRECFKNGLIVELGGRHSAVVRFLPPLNITEQESGAILAIFEKSVAEIALATAA
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CDS complement(4855803..4856825)

/gene="cphA"

/locus_tag="EFAGFIKM_04246"

/EC_number="6.3.2.29"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P56947"

/codon_start=1

/transl_table=11

/product="Cyanophycin synthetase"

/translation="MFPKGIHNLQNRLIISKAREMSITCEPLLEGCEDFLKLSVGDQE

IIINKTRSHRLPLIAGLLAKNKQACNMLLHEQGMPVPSFIVPEMGSEATDFLEKYGS

IVVKPLDASSSMGVTLDVRTREEELETAIHLASVHGSSIMLQQYVTGIDYRVLIINGEV

AAVNQYRPVYVEGDGTSTVRALIEQLNQERIEMTHIGEYEAPEVNAETERLLEVLHA

QGTTLDEVPTAGKEIELYNLRNSAAGKISEFYKDCTGIIHPENARMIIQAAKTLQIDV

AGVDVRCFDIRTPISRDQGGILEVNALPDLTHHVFPHGGTTRDVVRLYLEYLCQEQL

EYKIYSL"

CDS complement(4857399..4858220)

/gene="yusV_1"

/locus_tag="EFAGFIKM_04247"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32188"

/codon_start=1

/transl_table=11

/product="putative siderophore transport system"

ATP-binding protein YusV"

/db_xref="COG:COG1120"

/translation="MSILEAKELTISYGADPVIENLNLTIPIKGQITVLIGSNGCGKST

LLRTMARLLKSSSGSVLLDGEEIAKLPTKEISRRMSILPQGPTAPEGLTVNQLVKQGR

YPHQTWLKQWSREDERMVKLALESTHLTELADRPVDALSGGQRQRAWIAMTLAQGTET

LLLDEPTTYLDMTHQIDILLFELNEREGRTIVMVLHDLNLACRYAHHIVAVHNKSI

YAEGKPEDIVTQEMVRKVFQMECEIAVDPLFGTPTCIPHGRGRKLNGEQRYTQLA"

CDS complement(4858234..4859277)

/gene="yfhA"

/locus_tag="EFAGFIKM_04248"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31569"

/codon_start=1

/transl_table=11

/product="putative siderophore transport system permease
protein YfhA"

/db_xref="COG:COG0609"

/translation="MRKVLTSRNKKDTVSVQMERKSLFVIGICILLFLVAGVVGTSVG

SDFISPLDVLRTIFGLNAGEHDFVVLTLRLPRVLLSLLVGAALGMSGALLQGIIRNPL

ASPDVIGITGGAAVAAGFVTLGGAVSIKLLPLFAIAGAIVTALIIYVLAWKKGVSP

IRLVLIGIGVSAITGAGTTFMLILSPFYTAGQAYIWLTGSVYGASWTDVRTILPVIVI

VIPLGIWFARSLNAQEFGDDLATGLGVTVQRHRSALLLCSVLLAGIAVAVAGTIGFVG

LIAPHIARKLVGRMFGSMLIVSGLVGALLVFAADLIARTAFPLDVPAGVFTAGVGAP

FFLYLLFKNRNQF"

CDS complement(4859274..4860287)

/gene="yfiZ_1"

/locus_tag="EFAGFIKM_04249"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31568"

/codon_start=1

/transl_table=11

/product="putative siderophore transport system permease

protein YfiZ"

/db_xref="COG:COG0609"

/translation="MFPLFTKASAKIYGLVGLFILLLLACLASMILGRTHITFQMAWE
ALQFYDESSVEHVLLTERLPRTVIAAVVGASLAVAGGLMQALTRNPLASPSVFGINS
GAIFFIVIAIVVLSVSSLTMMWFGFAGAAVAAAIVYGLGSLGRDGLTPIKIVLAGTA
ISALFASFTQAILVLDGTGLQDVLFWLAGSVSGRTLEMLYPVLPYMTAAAIIVSLFMGR
AINLLLTGDDIAKGMGQNVLLVKVLMGIVTVLLAGGSVAIAGSIGLVGLVPHIMRAL
VGNDYRWLVYPYSIVGGAILLLSADVVARLVIMPQEVPLGVMTALIGGPFFVYIARKGV
TKI"

CDS complement(4860385..4861398)

/gene="yfiY_6"

/locus_tag="EFAGFIKM_04250"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31567"

/codon_start=1

/transl_table=11

/product="putative siderophore-binding lipoprotein YfiY"

/db_xref="COG:COG0614"

/translation="MYKVKKKLYIAALILMISLLAGCASGGSAAETTNTSSQAASSNE
SNNESDTTASATEDQSRVIKHAMGETTIKGPQKIVTLFQGANDVVVALGVKPTGVVE
SWVQQPVYEYLRADLDGVPQVGQESQPNLEEINKLKPDLIIATKIRHEEIYEQLSQIA
PTVVTETLFDWKETVKTVGEAMNRVEQSDKLLSDWDGRVADFKEKMGDRLPIEATITN
FRADQVRIFYMGYAGKILNELGFTRPAGHDADTWGVELTSKENIPDMNADMIFNFNSG
TETDAIQKNYDDWTSSPLWKNLDAVKNNQLVQVDEVAWNMAGGYTSANMMLDDLYKQF
NLN"

CDS 4861824..4862402

/locus_tag="EFAGFIKM_04251"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

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/translation="MKKSWVLSIIMSFVLLGGVFAPAGSYAAAADDLTNTYSEDEYYE

VDTSEEEPELTAEEDFLNYLDALDPAVYEKKAMDAVGGNTYITSSNRKSFYKLNN
TAIPNYTKYVSMLKQIKPENAEKKIHAKLVKGSYAQLEGYQLFKKSVAKTKVNSKLL
KQGNDKIASGKSIQQYHAEIKAYGEKLG YQM"

CDS 4862666..4864438

/locus_tag="EFAGFIKM_04252"

/EC_number="3.2.1.54"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q08341"

/codon_start=1

/transl_table=11

/product="Cyclomaltodextrinase"

/translation="MILEAIYHRPKLNWSYAYDRSTMHLRLRSKRGDLDAVIAITGDK

YAWDRITITHIPMHIFARDEMFDYWEAETSPPYRRLRYGFQLIQGEESVWMTERGFEQA

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TPVNFFGGDLQGVLDHLDHISQLGINAIYFCPLFEATTNHKYNTGDYMKVDPHFGTNE

QKAFVDACHQRGIRVVLDVFNHSGREFPPFVDVMKNGASSIYADWFIKDWPPRVE

DGIPTYDTFAFEPLMPKLNTEHPEVKAYLLEVGRFWIEEMDIDGWRLDVANEVDHQFW

REFRQTVKAIKPDAYLLGEIWHDSLMLWLQGDQFDVAMNYPFTNSVLDYTVHGKLDGLA

FANEIGKLLAAYSQPVTEAAFNLLGSHDTPRLLTCDGDERKMKLAVTLLLTYPGVPC

IYYGDEVGLDGGYDPGCRKCMEWDETKQNRELLEFFTRTIALRKQHPALRSTELKIVY

AKTGDPCLAIERLDSQTGERMLLVNAGDEPCTLELPLGDRNIWRNLFTSNTVEARQN

KLTLDEAYGFSLMQLEVKQPAEA"

CDS complement(4864919..4866298)

/gene="menE_3"

/locus_tag="EFAGFIKM_04253"

/EC_number="6.2.1.26"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00731"

/codon_start=1

/transl_table=11

/product="2-succinylbenzoate--CoA ligase"

/translation="MLNQFLLERFAEQGQQPALIWKEQEYSYRWLLEQVGIMSQWITA

EGLTGQLVTLEEDYSPYAAAAALVALLGQGCIVLPMDRNLVEAKREEYIQLAQVKWRLG
IEEGKLCIRQTCELSGEVPVLLSSLAQEGVGGLVLFSSGSTGVSKATVHRADRLRHGF
RRQVRPLRTIPFMMFDHIGGVNTMLQSLSSGGCLCIIADRSPEEVCRTIEKFRVQALP
VSPTFMNLLLLGRNDEGYDLSSLEVVSYGSEVMPESVLAAWNRRFPQLRTIQAYGMSE
LGILPTRSKEPGSLLFSIQDEGVKYRVVEGELQIRTETAMIGYLNAPSPFTEDGWLRT
GDEALLEQGYIRILGRRSEIINVGGGRKVYPAEVEGVLEEMECIEAAVVSGEQSGITGQ
RVKVTIRLATECTLTDLRRSIWEYCQDKLPSYKIPQKIVITQGALVSSRMKKIRKPMT
SIPFASAGK"

CDS complement(4866292..4867710)

/locus_tag="EFAGFIKM_04254"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIIPSFAPVLDIPYYPCNFPLIHEVLHRQGSITSLALLAASRL

YSLPSCGDNGLVKPYFHKLDYVEPIWEMYGQRQLESFEEGKTQIRQHIGEGELFLATG

TSYHLPYCEDYQNPEYIRKHVKQGTRLHLVDHWIAVYGLEDEHVHVYDPVPSKYKGKV

AQRAFHDFWKGNQNIPELAQAKRKEELRTFGTMDIRATVKLDSAGYREMLTQALTQI

EEFLTGRITQGERNYHFGHAVSLRLLGALHGANEGLANEMLISSLLFNMRWSRYFL

RDLLQESALWLGSPLDQYAREFSEIIVRWEKAYNMLQVSRIKQREQWKVQLTSVIKML

VTDEWQWYESLRQSIPQADCFPRQAVLMIGQEHREDLLRIVLDSCRELNAYHNTTIPL

GEGGNAPLYGRSGQLDSLELVSLLAVVEQGIEDRWGTGMGAALAEMAAASMPESPYQT

VDSLVDYLAQQWAPAGKEDARC"

CDS complement(4867780..4868394)

/locus_tag="EFAGFIKM_04255"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTHSVIECLEGIQASRLGNIRNIYVYLPPGYHEQTARHYPVLY

VHAGQRAFGPSRTGNETWNMDQAADGLIASGQIESLIIVGIAHVRPVTHNEFYHYIAP

EREAVSVGCSGIDYEHFIIHELKPIIDHRYRTLDPKSNTGLLGSSAAALCTLHMGMRN

PDVFGKLIMMSPFYVDVQLDETSESGLLEENMYRLPEAGISSDR"

CDS 4868842..4870998

/locus_tag="EFAGFIKM_04256"

/EC_number="2.4.1.19"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P30920"

/codon_start=1

/transl_table=11

/product="Cyclomaltodextrin glucanotransferase"

/translation="MFQMAKRVLLSTTLTSLLAGGALPYLPASAIHADADTAVTNKQ

NFSTDVIYQIFTDRFLDGNPSNNPTGAAYDATCSNLKLYCGGDWQGLINKINDNYFSD

LGVTALWISQPVENIFATINYGGVINTAYHGYWARDFKKTNPYFGTMADFQNLITTAH

AKGIKIVIDFAPNHTSPAMETDTSFAENGKLYDNGNLVGGYTNDTNGYFHHNGGSDFS

SLENGIYKNLYDLADLNHNNNTIDQYFKDAIKLWLDMGVDGIRVDAVKHMPLGWQKSW

MSSIYAHKPVFTFGWFLGSAASDADNTEFANESGMSLLDFRFNSAVRDVFRDNTSNM

YALDSMITGTAADYNQVNDQVTFIDNHMDRFKTSAVNNRRLEQALAFTLTSRGVPAI

YYGTEQYLTGNGDPDNRAKMPSFSKTTTAFNVISKLAPLRKSNPAIAYGSTQQRWINN

DVYVYERKFGKSVAVVAVNRNLSTPASIANLSTSLPTGNYTDVLGGALNGNNITSTNG

NVSSFTLAAGATAVWQYTTSETTPTIGHVGPVMGKPGNVVTISGRGFGSTKGTVYFGT

SAVTGAAITSWEDTQIKVTIPAVAAGNYAVKVASNGVNSNAYNNFTILTGDQVTVRFV

INNASTTLGQNIYLAGNVAELGNWSTGTTAIGPAFNQVIHAYPTWYYDVSVPAGKQLE

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CDS complement(4871325..4872611)

/gene="entS_3"

/locus_tag="EFAGFIKM_04257"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01436"

/codon_start=1

/transl_table=11

/product="Enterobactin exporter EntS"

/translation="MGMIPSEPENIGYQDGQAALHNTKAPRTLWRNVTFRRILYGYG

ISVFGDCFNGIAISLWVLQTTGSAKSMAAVQICNMAVSFLFGSVAGTVADRLDRRKLM

LTSDVFRGVMVAVLIAVSLFGWHAPFPVLLLLLSLSMFSSLFQAPAFHASVASMVGREH
IQQATGTIHMVDNLARISGLAAAGVAVAAFGGFVAILITGATFLLSAVCVLMAGRFPE
VQRSVSQQTTFAQEWRRSSFAYIYRKRLIRSIVLLNPVLILFFMSAMMLVQVMAVKVWE
ANPVQFGLIETCIPLGYMIGSALLIASGKRLKRRGRWVFIGLIVLGPLYIFLANVSSP
IMALPFIVGGGAMFACCTMLTQIMLRTAVPDELQGRVYGVVGTITSTAPILGLTVVSV
LADQWGAASVLQGVGILLLATGILAATTLKSIRTYH"

CDS complement(4872760..4873596)

/gene="malG"

/locus_tag="EFAGFIKM_04258"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P68183"

/codon_start=1

/transl_table=11

/product="Maltose/maltodextrin transport system permease
protein MalG"

/db_xref="COG:COG3833"

/translation="MNTRNNPLRLALSYVLLLIHAVSIYPVLWIFLSSLRPGAALFS
ERLWPEAFTLTHYGELFNNPSFMYGRWYMNTLKIAFFTMIFFSTLMVTLGMYALSRFRF
RGRKTILSTMLILGMFPSFMSMIAIYIILLQIKLLDTHAALILVYSSGAVLGGFIVKG
FFDTIPRSLDEAARMGDGASHLRVFTSIIPLSKPMLTYVALTSFTGAWMDFIFARLVL
RTKENWTLAVGMWDLVNRYQDSNFTMFAAGAVLIAIPITLLFVFLQRFLVQGLTAGAS
KG"

CDS complement(4873593..4874948)

/locus_tag="EFAGFIKM_04259"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQQQHVPVPVGPNNRERQHRMTAAIFSILQGLGQLYNRQWIKGI
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VLLVFFVFILYILNIRDAYVTGLAREEGKQTLGAAASLRNMMDKNFPYLFLSIPALG
ILFFTVMPIIFTITIAFTNYSAPDHIPPAKLVDWVGKTFSDLIQLKSWSQTFYGVLT

WTVIWAILATVTTYFGGVLVALLIEQRGIRFKKLWRTIFILPYAIPQIISLLLMRNLF
NGQFGPINTYMRAFGLEGLPWLTDPFWAKVTVIVNMWIGIPVSMVLILGVLTaipRD
LYEAAEVDGASAFQKFRIITMPFILFATTPVLIMQFAGNFNNFNVIFLLTNGNPLRGD
YQYAGATDLLVTWLYKLTDNNKFNMASAVGIIIFLIASFsiWNFRRSKSFKEEDMI
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CDS complement(4875206..4876492)

/gene="cycB"

/locus_tag="EFAGFIKM_04260"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07009"

/codon_start=1

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/product="Cyclodextrin-binding protein"

/db_xref="COG:COG2182"

/translation="MRKWQGATLSVMMAFTLAACGAGGGSPSPTTAGENPEEVVELTS
ENLQPEEGATLVIWEDKNQSSFIEQRAKKFEEKYGVTVKMEELPPTDQVTKLTTDGA
GLAADVVVFP HDKIGSASEAGLILPNDIFEAEVENTSDNALKAVTFKDILYGYPSV
ETYALFYNKALYPEAPKNFDEIISFAKTFNNVKSQYALMWELQQFYNYAFLASQGG
YIFGDNGMDSADLGLNNEGAQKGGQFLQTLKSEVLPLKMGDVNYDIKKGLFSSGKLAM
DINGPWTISDYRNAGIDFGVAPLPAIDGKPMTSFSGVKAYYVNAFTQYPNASKLLAAF
LSNEEAQMENFDLNGTLPANKNVAADPKLQEDPINKAFLEQFNNSTPMPSLPAMDSVW
GPITSAITDIWDTDKDVKASLDNAVKQIQESLATVQ"

CDS 4876938..4877972

/gene="malR"

/locus_tag="EFAGFIKM_04261"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A4T2"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator MalR"

/db_xref="COG:COG1609"

/translation="MITIKDIAKLAGVSPSTVSRVISNHPRISTKTSKVKQIMKELN

YHPNIIAKSLVSKTTHTLGIMLPRPAEELFQNYFFGELLRGIITHATRMNYELLTTE
TSSDNELHAISRLVHGRRVDGILLGSKRDDPIISFLEAEKFPFVLIGRSEAHNPAPM
VDNDNVQTAYDATHHLIAQGHTRIGFVSGPPDITLSHDRMLGYQKALAQAGLDADSDW
IVEGEFLQESGFRAMSLFMSLPDRPTAIVVIDDNVAFGVLRALAELHYLPEDISVVS
FNNIALSELASPPLSSIDIGTYQLGYTAVQVLLKILSGEPQLHNPVIIPHLIVRESS
LFSKPKPPSD"

CDS complement(4878146..4878904)

/locus_tag="EFAGFIKM_04262"

/EC_number="1.1.1.391"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C8WGQ3"

/codon_start=1

/transl_table=11

/product="3-beta-hydroxycholesterol 3-dehydrogenase (NAD(+))

2"

/db_xref="COG:COG1028"

/translation="MKLQDKVAVVTGAGSGMGKAIATLYAQEGAKVVVSDINEESAQA
VVNDIKAQGGGAIVVLANVAKEEDVQNLIDTTVSTYGTVDILINNAGIMDGMEPAADI
TDEKWERLFAVNTTSVMRTTRKVLPIFLEKQKGIIVNIASAGGLHGGRAGAAYTASKH
AVVGFTKNTGYMYAEQGIRCNAIAPGAVATNISASMTGISPYGAGRQQLGMAINPRIG
TSEIIAKVALFLGSDESSFVNGTVVTADAGWSSY"

CDS 4879097..4879690

/locus_tag="EFAGFIKM_04263"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSETLNSMDRRIKSKAALKDALIHLMQKHPFKEISITDIVQRA
DLNRGTFYRHYQYKEDLFNEIIDDVIQDLVTSFRKPYQDEEEFEVNLMPSSAITIFEH
VHQHAQFYTLVVKSEASSNFQRMICDVLRLDALQDLNHIFPPHINHEILASYQSHAIF
GMIMEWIRQDFKHSPAYMAEELFKIIHYKPDNVVLKN"

CDS 4879846..4880385

/locus_tag="EFAGFIKM_04264"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKSWIISLITSFVLLGGVLFSPAASADAAKVATSTYSDSDQSY

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KQIKPTNPQIKKIHFVKASYTQLEGYLLYQKAVSKNKVNYTLLKQGNAKVNTASVL

MDQCEQQLYAYARSLGYDS"

CDS complement(4880507..4881646)

/locus_tag="EFAGFIKM_04265"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSFSMEIPSQKEIQKVIEEEVKPVPAEVAELQQVANANVEMIMT

LDLESLEKRKEILQSIDGFGMNTMRSSSEKNALLQVSVGHLSKTGDEGGQVAKGLTEL

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NTTLEIEQQNLRELTKRLQKEIQLGVLMDESIDAQIEAAKVRNEDPEKVRFITEEVLF

PLRQRVMDLQQMLVVNQQGIMAIEVVIRNNKELIRGVDRAKNVTISALKIAVTVASAL

YNQKIVLQKIELLNQTTNDLIAGTSKMLKDQGIAIQKQAYEASISVDTMKQAFTDVLS

ALDSISLYKQEALPRMRETINQFRELADTGEQQIQRLEKGQKLGL"

CDS complement(4881666..4883354)

/locus_tag="EFAGFIKM_04266"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAKKGKFFFISIVMLVLVFGLVYAGITLTSNFGKSTTQVSTENA

GKELGKLYADIAPATAEPVKGQIDLPVDVAESLPDISKFIAIVENTTNDYVEIFSSP

EKSGSGVDGWLTEVGEEFNKANITVGGKQVSVKIRNIASGTATDYIKSGKYPDAFTP

SNELWGEMVEASGVKTEMVSERLVGNVPGIVISKAKYDALVDTYGSVNVKTVTEAIAN

NELAMGYTDPFASSTGLNFLVTALNTYDSANPLGEKAIEGFQTNVPFTASTTIQM
REAAKSGRLDAFVLEYQTYVNTADLKSGYVFTPFQVRHDSPLYALGQLPQNKQEIIQK
FAEFVTQAKYQQSAVEFGFNGLQDYKSELATVDGGTLLSAQKVWKEKKNNGSKPIAAVF
VTDVSGSMDGEPLNRLKESLRKGQKYLGTENSIGLVSYSSGVTNVLPIAKYDTNQQSM
FVGTVDSLQAGGGTATFDGIVVAMKMLEDYMAADPNVKPLIFVLSDGETNEGHTLKDI
RDLVETYKVPIYTIGYNADIKALESISSINEAASINADTDDVVKIGNLNFNVQM"

CDS complement(4883367..4884104)

/locus_tag="EFAGFIKM_04267"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNMIKYIKLLGLILGIVAVNVLAFFSPGFIGLNFEEGAFITALSV

TLLFGSAMALLYGSYTLLFRQPVVLPVKHIETHEDYVEALSFYRRIKVLEEDITLGLS

QLSRMKKKKETLLNVLHQRFDPGELSYKKFASVTLEVEKLLYNIRSVLNRLNVFDEA

DYANMMKSKSESIPQKLFQEKTKVYNDYLSYVKNALHTNEEILLKLDQLLLEISRLDS

FEAGDIEQMPCMQEIDQLIKHTKLYRQ"

CDS complement(4884755..4885198)

/locus_tag="EFAGFIKM_04268"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKSKKFRNISLTILSAVVYVGIWFSIVTVQYKPYTDAVPKNEF

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AFESMINENLEPIVNVDSPEKKNINEYKQMEMLFAKAREVWELE"

CDS complement(4885195..4885803)

/gene="glnQ_3"

/locus_tag="EFAGFIKM_04269"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34677"

/codon_start=1
/transl_table=11
/product="Glutamine transport ATP-binding protein GlnQ"
/db_xref="COG:COG1126"
/translation="MIEIKNLSKKFGDRLLFSEFNLIIPDGEFVIFSGPSGCGKTTLL
NMIGAIESYDEGTIVVDGIDLQSKKNHLHYFRTKIGFLFQNFALIENKTVNENLKLIR
KECKTELTEEALSRVGLESKLQKKVYTLSGGEQQRVALARMLKKCDIILADEPTGS
LDRQNAEIVLGILNDL NESGKTIVLVTHDDEIKKQGRGLISL"

CDS complement(4885800..4887779)

/locus_tag="EFAGFIKM_04270"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKS IKY LISFI TIVFLVSGESHIFKLENFYTGYYSTTFFLPE
NTTQDKMITEIKEAAKKN GIEVFVYERQSASPLNSSYHIYG TENVEKKINENLNIYTQ
EYSSLFLGKVSFDFHDLNELKDISNVYDYYIMGDKDQADQFKIELIDKYAGNFPQEGF
IYHNSEFMVLISWIVAIGIIIVLSFYDVLLQKKENVVRVTMGESIHRIYVKNISLDIL
AYVLSFLIAIVILNNFTFIFYKFTLALLLFGLLIVINSIIFLNLYSYRINETLKNSKQ
SRKILSLNYVLKSITAVLTILLISSNIAVIFESYEMYKQKPFFEKHENYFYTRIENKL
EVTKDGNITGNTDEDSVIQEKFYRTFFKKADATLLTDISGIVGKQAIYANKNTLAYLK
EHIHSLTTDISSKQFYFIVPESYKSSETDLLPNLTHAIEFYEGNNLETDKYDVIYYKE
NVKLISIDDLKPGSEFLLNPIILYNNISSDQLVGEISPRI PKLDFFNDIMYRISDNE
FNDFITKNGYSTQTVNKNVLEKFN EYWSVAKRLMYMNIIFTLLILALELIMIISIVK
LEYQVNAIELSLKKVFGYTLFQKNKKIYLMTIITNSLTLLAILVSFLASIGNPVHIA
VGGCLIFLTEILVISYYVAKIERLNIQ RVLKGETS"

CDS complement(4887873..4888223)

/locus_tag="EFAGFIKM_04271"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MNIKKLLATAGLTIAMLSVASSALASPVTTSKNSSGQGFTKSWE
LVASGPSWIMEYGFNKFAIDEDYVHTKHSGVSHSTALLSNGSNYSNSANAGNWA EVDVS
HQGT YVTYSIVYTP"

CDS complement(4888858..4891179)

/locus_tag="EFAGFIKM_04272"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIDTKKGFLGPEHVDLLNGVFQTSQEVGERYLLSLDIDRFLAPC
FEAHGLPARKERYAGWEARTISGHS LGHYLSALAVTYQATGNITLKERLDYAVTELAR
IQQT TSGYIGGLSEEPFHMAFRAENIGGFNIGEYWVPWYSVHKIYRGLIDAYKLTGN
GQALEVVTRFADWAVEGLLPMTEEQMQTMLQSEHGGMNEVFAHLYGITGKALYLEIAN
KFT HQLILRPLEHKQDDLQGKHANTQIPKVIGAAEIYNQDHTHESYRTAAEFFWNTTV
HHR SYVFGAT SISEHYEAKGMESLGIKTGES CCTHNMLHLTKQLFAWNHDSAYMDYYE
NAIYNHILGTQDPDTGNKTYFASTLQGHYKIYGTHDTAWWCCTGSGMENPGKYAEAIY
FEDEQDLYVNLYIASQLDWASQGLSLKLETD FPYSEKVTLTITGGNAS AHLRLRVPSW
LQEPMTATVNGDTEHPYTRMEPGYLSIDRTWTTGDVITITLPM SLRQYTARDDSHKVA
FLYGPIVLAGALGNEGLPEDTIVDETALNPKTAPVPVIWTEQDDVREWIKVVDADTLT
FELSKDVTSTGEAVKLIPFYDVHHEFYTVYWPFNDEGDALEKELNDITIDRVEADGQQ
DEIGHQLDSNCRGEHHNGSTTDGRKKLHMWREAFGVSGAYFSYQLAVDREATNYLCVA
YWGGDHSAFKREGTLYDRQFAITVDGTLIGEQR IHMKNKIGEVFYVTYDIPEAVTSGKD
SVKVMFQAKGDNGCAGKVVEVRTTRSKPESLIL"

CDS 4891362..4892126

/gene="araC_6"

/locus_tag="EFAGFIKM_04273"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A9E0"

/codon_start=1

/transl_table=11

/product="Arabinose operon regulatory protein"

/translation="MQKPLEHYLCGKFISEGNWSHMRRSMPVHEILMLEGEMYIAEE

EEQYVVRANDLLFLRAGRTHYGYQISDTPVSFYWVHYDAVQAEFNQFRTHATIQVPSM
ANQLFKQLLHVSSFSPGEADAALLLLFKELERNIEADYRPHNAIVDHICKWVDIHLHT
NITVSQIAENFNFNKDYISKMKREKGTGLKTYILTERIRRAKQLLLNTNSSVKEIAG
QCGFSDYKLFLRMFKQYEGNTPTEYRNHLYSTQLNR"

CDS 4892256..4892768

/gene="mshD_3"

/locus_tag="EFAGFIKM_04274"

/EC_number="2.3.1.189"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01698"

/codon_start=1

/transl_table=11

/product="Mycothiol acetyltransferase"

/translation="MTTAAVTIHPATEADHPEIVDILVASIAEYRETFEQNERWEAYL

KDIRESVVPYLTQLWIAKIDDQIVGTVQLFETARKAYPNFELPIDYPFIRLLGVDPK

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GKAICFRYDS"

CDS complement(4893132..4894175)

/gene="ydjJ"

/locus_tag="EFAGFIKM_04275"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77280"

/codon_start=1

/transl_table=11

/product="putative zinc-type alcohol dehydrogenase-like

protein YdjJ"

/db_xref="COG:COG1063"

/translation="MKAADVWYGHKDVHVEEREFPVAQADQVKIKVEYAGICGSDLHAY

HHGVGIQEGENHPLSGQKAPLTGHEFAGTVSELGSNVSGISAGDRVVVEPLYHCGKC

EYCIQGRYNQCTQFGFVGLNGDGGFAEYVVVEAYMVHPLPDNVTFEEGALVEPTAVAF

HAVRHSKLVGNKVAVYGAGPIGLLTILSAKAAGASEIYAVDVFEERLDLAAKLGAIP

VNSAKVNATEVILKQSGGIDVAYEAAGVQPTMDSAIAVVKKGGGEVVVIAAIPNPLQVN
FFDLLVKEANLTATLAYRHIFPEVISLIAEGSLDVKQVITKKIKLDDIVQEGLELLMS
DKSHAKILVEIGG"

CDS 4894508..4895419

/gene="gltC_5"

/locus_tag="EFAGFIKM_04276"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P20668"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator GltC"

/translation="MNLEQLEYVVEIAKTQSFSAASEHLHVTQSAISQSVHRLEKELG

IILFERSRQGTHPTPEGKQFIAKALDILQRIDELKSLNAEASSLSGELYVATFPSVMP

YLVQSAADMKREHPQLNISIEEKGSMEIIEDIRNNKIHLGFIAIYTKQLREFDGLHFS

RMYSGLVVGTHHLSELAKHSRVTPNQLKEHKLALYRDGFIEDFIQEFTYDHGPLSIL

FKTNNSEAINMVLNRNDIAATIGHDFSFHQNQLWKEGLVKMVEIAGIDQPKMQIGFVQT

ESKECAVAAERFARRFRQAIELDHLMV"

CDS complement(4895575..4897329)

/locus_tag="EFAGFIKM_04277"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIGFFRKRLVVRIVAVVTLVITIIAVGSMLLQVANMKLAAQEI

SSYNIQIAQSYVNQLDTASYAEFAKDPKENDEFLKIRDELDDFRVSIGAMYVYFVKID

DKGTPLIMVDGMKDADKASPINEVTDVPQEAVQKLLQGQTASSSIINNEEYGDYISSY

APMLDSNGAVTGVIGIDTAVSVIGSIESDIMKSSIPFYALLLLITLIGIAVVTWFIVR

GLRPLQPLKASVEKMAQGELAEANQILTSYRLRSQDEIGTTYQAMIHMSGNLNKIVSN

MVEGVAVTTDILSESTKEFNSTEEMLEMGKTVDQSVEQIRQGAHTQKQGASDSAHAM

EEIAKGITDISESSMVVSDAATSALATAESGKQSMTLMKTQMESISNVSGEVVAMVQV

LNNYSEEIGGALHTVRDFASQTKLLALNASIEAAHAGEHKGKFAVVADEVKLAEASS

TSMELISNLLLRIQQESQQIGSQMGVTATEIGQGVITITAEAEQAFHVVDVAFQLVTRR

IQEVSAAAEEISAGSEEEAAASVNTISQISAGVSDHSDEIYRLMREQSAMFNRVAQTST
MLEQQTNEMSEAVRKVKV"

CDS complement(4897510..4897800)

/locus_tag="EFAGFIKM_04278"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYKLMNVGDIFESSEHGTILVGINPDLDNLSDQIKKRINNYIF

VRTPDNKEFSIEVVSIIQISSSLMNKKSIGICVGKSSISQSEIPINSVVYTQNS"

CDS complement(4897821..4899128)

/locus_tag="EFAGFIKM_04279"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNNILKQHLFEIERQWDGSTKERFYVDFIVAQRVMDDFVSLSL

IAKELEGHAEKFRLADQQAVQSYDASCVPPPDECRAPATDTRHAFQKSADSLVELGQ

AFMQSADDRYQKRYDSVGGFLDYWTFGIPSGLVQGYVDRADKAFNSPNDAAANWLTFGI

HGTIQEATFPTNAWSSDHWANMIGLGGLMVGGGYASTMIKPHNLLTSSGGGAKINSFN

RPPGTGQLSGGFNGIQDQRLRVLDNIAESKKARESSKFSEYLEKEKEAGTGDYRQISS

DGLRNEIELTDAQKTELVSYSVRLGFPEENIVFREHWNTGMMYDRLYINTDVLPAESL

GIGTLSANTRVSGRATIAHEIIGHYEAFKSGKAFELYNLDDATYARNFALDEAQASIR

AARFAPELTSVERMTLLRDAITRLKNADLRVKDVKNELYIQHR"

CDS complement(4899316..4900668)

/gene="yvbW"

/locus_tag="EFAGFIKM_04280"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32257"

/codon_start=1

/transl_table=11

/product="putative amino acid permease YvbW"

/db_xref="COG:COG1113"
/translation="MAQTEGTLQKKLKPRHISFMAMGGVIGTGIFKGS AETIGLAGPG
VIVTYIFAGLLLLLVMAAMAEMATVYKNKNMKDFVQEAFGSRVSFVMGWMYCFLWLSV
CVIEVIAAGSFLQYWFSEVPLWMLSLACAAFIILVNLLSVGVFGEFEFWLAGIKIAM I
IIFIFLGAGLIFGIIPSDNTPYLQNYTQAGGFFPNGWSSIFSALLVVMFSYGGSELIG
LTLTETENAEKVMPIKIVGNFMLRIILFFTLPIIICGLIPWNEIGPESSPFVQVLAST
GLPGA AHIMNFILVTAVLSAANS GIYGASRMMHSM AVGGEAPKALSQTNRNGSPVNTL
LVCSVLLGG SLLGLFAQDQLFRVLLAVPGFVVILVWIC IASSQLKLRK RYPVQPTFK
VWGFPYITGVVVLCLSVI AVMFVFDEGNRFSISICLAVLALLI IWSLIRFRRTNGRTV
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CDS complement(4900804..4901085)

/locus_tag="EFAGFIKM_04281"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIYWWFDDMNPLFAVLVLCPIIAVVLGVCSYFAKW FRLWVALII
SFMLPLLYIASDLSTWGSNIGAWFVYGAVYSLLSWIVHRL LHAIVGYKT"

CDS complement(4901248..4901703)

/gene="ysnE_2"
/locus_tag="EFAGFIKM_04282"
/EC_number="2.3.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94562"
/codon_start=1
/transl_table=11
/product="putative N-acetyltransferase YsnE"
/translation="MEIKVDDL SGVQVKVLIAEHLQGMVGDSP PESIHALNLDGLKKP
EITFWCAWEAGDLMGCGAMKELNPEHAELKSMRTAS AHLRKG VARKMLAHIMDVAVER
GYKRISLETGSMDSFIPARKLYEDFGFEYCEPFADYTLDP NSTFMTKTI"

CDS 4901959..4902528

/locus_tag="EFAGFIKM_04283"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTLTTNNLFYSKRLKMTPRPEDVQTMLQWNEDPEYLRNVDTDL

AIPYSEKQLEDEGETKNKEVYFRLRTHEEDMLIGFVVVHSIEWNNRCGQLAIGIGLAK

HRNKGYGKEALNLILRYAFHEMNLDRLVGLDVIAYNAKAIRSYEKVGFQLEGRARSAY

RDGKRYDRLMMGILRPEWETHNQIHTEGE"

CDS 4902531..4902878

/locus_tag="EFAGFIKM_04284"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTKNAEVTAFIEQIQIPWQVQVAEQLRQLVHDTIPDVQERVQYK

KPHFLKNGKYAAVISPSKQAVSFTIFHATGLDLPDGIFEGPEERKTIKLKEKDTDPYE

WLAGLLKQASADL"

CDS complement(4903444..4904748)

/locus_tag="EFAGFIKM_04285"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTERIPCIREGCANTVLPATAAKTCGYCMPCKQKIEREERQRYI

EANRREVNLYAGITDPVEILKIMHKPQVRDPLIRYTPYEQSEEQVYLSLSVEQQDQMK

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RLLQQVKTDVNRNHILLMLAHIGDDVVQQFQQWRQSPPSWASELYVAPEHYTTEAG

WELAKDGQRRELFITPSYSLYKVKENEGPNKELTGDSLLMLNPSNNCCPWCGNALTSL

INLDVKHPALKNVSWHAQQLQITCVICSSYGVVYMEMDAAGEPLWSSHNVLPAGMDE

IDLDDYGKLAPDVGRQFRIVNASRHAFHASEWAMEPSLSQVGGHPGWVQDAEYPTCPR

CSTRMKAVAQMDWGEVEEYGEGBMYMFICEPCKMTAVSYQQS"

CDS complement(4904854..4906032)

/gene="alaS_2"
/locus_tag="EFAGFIKM_04286"
/EC_number="6.1.1.7"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O67323"
/codon_start=1
/transl_table=11
/product="Alanine--tRNA ligase"
/db_xref="COG:COG0013"
/translation="MTQKIYYDSAYTREWHHTITGRVDKEDGVYITLAETAFYPHGGG
QPCDLGQIGGI AVL DVNIEDGEVWHKLERAPEQTEVHCEIDWERRFDHMQQHTGQHLL
SAITLKLTEAMTSLFHLGTEYDTIDVAAAELGANQLTAIEQEVNLQIYRNARINTSWV
TAE EATQLPLVKQPTVTE DIRIVEIEGVEYNACGGTHVSATGEIGI I KLLKTEKV KGG
TRIYFKCGTRALNEFTATQNVLNSIMVKLKT SKDELLERIEKMELEQKQLQTELNALK
TTNDAYYAEELLAARQGLVIAQVFEDKSLKDMQSLATKLTADHEGLVLFV SISEAKVV
LAQNGQPPEWACGPFFKGNLGAYQGKGGGSEKMAQAGFSSSEDALAFYEFTKDQLGHH
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CDS complement(4906348..4907100)

/gene="fatE"
/locus_tag="EFAGFIKM_04287"
/EC_number="7.2.2.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q81XB3"
/codon_start=1
/transl_table=11
/product="Petrobactin import ATP-binding protein FatE"
/db_xref="COG:COG4604"
/translation="MIQINN VKKTYAAEVEIGPLNIHIPKAGLTSLIGPNGAGKSTTL
LMIGRLLDLDEGQIKVANMDVSTSKSRDLAKIITVLRQENHFVTRLTVRQLAGFGRFP
YSKGRLTDEDEAII SKYIDFLDLDLENRYLDEL SGGQRQRAYVAMVLCQET EYVLLD
EPLNNLDVARSVRMM EHLRYAANEFGRTILTVMHDINF AAKYSDRICAMKDGQIAAFG
TVEEVM DPEILTDIFETKIEIIDGPYGP IAIY"

CDS complement(4907097..4908161)
/gene="fatC"
/locus_tag="EFAGFIKM_04288"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q81XB2"
/codon_start=1
/transl_table=11
/product="Petrobactin import system permease protein FatC"
/db_xref="COG:COG4605"
/translation="MSDLASRNPLNIEIDSSHRPKRSARAFRTKKEEKRYWILLITL
IVLGVFASVGLLIYNNPVPVSSPSFIPVTRRVVALVSMIAICQSLSTVAFQSITN
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LSGKYGNLQLLLLVGIIIGTGLRSVSSFMRRLLAPSEFDILQARMFASVNNADSAYFP
IAIPIVIIAIIILLANAKRLNVLSLGKDVSTSLGTKHQSSVIYTLVLVSILMAISTAL
VGPLTFYGLVAILSYQAAQTYDHRVFPMALAIGFVILTGAUFIMNHVFNAQGVVSI
IIELVGGLTFLIVILRKGSL"

CDS complement(4908158..4909183)
/gene="fatD"
/locus_tag="EFAGFIKM_04289"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q81XB1"
/codon_start=1
/transl_table=11
/product="Petrobactin import system permease protein FatD"
/db_xref="COG:COG4606"
/translation="MQKNLIPKLAGVENSQPQRHNPKKLWTIPFIIAIIATILGITS
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MMLGAVISAFSTFVGLVFQITQNIESWFAGSFSSVQIGRYEYLWLIVLVTLIFVFAD
RLTLAGLGEDVATSLGVNYDRIILLGTALISLAVGIVAAVIGNLPFLGLIVPNIVSMF
RGDDLRSNLPWVCLLGMGSIIVCDILSRVIIMPFEIPVSMILGTVGAVVFIVILLRQR
RSTRVR"

CDS complement(4909200..4910237)
/gene="yclQ_2"
/locus_tag="EFAGFIKM_04290"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94421"
/codon_start=1
/transl_table=11
/product="Petrobactin-binding protein YclQ"
/db_xref="COG:COG4607"
/translation="MRKSISSKLMFIMVAALTLVLAACSSNEPATTDTEAATSDA
ATTATATTVEITDAHGTVTPVNPVKVVALDNRTFETLSTWGVKLAAPKDVMPADSP
YVADESQVQNIQNHREPNELELLASIQPDLVIVGQRFAGFYEDIKKLVPNAAVIDLNIEL
EETASPGENFVNGLKDATTNLGKVFEKQEEAAQLIADFDKAIEEAKAAYNGEDKIMSV
VVSGGNIGFSAPLTGRVWGPLYDIFGWVPALEVDKSSSDHQGDDISVEAIAQSNPDWI
FVLDRDAAVSAEEGAVPAQDVIDNSPALKNTTAITQKQIVYAPNDTYTNESIETFLEL
INNLTKALAKQ"

CDS complement(4910632..4912401)
/locus_tag="EFAGFIKM_04291"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKIINQAENVVMEMCNGIALAHPELEFLKKYKVIKRREIQADK
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KNYSGDMMNFKNAAHLAEEDGIDVQYVRVEDDIAVQDSLYTVGRRGVAGTVLVHKIAG
AAAEGRSLADVKSADKAAQNVRSIGFGFTSCTVPAKGTPTFEIAEDEMEFGVGIHG
EPGIRREKIVSADELAGRMIEALLADMKLDKDASAEIAVLVNGFGATPLQELYLLNNS
VQRELAGHAGLKVATTFVGNMYSIDMAGASVTILKLDEELKTLLFKESDTPAFKVSG
PPAAQVAYSEALEAVVGEDAPVSYEVETDASAAVIKGNQFSLDNVVYLIDKMGEIIIK
NEVPFCELD SHAGD GDFGMSVAKGFRQLKREWNHIINEDKKDIGSFLDACSLVIMEYC
GGASGPIWGS AFRAAGKAVGDKQQLNVAEFAEMIHA AVQGIQSTGERSFGRGAVVGDK
TLIDALVPCADSWTQSAESGDDFKTAFKGA AAAVEGAKKTEDIVARMGRAGTVGDRS

LGYPDAGAYALGVIFTESESMK"

CDS complement(4912401..4913543)

/gene="dhaD"

/locus_tag="EFAGFIKM_04292"

/EC_number="1.1.1.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P45511"

/codon_start=1

/transl_table=11

/product="Glycerol dehydrogenase"

/translation="MRKAFISPTKYVQGEDELLNLGYFVKSFGESALLIAHPDDVQRV

KAKLDATEAEKFNITFVESGFKGECSREEVARLQAIKEKGCDSTIGLGGGKAIDAAKC

VAEGEALIICPTIAATDAPTSHSAVLYTPDGSFDDYAYFKQSPSVVLVDTTVIANAPT

RFLVSGMGDALSTYFEARATAKSYSRVNASLPMGSREGYTSAVGTNAALALAKLCYE

MLLTDGAKAKVASDSNVVTQALENIVETNILLSGLGFESGGLAAAHAIHNGLTVLEGT

HHFFHGEKVSFGTIAQLVLENAPTEELHEVMDFCLEVGLPISLADIGVDTISQEELLK

VAEIACIPEESIHAMPFPITVPEVAAAIAAADRMGREYKAARREAK"

CDS 4913849..4914883

/gene="rhaR_36"

/locus_tag="EFAGFIKM_04293"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MIKEYLHINKILDLNKWKRLQDSLATVTKLAILTVDYKGIPVTS

HSSCQAFQCQNVKDPPELLPYCQKCDSRGGLEAVRLNEPYVYLCHFNIIDIAIPITIDG

KYIGAVMAGQVKLADPEKGSdleQIVTSKNVPMHAAKLEELKDDYAQLPVMTYEEIVK

ISNMLSLLCNIVEEALNKNLLVEMFEKASGNQETLNLSTILPGYSIRNIESIKKEMT

NAIADAYLKNSPSDTESSPVLQPAFEYIHSKSEQVSLKQMADLCHLSPSYFSRLFA

KETGENFTTYLAKLKIWKAKQLLEVTDMPVSQISDELGFNESGYFIKIFKKFEEITPA

LYRKYLQEKI"

CDS 4914989..4915978

/gene="yajO_4"

/locus_tag="EFAGFIKM_04294"

/EC_number="1.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77735"

/codon_start=1

/transl_table=11

/product="1-deoxyxylulose-5-phosphate synthase YajO"

/db_xref="COG:COG0667"

/translation="MEYRKLGNSGLTVSEISLGNWITHGAQVEDGIAEACVQAALDAG
ITTFDTADVYSNTKAETVLGQALKDVRRESIELCTKVCHPTGTGHNDRGLSRKHIMEG
CNGSLRRLQTDYIDVYYAHRYDYNTPLEETFLAFSDLVRQGKVHYIGVSEWNADQIAR
AAALAKELHVPFIASQPQYSMLWRVIEQEVVPASDQAGLGQITWSPLAQGILSGKYAP
NAALPTGSRAAAEAGAPFFNKLQAGWLREDVLTAVQQLVPLAKEIGLTPQLAVAWVL
QHSYVSSVIIGASRPEQVLENVKASGVKLDSEIMTRIDEILNLWIERDPAKTG"

CDS complement(4915975..4916853)

/gene="hcaR_2"

/locus_tag="EFAGFIKM_04295"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q47141"

/codon_start=1

/transl_table=11

/product="Hca operon transcriptional activator HcaR"

/translation="MDIRKLRYFITVAEELHFHRAAEKLNMTQPPLSQQIQNLEDELG
VKLLERTRKMOVRLTPAGAVFLEQARLILAQLDRSIQLTQKADQGIIGHITVAFVDSAS
GSIMVDVLRKFRAAYPQIELTLREMTSSQQQLQALEDGQIHIGFLRYQEDTRHVSFRPC
QMETLIAVLDPDHPMASQTQVSIRELADEDFILFPRHLGSPFHRLVLDYCGEHGVDPR
ITQEAIQMYTIVNLVAAGMGISIVPSSVDVFQRKGVVFLPLQENPPSVPLYTAWRTDM
NQEVSRSFMGIVDECV"

CDS complement(4916885..4917355)

/locus_tag="EFAGFIKM_04296"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTSIELKPIRDLLVKAYDTTMGNGCTPEKQQSIEDFEQKYNVKL

PAAYRALLLEFGACNFGDPALYSVKELSWAYPDFLEVYREYEKEYELPADLQPFPIGG

FGEGSTAILDQSSGKIMMLIHDAGETPLREIAVDFNELMTMLAESAIWIQEQMN"

CDS complement(4917470..4918570)

/locus_tag="EFAGFIKM_04297"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKETALTGDAFNQADFIVGGHGSRQVKVLQNVLDQIDGELFSD

HYGNGLIEEFQQQMADVLGKESAVFFPSGTMAQQIALRIWCDRKDVKR VAYHPLCHL

EIHEEDGLKELHQIESILLADKDRLIRLEDVQALDQDIACLLLELPQREIGGQLPAYE

ELEAISAYCRERGIKLHLDGARLFEITPYQKTPAEICSLFDTVYVSFYKGIGGIAGA

ILAGDPDVMQESKVWKRRHGGDLIGLYPYLSSQYYFNERIGKMELYEQAQELASLL

NACHGIQTLPEVPVSNMFHVHFALAAAEVEPILVQMAQQYGIGLTSYLNKTSGNSCAF

ELSTGDRYEKVPQDKLRAALEWLDEELRKQVR"

CDS complement(4918624..4919235)

/gene="yofA_2"

/locus_tag="EFAGFIKM_04298"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34685"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator YofA"

/db_xref="COG:COG0583"

/translation="MGNPPAGMLRLGAIETAASTFLTPLLAEYTSCTYPEVKHSLVTGG

THELNQKVIQHELHGALIYGPIDHPELNYMKMYDEELVLIAEPGVHEMYTLLSRPMLF

FEIGCTHRTQAESFLNDQGIHTLNIMEYGTLDITLNGVSAGLGVSLPRSSVTKAELR

GEIAVMSLPDPYCRLEVGFVYSRGEHISSALSALVEIITEPDL"

CDS complement(4919202..4919483)

/gene="yofA_3"

/locus_tag="EFAGFIKM_04299"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34685"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator YofA"

/db_xref="COG:COG0583"

/translation="MDAGDLKIFQAVAREGSISKAALSLNYVQSNVTARIKQLETQLQ

VPLFHRSNRGMSLTPAGENLLGYADRILELLYKQSRPRKWVTHQLACFV"

CDS 4919665..4920654

/gene="ccr"

/locus_tag="EFAGFIKM_04300"

/EC_number="1.3.1.85"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q3IZ91"

/codon_start=1

/transl_table=11

/product="Crotonyl-CoA carboxylase/reductase"

/db_xref="COG:COG0604"

/translation="MKAIVHSAQSGLAGLQYTESISRAPEAGEVQIQLKSAGINHRDL

FIMAGRGPQDIPLVPGSDGAGIIVAIGESVRGFAIGDEVIIHPTLGWEHASEVPTVPD

IVGGPMDGTLAQYITLPAENALPKPAHLSWEEAGVLSLSALTAYRALFTRGVLNKGEH

VLIPGIGGGVATYALLMAVAAGAKVTVTSRSEAKRNEALRLGATHALDSHADWSTQND

LEPVDIILDSIGQAMFPKYFDIIRPGGRIVMYGASSGDVLTLPIRSIFFPQISLIGTS

MGSREGFIQMLQWVEQHDIHPVIDGVYPLQDAAKAFERMEKGEGFNLAILME"

CDS 4921049..4921267

/locus_tag="EFAGFIKM_04301"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDNRLHLVELVRKLMDSEGTEAELDDMLTELQQQVPHAEISNLI
FWDDRDLTPEQIVVEALASRPILPPQS"

CDS 4921304..4921525

/locus_tag="EFAGFIKM_04302"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSDMNHNNNNVHPDFNENSGEENILVRGAAFAMLVGHQQVNGAA
SAESLQSNPDFGSSAMRVLHSHKQGSNNQ"

CDS 4921601..4922389

/gene="nirC_2"

/locus_tag="EFAGFIKM_04303"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AC26"

/codon_start=1

/transl_table=11

/product="Nitrite transporter NirC"

/db_xref="COG:COG2116"

/translation="METEALRNVEQLALKKKHKIYKQSLIRYLARSMLASMFIFGVIV
AFKTGNFFYMEQSPFTYPMAAITFGAAIILAYGGGDLFTGNTFYTYAALRKKLRWF
EVIKLWIASYSGNLMGAAVFALLIYLTGLFDSSQVNGFLLSVVEHKMEVPTMQLFFRG
ILCNWLVCMAFFVPMFMKENGAKMFAMMLFVFCFFISGYEHSIANMCTFAIALVLNHP
GTISFEGVLHNLVPVTLGNLVGGVLLMGFMYYAVNKPFLDEETH"

CDS complement(4922654..4923640)

/locus_tag="EFAGFIKM_04304"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTQIKVTPEQLETVSGQFAQAHQQLSGFMSTLDGKMSVMRSNWD
GMERERFYNDYSTAQGTMKSVLELVLSIQSELKKIAERFRTTDEEAVSQAIMTALTA
RALSTMGKNKGDDLDKTPGPPKNMDEWDEKDAEKYQNYEEMLKKAKEMGDEELAAQQIQ
ASMNIIRLQYEDVIYQTDPN TGKTVKITEDSIVGTYQVKS DKGETTTISLDKQGNVVD
YSKDTEKYRYSEQTH TTSQGEHLFGKAAQTATAYGIGLLTSKTGS AFTEHATGLGSS
FVADKFLFSVPEEGETRTMIYRTNKDTGKIENMIVVTRGDNDIEYTPWREYF"

CDS complement(4923662..4923763)

/locus_tag="EFAGFIKM_04305"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLVAA YREQDHD KLVG IWE RAVRATHWLTTGYK"

CDS complement(4923918..4925486)

/locus_tag="EFAGFIKM_04306"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNIRWRDHPKRG MILLIAAVCCVGAGIWLILNRNEQSIPPIAE
KQTAAEVWLTG DQ QNLLTPQKPI PITDQHDADTSSSQVTMQSADTPSAEFTIQIDPD
KTYQTM DGF GAAMTGSSAHLINELPEEQQEQLLKELFTTEGLNMDMVRHTIGASDYSV
DESGVASSYTYDDIESGTDYDMEHFSIEKDQEVVNMLERVAGLKPDLKVLGTPWTAPA
WMKYGEKTTNGWYLDYNDPRVYEAYARYFVKYIKAYQTKGIPIYGITLQNEPEFTSDK
YPSMSMGAE EQAMFIRDYLG PALQDAGLDTQIIAYDHNWDQAVEYTSKVLGDEQAAAY
IDGSAFH CYAGDPSAMSEVYERFPDKNIYFTECSGGEWSPDFGENLSWQMSNLIIGAP
RNWAKNVLLWNIALDPQGGPTNGGCENCRCGVVTIDSENNEITRNVEYYALGHISRYVR
PGAVRVASTQE QGKIENVTFRNP DGMTVLVAANTGEAEVSFEVMSGDSFRYLPSQS
AATIRWKPKTEVER"

CDS complement(4925632..4928343)

/gene="xyl3A_1"

/locus_tag="EFAGFIKM_04307"

/EC_number="3.2.1.37"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:D5EY15"
/codon_start=1
/transl_table=11
/product="Xylan 1,4-beta-xylosidase"
/db_xref="COG:COG1472"
/translation="MNRRLNLI FLKRWFMLLIIVAVAAMPLHAFAAEAESGADRPWMN
TSLSAEERTELLLKEMTLEEKVGFVTGKVNNYYGFYNDGLERLGIPALQMADGPAGVR
VANPDVQDKKSTALPAPIALAASWDTNLAKKYGDLIGQEAHDTTHNVVLGPGLDIART
PWGSRNFESLGEDPLLASGMGAAYVNGIQSNPVIATAKH YILNNQETERFTTNATASE
RAIQEVYARPFQAMVEKANLGSAMCSFNQVNGTYACENKEMLTNVLRDQFGFEGFVMS
DYGANFSTAKSANAGLDLETPGEPYGKWGDKLLEAVNNGEVSEQTIDEKVRRI LLQMF
DKGLFDSPVTNTQINAKKD GKQAREIAEESMVLLQNNDNALPLSKKNVKSIAVIGPDA
DNASAAGGGSSLVNPTYTVSPLQGIRNRAGNGVDVKY AAGTDPISAGDAFNGPSAVPS
TLLSPADAQESERDYGTDRAEYGLRAEYWTNKDMEGNPSLVRTDNQVNMNLGFYNYEG
FNAQSSKLPVPTPKFNAKMSARWTGAITAPQTGEYKLSLTS LGS AKLYVDDKLLVDNQ
GETLSTTKKEITFKEGESHNIRIEYRTDFPVQTNHDMGAQVRFGWEAPEDAVIDIKMQK
AVDLAKKSDVAVVVTRTYDSEGYVDRSDLELPNNQEQLIRKVAAANPKTIVVQMSGRA
VEMDSWQKEVPSIVQAWYAGQEQGNAVARVLFGDVNPSGKLPVTFPSDDSQTPVSTSE
QFPGVNGVGN YSEGIFVGYKGYDKEGMPAFAFGHGLSYTDFNYRNLHVKN TGKGDKA
TVEVSLNLRNTGKVSGAEVVQVYVGNLPTKVETPEKQLAGWAKVDLKAGKQQRVNIQL
DRSALSYWDETSHEWVMPKGKVQVYVGSASDDIRLTGSV NIGSKSGK"

CDS complement(4928899..4933869)

/locus_tag="EFAGFIKM_04308"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNQEEQVQVYMDGLQERAKSLTGVQLELAGYVVEIAGSTYL RGD
EKMFLNTDKLLGRLAAETQKPLFQPLLDVLQHLASESLVARFRYIAERATRF PYSNNY
ERRPFRSDPEQHVEQVIRKLMGLFRMEMKNFSLEEYVSLREYKLDYLHEIRWVLADC

IAYELDHQGGDMKQALHDIYGDNQTALLTHEMIKGIFMSDQADAYQMVGELLVAARL
QEGLRQSIVERMDEGTLEAYIYILKIIIDNNLIRFSSVVRALAWWTGIGIEAANQRVA
AQLIEQAYQALVQPEVREAWQQEANANKLFISLWATAVIEENELKSKIIEIMDQGGQLY
QKIVAQYVLANSQNRELRLDIARRYLEAQDTELMHWIVTNYDAMMYNWSFENGENQR
SVYVWPLPALGEKALRRQDFDRFKQMLAAIPKGGSGGPSGVLEYVHYRIDTDDVVKKM
LYLAAYDMDPEWIGEVIKDRLSPELRGELLSQFVQHPDNEVQRQFVFESLSDKXIS
NRESALAKAKLLTLTVDEMKQMEALMKLKTGSLRQKVIHVLLLQPV DQLAVSLKRLLQ
AKSELQRLGALELLTEIAADPERIDQQEQLQPLAQLIETPTAKEQKLLDKLTDQGSRY
TASNGFGLFDPKRREPLLDEKRD LKGHNPKDIFTISLDKTRPFLEGLSELVHEHRDHE
YQVEYYAGYKDTLLVGASLRSKVPYGERNEMKQMEQFPLHDVWENYIQHAGFSSVELM
QLYMAIQLREFNGNLSDHYSYFREQYDYDELQKIPLLEGWRKSFAEQIYPLDDIEKLQ
QMLDSLTYKDQVVALISA AFLDSDPIDTFEIAEKTWASIIASMPADRLEKESGMLHIL
TGPWNYVVRGKI HDDNSFKRFFQTAYQFTSLVESSQPLSLLSLEDFLRAYQLNLIDDQ
EIYRQVLVGGNRLLFIRDLTSTRTEGIANDPKLIHLRDTVVRILEIELTRGELSTEV
STLAMKLERIEGMEHWVHLVSAMDQDTFVRGYIYSYGDNTTRKETFSYLIQNCHPRDG
EDEKRLGELLQKYPVNEKKLLEAAMYAPQWMEIVAKHLGWEGLRSAAWYFHAHINERF
TAEKETIVAHYSPI SPQDFNEGAFDIAWFEEAYA AVGEERFNLLYDCAKYISGGSNHR
RSQLFADAALGKLRLDDMRDSVSDKR NKDHLLTYS LIPFAVNREQDLRERYDFIQKFL
MQSKQFGAQRRASEGVASQIALGNLARNAGYADVTRLMWDM EARRLDEMKSFFEPHAL
DADTTAQLVIDEEGQPEMVIVSKGKALKSVPARFKKDG YIAELKELKSDLVDQYRRAR
QELERSMTAGTSFTRQE IARLMQNPVIYPLVRTLVFKSDDKTGRFDVSSSGLVAPGPD
GTIQALAEQDQLLIAHPLHLYQSGSWSEFQRDLFTRQERQPFKQVFRELYLPNEDELA
NGTVSRRYAGYQIQPKKAVALLKGRQWTVSYEEGLQKVS YEHNLIANLYAMADWFSPA
DTEAPTLETVQFYDRKSYKPVALQDVPLTFFSEVMRDIDL VVSVAHVGGVDPEASLTT
IEMRHVIVNESLRL LKIDNVRLDGNYARIDGELGEYAVHLGSGNVFKQATGALHIVPV
HSQHRGRIFLPFLDEDPRTAEILSKVMLLAEDKKIKDPQILAQLQN"

CDS complement(4933894..4934313)
/locus_tag="EFAGFIKM_04309"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MNVWITVKS LGKRKPV LAKQAAELPETHTLRQLIENMVALQVK
ALQDKKKQSELLAYLMPDDIEAQGAAGKVGFGAVYNEGV PDLNVAMETAITAYEDGLY
KVFLNDEELQELDESLVVKDGDNVVFIRFTMLAGRLW"

CDS complement(4934657..4936789)

/gene="nasC"

/locus_tag="EFAGFIKM_04310"

/EC_number="1.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42434"

/codon_start=1

/transl_table=11

/product="Assimilatory nitrate reductase catalytic
subunit"

/db_xref="COG:COG0243"

/translation="MGLSVSSEPTASKLYVKETQCPYCSVQCKMTVEELAAPVPGQRR
GEYTVQGV PNEASQGR LCVKGMNAHQHALSGQRLMHPLIRRNGELEPCSWKEAIQTIA
ERFQDLKDSYGADTVGVYGGGSLTNETAYLLGKFARVALGTKYIDYNGRFCMSAAASA
GSKVFGMDRGLTFRLSDIPKAGCIVLAGTNIAECQPTLLPYFNQAKENGAFIIVIDPR
KTATAAIADLHLQVKPGMDALLADTMMKVIMDAGLVNPHFIDERTHG YEQLIQGLADL
QLEQAAQACGVDLALIRQAAMAYGEAETGMIMTARGVEQQTDGHMAVRHFLNLVLATG
KIGREGCGYGAITGQGNGQG GREHGQKADQLPGYRSIENEADRAYVASVWGVDPASLP
GKGVSAYEMIEKVHDQEIRALLVMGSPVVSNNPVRLVEEGLRKLDFLIVADMFLSET
ARMADLVLPVTSYME NEGTLTNLEGRVLLREQGRPAPGETLDDWDILCQIAAQLGKAF
YFEYDTAEDIFNELRVASRGGVADYYGITYERLRNGKGVYWPCSALEDQGEGLLFGER
FAHPDGKAAFTFESSPGWNDISSEFPLILTNGRVLPHYLTGVQTHRSPALAARELENF
VELHPATAARYRIHDGEWVEIQSTYGSFTVRSRIKDSIREDTL FVPMHWGGIQNVNRA
TRPELDPFCRMPGFKTAAVTIRPLRLVR"

CDS complement(4936811..4938925)

/gene="norW"

/locus_tag="EFAGFIKM_04311"

/EC_number="1.18.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01313"
/codon_start=1
/transl_table=11
/product="Nitric oxide reductase FIRd-NAD(+) reductase"
/translation="MSRSKLVIIGNGMAGVKCVEEIELEPDYEIVYIGNEPRPNYN
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AQGLLFTDGSKLEAQVVIVAVGIRPNVDLARRSGIATNRAIMVDDYMRTSVPDIYAVG
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GEGMQTAIQHLDGIQGTYYKKVLMQAGKVRGAILFGDTTEGTALLGLVQRGADVAELAP
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IYAGGHAEHPVKQGGIGVAETEVQAATLASACLQWYRQTAWYDEPLWAWTERLGFM
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CDS 4939348..4940580

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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42432"
/codon_start=1
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/translation="MMESKSFWKSGHKPTLFGAFMYFDISFMIWGMLGPLAVVIALDY
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ATHFGSWEVVFG LAIIPIVIVFILFSIFAKNSPNRPEPKLSQYGSLLKQKDAWVFCA
FYCVTFGGFVGLCNYLTIFFNTQYGLSPVRAADITTF CVIAGSFVRPVGGYLADKIGG
TRMLTFLYTGACVMLIGVSFMPPLPFVVVMLFLGMMCLGAGNGSVFQLVPQRF GNEIG
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CDS complement(4940710..4941948)

/gene="fabF_2"

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/EC_number="2.3.1.179"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P73283"

/codon_start=1

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/product="3-oxoacyl-[acyl-carrier-protein] synthase 2"

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CDS 4942087..4942950

/locus_tag="EFAGFIKM_04314"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNYDVRLQALSTFLKTQRSKISPESVGLPTGSRRRTPGLRREEV

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LLFDRKEFRRLAVNWEDFVSGFLAIFRAYYGQYVDDEWYNLFLDDMMNRHPDFHTLWK

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EREADPHLGKH"

CDS 4943085..4943759

/gene="regX3_4"

/locus_tag="EFAGFIKM_04315"
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/inference="similar to AA sequence:UniProtKB:Q9F868"
/codon_start=1
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/db_xref="COG:COG0745"
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SMQELKARIEAVLRRYSILNSSVVTEQESGISLDLARRTVLLNNQRVEMTFSEFEIMK
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GYKFTP"

CDS complement(4943781..4947005)

/gene="rcsC_12"
/locus_tag="EFAGFIKM_04316"
/EC_number="2.7.13.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00979"
/codon_start=1
/transl_table=11
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/translation="MLRDLVLNFTLILIFVFLIHLYLNHTNATRSTSITTRIIIGITL
SMLGTALYYFSIVLEDGTLNFRFAIVYLLAAYFGGSGSAFVTFTFMWMFRINMGRNPL
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EYLVLEGEMLSRLGLDMSSLKQDYKLGTLDPQEKVEFLRKQFNRAWEGESFFYEIE
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TELSFIVGEGHEQHVRVHLSPVKVLNSSEKIKAVIHDISDHYRRVKADKASQAKSEFL
AFMSHEIRTPLSGIINFSLLLQRTDLSPQQKDYLSKINASSQTLLALVNDILDFSKIE
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EPSTYRTYGGSGGLGVICYLLVTSLGGSLRVDSVLGEYSLFSFDLIFELADSEEESSF
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VSSMLMMMDMDAEETVNGSSWDSFMKRLNRTKFQMGYTHAFSENALWSEERSFRPDL
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PIIALTANSLKRDHELYLEAGMNAILTKPIHEQQLADILEIWIDLKGIREINGIDADK
AIRQMDGKPHILQYALTFRMEYGLFQKKLAIQLQQQIADAIRSVHSLRGVAANLHA
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CDS complement(4947199..4947504)

/locus_tag="EFAGFIKM_04317"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MQLELKAFLLLTDAVMITDEEGVILDVNSVYVTKTGFSRESTIG

QPARLLMDTHWRGNQTSWGVAKLMKVDQEVWEAQVTITSVHLDDSLFYISIFNDEFS"

CDS complement(4947577..4949574)

/gene="mcpA_2"

/locus_tag="EFAGFIKM_04318"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39214"

/codon_start=1

/transl_table=11

/product="Methyl-accepting chemotaxis protein McpA"

/db_xref="COG:COG0840"

/translation="MSRKNSKSTWFNKMHNFKTKLVVSFIAFLAIPSLSIGVLSYNS

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YVSAETKEITITIAKALEDQSGVVQLDLNLADISQLVSAIKVGEKGHILLDASEKYI

YHPTMEPGTDATEDFWTQVYTNESGNFNFTDQVDKVMYYATNESTGWKVAGTMFSSE

VEDAAAPILNRTIMVIVSFLVIGILIIWLMRSIVKPIRQLKVQAIQVSEGLTQTIT

STSNDEIGELSEAFGKMQSNLRVLIQNVENSASQVVISSDEMTQSAESTSAASEQVAR

AIQEIASGAEKQTEGIEHNNHQAMNEITIGITRIAERSIHVADLAKHTTVQAEEGGNTV
KQTVSQMQSIQETVEQTNQLIQALYERSHQISAITELIGNIAKQTNLLALNASIEAAR
AGTHGNGFAVVAAEVRKLAEQSGQSVNEITVLTAVQEDMAASVRMMEKVTSEVGEGM
DSTEAIRKFERILDSMRETPQIEEIAATSQEITAGVQEVSAVSNELAGIASGNAAT
SEEVAASSEEQLAAMEQISSSARGLSTLAEELQRLIRQFKY"

CDS complement(4949999..4950838)

/gene="metQ_2"

/locus_tag="EFAGFIKM_04319"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P28635"

/codon_start=1

/transl_table=11

/product="D-methionine-binding lipoprotein MetQ"

/db_xref="COG:COG1464"

/translation="MKAKMMLMLLAVMLVVAACGKKEETPAAEGTKEDTQAGQEVTLK
VATLIPPMTDVLDIVKPLLKEDGVNLEVVVLSDNVQPNTALANKEVDANFFQHVPYMT
QYNEANNANLVAVQPIYNAIYGGYSKKYKTIEELPEGATVAIANDPSNIGRSLVMLEQ
NGLIKLKEGVGFNATQADITENTKNFKFEEVDLLMLARMMDDADLVAMTPAYASPLGL
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AFK"

CDS complement(4950903..4951574)

/gene="metI_3"

/locus_tag="EFAGFIKM_04320"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P31547"

/codon_start=1

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/product="D-methionine transport system permease protein
MetI"

/db_xref="COG:COG2011"

/translation="MRLPESVLKYQHEIWQAIGETFVMVGISIAAAVLIGLPLGTLLY
LFRRGQRYQNQTLSTLGSVNVNIVRSFPFLLLVFMIPFTRIVVGTSIGTLAATVPLS

VIAIAYARLVEQALLDVPRGVVEAAASMGASTMQLVVKFLYVEARSGLVGLTTATI
SFISYSTVMGIVGGGGVGDFAIRYGYQRFETEIMVFTIIIMIILVQMIQFTGSRLSHW
LDRRS"

CDS complement(4951571..4952380)

/gene="metN"

/locus_tag="EFAGFIKM_04321"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32169"

/codon_start=1

/transl_table=11

/product="Methionine import ATP-binding protein MetN"

/db_xref="COG:COG1135"

/translation="MISLYGVSKRYIERGSRADQGFEALSSVSLEVGQGEIHGIIGSS

GAGKSTLLRMLNGLEKPDDGEVVVNGQHLLTQMNEQSLRQARRSIGMIFQHFNLVSNRT

VSGNVCMPLELAGISRTQRVERGLEVLRFVGLDKTDQYPAQLSGGQKQRVAIARALA

SRPDVLLCDEPTSSLDPQTNGILDVLRHINETLGVTVVTHEMEVARRLCHRISVM

KDGRRLVRTLSKAEVSSIPAPQPDLLTSLLAGDEYGLAGSSLFRQAEQEDKS"

CDS complement(4952512..4954815)

/gene="bamB"

/locus_tag="EFAGFIKM_04322"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00923"

/codon_start=1

/transl_table=11

/product="Outer membrane protein assembly factor BamB"

/translation="MKTGPDWQRTGYKWITMTGLSAVLLTGWMLLD SKMVVLGGQALA

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TTWSSEKSLTDKAVIVAKWK GYGVSIAPRVWDKESFTYRPG LFWIKAQAEQRMNVA

DGWFQQDASLPTSVIRHLTDI KLNKATTSKQVAGWLGE PDWKESSNLNFTGYSMSIG

QTWRYEREDAQFLVTFNKNG RLVRTRWNLAQDNRNAV VSDWNISR ADEYGF TTKIYGT

TLPTTIPWKPVWTNQGDIYNTFLQAATDDVLLMKGDDGGFSGDYEGSIYALDRHSGQ
QLWGINGGGFGRQQAQAEVDAERKYVTIYTDYDPDKKKYVDRIRHLNLKNGKVTWTYTPKQ
NFRLNGITAANKNVVVVDNPVVESSNSWLTVLDSANGKTLWTRKLTGYELLNKSADD
PYVLYWEKNKLVAVDPQSGRTVWSLKGKRSTIEQFWNDPYTGGIERLDPFATTNAERW
LSLDNQWLLLDLNTGKKLAQFPARVGQRFEELNDGMLLIRENKNKGHDHYGEYEDFTTTL
YDAKTGKTRWTLKGKIERGLVEEDQLYVIKNGYPAAVDYKTGETRWNAKDTIATLRHP
TNQGSYLVIDDQLLLPMDENLLVMNKKSGALLGRVHDVVMGNPEHRDRDAKNGTINRI
GNEVYVGSSNGRFRLYEASRLQEAIISP"

CDS complement(4954917..4955711)

/gene="ykoC"

/locus_tag="EFAGFIKM_04323"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34572"

/codon_start=1

/transl_table=11

/product="Putative HMP/thiamine permease protein YkoC"

/translation="MQLSFPHRETWLHNVNPGGLKMIILTMFMFVIVILIHNLNVMANVA

VAMMLLLCWTGHPWYRLMLYASPFILVFISTSTGMMMFGKGETTWWYKWGLIHTEESF

YRGLHLGFRSLMAAAGLLFGLTTKPVRLFYSLMQQWKLPKYAYSFLAAMRMIPILL

DEFQTLRYAIRIRGTQQRGSRWNVYGTALKRYAIPLLAQSIIRRAQRMVAMEAKGFTDG

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CDS complement(4955686..4957257)

/gene="ykoD"

/locus_tag="EFAGFIKM_04324"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34362"

/codon_start=1

/transl_table=11

/product="Putative HMP/thiamine import ATP-binding protein

YkoD"

/db_xref="COG:COG1122"

/translation="MNGEGNSQAVSVTNLRCKFPGEKALVFQGLSLSVRQGEKVLLLG
PSGSGKSTLLQILSGLIPRSVEIPMKCDDIQVPAKAGVVFQDPDTQFCMSFTDEEIAF
VLENRNILREEMPALIEYYLKQVGLSFEQNRVLIQSMSQGMKQRLAIASMLAMDPEVL
FLDEPTALLDDEGTSQVWDTVKRIASDKTIIIVEHKINKIVDMVDRIVLSTEGKIVA
DGPAQQVFTDERGKLKAYGIWYPGWDEHEQAAKEEEGSTSGELQVCVDHGISSLEAQ
QSSGLSDTTGISPISHVSSLSPVSPAYLPALDLQQFTGWRGKTPFIQVEQAKVWHGDW
IGIVGANGAGKSSLLLSLMNILKTTGLYEVDGQPSGKTEQLADRIAFVFQNPEFQFVT
NTVAEEVEFSLLGGRLTTEERLARTDHMLNQFGLIDLSEHPYQLSMGQKRRLSVASA
LVREQRILLLDEPTFGQDARNTFAMLAQLEQLRREGTAIVMVTHDCEIVKRYCTRIWT
VGEGRLTDATVVSSP"

CDS complement(4957258..4957851)

/gene="ykoE"

/locus_tag="EFAGFIKM_04325"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34738"

/codon_start=1

/transl_table=11

/product="Putative HMP/thiamine permease protein YkoE"

/db_xref="COG:COG4721"

/translation="MATTAGNKRLKLTDLVTIVIAVVFQVYKIWGPTYDLMKPFQV
HAEQMIYGMWFMAGTFAFVIIRKPGVAILAEVAASTVSAFLGSEWGMSTLVYGLLQGL
GAEIFFAAFLYRKTNLFVTCLAAIGAAAASLLLDYQYGYIDSLSAWNYTLFIGFRFIG
SILIAGVFAYYLAKALELTGVTRSLRPVSKQDYELD"

CDS complement(4958487..4959155)

/gene="pelA"

/locus_tag="EFAGFIKM_04326"

/EC_number="4.2.2.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9X6Z2"

/codon_start=1

/transl_table=11

/product="Pectate lyase A"

/translation="MKKMLTLLLSAGLVASIFGAVPAAAAPTVVNSTIVVPKGTTYDG
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WEDVGEDALTLSAGTVNITGGAAYKAYDKVFQMNAAGTINIKNFRADDIGKLVRQNG
GTSFAVNMTLDNSNISNVKDSILRTDSSTSQGKITNTRYSKVPTLFKGFASGKTSQSG
NTQY"

CDS complement(4959506..4960381)

/gene="moaA_2"

/locus_tag="EFAGFIKM_04327"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01225_A"

/codon_start=1

/transl_table=11

/product="GTP 3',8-cyclase"

/translation="MKTFKKVYIEITSICNLACSFQPTQRAKGFIDPEVFNNILDQV
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QMNFSLHSFDGHEGSTDRDGYLRHILSFVHEAVKHNVIIISFRLWNLTQDNFTNAQMNR
NRETLEVLEREFNLDRIEEKVVPKSGVGIAPNVYLNQDHEFQWPSLDAPEDDGKGF
HALRGQAAVLVDGTVVPCCLDGEGVINLGNVHEKSFSEIIIEGERANNLVYGFSKREAV
EELCRKCGYRQRFGA"

CDS 4960860..4961624

/gene="cmpD"

/locus_tag="EFAGFIKM_04328"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q55463"

/codon_start=1

/transl_table=11

/product="Bicarbonate transport ATP-binding protein CmpD"

/translation="MRNHVTIENVSFAPPEKKDSPVLANVSLQVQQGEFVSLIGSSGS
GKSTLFKLLAGLHEPTVGTIDIADVPPQQRLGRVAYMPQKDLLLSWRTVMENCMLPSE
LAPGRQDKDKLRANILAGLARFGLSGYEQAYPDELSGGMRQRVALLRTLLTGGQLMLL
DEPFGALDALTKREMRWLLELWEGFGQTVLFITHDIEEALLSDRIILLTPGGQGGQ

LREMTVPLPRPRHSDMIYELALVQMRQQLEEQ LHAK"

CDS 4961614..4962432

/gene="ribX_2"

/locus_tag="EFAGFIKM_04329"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A9WGD1"

/codon_start=1

/transl_table=11

/product="Riboflavin transport system permease protein

RibX"

/translation="MQNDRAEVSVWTWCSKWFSQYGLFILLMFLLLAIWEVIVRMGWV

PSFIIPAPTAIAGSLVEHRHLLTIHLPATFMEVVVGFVLSIVTGITLATGMHMNRSI

EKALYPFIVISQTIPLIALSPVFILWFGYTLWSKVAVVFLIAFFPIVVSTYDGLRQGD

PEQRELLLTMGASKWDIFRKLQVPLALPSFFSGLKMSVVCVVGATIGEWLGGSKGLG

YFSRRMSSNMNTDAMFAAILLSLLGIVLFVLIAWLEKRFSLRRHGHGGKRKVG"

CDS 4962486..4963559

/gene="thiY_1"

/locus_tag="EFAGFIKM_04330"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9K9G5"

/codon_start=1

/transl_table=11

/product="Formylaminopyrimidine-binding protein"

/db_xref="COG:COG0715"

/translation="MNNKGIYSLLPIVLISLLLIVSGCSTTNTSKNTPTTDSATNEQQ

TDKSATEPASNAKDKLSIMLDWYPNAVHSFIYVAQEKGYFADQGLDVEIQMPADTNDS

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GKTVGYSSIPLYEAMVRTMISHDGGNPDNMNLVDVGFDLIPSLASGQADAVMGGFINH

EQLILEKEGHAMKSINPVDYGVDPDYELVLTASEAGIEAKKDQLTRFVKAAQEGQKYV

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CDS 4963726..4964538

/gene="thiM"
/locus_tag="EFAGFIKM_04331"
/EC_number="2.7.1.50"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39593"
/codon_start=1
/transl_table=11
/product="Hydroxyethylthiazole kinase"
/db_xref="COG:COG2145"
/translation="MSYLERVRTQNPLVHNITNLVVPFTANGLLALGASPFMAYAHE
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TGKEDIITDGQSTFLTSNGHALLTQVTGAGCLLSSVIGAFTAIAESGADLIGSIVEAL
AFYGVAAELAAERTAHQGPGSFQIELLNQLAQVTPDLLAERAQIRQIRGGAV"

CDS 4964535..4965347

/gene="thiD"
/locus_tag="EFAGFIKM_04332"
/EC_number="2.7.1.49"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31620"
/codon_start=1
/transl_table=11
/product="Hydroxymethylpyrimidine/phosphomethylpyrimidine
kinase"
/db_xref="COG:COG0351"
/translation="MSIAQALTIAGSDNNGGGAGIQADLKTFQELGVYGMTVITAIAAQ
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VIDPVMVAKGGAPLLQQEAVKALVTDLLPHALITTPNIPEAELLTGMSITNLSQREEA
ARRIVQMGSTYALVKGGHDEGSGMIVDVLYDGQSFHYLENVRVVTRHHTGTGCTYSAA
ITAELAKGSPVLAAVTTARAFIQAAIEDELGIGAGHGPTNHFAYQRRQRGEQ"

CDS 4965347..4966012

/gene="thiE"

/locus_tag="EFAGFIKM_04333"

/EC_number="2.5.1.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39594"

/codon_start=1

/transl_table=11

/product="Thiamine-phosphate synthase"

/db_xref="COG:COG0352"

/translation="MRPWDAEAVRRAMQVYLVMGSVNITQDPVEVLRQAIAGGITLFQ
FREKGTGALAHEARITLAMRLREVCSQHGVPPFIVNDDVELAVAVEADGVHVGQEDADA
LLVRARIGDGRMLGVSAHSVDEARRAVQAGADYLGVGPMYPTRSKADAHAVLGPAGVA
ELRAACIAVPIVGIGGITPDTTAAVMAAGADGVAVISAIAGAADVRAAAQFAAAVRG
MQA"

CDS 4966333..4967076

/gene="mta_2"

/locus_tag="EFAGFIKM_04334"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P71039"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator mta"

/db_xref="COG:COG0789"

/translation="MAMKVKEVTELASISVRTLHHYDEIGLLTPDEVTSAGYRLYSDA
NLERLQQILFFKELDFSLKEIKNIITDPSFNPEEALNMHRLILLEKRQLDQMIATID
RTVLHVRGEIKMTAKEQFEGFDFSQNPYEQEARERWGDHAVDHANQKLHKSSTTDQKA
LSDQMNEIYKHLASLRHIEPASEEAQAGIKEWFTWLNQMGSYSPEAFRGLGQMYVDDE
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CDS complement(4967616..4968098)

/locus_tag="EFAGFIKM_04335"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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IGALTGYAVVLFSNKQIATVHKIIAVLFALVGILLGKYLTVVYFTSELFQDVSMELV
FDSEMISAFVETFQEYFSQPIDLLFIALAIVSAWQIPGRMARTSLATDASSSDHAPRA
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CDS complement(4968238..4968396)
/locus_tag="EFAGFIKM_04336"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MYFLGYIGYIDTMDNIPYTAIMLLEGCFMCQGNDYEMVVDK
TKMIYSSE"

CDS complement(4968415..4969071)
/gene="dck"
/locus_tag="EFAGFIKM_04337"
/EC_number="2.7.1.74"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37529"
/codon_start=1
/transl_table=11
/product="Deoxyadenosine/deoxycytidine kinase"
/db_xref="COG:COG1428"
/translation="MNNYGIPTNALITVAGTVGVGKSTLTAALAQRLNFKTSLEQVDH
NPYLEKFYHDFERWSFHLQIYFLAERFKEQKKIFELGGGFVQDRSIYEDTGIFAQMHA
DQGTMSATDFETYSSLFEAMVMTPYFPHPDVLIYLEGSLPSILNRITERGREMEIQTD
RSYWEHMHERYSVWIDQFTACPVRLRNIDEYDVHDPASVDAILAQIAAVIQPSKEVQR
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CDS complement(4969068..4969700)
/gene="dgk"
/locus_tag="EFAGFIKM_04338"
/EC_number="2.7.1.113"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37530"

/codon_start=1

/transl_table=11

/product="Deoxyguanosine kinase"

/db_xref="COG:COG1428"

/translation="MNTMKSAPFIAVEGPIGAGKTTLATMLSHLNLPLVKEIVEENP
FLASYQDIDEWSFQLEMFFLCNRFKQLEDTGVDHYEQNTPVISDYHIYKNMIFADRT
LKGTKRDKYRQIYHLLTDDLKPNLVLYIEAELDTLMYRINKRGRSFEQDMDPAYMEQ
LITDYKTGMDYLANSSNPPAIIKVNAEQQLDFVEHPEHFRQIVNQVKEYII"

rRNA complement(4969907..4970018)

/locus_tag="EFAGFIKM_04339"

/product="5S ribosomal RNA"

rRNA complement(4970103..4973023)

/locus_tag="EFAGFIKM_04340"

/product="23S ribosomal RNA"

rRNA complement(4973332..4974882)

/locus_tag="EFAGFIKM_04341"

/product="16S ribosomal RNA"

CDS complement(4975587..4976762)

/locus_tag="EFAGFIKM_04342"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKSFKDFLKVPQTKIGLVFALIVPLLFFVIWMTGYHQATERVDQ
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ELSAAIGQAMAKMNEGPVKAIEINKTNSVSDFATSMILGFIYIASMTMNIQFNIT
SNIMKRTHSKWEIFWGRQLLLLCIALIVPLIVDTVALQFTDVASSFGALVYHVLVSL
ACICFTQMSFALFGNAGPLFNVAMVPLQLMTAGNIIPAEMLAPFYRYIGNFLPASNGV
QGFMRLIYSGEAVGGYMHVHLLLSIITWAITLLRVGMQKAGNGQMTMTTPASAQAQH"

CDS complement(4976843..4977274)

/gene="mhqR_2"

/locus_tag="EFAGFIKM_04343"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31672"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator MhqR"

/db_xref="COG:COG1846"

/translation="MPVNMMDKNPLGQILSRITYLAYKKTTTRNLSEQDITPEQFAVLNE
LSKAGSHISQKKLAELTVRDQTTVGKIIDKLIRKGLVTREEDPQDRRAVLLCLTAEGL
EMNNDLTPKAKQQEQEALAECSPEELEAFMNMVMNRIYEKMK"

CDS complement(4977440..4977607)

/locus_tag="EFAGFIKM_04344"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSNAKGKGGTGRGTGKKGWNRWQAAANRAKSAPKPYKSKGTKKK
DDTETSSGKPE"

CDS 4977920..4978780

/gene="licT_7"

/locus_tag="EFAGFIKM_04345"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39805"

/codon_start=1

/transl_table=11

/product="Transcription antiterminator LicT"

/db_xref="COG:COG3711"

/translation="MIIRQIFNNNVIRAKNQVGHEFVVIGNGLGFKKKNGQPVEDDKI
EKTFVLKSDKIPQKLIDLIGETSVEYLKLADEIVGHAKQEMGDIFSDNIYISLIDHIQ
FAITRYRKSVGLKNSLLWQIKKFYKKEFGIGMNAVELIQEQFGIQMDEHEASFIAMHF"

VNARQDAQGMKQTVEITEIIDIFNIVTNHHHIALDENSFNYSRFITHLQYFVQRMLS
NEQEQFASGDNFLYEQVKDKYSNAFECTQRINQYLEERFESALSIDEKVYLTIHIQRV
TSRNELLDTE"

CDS 4978965..4980860

/gene="bglF_10"

/locus_tag="EFAGFIKM_04346"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P08722"

/codon_start=1

/transl_table=11

/product="PTS system beta-glucoside-specific EIIBC
component"

/db_xref="COG:COG1263"

/translation="MDHKKMGGDIVRLVGGEANINGLVHCATRLRFDLKD
SKKAERETLEKHDGIITVVESGGQFQVVIGSNVAHVYAEIMKNRDFG
GDSSSSAESTGEKTSLSKVFIIISGSFSLIPAMAGSGMLKALLTVL
TMLGWMSDTSPTYLILSAAGNAVIFYFLPIFLGITLGMKLANPYV
AGVIGAALMEPSFTGLMDKGSDVSFLGIPVVMNYSASVFPIFISI
SIYAVLDKLLKKIILKDLQLFLVPMIALMIMVPLSAMAFGPFGT
TVGDWISSGVTWLIGVSGILSGVVLGGFMTFMVVFGLHWGFTPI
TIQNIQVGGDPIEAMAAAAVFAQIGVAFGIFLKAKKNKTLRTL
AGSTSLTGLLAGVTEPIVYGLILRYKRVIPVVIAGAIGGAINGH
FGVKMTAYVFHNIFAIPVYTPTVVYVIAIACSFVAVALTMFGY
ESKTKDTVSETNESVSTSAESTPAELPVVLETKTEIKKEQIYSPL
TGTAVASTINDPAFSTGAMGKGLAIVPEIGEVVAPVDGVITSLFPT
GHAIGLTTNAGTEILHVGINTVALKGKHFSPVVQEGDIVRQGDLLI
QFDIDKIKEAGYETVPVIVTLTQQEVDVFETTQAQVQKNDVLL
TLVV"

CDS 4980903..4982312

/gene="bglC"

/locus_tag="EFAGFIKM_04347"

/EC_number="3.2.1.86"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42403"

/codon_start=1

/transl_table=11
/product="Aryl-phospho-beta-D-glucosidase BglC"
/db_xref="COG:COG2723"
/translation="MKHTQLKPFKDFFWGGSTSAYQIEGAWNEDGKGPSVIDMGNHV
EGVTDFKVTSDHYHMYKEDVALLAEMGFKAYRFSIAWTRIYPQGAGEVNPKGGLAFYDS
LINELIKYGIEPIVTMYHFDLPYALEEKGGWSNRATIDAFEQYAKTLYENYGDRVKYW
LTINEQNMLILHPGSLGTLDTTLVDPQKTLYQQNHMLVAQAKAMVLCHEMLPEAKIG
PAPNIGVIYPASSKPEDTLAADNYAAIRNWLYLDMAVYGRYNHIAWSYLEEKGYTPVI
EDGDMDILAQGNPDFIAFNYYTSQTVGESLNDGNDFSHTGDQHEIVGEPGAYRGSVNP
NLQKTEFGWEIDPVGFRSTLRQIYSRYHLPLIVTENGLGAFDKLEEGDVVNDPYRIEF
FNKHIEQIQLAITDGVDFVFGFCPWSAIDLVSTHQSSKRYGFIYVDREEFDIKELRRI
RKQSFHWYQKLIETNGEIR"

CDS complement(4982414..4983634)

/gene="tetA_3"
/locus_tag="EFAGFIKM_04348"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P02981"
/codon_start=1
/transl_table=11
/product="Tetracycline resistance protein, class C"
/translation="MALLTRNRGALLLLMFNIFLVFTGIGLVVPIMPAYMDLLHITGF
TVGLLVAAFSFTQFLFSPLAGRWSDTWGRKKIIVGGMLIFAVSEFMFGAVNAPVLLFA
ARMLGGIGAAMIFPAVMAYTADITTEEERGKGMGLINAAITGFIIGPGIGGYIADFG
IRIPFYAAGIAGLLASIITLIILPESARSTGEQSKPIPLTKVKAPGMVSQLLNSYRE
PYFFSLIIVFVMAFGLANYETVFSLFVDHFKFGFTTKDIAFIITFGSIAGAVVQVSLIG
WLLNRFGEKMVISVCLLFVAVFVLLTLFVSTYWMILVVTFIVFLGMDILRPAISTQMS
KLAQEQQGFVAGLNSAYTSLGNIAGPIVAGALFDVNINYPYVSAAAVLAICFLLSLRV
IRGAKAVKQPKAEM"

CDS complement(4983667..4984272)

/gene="qacR_2"
/locus_tag="EFAGFIKM_04349"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A0N5"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator QacR"

/translation="MNMNKKQLQTEQTKKKLADASKALFVQKGYKATSIEDIVAATGS
SKGNIYYHFKSKEGLFLYLIDEWDREWEESWAAKEHLYHTSTEKIYGLAEQLVLDDMN
HPLTKAADEFFTGEKKENDIEERISLMFERHIQFNKQMIEQGIESGEFKADNVDNLAL
ILESTIIGLSQMSRGMEDQALALYRQAASVFLHGIANDKA"

CDS complement(4984413..4984832)

/locus_tag="EFAGFIKM_04350"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVAIRAKQIFVNLPVQDLKKSVEFFTKVGFEFDANFTDESATCM
IIGENIYAMLLVEERFQSFISKKISNAADTTEVIVALSVDSREQVDVIVQAALDAGGK
PSNEPQDHGFMYGWSFQDLDDHLWEVSYMDLSAFPSE"

CDS 4985111..4985461

/locus_tag="EFAGFIKM_04351"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKNKINYADFYERVGRNGWNFSSMNLVSENIGWNFYDEVVRHT
RTSDLLLDIGTGGEAIIAEDALLVGIDLAQGMIIETAQHNLQTTGGHSNVRFLHM
DAEKLAFLLISSLM"

CDS complement(4985979..4988066)

/gene="pbp"

/locus_tag="EFAGFIKM_04352"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P07944"

/codon_start=1

/transl_table=11
/product="Beta-lactam-inducible penicillin-binding
protein"
/db_xref="COG:COG0768"
/translation="MKSKRKLMYGLLPILFAGGIGMYLYMQNNKEAEAKPQTTVNQYI
EHLQKKEFDQLYTLMTPASLQESGMNKEQFVEKYNAIYSGMEVSTVKVAVKPVDAET
TSDGSKTDAEKQNPDMYEVDYNLQLTTFLGEVSEHTLKLVRHELEDGGKNWQINWQP
SLILNDMVKGSKVRVRTLPDRGDIVDRDGLPLATKGMTNEWGIVPEKLGDNPDQMIA
RIASHYQVSEDAIQKALAQTWVKPEYFVPIGSTEEFDVPESLSGVTMQSKEIRYYPLG
NAAAHLIGYVRKATKEDLDKDEGYRAEDWIGKAGLEQSMEKQLRGERGGLIEITDE
SGNSRSELIRKDAVDGQNVQLTISSKQKKLYQTLSSGGDAGAMVLMPTDGNLLALV
SAPSYNPNKMVTGLTQAEWDAYSANEKLPFINRVTRYAPGSTFKAITAAAGLVEKVT
TADKTHDISGLQWRKDDSWGYYVKRVKSLSPVNMVDALVYSDNIYFAMEAIEMGSAK
FIDGIQKFGFGDNFGLDELYLKSSQYANEHLDSLSEVLLADTSYGQGEMLMSPIHLA
SSFTPFINEGKLVKPVLIEGKESTDPEVIITPEAANTVKDALGEVVSRRQGGTAHTLNS
IPGGLAGKTGTAELKAKKGEKGQENGFFVVFDTDSPTFLLSAVIEEVNRRGGSHYVVD
KLKPFLEKLEITQ"

CDS 4988244..4988648

/locus_tag="EFAGFIKM_04353"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEISYFLLPKAEVAYIKSTASMKDAIEQLESQHYYTAIPVIDQDG
KYVATLSEGDLLWKMRNTPGLTFDTMDQVQVHEINNRVYNECVFIEAEMEDMLTLAAD
QNFVPVVDVDRVFLGIIRRKDIIEYYTRNISR"

CDS complement(4988750..4989190)

/locus_tag="EFAGFIKM_04354"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MKDLTPEHAELERQIVETVEAGNVLDETQQHEQALVYYDQAWGM
LPEPKMEWEIASWIASCHANAHIDLKQYGLAKPWAEISLSTRSSDRSTSPLIDLGMIC
MRLEQHDEAYSYLHQAYEFGRERAFQGSPRDVLSYYIDERAKRK"

CDS complement(4989187..4989636)

/locus_tag="EFAGFIKM_04355"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLSNKVIDHCQEQQWWHEDVPAAYEEALRKLGIDLQSDFAQFYL
HAEDGPTFYSRHQELYQICWFMENVYMEDMDVAQLTLGLPEAYIPLDSFEGEGGFFY
NRQTGEVVLVELGESIERFLNGESEPQWADFNAFLEWYFVLEEETVQ"

CDS complement(4989662..4990210)

/locus_tag="EFAGFIKM_04356"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGQCFHEWVMENRAPYRSRRGVHLMNVNEHVIEQQSLTFVGIKR
TFSCVDGENLIEIPKMWQDALADGIEERLNGFNNGAIPGLVGICVDQRELKDNQMEYW
IATSYSGDVPEGLVSIELPASHWVVFEADELEPEAIQRLWHYIMTEWFPSTSYQHAGI
PELEVYKGDGTPPQVWIPVKS"

CDS 4990484..4991086

/locus_tag="EFAGFIKM_04357"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRITCSPGFPGSMIGSIDLQPLKYYSAPSMNSKITDYVDPELIT
IPYVEDPEFGLHFDAMKVMNGTYKDEMHVSYDVEFTIDVDKQGYITQFEHTFQLERYL
DLVRTQSYKVIKTNWRGQTFHVMTYSYLEEVIHPKNVLFKCNLAEDVFVVGELVSNRS
DESATEHGIRDLHFRALISARDDLYPLDYMCEPDFDLSLD"

CDS 4991462..4992442

/locus_tag="EFAGFIKM_04358"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNDSASNIDRLGHRRWILSPQLQRIGFGLATRSEAGKTYDQYY
SAMQVFDKSRTGGTSFNYSLFPNQGAFFIEAFGSTQAWSVQLNTDVFAPSLSEVQVE
MTRTSDQRTWTFNAKNQNSGFPTGYNVDPADKQWFNQAYFNVETGGYGYGYAIIIFRP
DDVQLLKNGDTFNIRITGLQKKNGTAAEISYSTRFFHVDGVQDRTLTRITPGQPNLKV
RVGEQIDLPSITAVNDNGTSYVPQSNVSFTTSDRIAIDGKVIQLQNGKAEIRIRFE
GKEAFVSVTVTGIPQLTVSIHIGRKMPFNGPFNRRWSVDTRMERSNPTIR"

CDS 4992394..4993188

/locus_tag="EFAGFIKM_04359"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVSGYEDGTFKPNNQVSEAEFLSMLFKLYANSHVIQSIDAVEGQ
AIKGDWSDRYTYASALNLKLDASKQNPKLNRHALNRTEVAVIVAGLGGKNYTQDED
AIRYLLNMGYSSGKTAATVQGYAGQESLTRAEEVFLQNLKEKGFELWSRPKNATEAT
ENEKNGGLPDQTMKAVYSADHTLVLQGTFPAYANQTMPIKIHGSPAVEHIQTQQVTT
DAYGNFKLTLSNLDVKELNLYVDVREDYSYWISVEAGRTAISDYTE"

CDS complement(4993332..4994318)

/gene="thrB_4"

/locus_tag="EFAGFIKM_04360"

/EC_number="2.7.1.39"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00301"

/codon_start=1

/transl_table=11

/product="Homoserine kinase"

/translation="MLKLYLFQHNDLAEMILNNWSYDPESLDMFQYYRISSNAMYPF
RDQGEVRLRFAPVEEKNQINLSAELDFRLRLTNQYGAMEAVPSHSGTELVEAYTPW
GTYVASVFKRVPGSQLG SINLND SILYSYGQALGELHHLSRAFMPEQKEKRWTYTDVL
DWMQEILKGFPGETAALNEVEFLQTYFATWPITQQNFGLIHYDFELDNV FYDEGSQSC
YAIDFDDSMYHWYAMDVEQSLDSLREEIEPEQWEQKKQLFLNGYWSKAGERYDLESMF
PACRRFANLYGYVRMLRSVAEQWSHEPEWMSGRLRARLARIMTEKAEQFGHP I"

CDS complement(4994727..4995275)

/locus_tag="EFAGFIKM_04361"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRKNKYFTSVTILLLLVCSVMLTACDVITAQNITKTGSAQGMNG
GGMPNGGGLGMNGGT PRGGRG TAGMNDRTGSPGMTQGMMNADITGRVISVNGNTVTLA
LLEVQDTSSPSMEWKDTG MEMKLNIGDDVAITEGMGTPGSGNSSPRANWSIQVSDLQK
ENIVMVWYKDNTETVERVMVVQ"

CDS complement(4995280..4995603)

/locus_tag="EFAGFIKM_04362"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MITEVLQGDSAYRTG LLWIVYVMNFLMYCFIFIRLVGGLRRKRY
DEVSLILVILGFIGFYILWEIKSRYIYPVYPLLVL SYMGFKDTYDFIFHRKGT LERY
SLRKR"

CDS complement(4995600..4996862)

/locus_tag="EFAGFIKM_04363"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKVLHKS FYLILLVFVAVFIASSLLVRAQYNYALYGDNPILGM"

QQWSIFLPVILLLLGSGVGLYALCLKLNKYSPKVVIPIVLLCSLVIQIIIFVFPRVP
TDDSQTVLSLAMNMLYDKDYSSFETGGYLHMFPFNYSIVLYLKTLLYLFPDNYLVIKL
FNILFSTLTTFMIYLIYKQVNDRSTERDYGVLVFAATYLPSTLNNLIYNDVIATAFL
TSCLYFIIRFVHEKSWKTIVIAAVFLAMGNYFRSIGVIVLIAAIYILLNMRSIGMKK
VIISIAVLAMLFNVPTWTQNAVLQSSGAVSEPVGENAEPVYMWLDMGINLERFGFWDN
MESYQIYQRQANYSKAESAELEFKQEIGNKLSEASADLVQMYKRSYGP GPKGHTRW
DTESAMKVPWVPEEEGEAESQAPTVIPM"

CDS complement(4997061..4997270)

/locus_tag="EFAGFIKM_04364"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIKVHLSRIMGEKRINIADLSRLTGLHRNGIAKLYNEETDGVKF

NTLNRICEALDCEIQDIIEFIKDEK"

CDS complement(4997559..4997945)

/locus_tag="EFAGFIKM_04365"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAESNHYSVLVDEYISEFAPDVQVRLQAIRQIIREAAPNAEEKI

SYQMPTYAQHGNNLVHFAAYQHHIGFYAPPRGIQAFQEELSKYKGGKGSVQFPLDQPLP

EDLIRRIVEFRVKENVEKAREKKQKK"

CDS 4998130..4998450

/locus_tag="EFAGFIKM_04366"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNESMGNQKVIDIFENLSPYLQGLGDPVRQRIISLLIDQESMNV

SQIAEHVPMSRPTVSHHLKILRQSGLLSVQKKGTEMYKLEFNDAIELIKQLVHLVEV

ECQS"

CDS 4998550..4999632

/locus_tag="EFAGFIKM_04367"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNRKRVLIAAGGYGAVGAQLARILHDRHPDLELVLGGRSAGKAAP
FPSNRVQTVVVDYADDPLIHAGENISLIINAVNDLDDRLLVSAVRRKIPLIDVTRWT
EVFNQAIRTVEQEELHAPVVLSSGWMAGTASLFAMILSNSLQHVELNIHALYSLRDKA
GPDSAAFMDRMSIPFQVTESNTNRLVYPMTDPIKVHFPNGYTPCYRLDTPDHVTLPH
TSHIDSASFRISFDSKVSTYALAGLVKTGVWKMISGERFQPFRRKLLYNPGTGSAAHHL
VIQLKGLDAKNQVERTMTVSDPLGQTHMTALGAAVQAEKILMMPMDKPMAPGIYYSE
HLFDDRMDMDAVTHFFTQYGVQVTHS"

CDS complement(4999748..5000410)

/locus_tag="EFAGFIKM_04368"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLTIELNNHSINCHIYQYGKRKKVSITMDLPYMTIKAPNGTSED
MIRQLVEQHGDVILKKSALMQRALDGPQAKEYEDEGKGKFLFGKEHALHELIPVEGL
TEEELRANLKKFYFAECKRMIGERIGRYQQELKVPKSVEIVDSPTKWGSCSWDKKLT
FNYRLAMAPLEVMDYVIIHELCHIIHMHNDRSFWRRIGSIMPDYKTKEDYLMRNGRAM
TL"

CDS 5000559..5001314

/locus_tag="EFAGFIKM_04369"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTHSIDSEHKTIEELSLNHWQPLSTLLYDGWVLRFAKGYTKRAN

SVQPIHYSTLDVHEKIEECERIASNQLNTIFKITPFIQPDHLDQLLQDKGYGVVDT
RIQTRSLEEIKEPVHQSVQIDEQLTTTWLDHFCRLNQVNDLQRGTTELMLDNIRTKVG
FISLLIDGQVVACGFGVIERGYIGLYDIITDANFRNRGLAEQMILHLLHWAKKQGATS
SYLQVVANNVPALKLYAKLGYSEIYSYWYRVKE"

CDS complement(5001500..5003878)

/locus_tag="EFAGFIKM_04370"

/EC_number="2.4.1.321"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8P3J4"

/codon_start=1

/transl_table=11

/product="Cellobionic acid phosphorylase"

/db_xref="COG:COG3459"

/translation="MIKATEDNQYVELTSPTSLPKASGFLWNEKMMIHVNCRGYAVAQ
FMQPEPAKYSYAPNLEAKTFMQPEQPYAHHPGRFVYIKDEISGEIFSAPYEPVRKQA
DSYTFAVGKHDIHWKVIQDDICIEMSLRLPKEDVMELWRVKVTNLSSGKRKLSIYPY
TVGYMSWMNQSGSYVEDLQGIVCSAITPYQKYQDYSKIKNYSKTYLLADHQPTGWEV
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ENGAVYNHAAAFYIYALYLVGEKEKAYRLLRKMIPGPDGEDILQRGQLPVFIPNYYRG
AYRQFPRTAGRSSHFNLTGTPWVYRCLIDGLFGLQGHAQGLQVRPQLPEDWNKASVT
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CDS complement(5004008..5004427)

/locus_tag="EFAGFIKM_04371"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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TRTPSDYADHVREMIEAYGEFSLEILELLTEGDKVYVWRWQTGTHVGEVDGYSPTNLP
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CDS complement(5004692..5005687)

/locus_tag="EFAGFIKM_04372"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MAKNVLKLGDPVISTYTSYGTLSVMHEDLWPWIFNNFIQIRYA
HGWGIFSFDHQFLLSTCPGISFYNLPQEIVISKWGTSLKQVITEAIDMGYYLIYAD
RYYIACTDYYQKEHLMHELLVYGYDLDQNLIIYADNLDDGKFIQTVCSLDELEKGYWT
MSNEYSFWTEVRFLKPIQNINYAIHVEQIITAMENYLNSSSETYDLVRDQKYDFGMQAI
QRIFTDIEQAALVGEALDSRVFHLLEYHKLMLRLSYLMEKLIIEPDATFMELSAVL
KQDYFKLRNIVLKYNITRDASTLSKISERLQENLMKEKAFISSFITRLQQVKSMA"

CDS complement(5005944..5006846)

/gene="yghA"
/locus_tag="EFAGFIKM_04373"
/EC_number="1.-.-."
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/inference="similar to AA sequence:UniProtKB:P0AG84"
/codon_start=1
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/product="putative oxidoreductase YghA"
/translation="MANQDQHTMQDPTTQYPKATSEWRQQQDEPGLQREMTPVPDAGE
KSYKSGSRLTGRKAVVTGADSGIGRAAAIAFAREGADVVLAYLPREEADAQEVVKLIE
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ATFKTNVYSMFWLCKAAVKHMKPGSSIINTSSIQAYKPSPILLDYATTKASINTFSKA
LAQQVGSKGIRVNVVAPGPVWVTPVQVVGQPVVEKLADFGSNTPLGRAGQPAEMAPAFV
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CDS 5007198..5008202

/locus_tag="EFAGFIKM_04374"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNHEVISLNANKEPYSIGEAAKLIGSTVKTIRYYDEIELLQPSS
HTEGGHRLYTTQDLWQLELITTLRYLNFSIPDIRKLMSGELAVAQALDLQIEALETQI
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LDSIPQEWVRVSFLHFFDKYMMKDKLTAQQTALWKEIQELINDPAYWADLAQLEVPPF
IMANQPQVEADVWVKKMEAIRIRTEALDKRWIDSPAVQSMVWDFVLMYASVEHAET
PEVFFRKQARYMLDSVTDRILRFNKLCKVMNPEWSQIVDGINLLQEGMRLRLKQMEAD
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CDS complement(5008229..5009758)

/locus_tag="EFAGFIKM_04375"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRTVEWIYLIFNLLMLVGVIIGIGKQSQHFRKMVWGGFAISGVLL
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SDLYLISPLLEWTQGVDARGTQQLVNDTTIDFFNHYLKGGQSLHLDTEVGEHESYSLKK
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CDS complement(5009941..5011320)

/gene="yifK"
/locus_tag="EFAGFIKM_04376"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P27837"

/codon_start=1

/transl_table=11

/product="putative transport protein YifK"

/db_xref="COG:COG1113"

/translation="MESKQLSRGLKPRHVELIALGGTIGVGLFMGSASTIKWAGPSVL
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AMIVIGTGLIFFGLGNGGEPIGLSNLFSGGGFFPGGIKGLFALCIVTAAYQGVEMVG
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GIVAAAGIINFVVLTAAMSGCNSGIYSAGRMLYTLAENGQAPAFFKKLSKGGVPRNSI
VITISLLLIGVVLNYLMPDSKLFYIYSASVLPGMVPWFALAFSQFRFRKRWGNEMAD
HNFKSKWFPISNYIIIVYLILVIIGMAFNPDTRLPLVVGATFMAIVVAGYFAFGIGKR
QRIDGGEDR"

CDS complement(5011654..5013006)

/gene="hssS_3"

/locus_tag="EFAGFIKM_04377"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A6QJK4"

/codon_start=1

/transl_table=11

/product="Heme sensor protein HssS"

/translation="MIKTLYVRIICTFLVVIVFSLLTSFFMGIFFFKKEVNHIGQNDM
ISVGEELIRLYEQTPEDRDAFIKSMVKVSTYPIHLYDVSGNVTIFYDL DHTETVEIAP
EVVQMV LQGQIYRSPGEVEQTFIGLPFPYKGEPQAMFMQYSPQENIINRMILLVLLF
ALLIGSFCILIAARYLVKPIQVLTRATKRLAKGDFNVEIQTKRVDENGALTQSFNEMA
SELKQLEQMRQDFVSNVSHEIQTPLTSISGFAMALKNSSLVAEADRNYLDIIITESG
RLSRLSDN LLELASLSDSDHHPFETTTYNLDEQIRQVVVTCEPQWSAKGIPVHLELADG
IKIRADQDQLNQVWMNLLGNSIKFTPVGGRIEIRTSQSVDGIIFTITDSGIGIAPEQL
DYVFERFYKTDLSRDRSISGNGLGLAIVKKIVMLHHGTVEMKSQMGVGTVMVHLP SG

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CDS complement(5013003..5013677)
/gene="hssR_4"
/locus_tag="EFAGFIKM_04378"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A6QJK3"
/codon_start=1
/transl_table=11
/product="Heme response regulator HssR"
/translation="MTKILVVDDDVHIRELITFLRNEGFEIVVAKDGAEALEIVGKS
PIDLVILDIMMPRLDGWELCREIRMDLNMPLLMVTVKGESAQKVKGFLGTDDYLT
K
PFDPLELVMRVKALLKRYLIVSSQTIQLGGIMLNRRSFQVIRGEETINLPLKEFELL
F
MLANQPGQIFTREQLIKIWGSDYEGDDRTVDVHIKRLREKFAGDAHFFQIETARSL
G
YRLVIT"

CDS complement(5013732..5015705)
/gene="dap_3"
/locus_tag="EFAGFIKM_04379"
/EC_number="3.4.11.19"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01960"
/codon_start=1
/transl_table=11
/product="D-aminopeptidase"
/translation="MSSLIRKIFGKMILLVLLGMILGATGLGTMPLSAAVSNQGLNS
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NI
EENKVPDPETSLFRIASTTKLFTWTAVMQLVEAGKLDLDTDINTYLKTVKIPKTYE
EP
ITLRHLMTHTAGFEEGGVGYQITDTPGKLPVSIAETMAKHMPARVKPPGEMLSYS
NYG
ASLAGLIVEEVSGVAYNDYIQKNIFDPLGMNYATVEEPPASLEPYAALGYARANG
EF
VTKRPTYEGGFRPAGSGSVSANDMAHFMAIHLQDGRYEDKQILKPETAKLMHSPA
FQF
DERLPAMD LGFYELNMNGLRVISHGGADELFNTALYLPDKKVGIFVSYSGGEGGT
AA
EGLAQAFFDRYYPVHATEQPNETSIELGESLEKYAGSYQFTRRNHTKIDKFFSFLT
QI
NIEFSDNRLFIGSGADQQVYTPIGVNLFQEVGGTHQMGFRTDAEGKVTYLFLDIL
NPM
PLEPAPLMNQSKFWLLLLGISVVLFITVLHGFVYRRREIRVMPKAQKWAVRLSAV
TSV"

WALLTLGATLLVMNMDLIDRLSHIPVSLRLYL FMPVILVGLTAAIFIMSVLAWKNQYW

TLLKRVHYTFVMVAAVILSLFFYHWNLLGWHFG"

CDS 5015874..5016239

/locus_tag="EFAGFIKM_04380"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPDFLLVLFLFNLSLFLHEMDAIRRSEWKLFMVLLKDMEDDKAY

RYFTWIHLPMYTIILSLLFSSYQTITFWVLDIFFIIHTVLHFFFEKHPRNEFKNGFSR

SLIYPMGITALIHLIFLII"

CDS 5016398..5017303

/locus_tag="EFAGFIKM_04381"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHRLAALLYAAENKTADGEAIRQSHELKQNTKLFSAFRGNSAI

SIAAMLSLTDAETKLADTLHVYDLMKEIKFRNSDYLVIAAYQIATQTSPDQFQPTVE

RAKSFYDGMKAEHRFLTQDDYIFAAMLALSDLNVDTGVARMEQLYGELKPEFSSRNS

VQALTQVLVLGDDPPDAGARVIALNEAFRKRNL RMDKTYTLASLGILSLLPSDRDSL

DEVAETNDWLRTQKGFGAWSIDKQELLLFSSALVAIQHVENLRNGVLTITISTITNI

IIAQQAAMAATAAASAAAASSSSSN"

CDS complement(5017431..5020781)

/gene="rcsC_13"

/locus_tag="EFAGFIKM_04382"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00979"

/codon_start=1

/transl_table=11

/product="Sensor histidine kinase RcsC"

/translation="MNKRTSFLYYIIPVMLFFLIFTVLILFELPSNQMNAEVQDGRLT
ITSEALSSGEGSRLDGEWAFYWKQFLEPKDFASERTGPVSYVNPESWGNYEISGHKL
DNTGFATYRLVVDLPEQDIELGLLTSGITSAHRLWINGKLVSESGIVGRTLKESSSYK
VPALIRMEAGQTQADIIIQVSNYTHRKAGLFGSLTIGEYNQLNQSMKYKMSSESMIIG
CMLIMGLYHILLYTLRKNRESLYFGLICILLAMKNSSDSQYILSELIPGMSGDTFLK
VEYLGFLGSSPLALLFCYSIFPNEVSKRLRDIFWIPGLLFTLFILFPAQVYTKFALF
MQAYVILIGIVIIQNVVRAAMKKLAGAHWMLAGTIVFFITVNDILMNNGIIQTGIYF
SYGLLFLILCLSIIVSTKFSNAMKTNERLSSRLELDRVKDEFLANTSHELRTPLNGI
IGLTQSLHSMDDRLEDNQRMHLNMIVSSGQRMFLINDILDYALLKNNDVRLNRTKI
NLHQLVQVVLTVVKPLITGRDLLYNRIDPHFPPIEADENRMQQILFNLVGNAIKYTP
SGHIVIRAQIVQGDVEIQVEDTGIGIPEDKFAMIFNPFKLESIDNTGAGLGLKITKQ
LVELHGGEIKVQSKVNQGSLSFTIRQHKKNVPTALPDKQNNESIQNGASTLRSVAEA
KKASSHALSREVSSAKESEIQPYRVLIVDDEPVNLQVVIQQLAPLACVFEIANSGETA
LVRMNELQNFDLVITDMMVMGMSGYELCGLIRERYSLIELPILIMTASNRDDTITACF
AAGANDYISKPIGRNELISRVRTLLLLKRSAQELSLNAQQLEELNQQSELNTNLEYR
IQDRTVELEQKNKDMGRLELSRRRLLSDISHELRTPMIAIQGYVEAIVSGLVDNEDDQ
KVYLQMVVLKALGLNRLIHDLFELSRLSESGKSEMIFIMMSLQDLMDTIQDKFRLDIAR
ADMSYEFQMNITTAQRSYQVVIDMDRITQVLTNLVFNAIQHTGAGGMIRLHCSIEEW
ENDGDSPGRLTIRVEDNGAGIMEESLPFVFDRFFREKHDRHVQSGSIGLAIAKEIIQ
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CDS complement(5020871..5021830)

/gene="mltF_3"

/locus_tag="EFAGFIKM_04383"

/EC_number="4.2.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_02016"

/codon_start=1

/transl_table=11

/product="Membrane-bound lytic murein transglycosylase F"

/translation="MIRSYGRLCILLFFMLTIGLILSSCTSVSRDAVSTIASPQTETA

QSRAAETDITAAKAAKGREPRVYTAEELGYGPQDIRDILSRGKLRIGLKVEERYPPFY

TDEEGLLRGSDVELANDIALKLGVKPEYIRTADSFDEVIDQVSSGEVDVGISKLSITL

ERAKRVLFSNAYLHFKQALLINRLQLAELGKKNEFPDVLTLQQRGTQIGIVQGTSYV
GFTRELFTQKQIAYKNTSELDHVRQGEVIAAVYDAFEISRYLDQNPAYSLDLQYVQ
LEDQDDDIAlAVDPRRMHLHQWINTYLHMQEKNIQRWLENYGI"

CDS complement(5021833..5022048)

/locus_tag="EFAGFIKM_04384"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGYQQNGNDAEQENRQSDELLEEELEEVVGG LATVSIARCKVCH

IRIAVYEMSVCAACFRKTQLPLAGEGG"

CDS complement(5022097..5022828)

/locus_tag="EFAGFIKM_04385"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKTAYVHHAESTAMQMMVVYLLHRGLQITASFATSEQAEQFHSD

LSVHDQKNCLTIVAPDLGMKGIESVLSASAEHMQGLDFYIHGSSWVDELSELQSDPAA

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GLLLDYGQGMSGQNITWGYGIPSVL"

CDS complement(5022866..5023609)

/gene="fabG_10"

/locus_tag="EFAGFIKM_04386"

/EC_number="1.1.1.100"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P99093"

/codon_start=1

/transl_table=11

/product="3-oxoacyl-[acyl-carrier-protein] reductase FabG"

/translation="MTRFDHVVVVTGVTRGIGRAIALRFIAEGAIVAGIYVRDDAAAD

RLTEAVSAAGGRMRLFKGSVADHAFVADVMKEVFDTFGRVDVLINNAGRSSDQMALRM
EEQQWNEVLDTNYVGACYCSQEAVSYMVLQDSGSIINLVSVSGIYGREGQSNYAASKG
ALMGLTKLYARQYATHNIQVSAIAPGMIDTEMTGEVSQEKLNDFLRHTLIGRQGYAEE
VAEAVIYLAGPAARYHTGQTLKLDGGFLR"

CDS complement(5023606..5023911)

/locus_tag="EFAGFIKM_04387"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTVNYESVEMDEIKQTIKQTLIDRLKLEDITAEITDDMILFGE

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CDS complement(5023949..5026411)

/locus_tag="EFAGFIKM_04388"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSDRENTNTKDRIVITGMGVLCALGDHPQMUYERMLAAETGIRE

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AGFNVLRALNSRPSPFSTQYGLNLGEGAAFWLERLDAALERGATYAEICAYGLSN

DAHMTASHPEGAGIQRAVEMASLAGVSKTDIEYVNAHGTGTQANDRAEISGLQGSF

GPNLSIPISSSKAYFGHTLGTSAALELVTSLYAIRQGYVPATLHFEEAREGCEDVDII

QHSMRPMRPEYMICNNSGFGGHNVSLLVLRNTGIEEERYSGVQNPERENSLAGHPGEAV

PRRRVITGVGAVSKGDIRKGNVLGAFGKDTKQVTETSTFFSLKDYDKSKYERRMNQLT

QNTIGAVLAAMEDAALGESQREHTGFIYGTARGSTSSISNFLESVFKGPEYASTIYF

PHTVINSIAGQTAEKLQFKGFNSSFSTGGNEGLTAALYATGKIREGALTSLIGAGDE

RSQLAEDIDRAKGLQDSRYEMTEGSVCMVLSLEEADQTRSGIYAELSGLGVASGAAQ

DASRQSEALIRAVTDALHEAISMGMQMDLILLNSVGRPGELEMEQVAVSSIGEAVVAV

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CDS complement(5026428..5027318)

/locus_tag="EFAGFIKM_04389"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MITIKRLTLQDRLKYKSFMFQWLYKQVEQSLNDPMESERFILIG
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FLWADQEEGQLRQSIETGELDFPSFLSPFKTFAPLELSNSFGIQSAQGIQGWSMTYRL
DEDTILYDALYIAPEYQQFGLAFQMLGRSIRVQTEAGIPHAMFTVNQSTPIMMKLSRQ
WLAPYSWKTSEKRSSYIRLG"

CDS complement(5027272..5028576)

/gene="gltP"

/locus_tag="EFAGFIKM_04390"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P21345"

/codon_start=1

/transl_table=11

/product="Proton/glutamate-aspartate symporter"

/db_xref="COG:COG1301"

/translation="MSRKTAFLSKWIKSFWMIVLCMVSGIAAGLYVPELAHAVSRFGD
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NTLQILFFSVIVGVAVGMMRTPQGDDVLKIADVLFQAFQKVISWSMYALPFALFCMMA
GQFATLNLDILPAMMKLIMMFYISSVILIVLSIVIMAVTLRKPVRVVLKDALILA
FGTRNSIATVPTCMEALSMKLQQDPRIVQLVLPLGMIMCRYSMVLVYTLGITFTVQLY
DFDFTLSQWIVVLGAVVISIAGAGSPGVVSIGMIAVIAEMLGLPSEVTIILLAMNP
IIDPIITAANVSIQCLTTSLLSARKDNYDHYQTANTPGQVEV"

CDS complement(5028745..5029113)

/locus_tag="EFAGFIKM_04391"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSWTEEQIQETVNAVMTKASSDAAFRALAVSDIYAAIQQETGQE

VPREFKINVVDGTGYHATIVLPEARGEADELTETELESVAGGSKDGATDFFNGVGSIA

EDAARAAIRVGENVGNSYAK"

CDS complement(5029215..5032133)

/gene="btuD_11"

/locus_tag="EFAGFIKM_04392"

/EC_number="7.6.2.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01005"

/codon_start=1

/transl_table=11

/product="Vitamin B12 import ATP-binding protein BtuD"

/translation="MAEPIRPKMESFFTKVGTIHDVEGNNPILITDENS VWYVASGYV

DVFAVVMEGENAGTRHKRRYMFSLDEGALLFGFDNGQMVERMGLLLTASVGTKVFRID

KELLLNRRVNDQWDNEWLASRVDQWVGWSAALNVRNSPLEFTLLEPGEDQNLIPDQT

WRPMRTVWIKVQDGMVLWGKEHPVTTEDACYIPVTSSGWLETQQAAVVDVRATQSWLP

TDPSLHGLYAFHQLIASRLAVVAKERLQEQLRQRTTEHDDSLMDHALKKLIAVTGP

DEQQVVSFYSTDPLYVPGKIVGDYAGIVLKPVTRKLKSQSKRSPVQEMAEASGVRSRQ

VALKGEWWEADNGPLVGYLETSGEPIALIPAGANSYRWENPLHGNGFVNDEMAATIQ

PMAYMFYRPFPAARELGKIDLLQYGAAHHSVRRDLVMVILMGALAGLLGIMVPLASGILV

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LPVSFFRNYSAGDLASRAGSINAIRQLLSGAVISSLLTGVFSIFQFALLFRYSPVLAL

VAGGLVLISMSFTFAFGLLQVRYQRRLELQGQIAGTVLQLLNGMSKFRMAAAENRAF

FLWARAFAEQKKWSYKVRMLDSFSSVFQAFFPLLTSMVLFYLVVSTRSEMSAGQFIAF

FAAFTSFLMAMLGMATALLSVVNIVPLYERAKPILKTLPEIHDQLEDPGEVSGAIEIR

HIQFRYEEDQALVLNDLSMDIKSGQYVAFVGASGCGKSTLMRLLLGFEQPQSGSIYFD

GQDLRSLDISLLRSQFGVVLQNSKLMSGDIFTNITGTSNLTIQDAWEAATMAGFDDDI

RSMPMGMHMTVISEGGGTLSGGQRQRLMIARAIKRPKILFFDEATSALDNRTQRIVSE

SLSKLQVTRIVIAHRLSTITQADHIYVFDKGRIIQSGTYQELMEQNGLFAELASRQLA

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CDS complement(5032159..5034315)

/gene="lagD"

/locus_tag="EFAGFIKM_04393"

/EC_number="3.4.22.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P59852"

/codon_start=1

/transl_table=11

/product="Lactococcin-G-processing and transport

ATP-binding protein LagD"

/translation="MARRRVKTPTVLQMEAVECGAASLSIVLSYYKSFIPLEELRISC

GVSRDGSKANNILKAARQYGMEAKGYRKNPEDLRNMPWPVIIHWNFNHFVLVLEGIQKD

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ALVYAIAGLFLVLPGLVIPVFSKIFIDQVLLGHLNNWLFPLLVGMGITALLRALLIW

LQRYLLRLEMKLALSSSSRFFWHVLRLEPIEFFSQRHSGDIASRVAINDRVAQLLSGQ

LAVAALNCVMILFYLLLMLQYSVLLAVTVGVSLNLFVFMQFTRKRNDQNLRLQES

GKMQGVSMNGLQVIETLKSNSSESDFVFWKWSGYQAKLLQSNQQFGVSNQFLMSVPTLL

TSLGAVAVLFFGGFQVMDGALTIGSLVAFQSLAASFQPVNEMVMLAGTIQEAGGSMK

RLDDVLQYPVDRQIQSDLDQADEQKDSAKLSGQVQISNLTYGYSKLEAPLIDQFNLSI

QPGMKVALVGGSGSGKSTIAKLIAGIYEPWEGEIRFDDLRRDEISRHRMGNSLAVVDQ

EIVLLEGTIKENITFWDATIPETDIVRAAKDAVIHDHIAERSGGYDHMISENGGNFSG

GQRQRLEIARALSGNPSILILDEATSALDPATEKLVDDSLRRRGLTCITVAHRLSTIR

DADEIIVLERGKIIERGTHFLMEQNGYYTRLIQSQ"

CDS complement(5034359..5035318)

/locus_tag="EFAGFIKM_04394"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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ALYWGIFGTMTRAEGQGVLRPGGLKTVHTSSEGAISDIAVVENDTVQQGEVIGRIE
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GKVTEVLVKNGMYVGEAEMFRMETYGSQTDELIGVMYVPVNQGKQLLPGMEVRVSPS
TVNREEYGSMIGQVVSSEFPVTVQELQSTLGNEGLVEQMASQGLSLEVRVNLSPNSE
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CDS complement(5035311..5036531)

/locus_tag="EFAGFIKM_04395"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8YEE8"

/codon_start=1

/transl_table=11

/product="Leu/Ile/Val-binding protein"

/db_xref="COG:COG0683"

/translation="MNGSGGNRLKWVLWSVALLGALVISGCSSDTAPDQIREKTLGSS

SNEVIVGAVWPFQKNEQFREGLQLALEQINKEGVLGGEKIKLLEMDDGASTTKGMAI

AQQFADNPSVSAVIGHRGSSVTVPASRIYANAGIVLLSPASTSPKLTDVSSPYIFRNI

PNDNQIGQSLALYAAGTKHENIAIYYTDDEYGRGLANAFERQATLSGQNVVDRVSGYK

DGADMMRIANKWETLDTDLIMIATRADEGITFVKAIRAAGMDTPIIGGDALDSAEFAQ

GGGSVEGTIVASVYDDQGQSTLNQDFRSTYIEHYGKAPDKWAAQAYDSLKLLAAGIDE

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DSSRDSAKGGGQDE"

CDS 5036789..5037508

/gene="phoP_5"

/locus_tag="EFAGFIKM_04396"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P13792"

/codon_start=1

/transl_table=11

/product="Alkaline phosphatase synthesis transcriptional

regulatory protein PhoP"

/db_xref="COG:COG0745"

/translation="MSLKNTILIVDDDHEINELLTMSLKREGFQTVSAYNGVEALRAA

QEHSPDLVLLDVLLPGMDGFQICSEIRKTSNVPILFISCKDEATDKVIGLGLGGDDFI
SKPFSPIELIARVKAHIRRNNMPQKQEEQVDETLVFDQLLIDPATHRVLVGDKPIALS
AKEFKLLFHLAKNPNRVYKNEQLFSLLWDDVHMGDTHTVMVHIYNLRKKLEQNPAPKH
YIRTIRGVGYKFNDKPAEFAE"

CDS complement(5037609..5038598)

/gene="thrB_5"

/locus_tag="EFAGFIKM_04397"

/EC_number="2.7.1.39"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00301"

/codon_start=1

/transl_table=11

/product="Homoserine kinase"

/translation="MSIQPTALRSVLNPRYLESALRNQYDIGTWEDCLFWLRGLNDTY

RVRTSSGMYILRIYRTEITEADVQYELSQLKNVLGSAEHTDIGEYIEKKDHTGYT

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KLLIDEPLERIIHYIGENNEAAAFLLHTFATTLKERIVATSRQDLDFGLCHGDMHGNNN

AFQQEHQFIHYDFEWAAKGWRAYDLAQVKVRKRQSDERKAALWDALMAGYRSVRSFSV

EDEQAVDLFIVARRFWVMGLDVAFIESDMGALDYGSDWLDSFVEEFREADIVS"

CDS complement(5038731..5040455)

/gene="dauA"

/locus_tag="EFAGFIKM_04398"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AFR2"

/codon_start=1

/transl_table=11

/product="C4-dicarboxylic acid transporter DauA"

/db_xref="COG:COG0659"

/translation="MKWMGRYAGYNAAFRKDLLSGLIVGIIAIPLGMAFAIASGVKP

EYGLYTTVIAGILISLLGGSKFQIGGPTGAFIPILFAIVMQYGYENLLIAGMMAGLML

VLMGVFKLGALIKFIPKPTIGFTAGIAVIIFSGQITNFLGLRGIEKHEDFWSNMKEI

GMHISTINIYSVLTAGICLAVLLLVPKFAPKVPASLVGLVLSTVVAFFFFEVQVATIG

SSFGAIPNSLPQFHVPEITWERIVNLLQPALVIAMLGGIESLLSAVVADGMTGSRHNS
NRELIGQGIANMVTPFFGGIPATGAIARTATNIKSGAVSPWSGVIHGVVLLVLVLF
PYASHIPLASMAPVLMVAVWNMSERRSFIHVMKTKTSDSLVLLITFLLTVFTSLTAV
EVGLILAVLLFVKRMSEMLKVAKVLPDPDHKHEKVMAMHVREGHDCPQISLYTIEGPL
FFGAADMFEKSVMDSIHRRPGTLLLRMGKVPFMDTTGESNLARVVKHMERSGGRILLS
GIQAQPLELLKRTGLIERIGSDHMF EHTGEAINYALVYLDVQKCRGCKHF AFRECAAL
SREGAIGV"

CDS complement(5040623..5040952)
/locus_tag="EFAGFIKM_04399"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P9WMI7"
/codon_start=1
/transl_table=11
/product="putative HTH-type transcriptional regulator"
/db_xref="COG:COG0640"
/translation="MNQSIQQFKADFFKALAHMPMRIQILELLSEGAKNVNELQSILGS
EGSAVSQQ LAVLRSKNVVHGIKEGTTVTYSLRDPLIKDLLAVTKQIFDNHLVDAISML
EDIRKES"

CDS complement(5041366..5042943)
/locus_tag="EFAGFIKM_04400"
/EC_number="3.2.1.55"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A7LXT8"
/codon_start=1
/transl_table=11
/product="Non-reducing end alpha-L-arabinofuranosidase
BoGH43A"
/db_xref="COG:COG3507"
/translation="MNNATQSEQCTFNNPIMPGFYPDPSVCRVGEDFYLVSTSTFAYFP
GVPIFQSRDLVNWKQIGNVLD RPSQLNLQGAGHSQGIFAPTLRYHEGTFYMITTNVSH
GGNFVVTATDPAGPWSDPYFIEGAEGIDPTIFFDDGKAYYLGTRPCSEGVRYNGNWEV
WLRELDLGSMKLVGDSYVLWRGAMVDVIWPEGPHLYKID EYYYLLIAEGGTGPNHAVT

IARSKSLTEGYVGNPNPIITHRHLGKRYPVVNVGHADLVQAANGQWFMVMLASRPYG
GSYSNLGRETFLASVWVEDGWPVVNEGRGILEEQGTLDLKPVPVEPQLRFDHFDSDKL
GLQWMFLRNPQEDLYSLTERKGYLRLLKLPQTLKEKENSSFVCLRQRHMDYVAATAME
FVPGNANETAGLVVIQNDQYHVRIERALADKQQVLRVVTVIDGQDSHIAQIALEGDVS
RVYIKLAATGQQLNFYYSTDGSQYHLVAEQVDTSSLSTEVAGGFVGCCIGMFSSSNGT
SSDQVADFDWFEYGSYK"

CDS complement(5042940..5043839)

/gene="araQ_27"

/locus_tag="EFAGFIKM_04401"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MKRFSRKRSLGDSIFSITNGIFMLLMVVTLYPFLNTIAVSFNN

GLDTIRGGIYLWPREWTLQNYVSVFQNPNTQAAFVSVARTVVGTVVQLFCTAMLAYV

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IRTYIQGLSEGLIESAKMDGAGDFRIFMRIVLPLSKPVLATVALFIAVGQWNSWFDSM

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IVLLYPFLQKYFVTGLTIGGVKE"

CDS complement(5043855..5044829)

/gene="yteP_33"

/locus_tag="EFAGFIKM_04402"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system

permease YteP"

/db_xref="COG:COG4209"

/translation="MAKKELQPSLKTSHIPAGTSWIGYNLSRMKSQRQLMWMSFPFIA
FIAIFAYGPLWGWLMAFQNYRPGIGFMEQDWVGVDHFRTLFTDPTFLRVIRNTLAMSL
ISLFLGFVGSIGLALLLNELRMVLFKRVVQTVSYLPHFLSWIIVTGIVANVLSTETGI
VNVLLTKLGLIDAPINFFAEPKYFWGIVGLSSMWKEIGWGTIIYLAAMASINPSLYEA
ASIDGAGRFRKMFNVTLPSTIKPTIIILLIINVGNVLNAGFEIQYLLGNGLVQDVSETI
DIFVLKYGINLGNYSLATAAGIFKSVVSLVLIFIANGIAKSLGEERLI"

CDS complement(5044966..5046636)

/locus_tag="EFAGFIKM_04403"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKDVRKRIKYSALLALILVIALTGCTPGSSSKGEKTADGRELK
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DGSDGTQQLVAAGALVPLEDYIDKYPNIKNYLGEDWKKMKNTTDGHIYFIPQFGNIQE
KSMKVSHDGEAFWIQKAVLEWDNYPTIKTLDQYFDLIERYKAAHPTVDGQPTIGFEII
SYDWRYFALENPPLFMAGYPNEGAAIVDKETLTAKNYNTIPEAKAYFKKINEVYHQGL
VDNETFTANYDQYISKISTGRVLGMVDQGWQFLDAEASLVKQKLYDKTYVPLSITLSE
DVKGRYQNNPILNVNGGLAITKSCEDIEGALQYINDLLDPEMEVLRTWQGEGVDYQVD
DKGVFSRNEEQRANSKDPDWVLANTGSPLVYFPHHEGMTADGKNALDPKEQPPEYLAT
LNDIDKKVLKAYGYTKFTDFLEPAEENEPWFPIYTYNFEPNKPETIARQKMDDVKRKW
LPKVIMTSPAEFDKAWEEYQATLKESADIKAYEDALTEEVRRRMELWG"

CDS complement(5046815..5048389)

/gene="cheB_12"

/locus_tag="EFAGFIKM_04404"

/EC_number="3.5.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00099"

/codon_start=1

/transl_table=11

/product="Protein-glutamate
methylesterase/protein-glutamine glutaminase"

/translation="MINVLIVDDEPFIRQGLLLIDWESYGFQICGQASNGMQALECI
RAMQPDLVISDIKMPMDGLQLAKTLYEQYSGDIKLILLSGFYEFYAKQAIKYQVDD
YILKPIVKTELQVLEEFRAFNARTEEKRYQQKKDRIIMAQHMQSILLGVAEEDAVT
SLQPHYQDVGILRCILIEAEAGPDQGTDWCARVEAWVGKPLPGQILKPFTGDKNAVLL
MVTDLMVNREAVTLEQYLTRLHADLSHGQEAACIACVVGKEVHELEALHESYQSCGIMK
SLRFFTTCPRIYYFELMDTTLFVNRPQGFEKQLFDGLVKSIEEQQTDELYSHAKAIFQ
FFLDERIEPGMVRIHLHYLAYTLLDLVNNDTVTPDSGLMESTFLKVNYAMLSMEENIE
HLCEFSLMCAEKLKEQQKSNAMGVLAKIEAFIHEHYRENISLKLGEQFYMNSAYLGQ
IFKKHFSISFSDYLNQLRIEEAARLLRRTDQRVYEIATMVG YRDS DYFISRFELMGE
TPAQYRKSAHAAYS LD"

CDS complement(5048401..5050203)

/locus_tag="EFAGFIKM_04405"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSRKTYCKRIQFLDDWSLTKTKLYILFIFCVLPVLTNTVFYLS

IKGNIEEKEHSR FNEMQQRIKFNL RNSIDNSLYVSNFLYTDGTLNRFMEFKYRDQEDY

YSAYYDMLSNNNLVRYYYSYQQVNQITFYVGNDTFVNGGNFIKLDDEVKKSDWYQALM

NTSDHIMIYSYFDKQQAEMSQSQGGRKVSIRKLDYFGEQQVEKVLKVDLDYAFINKS

LKNEGANGKVYVVS DGRVIFSND SKMNQMRKPFNL IANSPIDPVQSMQSIPVVS EDWQ

IVVSTEKLDVLSEIINSKLNLTLLIILNLLVPTLLIWLISRSLVIRVNRIAKHLDQVK

HEKFEVISGPVGKDEIGSLTHSYNMMVIKIKNLIEIVFKGQVERQALELSKKQAE LKA

LQSQVNP HFMFNTLETIRMRS LIKDELETS DVIHRLALLLRQTINWGDDLITIAEEIN

FVESYLSIQQYRFGEKLQFAIRITDESIAAMMIPKLT VLT FVENACIHGIEGTSNDGV

VEVLFEIRSNELYISIRDTGVGMDQDKLASLRKMMQDPSMDRMSELSSIGMMNAYIRL

RM YFDDFVQVHIFSEKKGTTIGIQIPLMQASQE"

CDS complement(5050404..5051252)

/locus_tag="EFAGFIKM_04406"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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GYHPEISMGAFKDERMVG FVINGLR SWNGKTTAYDLGTGVVKDCRRQGITSNLLLNIQ
KLLKEKNVEQYLLEVIQSNESAVQLYSKQNFKIQREFSCFQLQKDQFIPQTTCMVECV
ERIDLEQFKEFWDVPSWQNSIDSIYALPEAFIYVVARQDQSIVGYGIIDQKTGDVPQ
LAVNQNYRGKGIASSITEMVQRTESPRISVLNVESHKPMQDFLLVKSGFAYHVGQY
EMLLKL"

CDS complement(5051463..5053643)

/locus_tag="EFAGFIKM_04407"
/EC_number="2.4.1.247"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A9KHK4"
/codon_start=1
/transl_table=11
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/translation="MSKLTKGSFTLPGESGYEALTLELANRWGADVIRDS DGTKLSDE
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FRVND SKEAFKYWQVYDR TTGEEVPRGQWNYERESGNVVITGVAPWHKYTVSFMVYRI
WEEISMYNHTTNNWDKEHLMQIDPIYTD TQTYLLDWMEKWCQDHPETT VVRFTSLFYN
FAWIWGS DERNRHLFSDWGSYDFTVSSRALDLFAQKVGYSLSAEDFVNGGKYQVTHMP
ADQRKLDWMAFINDFVIEFGKKLIDIVHNHDKLAYVFYDDSWVGMEPYNDRFQEFQFD
GMIKCVFSGYEARMCSGVKADTHEIRLHPYLFVGLGGLPTFKEGGDPTLDAKKYWIN
IRRALLRESIDRIGLGGYLHLVEPYPDFVDYIEKIAHEFREMKE LHQEGKPYQIKTKV
AVLH SWGKLRSWT LSGHFHETHMHDLIHVNEALAGLPVDVQFIDFDDIRQGALKDVDV
VINAGSAGSAWSGGEHWS DHKSVDLLTQWVYEGGTFIGINQPSAMDGYDSFFRMAHVL
GVDEDTGARVVHGKWSYEVNDEYGLVPEGASILPKNNIYLT DGSAAVVSETDGQITLS
THAFGKGKGIYLP SFEFSWENTRILLNIRFAGNEFHETKYITDNLYTECAYYPESNI
LVVINNSDQVQSTTINTEHGKQTVEMEPYDTVVTKIGLTKSVSP"

CDS complement(5053657..5054676)

/gene="yesR_2"
/locus_tag="EFAGFIKM_04408"
/EC_number="3.2.1.172"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31521"
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/product="Unsaturated rhamnogalacturonyl hydrolase YesR"
/db_xref="COG:COG4225"
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DYLQNHALRFGDNVLQHTVSVSNDPFPEQAWADTLFMAAFFLLRVGSKLKDEAMIQDAL
NQYYWHIKYLQDPSSSLWYHGYNNINKDHMSGFYWGRANAWGAYTMSQVKPQLKDWYL
YPQCMDVECALRDQLAALKLVQTENGLWRTVLDDSDSYEEVSASAGIAAAMINNGNPL
HTKYVQKALEGILNNISEDGRVLGVSGGTAVMKDRDGYRNIPKDWIQGWGQGLALAF
SDMLR"

CDS 5054848..5055795

/gene="rhaS_36"
/locus_tag="EFAGFIKM_04409"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaS"
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GLLSLYIELLRMHASSERLSSQDQERERDLQGDLVISPVLEFITKNYMPVTIDHLA
DLCHLSTTHFRRKFHEIMGTTPLDFLNSTRIEEACKRLKSTEASILSISEQVGFRSIS
SFNRCFSKLMGESPKAWRKGATEAQSAKASILEFTGWV"

CDS 5055916..5059047

/gene="rcsC_14"
/locus_tag="EFAGFIKM_04410"
/EC_number="2.7.13.3"
/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00979"
/codon_start=1
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/product="Sensor histidine kinase RcsC"
/translation="MLLKISGVLTVVLAITVLLLSTIREPQSAALHARQGVLDLSAW
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SPQIGFFPYHGGDIEILIRVANYDYTDSGIPGPLFFGEQAAMLKKHQFNIAIEFGTLA
VLGTISIIFLVSYLGSALYRNRDDSLLLIGLICLLYALYNGMISERVLSMAGTEISFS
TLYKLKDFCSVACLGLLTFYFYRFGTGILSGLLTAVILIIFGAYLCMVALLPISYGL
AAPYVVVMYTLMFLWLLYQCAKQFLTSEKGERLSTFLWYAALLSIVLYCLDINLFSIS
LKENMNIGQASIVLFSILMLFLAVLRFFEAYRTVRTLKDQLLLLDKVKDDFLSNTSHE
LKTPLNAIVNISESLKGAEGPLTDEQAHNLAIVTGSGRRLTYLVDEL LDYSKMKHGD
IPLHRSSTDLYSFVESVMRMHSFLLGAKKVELINRIPAHFPPIYADGNRLIQILHNLI
GNAVKFTERGTVSIKAAVVQGKAEIRIVDTGRGIGTDKLEHIFLPFEQEADTGPPVAG
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LDKLPVHLVIADIMMPDMSGYELLERIRERYSPSELPVLMLTASNKAHQKLKLALEKG
ANDFVSKPFES EELLARIGGLTRMKTSVQAARDAEISFLRSQMNP HFLYNALNAIAEL
CVDAPNRAEQ LILQLSSYLRRSVHFKHLD SKTSLMNELEMIEAYVAIEQARFGSRLEV
IIDVDADVNRNMDIPPLTLQPLIENAIRHGLMSSIRGGRVMLSIRNLNDTETRFTIED
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QRLSTVGNNGGYET"

CDS 5059044..5060162

/gene="cheB_13"
/locus_tag="EFAGFIKM_04411"
/EC_number="3.5.1.44"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00099"
/codon_start=1
/transl_table=11
/product="Protein-glutamate

methylesterase/protein-glutamine glutaminase"

/translation="MMKVIIIVDDEDLSLKRLNRILTESGEVEVSRTFHDPEEACEYAA
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PKTEELLAFLLYAKSTTRDALADTLWKDLSPQKAWTNINSTLYYVRRRAIGDNSDVPII
LKDRNGIRIDREAINCDLYEFETLFRQMRQASAHRPelfERMDTLYTGELLKGRHYEW
AFAWSRQLELDFIMTmetaAHYHAKedePLRALYYFERILQIDSIREDIHREIILLYL
SLGRRTEAQRQYLVLEELLKEELGSSPAADIKQLLRQS"

CDS complement(5060280..5061461)

/locus_tag="EFAGFIKM_04412"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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DLMLLLVDRLVDTKFERDMVATFVRGQYYLPTKARNEATEESEKNEVFAHPFILCSV
NSTEKQRKTLLFDYVEREFKYNIIVDPIIKLSTPEQGFLYPSVTDNYSDVNRVLYCTG
KSNFPDPHFVENVLNGERSVTALEERAIFEDIVKEVAGEQLDSATIAHVYEEINRVIE
INEESHEEEPPKLDYKDLERVLTASGIEDLTTEKVERAFETIVDNKNYEMKATSVMPK
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CDS complement(5061684..5062391)

/locus_tag="EFAGFIKM_04413"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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KAVEKGRTGFKRKYVRC"

CDS 5062909..5064072

/gene="agaA_4"

/locus_tag="EFAGFIKM_04414"

/EC_number="3.2.1.22"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:B3PGJ1"

/codon_start=1

/transl_table=11

/product="Alpha-galactosidase A"

/translation="MSNNQVLGFAPALGWNWSWNTFTWDINEQLIRDVADV FVSEGYLA

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FSACNWGADDVYDWIRESGAHMYRSTGDIRDNWDSVKELALSQLGKQSYTGSFCHNDM

DMLIVGMYGGSNNDYIGSIGGCNDIEYKTHFSLWSMMGSPLMIGCDVRKANQITKDIL

LNPDLIAINQDVEARGAYRIKPEPQWFHTDDVFMLVKVLTGDGLAIGFFNLSDSQREL

SLQFWDMLPYAAGYALSLYDCWEHKEIGVFRERFAPVVAHDCLVVRAKLVK"

CDS complement(5064279..5065088)

/gene="araC_7"

/locus_tag="EFAGFIKM_04415"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A9E0"

/codon_start=1

/transl_table=11

/product="Arabinose operon regulatory protein"

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GQGTLETGGRVFRVLVTGESFIIFPQKEIYYYPDPQDPWEYVWVEFSGEDAGRLLGLTQ

LSEVQPVVTVSPETLQPFHFLAWNAGASSYELLRADARLRLLLSYMEHYPKEPQVDA

KDYVWLARKYIEQNYWKPTLTVTEIVKAVNLERSYLFRLFKAATGKSVLEYITSCRIE

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CDS 5065170..5066705

/gene="pnbA_1"

/locus_tag="EFAGFIKM_04416"

/EC_number="3.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37967"

/codon_start=1

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/db_xref="COG:COG2272"

/translation="MLRMVTEHGVQGLPAADPRITSFKGIPFAAPPVGENRWRAPQ
PQSSWEGVLQAFDFAPISIQAPTVIDDNNIYTREWAVDPDLPMNEDCLYLNWVTPAKR
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ESPHAPANFGHLDQQAGTQWVKRNIAAFGGDPEQITIGGQSAGGGSVLSQMTSPQNK
LFQRAVIMSGIATELYPKVRVPSVRSTLRDAEQAGVEFFGFLGVSSLAETRQLDAEYL
RDKALEYKSWGTVIDEQFCAGDPFTRFVQQEREIPVMLGHTSSEFWTRPAAANLEE
LKQMAVELFGEDAPAFLLQCEADTGQIEHALQQASVRMIQHAILAIRANS
GHPSETP
LYYYNFD
AEIPGWDQPGTFHSVDLWFFFETLAKCWRPFTGKHYDLARQMCNYLSNFIA
TGNPNGPDSTGKLMPHWTPCTTEQPYLMEFGDQAQLQKAEPGPMLAFLIEQYFKKQNA
PVV"

CDS complement(5066900..5068243)

/locus_tag="EFAGFIKM_04417"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNRLLIGKKLKIKLVAVVISLVISALVILQVVGETVLD
SYL
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VSTRDHEQLSAWIRHERYLNLYIFAKDKLIFSS
NTEIDPAINEELLTQFVPSKIPITTIHFADQDAQIYLVSFYEYQYYNLILIGVFIAA
IVFIVSFLMINKKTSYIGVLEQEIKILEGGNLDYSITISGKDELSSLAQSIDEMRKS
FVERLGSEERVRIANRELITAISHDLRTP
LTILLGYMDIILNKYKTHEDLLQYIHNS
REKAYQIKVLSDKLF
EYFTVSSAAEEEEVEFEMYEGRALIDQLIDEQLVVLEDIDVQV
QTDAHHEEFLL
EINLVAMRRVMDNIFSNIRKYADPGHPVHIQISLKQQWVILAVENKI
KHVGRKKDSNEIGLVSCQKMIQQHNGTLTVS
QEKDIFSLQIMLPVIFNKPTQTHI"

CDS complement(5068236..5068928)
/gene="walR_4"
/locus_tag="EFAGFIKM_04418"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9RDT5"
/codon_start=1
/transl_table=11
/product="Transcriptional regulatory protein WalR"
/db_xref="COG:COG0745"
/translation="MSKKILIADDNSEIREIVRILLESENYEVIEAIDGQDAIDKVNE
ETDLIILDMMPNKSGLKACLEIREKTSAPILFLTAKTQDSDKQLAFSSGSDDFLSKP
FSYTELVSRVKALLRRYYVYRGKEKTEEQDQIIVKDLTVHQDSKAVFVGEKEIALTEI
EYQILLLLVKKRRKVFSAENIYESVWGQPYFYTCNNTVMVHIRNLRGKLEDDPQNPKY
VKT VWGKGYKIE"

CDS 5069088..5069849
/locus_tag="EFAGFIKM_04419"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MPQTSKKVMINILLGLFIMLSIGLLVYYSPAIIKIMSSMDNFRA
YIHSTGHWGPVMFILFQILQIVVAPIPGEVVQIAGGYIYGVTLSLYTTIGLIIGSAI
AFYFTRFIGRAYISRLMHKKNNKWMSLIHDEKKFSAFLFIFFVIPGLPKDMLVFVAAL
TSISSFRFFTILIVGRLPWIIASTVVGSTIHMQQYTIAIISVIAVTGFVLGYIYREK
LVGLFSRSDSTKTKPKAIPSYSTNRESRKIKRDTT"

CDS 5069894..5070472
/locus_tag="EFAGFIKM_04420"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQILKTNRLILRNFTVTDAAGLLEYTANPRVNCFMDQRISTLED"

AAAEVAKRSSDDSHIAVCLKDSNELIGELFGMREDRDSDDKDSNSDTYSIGWNFNGR
YEGKGYASESANAFIENLFMEQGIRRLYAYVEDDNFRSQKLCEKLGMRREGLFMEFIS
FVKNEDGTPKYENTYQYALLKKEWLAQRESQK"

CDS complement(5070663..5071829)

/locus_tag="EFAGFIKM_04421"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTDKFQIVGSLLRPDELLKYKTQIEHNDDIQYPFYENYEGYEKC

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NIGGTDSVYQNIQELKEGLVIAYKEFVEEFAAVGGKILQFDDCLWELFADDNPNSPFT

GENINQDEVKGLATEFIDINNTVIDFGHSLGLKMWTHNCRGNYDSRNMGGGSYAKIAN

LFLKQLKYDRFFLEWDDDDRAGSIEALEVFKDRPETEIVLGLLSSKTSTLDDEARVVRL

LDEASKIIDKDRLLLSHQCGFASCDGGNELSEAQQWAKIDQGQKIAKQYWGSTV"

CDS complement(5072000..5072569)

/locus_tag="EFAGFIKM_04422"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSWSKCLKQQLLESFLSPALVGSVEYRATSYSPDKSGNCYITVD

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KKRILNMSEQVKLHPAVQYFYELRRRTV"

CDS 5072822..5073877

/locus_tag="EFAGFIKM_04423"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MATKKATLPAHMEKLVKDNDIATVKEIFEQCEWDARGGYSKGTA
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QNETPLHAAVNGYRTKVQELVNQGATINVENKQGNTPLAKGLINCRNSDIVNLAEIS
AILLDAGASVTPDMKESVKRIGKDFEFVREKFNKDKVDEVSDALIKLYQLFDVEQVAN
RIMHDGNTPIQVKATTWTKQHQLWEYLIPAQGHAAQTVQGEVIRITGRVSHEVLDNGG
GNWDAEYRKMLDALIRHLGSGAPLAPALLQEAADLVSRHLDGYDFDAPARLSELAVLW
VLANPQPVAMEKPAYTR"

CDS complement(5073971..5074945)

/gene="dus"

/locus_tag="EFAGFIKM_04424"

/EC_number="1.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P67717"

/codon_start=1

/transl_table=11

/product="putative tRNA-dihydrouridine synthase"

/translation="MTKENFWRELPRPFFILAPMEDVTDVVFRHVVGGEAGRPDVFFTE
FANTESYCHPEGHHSVRGRLTFTADEQPIVAHIWGDKPEFFREMSIGMAKEGFKGIDI
NMGCPVANVAENGKGSGLICRPALAAEIIQAAKAGGLPVSVKTRLGTFTEVDEWRDWLT
HILRQDIVNLSIHLRTREEMSKVDAHWEILPEIKKLRDEIAPNTLLTINGDIPDRETG
LRLAEQYGVDGIMIGRGIFQNPFAFEKEPKEHSSTELDLLRLHLDLHDQYSELEPRS
FSPLARFFKIYVRGFRGASELRNSLMNAKTTSKVRELLNEFESNEQVE"

CDS 5075334..5075540

/locus_tag="EFAGFIKM_04425"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEISLDMIKDKVECLQAYDFRELERAI EERIGMNKALMLRVKQV
QHQVTFDPFRNKMLYSAIVHFAVD"

CDS 5075741..5076622

/locus_tag="EFAGFIKM_04426"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQELIFMKNYKNNEVLRKSFFELAINTEINFEDWYQQGYWGER
YIPYSYVDGDLVIANVSVNILELIIHGEKKKAIQIGTVMTHPDYRGKGLSTRLMNKNVL
EEYENKYDYMFLFANESVLDFYPKFGFNPVEEHLFSMNYTAKKSSEPANIRKLNVTNA
DDIRLIQKLASERLPVSQHFATNHAQGIFMFYCLNVFSDDIYYLENENVIVIIYQKEDN
HIELFDVSLNELNMKDILDKIADEDETEKITFHFTPDATDDIVLKSSITNEGLFVRTH
GEHLYPVQVKHPITSIA"

CDS 5076807..5078672

/locus_tag="EFAGFIKM_04427"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAFIPLNCPNCNGRIEYKKDEVLKCPYCETELLLKQNHVYYVDQ
TINHYHGTTPPKAPLKQTASVKVMLILMFVLAGAIGTYFYYSNSSTYSKTEANLTVRKM
PESEVLLSFLRDIFDKGSALPTEEELARIRYLTVEHSENDQWKFTYSLSDPFSDEQAE
KITYITQDKKLNSQRIDQRDFEAFKGLTALDNTYEISQTDQTTLAHMPGLKSYAGA
FNESFSTFSGYFGDKSKITELSTQLRSNQELAMLLEFPNLSSLSITYVDESVTDFHLL
NQLPIKSLSLTFVDELGWLSSMTGLSSLSIQYSETDLQPLYALTQLQELQLSYLTNV
KSIDFVQNMPALQTLDIENVNFSSLERLTGKNSITTLRLASSELGSVKAINSLPSLR
ELTSLSGYYENAEALTLPKVERVEIPSSFLPGLKAPVTTSLTRGGSGELNLATLGKFP
KLEQLSLWEIDEITRLAALDGLSLLETLNIDSSSLFKESDALFRLKQVKSVCSECRL
NFEQKAAAENSVLEHLTLEQPYFSINNTSVTEVDQMMPYFANMSALRSFTLQDSNLAS
LEFMSKWKAIEELHLENNANISNIETLSQLPNLHKVYLSGNSVQNKYVLGTGVHVY"

CDS complement(5078811..5079392)

/locus_tag="EFAGFIKM_04428"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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STFYQYFTDIYELLDCVEERILKSIKEEMAGREFSTHTIQDALQCLENAAEEISVLKAI
LGDYGSVHFVERLKREIPFERLIVDFPTDDVLAPYIIEFYISTLISMFRLWIHRDKDL
SSEELIKLIDSLFSKGITPYHIFGTVNPQRSGV"

CDS 5079542..5080468

/locus_tag="EFAGFIKM_04429"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRILFFGRGVISTQYAWAFEKAGHTVEFYVRKGRTETFGSHIAL
EMWDARRRKHLIQESWKVKLHEEISPNYDLIIASVNTKQLPEAAQLLSITAGNTPILI
FNNIWQDLESSILPLSMNNVVFPGAGGGIEDNLTGRGGFLKMIFLEKPRVGTEQINN
KVKELFESTHFKINWIKDMQSWLWNHFAMNAAMETEVLKRGSPFPEIMNHSDSFANVGK
SMREMAPVLKTRGAKMDAITLLLTKIPSGLLGTLFNKVIFAKGSLPRLFIEYNNSKAG
FAVLEVVREAKKLGIPRLTVALENTETTQS"

CDS complement(5080595..5082307)

/gene="rlmCD"
/locus_tag="EFAGFIKM_04430"
/EC_number="2.1.1.189"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31503"
/codon_start=1
/transl_table=11
/product="23S rRNA (uracil-C(5))-methyltransferase RlmCD"
/db_xref="COG:COG2265"
/translation="MSNTNRSGRGKNRRNSAASQGQGNASASRQPSQSRRPSTRQQGK
EVRPQGASLSAVRPKGRARESAPIEGLPVSKNEETVIDIIGMNHGDGEGVGRANGYTLF
VQGALPGETVRVRVMKTKKQYGYAKLLEIVKASPDVRSAPCPYDQCGGCQIQHMSYA
GQLAWKRQLVVDNLQRIGKLNVMVEDAETLASNVQEDASVGEANEAKMIGSNRIRLRL
EGVMNEEDTEQGIRVLPMTMGMDPEWRYRNKAQVPIGAAEGGLVGGFYAKGSHRIIDME"

SCLIQHEHNDEVVAKVKEIGSHFGISAYNEETGRGLLRHVWVKAFRTGEMMLVLVTN
GRDIPYKDEWIGSIREAIPHVASICQNVNKKQTNVIFGDETRVLWGRDVIYDYIGDVQ
FAISARSFYQVNPVQTEVLYGKTVEYAGLSGKETVIDAYCGIGTISLFLAQHADQVYG
VEIVPEAIEDARSNALLNEMRNVKFEVGASEDVIPRWKEQGIEADVIVVDPPrKGCDP
RLLETILEMKPERVVYVSCNPSTLARDLRVLEDGGYRTVEVTPVDMFPHTVHVESVAM
LVRV"

CDS complement(5082936..5083817)

/gene="dagK_1"

/locus_tag="EFAGFIKM_04431"

/EC_number="2.7.1.107"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31502"

/codon_start=1

/transl_table=11

/product="Diacylglycerol kinase"

/db_xref="COG:COG1597"

/translation="MKKARLIYNPTSGREEMKKRLADILQRLDQGGIEASCHATTGEG
DATREAELAIERGYDMIIAAGGDGTLYEVIINGMAERENRPPLGVFPLGTTNDFARALG
IPRQWEDYVDLVINQQLRPLDLGKANDKYFINIAGGGSLTELYEVPSRLKTMIGQLA
YYMKGIEKMASLSPQELIIRADGQEEIHDEFMLFLIANTNSVGGFEKLAPGATIDDGL
FDVICVRKCNLADMIRLVTLALRGEHLNDKKVVFQTSHEMTSPGYVQLNLDGELGG
TLPATFTNLRHHLMLYR"

CDS 5084343..5085059

/locus_tag="EFAGFIKM_04432"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKIVLMLLVFLMACIPWVTVEAAEINHDAQVVGFEVSPVTVM
QQAAKRFQPFVKVYHGCVPFPAVDQQGNTSAGLSTSGSSNGNCSSNTGQIYSRSAWHN
GVWAIMYSWYFPKDSPSSGLGHRHDWEGIVVVDNPAAANSKILSIAYSGHGQFTKVT
PSNNNTQGNHPLISYNSTWPLNHELGVTVNAVGGTQPLIGWDDLTSAARNALNTTDFGS

ANVPFNDNNFTNNLNKAWFR"

CDS complement(5085156..5085572)

/locus_tag="EFAGFIKM_04433"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MREVPMSYVKANQVGIVLFVILSFVFNPIVVLGALWSIQVVGLA

SSGKLNLFVQIGKAVLTGKGTETQAVELQRFNNILAVLFLSLALISFSLGWVAAGYVF

SVMLLAAASAALLGYCVGCTVYFWYKQLRAGRKIGF"

CDS complement(5085644..5086570)

/locus_tag="EFAGFIKM_04434"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKILVYGAGVLGSQLAHVLVRGGNDVTVLARGKRAEELEKDGWV

IRHVFQFKTTVDQVRVARTLEVDDQYDLIFVVMKYNDFSSVLPILAENQSSNIVIVGN

NADARSMQNFLEENSRVAKQIAFGFHVSAKGKREKDRMLSVGGGNGQMVIGSLDGEIGF

KPLLDQAFQHVKYKLNVLSDIDAWLKSHIIPILMLNVVSFNEERELIKLDGNRKQIQH

MIRAMDEGFSVLEAMGITIPEIQAKMIRKHQRMLYLLKKIYSMLPVBHKLKLVAGSFGEI

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CDS 5086739..5087308

/locus_tag="EFAGFIKM_04435"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDRRVLKTRKAIEAFVGLLEEQDFEQITINEIADRANVNRGTI

YLHYADKFDLLDQCIETYLQRLLDACMIESPTTTPVTAKDALLRTFCYLEQHATTYTT

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CDS complement(5087455..5088240)
/locus_tag="EFAGFIKM_04436"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKPGVLIISHGSQEQTWVESVDDAISRLNLPVPLPVEAGFLEL
VEGRLIQDGDIDRLEAQGVTDILVVPLFVSSGSTHVDEIEYAIGAKETPDRETDLEPFD
VKARVHFGYPVDNDPDIALMVWDKVRLLSQPEKETILLVGHGSIHDGFRERWEAGIS
SLTERVQEVSGVAHTDYALLNPESVYDKVKYWSEERGNRVIVAPLFLSAGYFTRNVIP
DRLRELNYYVSGETLLPHPLLQWLERQIQILLERCNEVKASS"

CDS complement(5088242..5088532)
/locus_tag="EFAGFIKM_04437"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQLKKLNDKSIEQLFEAILTLKDIEECYVFFDDLCTVNEIQSMS
QRLEVARM LGKGNTYNQIEAETGASTATISRVKRCLNYGNDGYKMTLERLGR"

CDS 5088986..5089621
/locus_tag="EFAGFIKM_04438"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MPQHYYHRQPAPRQRPSSHAHRQAHTSAYMPPGVVPRSLNETQI
QPMYPGVEPHYPGFGEVEASAIVPYGQGAPGGNFYGGAAQVLPPAPVPAPATGSSGFS
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AADADYEEYKPSRKRKSKRRNKATNVPRRRNTTPTRRKSNSTKRRPKSRKG"

CDS 5089755..5090843
/gene="yhaZ"
/locus_tag="EFAGFIKM_04439"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07541"
/codon_start=1
/transl_table=11
/product="putative protein YhaZ"
/db_xref="COG:COG4335"
/translation="MELIKDKYTPALIDRTGEQLRQFYPKLDTQQFHELVFAEGWEQL
EFKARIRRITLALTQVLDPDNYEEALHIIIEQAAPTMRGVEYLFVPDFIEVNGLDPEDYE
LSMKYLTFTPYSSSEFAVRPFIEHYPIQTMKHMMAWAESNNEHFRRLASEGSRPRLP
WGAKLQNFITDPTPVLPIHLALKQDESLYVRKSVANHLNDISKDHPELVMDLATTWYG
QHVHTDWIVRHASRSLKKGHSKALSFLGYNEQDSIHIEQLQLVQDTISIGEDLHFSF
DVVNESGESQMLRIEYEMGYMKANGKQAPKRFKCSDKMYPTGRTKVATKQSFKIITR
KYYAGLHTLTIVVNGKEAATTSFVLEME"

CDS complement(5091085..5092044)

/gene="corA_2"
/locus_tag="EFAGFIKM_04440"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9WZ31"
/codon_start=1
/transl_table=11
/product="Cobalt/magnesium transport protein CorA"
/db_xref="COG:COG0598"
/translation="MIRTLAITREHQVSVNVPLTQLDLNDYAWWWADFNQPTEESRL
LDTYFHFHPLAIEDCLHVLQRPKLDYYDNLQFLVLHALNPSTLEAEEVDLFLGSNFLV
SFHHGVLEEVEAWERLLHHAHERTIWARGPVAAAYTVMDKLVDPHYFPSLFAIEDELA
ELENRGGQESVEDLMNQVFDLRLRLLKLRRTVVPMRDLLYRVVNSQHVQRTGEHTAYF
TDIYDHLLKLTDMEADREMTADLRDSYISLNSNRMNQIMKTLTVITTVFMPLTLIAG
IYGMNFAYMPELQWKFGYGAVLLLMFVLGGSMVAWFVKRGWFK"

CDS complement(5092352..5093341)

/locus_tag="EFAGFIKM_04441"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
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IFAKRSPHNVNKGFRTVQIFTAALQAFTHGTNDAQKAMGIITFALVAAGVQDNLDVPL
WVKISAATAMALGTSIGGWKIIKTMGTIKFKIEPINGFAADISAASVIFTATLLHLPV
STTHAITSAILGVGSAKRFSVAVKWGLAGRIITWFITIPITAGLAGLLYWIIF"

CDS complement(5093356..5093976)

/locus_tag="EFAGFIKM_04442"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MKLKKKKDIFFETLENMADTVVQAADYFSQHVSNLQDVTLFANE
MKKYESKCDDYVHTIITELNKTFTPIERDDIMELTTTLDDVLDGLEATASRFYMYQL
TDPDDEFVIQFAEILRQSAYEIQKAIHLLSQKKLLAIREYTIRLNDLENQGDEVLRMC
IKHLFATVSDPIELIKRKEIYERLETTTDCEDVANVLESIIIMRNS"

CDS complement(5094294..5095367)

/gene="yerB"
/locus_tag="EFAGFIKM_04443"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34968"
/codon_start=1
/transl_table=11
/product="Putative lipoprotein YerB"
/translation="MKLFWKKAASAASLFILSLSLVACQNQEVAQLPVQPEPTPAPI
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KQHMDEISNGGPYFWRSSDRKAPHNLYTSADKLREGSDIKGYSHDFKSPVYNYNEEGA
TSVGEAVKQFDIHYLLDSYRVTYDYDEVSGRYMRMVNGKADQDLNQTQLGAANIIVA
GADHKVLDSVGRLSVNLEQGGEAMLFQKGKMIRGQWVKKQGDIIIRFVQGGSEVALVPG"

KTFISIVPNQPEFSSHVKLAVQQ"

CDS 5095705..5096244

/locus_tag="EFAGFIKM_04444"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFSTNQWLRENKVAMWILTVLRVYIGYDWMTHGWSKLTGGFQAG
GFLAGAVEKATGDHPAVQAWWATFLEKFAVPNAGLFDVFIPLGEFLVGLGLILGCFTT
LAALMAMVMNFAFLFSGTVSTNAQLVVMEIFLVVAGANAGKIGLDHWVLPYLRGLITR
NKGNHPKDTPPTISPTQKTA"

CDS 5096400..5096612

/locus_tag="EFAGFIKM_04445"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPTQRRLETDADFQEAMNMKYKVRVFKDNHQIDSGGIIIRFDSN
TVVVQSSVSELAYHSRTDCELF EIRK"

CDS complement(5096785..5097570)

/gene="ygiD_1"

/locus_tag="EFAGFIKM_04446"

/EC_number="1.13.11.29"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P24197"

/codon_start=1

/transl_table=11

/product="4,5-DOPA dioxygenase extradiol"

/db_xref="COG:COG3384"

/translation="MTLPALFIAHGSPALAVESNDYTHFLNQLGDRLPAPKAIVVFTA
HWDCPEPSVTMDDTHQTLHDFYGFSTMYTMEYPASGQPDLANEICALFTRSNLAHQ
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IRGRGLDHGVVWVPLLHMYPEANIPVIAVSVDLSLRTPQEYDIGRMLEQLRHDDVLIIG

SGGTVHNLRLLGNTDEPQEWAVEFDNWIGERLQQWNTRELFQYEKKAPHARTAVPSYG

TEHIAPLFYAMGTADMSRSKRFLQSYPGTSLNLCWQFGDGV"

CDS complement(5097674..5098504)

/gene="menH_2"

/locus_tag="EFAGFIKM_04447"

/EC_number="4.2.99.20"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01660"

/codon_start=1

/transl_table=11

/product="2-succinyl-6-hydroxy-2,

4-cyclohexadiene-1-carboxylate synthase"

/translation="MERQISIRHGQEELTATIHYPVVKDIKEEKSQQRVPLAVICHGF

VGSRIGVDRLFVKTARELAEDGYLVLRFDYIGCGESSGEYGAEGLESMVLQTRSVLDY

AVNCSDVDPTRVTLIGHSLGGAVALLTAVRDKRVKNLVMWSSVGYPFNDIVKITGREV

YDEGVKLGAAADYLGKFTPTFFESLAEQQPFQEAVKFSGDVLVHGTSDIIPVDYAF

LYQKVFWMRQEGRCDKEIIFQGDHTFSSGKEREQLITRTREWLGERQKIEQDWQHWMI

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CDS complement(5098759..5098992)

/locus_tag="EFAGFIKM_04448"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDKQTELTRKLLNSNSRGVVDEVVSFEENLEDTEYAEELTDGN

LKGRSFDWNTDSGHEHEWNGRVETHEMFRRSYE"

CDS 5099405..5100217

/locus_tag="EFAGFIKM_04449"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGISYKKLKEIQNRQITEMSRMTPEHVKLYDEISTARHAPADE
RTQEEWILSAGKAIVQAQRDNKPARELYGPDLEQDIHAQLGITNTAPEKTA AVEVGKS
SPTRDNSSTASSKKNANAVEPQPTENPEPVKRTPMWYAMIAWAALS FVMLIQGCVGLF
VGWTGGDTEPFQHISLFSLIVA AVGGIALVEMLRRLAERP DDEGADKNTVPKVN LKGI
IIYIVIVVLVLFVGYPLRDKLPVFALAPWVSAVIGVVGLATVRPLFGQK KTA"

CDS complement(5100244..5101149)

/gene="rhaS_37"

/locus_tag="EFAGFIKM_04450"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MLAFRLTGLPDSRLPLYLYCVGTQEEKVLHRPDGFPVYQLFLSR
GGEGQFKITGKGTWTIGAGQLFIVEPEVAHEYVPHSKSKGELGYIGIGGTSAGSVLQS
TGLLQNEPCHISGFVWSRMTNLWHALDQGATEMWNTSTLIYQLILDIAQLKISSDV
GIGDIGSSRAQDGTVKHSNRES DPSKDALVRAVALMH THYQDDLLLKHVADAVGYSVQ
HLNRLFHQHYGVTGHQYMQRLRLQKASDWMDKHPRASVREAAETVGMEVNYFIRIFKR
EFGETPGKGIKHRNQLQMEKDLTNS"

CDS complement(5101370..5104540)

/locus_tag="EFAGFIKM_04451"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKVMSALAVSAMLMSALPTSVMDAAARISYINDAELSSAQAP
VMKGGRVLVPLRSIFEGLD AKVQYTNRTKTIVATRDDQEVTLKLGSKTAYINGE AISL
DVPANTIKGNTMVPIRFVSEAFGEKVFWNSRNQRVDIKTTATPPVDETQYAAWNIYGS
VSGSNGDGRDLTVSFTRPTSEKAVSAYRIMLVKTRDVNSFTESSATAVPSANYTSVTP
NGSNPKLTLNAQTRDVNGDFLNSNETYRLYVLTVGNSSNNYKNALNWSSQALKLNNVK
STVQAVTSLRAADISDYGDGRDLEINF TQPSTTSNITYYRAFVVKAKDSSAFNLAAAN
KVSSANSTIIYKGNSTAVKSQ L TSSTRDTSGEMIKSGTAYVVYILSVSTNTTTDSKLS"

AASSSLTSLVNTATSPVITQVKDNSDYGDGRDIQVSFNRSSDESKVANYRVFVVRNSV
ASSFNLTTASNLSSSLYYTVNKTGNNITTTLPSSMKDTSGYNVTNLQDYRIFVMAVGN
QQNGYTNALSASSTVLRLLTNGNAGVISNLAVADISDYADGRDLRVSFNKAADSRIS
AYRVYVVRSANVGSFTLSAANASNNTQVNKTGGNLSVTLPNYAVDTNGYTITNNVAY
RVFVLSVNNNGNSSQNALSGYSSQITLTQNAAITAPSNVTATDIGDNGDGRDIQVTFN
KSADETNVREYRVFVVKANSTLSLSTASALNSAYYTSVGKTGNNRSFTLPSGTIATDG
SKIINGVEYRVYVLAVNNNGSLSNALSSASGIIKLNTTSTVEAVSSVKATVKEASQAT
GDATDILITFTKPRNDTGISNYAIMIVPSSQVDVFNLSAKAVLKLNKYLSVSKNGSS
TDVQPFVAVTTDVNGAPIDSSKSYQVFVLSVSDSNTRESSLSGASNIIKVNPKQQQPVE
VKAASLTATDATGAQGPAIKINLTPNATEQGISQYKVFVKNVSNFTLPVANGVNNTD
RFQILVTGSKEDLTLTLSKDTDGDAIVAGTSYQVYVLSVADQQQATINALSAPASVQL
AAAQQPATGSPASDTPVVDPNNTTSP"

CDS 5104857..5105825

/locus_tag="EFAGFIKM_04452"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTSSFQSAKRTGMRTFITATAILMLLQTAVAPLSVVAATSSST

DTKVTTASSTTIYKTFQSMLYKKNGLPAADTYLESHIKKVTKHHATLMVLQLENARLK

ALSAMTDRLLVPNVQDKMIKAYKLNDSTKLMERTQDSDLLALLKEARDSGYRLVMLE

GSLYPIMNYAAFVKYTSVIKEDISSYISIMTKETKNLPEDDGALVIGYQEILLRALSQ

ERFLELHPKSNRAKQVQNLLNSYTYFYGLNNTPLFDYDTNKMVANAQRGYNGVLQR

LASVDSEFLRLDAFMDVVKESKYEKTAVEKWLEQNPVSDYANY"

CDS complement(5105976..5106578)

/locus_tag="EFAGFIKM_04453"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNNSKMPSDHQETSPLIRPARIEDADQVIPLLYQAIGDITYSLA

GEADHEKAMQILQEYVQEDNRISYRHVTVMERDGLIAGILVAYDGGEADRLDQPILD

RPGRSQEEKYALVKETRPGEYYLDTLSVSEAYQGQGIGRALMAAFEQQGRDLGHSQVS
LIVERDNGRALMLYERQGYVKDDVIVIAGHEYNHMVKPIQ"

CDS complement(5106578..5107870)

/gene="ilvA"

/locus_tag="EFAGFIKM_04454"

/EC_number="4.3.1.19"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WG95"

/codon_start=1

/transl_table=11

/product="L-threonine dehydratase biosynthetic IlvA"

/db_xref="COG:COG1171"

/translation="MKPVEQEPTGTTSPGRASVGMEDIVRAHHVLREVIVRTPLQRDA

VLSAKYNCNVYLKREDLQVVRSFKIRGAYNMIRSLTPAEMEKGIVCASAGNHAQGVAF

SCNALGINGKIFMPSTTPNQVKQVRRFGGSNVEVVLIGDTYDDAYAEAMRACDEQGM

TFIHFPDQPKIIAGNGTVAMEIMESLDENADYVFVTIGGGGLAAGVGTYMKTVPETR

IIGVEPLGAASMSEAMFRKQVVTLDIDKFVDGA AVKRVGDLTFDICNSILDDIVKVP

EGKACTTILELYNENAIIVVEPAGSLAVAALQYREQIVGKTVCVISGGNNDIDRMQE

IKERSLIYEGLKYYFMVNFQVRAGALREFLEEVLGKNDDITRFEYTKKHDKENGPAV

GIELMYKEDYHPLIERMNRKGIAYTELNKNLNLNMLI"

CDS complement(5107934..5108824)

/gene="rutD_6"

/locus_tag="EFAGFIKM_04455"

/EC_number="3.5.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00832"

/codon_start=1

/transl_table=11

/product="Putative aminoacrylate hydrolase RutD"

/translation="MNPNPSSHTFGSSAFVTRDGRKLHYMSRGTGELTVVFESGMGA

SRSNWGLVAPAI AEHARAVVYDRAGAGRSVD SAPRSLERIAAGDLGELLTALGP GPF

LVGHSWGGPIVRAAAAAHL SRLRG IILVDP SDEHCEMYFSKLT KKSFAINGFIIPIMA

RTGLYKMLGSKAGSVQPDDVAADHLKEDFTVRAASTMLAEGKTFLLDDMAALLEHPPAL
GDLEVSVISGTPGKGEGKIRPALITAHRTQTVSQLSNARWIGADQSGHVMYTDQPVI
INEIVRMINDVSSGARTEQK"

CDS complement(5109191..5111482)

/gene="bglB_2"

/locus_tag="EFAGFIKM_04456"

/EC_number="3.2.1.21"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P14002"

/codon_start=1

/transl_table=11

/product="Thermostable beta-glucosidase B"

/db_xref="COG:COG1472"

/translation="MERNIKELVQRMITLEEKAGMCSGLDFWHLKGVERLGIPSIMVTD

GPHGLRKQDGSADHLGLTSSVPATCFPSAAGLASSWDKELARQVGVALGEECQAEDVA

VLLGPGVNIKRSP LGGRNFEYFSEDPLLSTQMATGHIQGVQSQGVGTSLKHFAVNNQE

ERRMSIDAVVDERTLHEIYLASFEGAVKDGQPWTVMCSYNKVNGTYAGENEWLLTDIL

KDEWGHEGLVSDWGAVNERADALAAGLELEMP TSGGIGERKVIDAVESGQLPLDKLD

RAVERLLTLIFNAVDQKQDGATYNKDEHHQLARKVAAESMVLLKNEEGILPLGREGDV

AIIGAFARKPRFQGGGSSHINPTKVDDIVEEMTQVAGESVTFSYAPGYRIEADDVDET

LMHEAVQAAQSADTAVVFVGLPDRYESEGYDRAHLRLPDNHIRLIEEIAKVQSRVVVV

LSNGSPVEMPWLPQVQAVLEAYLGGQAVGGAIADLLYGEVNP SGKLAETFP AKLSHNP

SYLNFPGEGRVDYREGIFVG YRYDKKELEPLFPFGYGLSYTTFEYADLKVDRTLT

DQDEVNVQVRVTNTGDRAGKEIVQLYVSDVESTVIRPVRELKGF AKVALEPGESKVVS

FTLNKRSFAYYNVDMKDW HVETGEFEIQVGSSSRDIHVHTRVNVESTATFLPTYTRNS

TLGDIQRDPAHKQLLDQALQQFQEASGFGGDDAGDHADMMMDAMMKY MPLRALVAFSGG

AMTEEAMNELLEQLNNKDHGIRG"

CDS complement(5111699..5112322)

/gene="mhqD"

/locus_tag="EFAGFIKM_04457"

/EC_number="3.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34842"

/codon_start=1

/transl_table=11

/product="Putative hydrolase MhqD"

/db_xref="COG:COG0400"

/translation="MTTNTMKHIYKAGAQPDAPTILLHGTGGTENDLISLAEMIAP

GAGILGVRGNVSENGMPRFFRRLAEGIFDEEDLIARTAELGSFVDAAAVEYGFDRSNV

YALGYSNGANIAASLIFHQADVFKGAILHHPMVPLRGLELPDLKGLPVFIGAGENDPI

VPRRETEELASLLSGAGADVNTHWERQGHQLTRTEAEAAAAWFKQAQ"

CDS complement(5112319..5113269)

/gene="mhqO_1"

/locus_tag="EFAGFIKM_04458"

/EC_number="1.13.11.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P96693"

/codon_start=1

/transl_table=11

/product="Putative ring-cleaving dioxygenase MhqO"

/db_xref="COG:COG0346"

/translation="MFRTSGIHHITAFVDDAQKNVDFYAGVLALRLVKKKTINFDA PDV

YHLYYGNEQGAPGTIITFFPQQNSRRGVIGSGQTGVTVYAVPVGSLPFWKERLASFDI

PYENKTRFGEQYIRFFDKGGLLLEVEREGGQPSNWSFNGVTPEHAIKGFGGAVLFSH

VPEKTM DVLVSKLGLEQVGEENGLRLQASGNIGQIIDIQSTGIQRGIGGAGTVHHIA

WRAKDYVEHEQIQQDLEQSGYHPTPVIDRQYFNAVYFREPGGILFELATDPPGFARDE

PAESMGKLM LPEWYEPQREQIEQLLPRIEVREWKGESKS"

CDS complement(5113523..5114605)

/locus_tag="EFAGFIKM_04459"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WLQ7"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/db_xref="COG:COG1253"

/translation="MDGIILNLFVAVFIGLTAFFVGAEFALKVRMSRIDQLISEG

NKKAVLAKKVAHNLDYYLSACQLGITITALVLGALGEPTVEKMLHPLFERLEVPAALS

TVLSYGIALAIITFLHVVIGELAPKTLAIQFAERMTLLLAPPLYWFGKIMNPFYALN

GAARLLLGIFGVKPAGHDSVHSEELKLIMAQSFESGEINQTELDYLNIFAFDERLL

QEIMIPRDKIVTLNKEMPIDQIIETLNRHEYTRYPVIANGDQAHFVGFINTEMLTSV

AAGRDFNMETFVHNTSPFSERSPIKDVLIQMQQSRVHIATVKNEAGATVGMVTMEDIL

EEIVGDIKDEYEHKDLVNPPKRMKLV"

CDS complement(5114889..5116226)

/locus_tag="EFAGFIKM_04460"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WFP3"

/note="UPF0053 protein Rv1842c"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDIITILNIALLIILIALTAFFVASEFAVVKIRTSRVDQLVAEG

NKKAVLAKKVVSOLDYYLSACQLGITVTALGLGALGKPTVERLLYPVFNYLDVPASIS

SIASYAIAFILVTFLHVVVGEMAPKTLAIQFSEKLTMLAPSLYWFGKIMYPFIWALN

GTSRVLLRGFGVKPAKHDQAYSEDEIKIIMNQSIEGDENNKTLSYLENVFVFDERDA

KDIMVPRTLVTLTDQDMTYDDIIPILDEHNYSRYPVIEDGDKDRIIGVVNVKKILPDM

VAARSYQLSEFVREIPFVSEVTSIQDAMIKMQQERVHMAVVVDEYGGTSGIITMEDIL

EELVGEIRDEFDADEVADIQETGENQYLINGRVLLDEVERQFGLIFEGNEEMDTVAGW

IQYQKGVGVEKGDTEHGDYVWTVVDTENYHIKQVLLERVNGAQVEEATSDLA"

CDS complement(5116934..5118199)

/gene="purD"

/locus_tag="EFAGFIKM_04461"

/EC_number="6.3.4.13"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P12039"

/codon_start=1

/transl_table=11

/product="Phosphoribosylamine--glycine ligase"
/db_xref="COG:COG0151"
/translation="MDILVGGGGREHAIWALAKSPKVDKIHCAPGNAGIAQLAECH
AIAVNEFDKLTALAVELKVGLVVIGPDDPLADGIVDTFDSTGIPVFGPRRNAEEIEGS
KTFMKDLLHKYNIPTAAYEKFDNYEQAQAYLNEQAIPVVIKADGLAAGKGVTVAYSRE
EADQALRSIMVEKVFGEAGAKVIIIEFLAGQEMSILAFVDGETVRPMAAAQDHKPVFD
NDQGPNTGGMGTYSPHIPASIIIEAVETIIKPTAKAMVSEGRPFQGVLFAGLMISP
DGKPKTIEFNARFGDPETQVVLPRLKSDLFDIFWATVHGKLADIEIEWSDEAAVCVVL
ASGGYPGPYAKGVVIEGLDQVDDAVVFHAGTARSEAGDWVTNGGRILGVVGLGANIAE
ARNKAYQQAERIHFDGKHQRTDIAAKALV"

CDS complement(5118328..5119875)

/gene="purH"
/locus_tag="EFAGFIKM_04462"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P67544"
/codon_start=1
/transl_table=11
/product="Bifunctional purine biosynthesis protein PurH"
/translation="MSIKRALVSVDKTGIVDFCRELSQMGVEIISTGGTSSLLSKEG
VPVIGISDVTGFPEIMDGRVKTLPVAVHGGLLAVRDSEEHKRQMEENGLGYIDLVVVN
LYPFQDTIAKPDVTYEDAIENIDIGGPTMLRSAKNHTFVSVVVDADYGVLEEVR
NGDTTLETRKRLAAKVFRHTAAYDAVISDYLSNLNGDPLPERLTVTYEKLQDLRYGEN
PHQQAIFYRKPLAAQDTLTAEQLHGKELSYNNINDANAALQIVKEFEPAVVAVKHM
NPCGVGIGASIYEAYS KAYAADPTSIFGGIVAANRIIDS DTAGKLSEIFLEIVLAPDF
TQEALDILTKKKNIRLLKTGELNAARKRESQFVVTSIDGGMIVQQSDVHSIEASELNV
VTDRAPSEEEELKQLLFGWKVVKHVKSNAIVLAANDMTVGVGAGQMNRVGA AKIAIEQA
GEQAKGAILASDAFFPMGDTLELAAKAGITAVIQPGGSIKDEESIKVAN EYGIAMVFT
GVRHFKH"

CDS complement(5120210..5120827)

/gene="purN"
/locus_tag="EFAGFIKM_04463"
/EC_number="2.1.2.2"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P99162"
/codon_start=1
/transl_table=11
/product="Phosphoribosylglycinamide formyltransferase"
/translation="MANYRIAVFASGEGSNFQSLVDAVRNGGLDVSDLLVCDKPAAR
VVQRAQDAGVDCHLFTPKNYASREAYEAEIVEVLESKKIDLVVLGYMRLTTSVVVDH
YAGRLINIHPSELLPAFAGKDAIGQALEYGVKVTGVTVHFVDGGMDTGPIIAQHPVPIL
PEDTPESISRSIHAAEQQLYPEVVSFWFAQGLVQLDGRHVTVNKPV"

CDS complement(5120827..5121867)

/gene="purM"
/locus_tag="EFAGFIKM_04464"
/EC_number="6.3.3.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q81ZH0"
/codon_start=1
/transl_table=11
/product="Phosphoribosylformylglycinamidine cyclo-ligase"
/db_xref="COG:COG0150"
/translation="MSEAYKKAGVDIAAGNEAVERMKKHKVTRFRPEVMTDLGGFGAL
FGLNKDKYDEPVLVSGTDGVTGKLKIAFAMDRHDTIGIDAVAMCVNDIVVQGAELFF
LDYLACDKVPEKIEAIVAGIAEGCHQSGCALIGGETAEMPGMYSEGEYDIAGFTVGI
VDKAKIINGTTIAPGDTVIGLASSGVHSNGFSLVRRLLLEDAGLDLHDEVAELGGKLG
DSLLEPTKIYVKPLLSLLEKVKVKGMAHITGGGFNIENIPRMLPSNVNVDIDYGSWPIL
PIFNLLQKEGAVSNRDMFTTFNMGVGLVLVNEADATEALQQLKTSGEEAYIIGRVTE
GDARVTLTGADV"

CDS complement(5122283..5123761)

/gene="purF"
/locus_tag="EFAGFIKM_04465"
/EC_number="2.4.2.14"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P00497"

/codon_start=1
/transl_table=11
/product="Amidophosphoribosyltransferase"
/db_xref="COG:COG0034"
/translation="MSHELTGTLWTGDYYNEGSGKEGLDKLKEECGVFGVFRHPDAA
SLSYYGLHALQHRGEESAGMCVSDGSQFNYHRGMGLVKEVFTKDLMQTLTGDISIGHV
RYSTSGDSKLTNAQPLVFKYRDGDLAVATNGNIVNAPTIRRELEQSGSIFQTSDTEV
IAHLIARSSKGLVEAAKEAFQRIVGGYAFLIMTNDKLLVASDPHGLRPLTMGKLGDAY
LFASSETCALETIGAEIRDIEPGELLVLDADGLHEDRFDHHKHKALCAMEYIYFARP
DSDMNGTNQHAARKRMGSRMAIESFVDADLVTGVPDSSISAAIGYAEQTGIPYEMGMI
KNKYTGRTFIQPSQELREQGVKMKLSAVRRVVEGKRVMIDDSIVRGTTSTRIVNMLR
DAGATEVHVITSPPFKNPCFYGIDTPDSRELIAQLSVEEICREINADSLEFLSPDG
LIASIQGDNQDDPKGGCLACFDHDYPTRLDFGGEEKFGCSC"

CDS complement(5123746..5125989)

/gene="purL"
/locus_tag="EFAGFIKM_04466"
/EC_number="6.3.5.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P12042"
/codon_start=1
/transl_table=11
/product="Phosphoribosylformylglycinamide synthase
subunit PurL"
/db_xref="COG:COG0046"
/translation="MTQQLSAKEPTAEQVAEHKLYAQMGVSDSEYALICEFMGRKPNY
TEIGVFSVMWSEHCAYKNSKPLRRFPTGPRVLMGPGEAGIVDIGDNQAVVFKIES
HNHPSAVEPYQGAATGVGGIIRDIFSMGARPVAILNSLRFGKLESDRVKYLFEHVAVG
IAGYGNCIGIPTVGGEVMFDESYEGNPLVNAMCVGLIDHDKIQRGVAKGVGNPYYYVG
PPTGRDGIHGATFASVELTEESQRTAVQVGDPFMEKLVMESELELIDTGIVLGIQD
MGAAGLTCSSAEMASKAGNGLELYLDQVPQREEGMTPTYEMMLSESQERMLFVVEPKDE
AQAMEIFERWGVICAKVGKVTDDGRLKLIHHGEVVGDMPTALVDECPVYDKPSSVPA
YYEQSASIDTLRYDEVTDLGGALKQVLASPTVASKKWIYDQYDYMVRTSTAVRPGSDA

AVVTIRGTRKGLAMTTDCNGRYVYLDPEVGGRIAVSEAARNIVCSGAEPLAITDNLNF
GNPEKPDIFWQMEKAVDGMAEACRVLDTPVIGGNVSLYNENAKGSIYPTPVWGMVGLV
HDTDHITTQAFKSEGVDVILLGETKAELGGSELQYAVHGGQTEGRPPELNLQTEKALLS
TVLEAIQSGLVRS AHDLSEGG LAVALAES CISGNVGAQVNVETALRADHALFSESQSR
ILLSATPEQAGKLEAFVRERGV PVAVIGRVEGSNLTIELNGTSAVSEPVGG LAQWED
AIPCLMN"

CDS complement(5125967..5126656)

/gene="purQ"

/locus_tag="EFAGFIKM_04467"

/EC_number="6.3.5.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P12041"

/codon_start=1

/transl_table=11

/product="Phosphoribosylformylglycinamide synthase
subunit PurQ"

/db_xref="COG:COG0047"

/translation="MKFAVLVFPGSNCDIDCYKAVEDAIGQEVDYVWHTATDLSAYDC
ILVPGGFSYGDYLRCAISRFPVMNEVAKAAEQGKYILGICNGFQILTEAGLLPGAL
IRNTSLKFRCHDTV LK VANADTPFTRDYVPGEIIIPIAHGEGNYCDEETLASLQAN
NQIVFTYGTNPNGSLGDIAGVCNEAGNVVGMMPHPERAVDSLFGSEDGKRMFTSILKA
WRDRHDAAAIR"

CDS complement(5126661..5126906)

/gene="purS"

/locus_tag="EFAGFIKM_04468"

/EC_number="6.3.5.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P12049"

/codon_start=1

/transl_table=11

/product="Phosphoribosylformylglycinamide synthase
subunit PurS"

/db_xref="COG:COG1828"

/translation="MIKATVYVTIKQSVLDPQGVAVQGALHSMGFNEVESVRIGKVME
LNLDTTDRAEAEKRLKVMCEKLLANTWVEDYRYELEG"

CDS complement(5127479..5128351)

/gene="purC"

/locus_tag="EFAGFIKM_04469"

/EC_number="6.3.2.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WHN1"

/codon_start=1

/transl_table=11

/product="Phosphoribosylaminoimidazole-succinocarboxamide
synthase"

/db_xref="COG:COG0152"

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LDPVPEKGNVLNKLSSFWFELTGGMMENHVVHTDVNQLGDLITNPELLRDRIMVTRK
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DEDIPMDRMKELVGDALAVELQEKSRLRYEFARDYCDQRGILADCKFEFGIVDGKVI
LIDEIFTPDASRFWAKENYELDIEIDSMDKEPVRTYLAGTDWDKNSKPDPLPQDVVET
TTARYVDIYNRLTK"

CDS complement(5128601..5129899)

/gene="purB"

/locus_tag="EFAGFIKM_04470"

/EC_number="4.3.2.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P12047"

/codon_start=1

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/product="Adenylosuccinate lyase"

/db_xref="COG:COG0015"

/translation="MIERYSRPEMRAIWTEENKFQSWLEVEICACEAWAELGVIPKEE
AALLRQNASFIDIRIYEIEKETRHDVIAFTRTVSESLGAERKWWHYGLTSTDVVDAL

GYVLRQANEILEKDIVNFIEILREKALAYQHTPMMGRTHGVHAEPTTFGLKMALWHEE
MKRNLERFRHAADNVQYGKISGAVGTYANIDPFVEEFVCEKLGTKPAPISTQTLQRDR
HAEYMATLALIATSLDKFATEVRALQKSEFREVEEAFAGKQKGSSAMPHKRNPISSEN
ISGLSRVIRGHMVSAYENVTLWHERDISHSSVERIILPDATMLLNMYMLNRFGNIVKNL
TVFPENMKRNMERTYGVPFSGRIMTKLIDKGFSREQAYDTVQPRAMQAWEEQRQFQDI
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CDS complement(5129896..5131098)

/gene="purK"

/locus_tag="EFAGFIKM_04471"

/EC_number="6.3.4.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A695"

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synthase"

/translation="MSSTGKQSGIAEELKKVLLPGKTTIGILGGGQLGRMMTLAGTAM
GYRFVTLDPAADAPCGQVARQIEARYDDAKAALELARQCDVITYEFENVDAEVAGLLE
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TVTGGYDGGKQQRVIREASQAVTAYEELAATGAELVLEQFIKFECEISVVVARSTNGEI
KTFPPAENIHVNNILHASIVPARVAADIQIEAQKLAAVAESMKAVGLLAVELFVAAD
GRLYVNELAPRPHNSGHYMEACATSQFEQHIRAICGLPLGDTSLSPVVMVNVLGEH
LEGIIARTGQPDAEAIELGVIPKLHIYGKTEAKTGRKMGHVNLLCQDVEEGLQWIEQT
NLWRNTNS"

CDS complement(5131095..5131580)

/gene="purE"

/locus_tag="EFAGFIKM_04472"

/EC_number="5.4.99.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9WYS7"

/codon_start=1

/transl_table=11

/product="N5-carboxyaminoimidazole ribonucleotide mutase"
/db_xref="COG:COG0041"
/translation="MSLQVAVIMGSKSDWETMKHACEVLDELEIGYEKKVSAHRTPD
LMFEYAEQAIDRGFKVIIAGAGGAAHLPGMVASKTMLPVIGVPVQSKALNGLDSLLSI
VQMPGGIPVATVAIGKAGATNAGLLAAQMIGAFDPDVQRRSEARRERIKQEVLESSEE
L"

CDS complement(5132146..5132580)

/gene="nhaX"
/locus_tag="EFAGFIKM_04473"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07552"
/codon_start=1
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/product="Stress response protein NhaX"
/db_xref="COG:COG0589"
/translation="MLFSKILVAYDGSKASNKALDRAIELAKVSPNAVLDVIHAFDFP
RVFIGEGLAPLPPSLNNDYYNLAVQTTDEAKERIQAAGVTANVDLIQGAAAEVLLDFS
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CDS complement(5132750..5133013)

/locus_tag="EFAGFIKM_04474"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQTGLILWFLFINVVGVLVMSDDKRRAQQRRDRTPERTLFLLAF
IGGALGVWIAMYRKRHKTKHPSFTIGIPLLLFLNAVIYGYFIQ"

CDS complement(5133140..5133277)

/locus_tag="EFAGFIKM_04475"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MPHNKPEKIHNNQKNKDSIREESIAVRPDKAAKRAPSLNGIPKQE

S"

CDS complement(5133442..5135571)

/gene="topB_2"

/locus_tag="EFAGFIKM_04476"

/EC_number="5.6.2.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P14294"

/codon_start=1

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/db_xref="COG:COG0550"

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PYASLARPVLRKNLNITKRIVDDSKVTDHHAIPTEQTVLLNQLNPEERKLYDLIVRR

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HERALLPDVQQGQSVTVQRCHIKSGRTMPPKRYTEAALLSQMEKHGLGTPATRADIE

KLVSSDTIDRQGNMHPGTGKGKQLIELAAPQLRSPDLTARWEAELERIARGQGKPGPF

LDSIRSMKELVSTVKGSKAEYKPHNVSNHCPDCNARLLEKKGKRGKFLVCPTEDCG

YRRSAEKRLSNRRCAQCHKKMEIKEGKAGLYVQCLPCGITETLDKDKQHVNKRDDQKL

VKQYAKQESIGSNLGELLKAAMEKKGE"

CDS 5135942..5137876

/gene="QRSL1"

/locus_tag="EFAGFIKM_04477"

/EC_number="6.3.5.7"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00120"

/codon_start=1

/transl_table=11
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chloroplastic/mitochondrial"
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VAAVSKGKAPATPAAFVQAMEEAATLAGVPFTMDKLSGTTVQRKDAVALQQWLKLD
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PFVLEEATIMDLQTAMTQGKLTSKELVQKYLDRIVKYDDQGV SINAVLT LNP DALQIA
EQLDEERAAQGARGPLHGVPILVKDNFD TNDMP TTAGCICLKDSVPAHDAEQVKKLKA
AGAILGKTNLHEFAFGITTSSSLGGQTLN PYALDHYPGGSSGGTGAAIASNFAAAGM
GTD TGGSIRIPSSFNSLVGIRPTIGLSSREGIIPALTQDVGGPMARTVSDAAIMLDA
TAGYDKKDVATAYAVGKIPSSYTDFLDVNGLKGAHIGVATELIPSTKAEEKAVADVIN
TAVEELKSLGATAVPISIPNLTEINKYPSLSGYEFKFQLNDYLD SLGADAPYHSLSEI
IASGEFDKSQEQSMKTRDARQTLETTEYKDIVLKRTQVTRESLLKVMADNNLD AIIYP
TSTQAAGVIGEGQNSGGNNRLSPFSGFPAITVPAGFTTDGLPVGMEFLGRAFDEGTLI
KLAYSIEQGTHHRQAPKLTP"

CDS complement(5138050..5139057)

/gene="fabHB"
/locus_tag="EFAGFIKM_04478"
/EC_number="2.3.1.180"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07600"
/codon_start=1
/transl_table=11
/product="3-oxoacyl-[acyl-carrier-protein] synthase 3
protein 2"
/db_xref="COG:COG0332"
/translation="MNHQSKATITAMGTYVPDRILTNADLEKLVETSDEWIVQRTGMR
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KIPHTGVLDLNAACAGFTYGLQLADSLVTSGMYRKVLVIGAETLSKITDYTDRTTCVL
FGDGAGAF LVERSSGTEGDFMAAISGTHGEGGLHLYKSGLSSEMNGVPLQGEGCLVQN
GREIYKWAVRTIPEQLGKLITKAELSPDQIDWFVPHSANMRMIEAVCERGPVPLERTL
TSVEYRGNTSAASIPLALQLAVDEGKLKEGQSIALFGFGGGLTYAGLV LKWGVDPDKIQ

E"

CDS 5139359..5139913

/gene="chrR"

/locus_tag="EFAGFIKM_04479"

/EC_number="1.6.5.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AGE6"

/codon_start=1

/transl_table=11

/product="Quinone reductase"

/db_xref="COG:COG0431"

/translation="MKKELNILAISGSLRNQSSNTLLMHAMIKLAHTNLKFEVYDGLN

DLPHFNPDLDVEEGPESVQNLRAQLKHSBGVLICTPEYGNVPGVLKNALDWWVSSGE

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DSETQHALQNSLTILGEACNQMKV"

rRNA complement(5140100..5140211)

/locus_tag="EFAGFIKM_04480"

/product="5S ribosomal RNA"

rRNA complement(5140295..5143216)

/locus_tag="EFAGFIKM_04481"

/product="23S ribosomal RNA"

rRNA complement(5143529..5145079)

/locus_tag="EFAGFIKM_04482"

/product="16S ribosomal RNA"

CDS complement(5145580..5145678)

/locus_tag="EFAGFIKM_04483"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIYDLLVVYLMKSSVNKFYNVMSMYCIKHEFF"

CDS complement(5145849..5147225)

/gene="adeQ"
/locus_tag="EFAGFIKM_04484"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P31440"
/codon_start=1
/transl_table=11
/product="Adenine permease AdeQ"
/db_xref="COG:COG2252"
/translation="MDRFFKLKENGTVNVRTEIVAGLTFMTMAYILFVNTLFLGQAGA
GMSDNAVFFATAVGAGLMTIIMGLFVNIPIALAPGMGLNAYFMTVVLSSNGAITWQAA
LGAVFLSGIVFIILTVTKIRQMLLVAVPQSIKMAITVGIGLFITIIGFKLANLVAVTV
NVAPDADLSQPIPGSSFNLSLGNFVTHHDALLALIGLLLIAILMVMRVKGALLIGIVA
TTLIGIPMGVTNLSGLSGASWLPNFSDLAVGQLDLKGAISLGLFEIIFITFVELFDT
FGTMVGTATRMGIMKDKKKGEKTIGKAMLVDAVGVSAGAALGTSTITAYVESASGVEA
GGRTGLTSVTTGLLFILALFIAPLALVPSAATAPALIIVGVLMMSQVRSIEWDDFLQ
AFPAFLTIVLMPFTGGIANGISAGIVSYVILAVFSNLVTERKVKIHWLMWILALIVVC
RYVFIGGE"

CDS complement(5147899..5148150)

/locus_tag="EFAGFIKM_04485"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRKTDYMSKWKMIGISAFLMVMLAGCGSGMQDLASGSGDFPFVN
LEAADASSDQSSNQELSSDSTNTNQQEQEIQDAPQTEI"

CDS complement(5148396..5149934)

/gene="guaA"
/locus_tag="EFAGFIKM_04486"
/EC_number="6.3.5.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P99105"
/codon_start=1

/transl_table=11
/product="GMP synthase [glutamine-hydrolyzing]"
/translation="MNKQNEIVVLDFFGGQYNQLIARRIRDLGVYSELLPYNTPAEKI
AEMAPKGIVFSGGPSSVYAENAPHVDPGVYDLGLPIFGICYGMQLMAQQLEGKVERSE
KREYGKADLEFAAGSTLAKGIEGEHTVWMSHGDHVVTLPPGFKLDAGTESAPIAAMSD
DERKLYAVQFHPEVRHSVRGNDMIRNLFCEICGCEGNWTMETFIDDTIKDIREKVGDS
KVLCAISGGVDSSVVAALLHKAIGDQLTCMFIDHGLLRKGEAESVMETFVGKFDMMKV
KIDAQERFMSKLAGVDDPEQKRKIIGNEFIYVFDEESKQFDDFAFLAQGTLYTDIVES
GTATAQTIKSHHNVGGLPEDMNFKLIEPLSTLFKDEVKRVGTECGLPDEIVHRQPFP
PGLAIRVLGEVTEEKLTIVRDSDYILREEIAKAGLDREIWQYFTALPNMKSVGVMGDA
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IEWE"

CDS complement(5150324..5152687)

/locus_tag="EFAGFIKM_04487"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MWERKGNQQPNSTVANLESTDRTMRMESAYSVYKAVNQNSVTDIK
DEGYVSVPVLYKIFISAILLISLEWIYPVTSSDQQGSEFLSVMAGLTGALLLAGLI
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SISTE
TRGLFMMCGWSMLMASVQSLVLLRRSVMLFGSATLLYLLLESFAGLDVYASVIRSVL
WTFLIQALLQLRLNGGVTTSPYRGSPYGRWSAVTIVVSAGMVLLSALPGQFTSIPQP
ERISLEQMGERLARWAGYTQHSSIPAATAVTGYSTADAPMGAPLVQGNSIFFIAKSPK
VTYWRGETRSYNGSTWSDPGQS FETASPSGMLRADGWENPTYWSRIRQTVTMQREW
K
GPNPLFTGGIPVNVSFQDKNKDNQENMFSLLSNHDSATLWLAGSGKDKMVKNYSADVM
VPVATAEQLRLLEETNKGKDPAAIRRTYLQLPASLPGRVQTLAKEIIQGSETRYDAVQ
AVKTYLAAHA EYTL DTRMPPRGTD FVDDFLVTRQGYCNHFS
TAMIVLLRAEGIPARW
VKGFGPGVADPDVPGQYLISQGD AHSWVEVYFPGAGWMPFEATPGFTMAQGAGEGVAA
LAGPQPVAENPPYMSGGVGYAGAWLLARARAIAAEPWLAAAALVAAALLGAAALVRMRR
LRPALRIRLLLAWPRSSFPDRERLLGAAAPVWAALARRYGPRPPGMTLREYAASPALA
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CDS complement(5152674..5153939)
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/inference="ab initio prediction:Prodigal:002006"
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LPDITDLASLGILVYEGASGYDVKQRENMDAPAFEQVVRAAARWIHTAERDDIPYHLW
MEGGDKNYDAQDQWKHGPFHADDENHGLDKLAGARISKAQSGSVSLRTEMLDGLTSGS
RIVVLTGKMDQVLAEWIITAIGSGYRVEVQLTEANQDQLGSTDRLMNGLGYDSLRLER
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CDS complement(5153936..5154925)
/locus_tag="EFAGFIKM_04489"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSYIRMEHEHAVELLNRVMKRVESVIIGKKTEIRYVLTAMLSGG
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GTYRLPEAQLDRFIMRIGLGYDPPEQELELLTRMQGREALDELRPVLLAEEVVAMQRE
VKQVHVDPVVKQYLVAVAVASRSLPAVRLGISPRGTLAWMAAAQSFAYLQGRSYVIPD
DVKEVAVPVLSHRIQLKAQNRAEVWGQVQVIEEALSSVPVPVQMASQGRGRRRQ"

CDS complement(5155028..5156329)
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/inference="ab initio prediction:Prodigal:002006"
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/translation="MVQRPEFIIKEIGGNSATTIHTFLSGQWYVILVRIALLCAFAV
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RPNLVRAPGGTYGHFDQSYFDLLQLGGYTVMDWNVDSGDSKRKGVPAPKEILSNSTKVP
AGARSVIVLMHDGGAHAETVKALPGIIKYYRDHGYRFDTIKSTDQPVQFRVHPDGKYK
ARKVPGKAWIAEHVEANATLWLANKKLKVEVGLAAATLQPGEFRMEGKRIMVPLRTFM
KKFGGSTRWDSETRTAIAVWKERTIHADSVSGTLTTTGAJETGAVQSQGGTIWVPLRE
LLEQMGLRVNSLTSNEAEWTVKAGTSRSISAMNNIFYKMI"

CDS 5156570..5157217

/locus_tag="EFAGFIKM_04491"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MELLEKIQLHFGSYGYSLFFGLLLEFIALPFPGETTMAYAGFL
SYKGHLDFGILTILAF LGTTIGMTITYFIGAKAGLPFITRYGKWFLKQDKLDTQKW
FAKYGNALIFIGYFIPGVRHFTGYFAGIAAVPFRKFVLYAYSGALFWVVLFLGIGKIF
GPQWNAVFHLAHQYAAIVGGIGLLLIVAVLYRYRKAWTARSTVSKPAPVRQRQK"

CDS 5157351..5158865

/gene="gerBA_4"

/locus_tag="EFAGFIKM_04492"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39569"

/codon_start=1

/transl_table=11

/product="Spore germination protein B1"

/translation="MSETSPERQDQRQISPDLSENMEYCKQVMGNSNDLMMRPLQCLH
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DNMEDVLNALLSGSAILLLEGCARGLKIAAAGWEDRAVGEPISQTVVRGPMEGFNENL
RTNTSLIRKRIRDPHLWIEEKEIGRITKTRVAVLYLKHTVDPEVVEELRRRLDEIDID
GILESGYIEELVQDETRTLFPTVYN SERPDTVCAALLEGRVAIIVDGT P FVLLVPALF
VHFFQSPEDYYQRADISTLIRLIRYLSFFIALLAPSFYIAITTFHQEMLPTNMLISLA

AQREGVPFPAFIEAILMELTYEILREAGIRIPKTVGQAVSIVGTLVIGQAAVDAGVVS
AAMVIVSITAISYVIPENGLSISVRILRFVLMILAAAFGYGILIVLLITVTHLCS
LRSFGVPYMSPFAPLIQKDLKDTLFRVPWSHMKTRPFSTGTPNKIRQASKKMKR"

CDS 5158886..5160088

/gene="gerBC_1"

/locus_tag="EFAGFIKM_04493"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39571"

/codon_start=1

/transl_table=11

/product="Spore germination protein B3"

/translation="MNKCFRLIVCIVFLLPLLTGCWDRQELNELGIMLGLGVDKDGD

LKVSQVVPNEVSSKSGGGNGTPVTLYEASASTLFEAIQKLTETSPRRIFMAHIRVL

VFGEEYARKEGIYDVMEALMREPTARPDYYVMVARNTTASKVLDVLTPLNIPAEKLF

NSLDVSAKTWSPTTTVTGDQLIEYMLTPGIQPVITGVEVVGNLARSGSKDNIGTIKSP

ARLNSTGLSIFKKDKLIGWLTEDESKGYNYIRDNVVSTISHMPCRKGGNVTFKALRTK

TQRKAKVINDQPVIHIKLNKVNSSIGAVECGIRIGSMKTLKELEKDSEERLIDLMEKSV

NSVRRKFHIDIFGFGQEVYHADPKFFKKIEKDWDQYFENLDVKYEANVQIKRVGTLDD

SFKEDLKE"

CDS 5160095..5160331

/locus_tag="EFAGFIKM_04494"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLITITVIVIGGLVGLFDLPGLIRRKEWRETAVYSGMLVIATGF

SVIAANLWDFPSPLYIIMWIYEPVNQFLAHLTG"

CDS 5160350..5161474

/locus_tag="EFAGFIKM_04495"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MLEQGRLGTRQLTTLIFMMVVGDMMLIYPSVITSYAKQDSWICA
FIGVPLGMALMAMILKLCSLHPEKNLVQMARSILGFWPGTFFSCFYLFFFIIGASTHT
REVGDFMTTQIFPYTPIRIIILMFVIVIAWGVSHGLETMGRSSELLMPVVIVFIVVLA
VCLLPQIDTRNLKPVSDTSVVSISQGILVSIYPIGEVVPIMMILPYVAKQAHRTDI
IIAAGLGSLVLATLVLTISLLVLGAFLTQHNIYASFVLSQKISIGSFFERIEAIMASSW
LISTYFKAMIYLYAFIVGCAELFKLKQYQILVLPASILVFGLANLISPSITFIVITIV
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CDS 5161573..5162700

/gene="yndE_2"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31809"
/codon_start=1
/transl_table=11
/product="Spore germination protein YndE"
/translation="MLINEKITIRQFAVLTLVLMVGDMILLYPSVVTASGQQDAWICS
LIGQPIGLLIWVLYKLHQTHPDLSLIEICQKILGRWAGSVLSAAYLFYFAIGAAICI
REVGDFMTTQIYLQTPIRVILIILMCALVWGLMHGLHTIGGSSELLTPIVVAFMILLF
LGLMPQVNSSHLQPYLNTPWHLHMQSIIRGAFTSFGELIVITMVLPYVMSGPHIKRDM
LLATLCGGLLLTLLVISLMIFGPFLTQHDYISYTLSQKINIGNFFERIEAFMATAW
LIATYFKSLLYMFSFVLGTAQLFRLKTYKPLILPSAMLLFALAVLISPNVIFYTNTIM
PAWVDWDITVSFIPLFLLLHRLRSGKSKNNSTNHKRLPT"

CDS complement(5162792..5163256)

/gene="bcp"
/locus_tag="EFAGFIKM_04497"
/EC_number="1.11.1.15"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q83CY8"
/codon_start=1
/transl_table=11
/product="Putative peroxiredoxin bcp"

/db_xref="COG:COG1225"

/translation="MTLKVGELAPDFELPSSTGESVKLSDYHGKRVLLYFYPKDMTSS

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GVWQLKKMYGKEYMGMVVRSTFLIDEEGKLIKDWSKVRVKGHIEAALEALKTL"

CDS complement(5163302..5164087)

/locus_tag="EFAGFIKM_04498"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYYMGLIWEYLKNYMKTRLTYRADFWVEILSDLLFQATNLIFIF

VVFRHTDNLGGWSESEVLFVYGYFMVPYGFSCFINLWGFSEYIVKGEIMDRILTRPA

HNLFQILLENDPPALVGSFIGLIIMIFSGAEMGLMLEWWHIPALIILALSSVMIYAG

IYTTLSLSFYSDAPTGILPLMYNIQGYGRYPVTIYNRAIQVLLTWIIPFAFVGIYPA

ALFLERSEMHMALLTPVMGLVFGSMGLLLWNFGVKRYRGAGS"

CDS complement(5164093..5164887)

/locus_tag="EFAGFIKM_04499"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNSAFIDFMRIRFLTMLAYRVNYYSGILIYTLNIGVYYFTWQAI

YGSSGELGGFTAAQMTTYIAVSWMARAFYFNNLDREIAADIRDSIAIQFIRPINYVM

VKMMQGLGEGIFRFLLLMIPGMLIAILLFPVELPTAPSAWIGFLVMLFFSFLINSQIN

VITGLAAFFVENNEGMMRMKRVVVDLFSGLIIPISLYPGWMSAVMKVLPFQAITYLPG

SVFTGRVEGTAIWSVLGIQVFWFAVLLLPMVLIWRKARKRLFVQGG"

CDS complement(5164889..5165935)

/gene="btuD_12"

/locus_tag="EFAGFIKM_04500"

/EC_number="7.6.2.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01005"

/codon_start=1
/transl_table=11
/product="Vitamin B12 import ATP-binding protein BtuD"
/translation="MLAIDVKDLRKSFSVQKSRGGLKGAFQDLFARQYQEVLA VNDIS
FQIPQGEICGYIGENGAGKSTTIKMLTGILVPTSGQISVGGYVPYQEREK FVQNIGVV
FGQRSQLWWDIGVIESFHLLRKVYRVGEVD FRKRLDE LVERLQLQDLLSRPVRKLSLG
QRMRCELVAALLHNPSIVFLDEPTIGLDIVVKSEIRDFLKDMNKEHGTTILLTTHDLQ
DIEALCSRVI ML DAGNI IYDGG LDHLKSQWGKEREIRFKFGSAHNISQM QE WTAALPV
RWTVENELSASVWIPL ELNVSDVLGRVVGQADITDIQIIEINTDEIVRSIYQSGSAER
PEIVGAGKEAVGVS"

CDS 5166148..5167191

/gene="tagU_5"
/locus_tag="EFAGFIKM_04501"
/EC_number="2.7.8.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01140"
/codon_start=1
/transl_table=11
/product="Polyisoprenyl-teichoic acid--peptidoglycan
teichoic acid transferase TagU"
/translation="MTRKTKRTIWISLAAFVLIIGGAAAYYFGSILNQ LDGLAKDGDD
SPFAGIENVEKVNTPDPPKWE GTETVNILVMGVDARGLKKGEVPRSDSMMVVS LDPLT
KKINLFSILRDTYVNIDGYGKERINTAITHGPNAAMQAAGDLLGIPVQY YVYTDFQGF
IKLVDAVGGVDFDVEKDMHYTSKADNNEYDIDLKKG YQHLDGETALMYVRFRHDAMSD
FARSERQRELLKAVTAKMQSTTTIAKLPAILEQVNPYVD TNLTLSDMWKLGG LGYQSS
MNGSEQIPPMNLLKEERTAGGAQVLTVTNEEKLKQHIQDI IHPPATTD DTTSTEDKT
ASGDDQKSEQPAQ"

CDS 5167323..5168642

/gene="hemL1"
/locus_tag="EFAGFIKM_04502"
/EC_number="5.4.3.8"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81YV0"

/codon_start=1

/transl_table=11

/product="Glutamate-1-semialdehyde 2,1-aminomutase 1"

/db_xref="COG:COG0001"

/translation="MNTSRSRSELLYAEALEHIVGGVNSPSRSFKAVGGGAPVFMKKA

QGAHFWDVDDNRYIDYLAAYGPIVTGHAHPHITQAITEAAANGVLYGTPTELEIKLAK

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GPSTLGIPDSAGVPASIAQEVITVPYNDLEALKDALERWGDDVAAMVEPIVGNFGMV

MPEPGFLEGLCAMTRANGLSVIYDEVITAFRFHYGSTQTYAGLDNHAEIEPDLTALGK

IIGGGLPIGAYGGRKHMVEQVAPLGPAYQAGTMAGNPASISAGIACLEVLQGAGVYEE

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FRHMLDRGINLAPSKYEAWFLTTAHTDEDVQATLEAAEASFKAMAE"

CDS complement(5168781..5170166)

/gene="norG_1"

/locus_tag="EFAGFIKM_04503"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2G1P1"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator NorG"

/db_xref="COG:COG1167"

/translation="MRKYEVIAEALKQWIQEQMQQDQRRQWADKGIRLPAVRVVAEQY

QCSVSTAIRAYEWLEQRHLVYAIPQSGYYAVQNGTGAQDMDWQGALDFASAAPDPRVF

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QQALAVLALMPFPNGKRKVLLELPTYHNMPSSLGLDVPIAGVVRTLDGLDWASLERQ

FTEGDIKFFYVMPRFHNPIGTSITVADKKRLRLAQRYDVYLVEDDYLDLEDNTKQD

PLWSYDTEGRVIYLSYSKILFPGLRIGVAVLPSPLIQSFGAYKKMLDIDTSVLSQAA

LEIYVHSGMFAHHRKVIRNRYAARMNTVHEQLDTYPDFAPFMEAPRTGGEHTVLPLAG

DMPLRVLLPRLQKRGVIVDTTERYYPEGTYQVHQDQMLRLNISNVPKQRIEEGIQKIR

EEILKLQIRQK"

CDS 5170335..5171282

/locus_tag="EFAGFIKM_04504"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNITHTRGYAYIAAVLYAAIIGLSFLFVKMTVTVAHPIDVLAHR
FALSLIVVSIPVIFGWIKIRLSLRDLWRIIPLGLLSPVLFFAFQAFGLVSSNSSEAGI
IQAMAPVFTLVLASVFLKERTSTMQKLFLLLSVAGVVFIFIMQSGMSIGNLKGIALL
LLSTVCFAGYGVLARPLTQKYKPMELTWVTLMVGCIVFNAASLRHASSGSMMDYIKP
LGDTSYLGALAYLAILSTMISTLLASYALTHLEASQMSVFSNLSTLISIVGGAWILHE
PVGSYHYIGALLIAGVLGTNMSGRKHKLVSGIKSNSPY"

CDS 5171490..5172596

/locus_tag="EFAGFIKM_04505"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKRTQPSFLQAMMLIMLSVGLISHVLIIPALLAAAKRDSWISVL
LSAGPFLIFALMLAYVSRFLQHQTLEWLTSLRGKPIGLFFRVGNSLFFLSAIYFTLH
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VNTQYKDYSRLLPVLEQGWHPVLNGMIYSLAGMFELLIWYIQPHLTKRIRVWQYLML
ALILVGLTVGPLIGAIVEFDPFEAAKMRYPAFEEWRIASLGKYIAQTDFFSIYQWLAG
SFTRISLAMYIVVEIWNIKSSTRRLISCISLGVFFILTMLYPLDDMTFEKLLVEYIFP
FNLVYLSGLAIIATTVAFIHSRHQRRKHHGASSD"

CDS 5172577..5174046

/gene="gerXA_2"
/locus_tag="EFAGFIKM_04506"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9ZFB4"
/codon_start=1
/transl_table=11
/product="Spore germination protein XA"

/translation="MEHQAITTSHETLLASLKEQFNPCADVVIQTFPVKDESDQPVI
LLYCDGLVDGKQINQFIIPRLEQHSLIIEESHPKELGLTLNPLDDLTDTNKLNMLIFS
GQLLIIFGNGVQSCSVDIADIPGRSPEESAIETSVKGPDRDGFTEELTTNVALIRKRMK
TSSMCYEKYVKGGRQTQTAIGLLYVKDIINPDILKEARHNLDQIEIDGILGTSIMERAV
MGGIRSIFPLTDNTERPDFVVDSSLNGRFAVLIEGSPVAVIAPTTLFNQLKSPEDST
PFFIVTFERILRISGLLIACFFPGFYIGLTSFNVEQIPLPFLATIAGTRMGLPMPVTL
EAFLMIFMFEIFNEAGRRLPRALGQTVSVVGGLIIGDAAIRAGITSPTIIVTVAISVI
SSYILVNTVLSGATAHVRIGMLLISSILGLFGFMIGLFALLVHLVSLECYGVSYLAPV
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CDS 5174043..5175200

/locus_tag="EFAGFIKM_04507"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIRWTSMSGLLAGCLILLTGCWDSKEVQSINFITAIGIDYVDNQ
YIAYAQLIDFSSIAKQETPTSRETRDIWTGRGEGTTLNMAINDLYETSQQTLWTHVK
AIVLSKKVLDDRLEDIFNTLLHSGQLRYTPWIYATEHNIPDILSPSALLNQSAQTIEL
FEPMRLYKQHSGYEPIRLHQLLDGLREPASVLLPSVSTRNETWFNGDKTPPLVRMDG
FYVISKGTSQGRVAGADADGTRYVNYERVHQYPLYVYGNGGKTPDLTLMLRHPKTRIT
ARKQGDGVTFDLVTSAKSFITEDHGAPRSPHAMEQEAEKQIESQIRGTFEKTKLRKID
SYGLVEHLYRHNLPWQQEVYNRADPLQRFKLGKVKVHVDILNASTYKYSE"

CDS complement(5175287..5175703)

/locus_tag="EFAGFIKM_04508"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTPDQTESATSASKNVSAATGHTYWWIPDGYIPLESRGTLSEH
SICVLNTSATDAELHITIYFEDREPLEGIVAEVPARRTKHIRTASLRSGEQSIPPGVP
YAITVSSNIPVIVQYSRLDTTQPELALMSVMAYPLG"

CDS complement(5176188..5177429)

/locus_tag="EFAGFIKM_04509"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNKAQGSQAVVMGAAAEQAVSVTSWKFNFGPDSGRADETGDYL
KVTATTAYEERGGYGFEAGSLVYEKQRIGDDDPDPTKQHHNNSGQTTMSARLRSGFC
IPLKASFIVDPDGTQVLLVAGDELAETVTRVKAGEGRLVLPITRTLPGQYAEVRFS
VVVRGGRLRLSFGSPAPRINALEITLVNQTMVFLAGDSTVTDQSESGYPYCGWGQLL
PAQFKHDVAVDNHAQSGRSSRSFINEGRLSTIMERIKPEDFLFMQFGHNDEKPDPERG
TDPFTTYKEYLKKYIDSAREAKARPVLVTPVHRRYFADDGTLTDTHGDYIIAVRELAE
EEDVPLIDLAERSRLLEQAGVEGTEKEDFMWVLPGEYVNFPSGVEDNTHFQERGARRL
AQQVAEAIRELQLQLQMYLR"

CDS complement(5177502..5178341)

/gene="araQ_28"
/locus_tag="EFAGFIKM_04510"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94530"
/codon_start=1
/transl_table=11
/product="L-arabinose transport system permease protein
AraQ"
/db_xref="COG:COG0395"
/translation="MVWRNVKWPIYHLFVAALALLMLYPVLWMLFSSFESRTIFVTA
DTLFPAEWIWSNYVDGWKGTAGRPFMDYITNSLVIVVISTIGAVISSSLIAFGFARLN
FKGRTFWFSLMMLTLMLPHDVVLVPQYIIFTKLGLWNTILPIVVPTFFGMPFFIFLMV
QFIRTIPKELDEAATIDGCNKFRLYIQIIMPLIKSSLATAAIFSFWRWEDLLGPVLY
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LKG"

CDS complement(5178344..5179246)

/gene="lacF_9"
/locus_tag="EFAGFIKM_04511"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P29823"
/codon_start=1
/transl_table=11
/product="Lactose transport system permease protein LacF"
/translation="MRQYSSLRRNLTGYAFISPFIIIGFLGFTLIPMFVSLYMSFTSYN
LFTSPRWIGLDNYTKMFFDDPKYWNSVKVTFLYVFIGVPLRLIFALFVAMVLNTGSRM
IGTYRTLYYLPSIIGGSVAVSIMWRNLFSNEGVSINSALTAIGIGPISWFGDPNASLVM
LISLSVWQFGSSMLIFLAGLKNIPTEMYEAAGVDGANPIRKFFSITLPLLSPIVLFNM
IMQTIGAFMTFVPAYIISKGEGGPMDDGTMLYSLYLFRQAFMFNNMGYASAMAWIMLIM
IGILTVAVFLTSKYWVFYESEGGK"

CDS complement(5179386..5180669)

/gene="yesO_3"
/locus_tag="EFAGFIKM_04512"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31518"
/codon_start=1
/transl_table=11
/product="Putative ABC transporter substrate-binding
protein YesO"
/db_xref="COG:COG1653"
/translation="MVKKAIFLMMAALLVFTAACSSGGGTEGASGDDSVTLRIAWWGS
DARHEYTKVIDLYKTKPNVKIDVEYASFDDYWKKLAPQAAANQLPDIVQMDISYIS
QY AQNGQLEDLAPYLG NQIKVDDVSENVISTGVINGKQYGV PAGVNV LGFQYDPALLQ
KAGAEAMPENMTWESYEALGKQAAEKGLYLDGGVAPDIFFFHYFLRTKGHSLYNAEGTG
LG YDDDQLFVEFFGLMRRMIEQDAAPTPDIANQTKGIIESDLVKGKG VGIWQWSNQF
VAVQQVADRPLEFAPMPGPDMEKGLYMQPSMYWGVTSNSKVKEEAAKFIDFWVNDVEA
NKLIKGERGVPISGAIKEAIAPELSDATKQVF EFVAAMEPKASPMSPPPVGSPEVIS
SLADVVEELNFGKITAEQAAETFRKNAESVLANNK"

CDS complement(5180890..5182443)

/gene="cheB_14"
/locus_tag="EFAGFIKM_04513"

/EC_number="3.5.1.44"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00099"
/codon_start=1
/transl_table=11
/product="Protein-glutamate
methylesterase/protein-glutamine glutaminase"
/translation="MYKVMLVDDERVILEGISQVVDWAAAGTELVGTARNGIEALDKI
GQSRPDIITDISMPGLDGLGLIEKASEAYPGVRFIMLSGYKEFEYARRAMQYGVKHY
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YGPVDLEYYQELFDLELEENAVRLLLFRIVDEHDYSHLFAIKNIASDLLPHVLLSTTI
EGKLLILLADSADPAGLKESIEEVRAAFTRLYKLEVTAAALSEADRMISRRRLFREALQ
YLNHRFFIGEGKLITKNDLVLAGECDGVHVEQDAEQLCQLIKSGNTEETAVEVERLFD
LLSRQQLEIEVTRSYVVQLYSAMVHVCPPEEATEFTQRMAELPHIDTL SGLKSFVASS
TARLTSGYYKNHISRQSSAVEKMMDIVDRHYGEADLSLNGVAHQMLYMNPDYLGKIFK
KVTGENFSNYVNRLRIERACDHIRRGDVKVFELAEFGFGGNSQYFSQVFKKWTGMT
PTEFRRIGI"

CDS complement(5182418..5184205)

/locus_tag="EFAGFIKM_04514"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MNKIKNAFTTLPIHHKTILLIGILMLISFTFYASVLRVFSIYD
RQIYEKSSQVLNMSSVGIENQLREVSNL SFKVM SDEPLQQYLLQLEKAETGYERNGLR
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WHTSGDKQARLLSVRQVKSFTGGAFTLDKLGTLIIRVRLDRIVQDQM QEPAEDSQLLI
SDGKEVIYPTESSVSEAEIESELKRTQPYGIAMFEQGRHFVARANSSYTDWTYLYTTP
FDQMFKKIQFVKQLVTVIFIMIFLAALIIGAKFSRSITHPIAQLIKKMRNIEKGDLDK
LEEAALGNVPMSPQNEVGLLHRTFKMMLQRIRELIDENYAKQLVIRETELKALQAQIN
PHFLYNTLESINWMAKVQKQRQISEMVEALGFLLRSSVNMTEKWITLERELDIVRSYV
TIQRTRFEERLDFDMEIAPEVGTARIPKLTLQPLVENAIHYALEPSIDPCRIRIRARA

DGDRVIIIEVEDDGPGMTPEFLEQLHEGRIQTRGQGIGLSNIQERIRLTFGDEGGMVMS

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CDS 5184242..5184466

/locus_tag="EFAGFIKM_04515"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLCISGFIVSYFHIYTSIGHLTRYIYATFQVIREGIIHLCQQLKK

NTKQPEYLEQIKVFWPLNNIMLKYEIQFTD"

CDS complement(5184456..5185778)

/locus_tag="EFAGFIKM_04516"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRKRIWENTAAGLTVSMLAGMLFFTSSALPAHAADTKTGVLP

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GEGTMTHMIKDRDFHPNQFGYAAIAEVFAKTIWGDYTKLTAPATGPMNIIVSGKTLN

TPYKPIIRNGKNFVAIQDIVNAVGA

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CDS complement(5186166..5186456)

/locus_tag="EFAGFIKM_04517"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDESKELERRLS

ERDPIVEETLKYRKMALEVDDRYDRYLERATGNKPESDTGHSNSED

CDS complement(5186481..5187344)
/gene="suhB"
/locus_tag="EFAGFIKM_04518"
/EC_number="3.1.3.25"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0ADG4"
/codon_start=1
/transl_table=11
/product="Inositol-1-monophosphatase"
/db_xref="COG:COG0483"
/translation="MNEKEKTPYVVTSSYTA VAINAASKAGEWIKSRLGTV AELGTK
YSPQDLVTEVDKGAEQMIRRLILTHFPHHAILGEEGV EPGPEASAKALKEAEEEEFLW
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MLVSGEQELAQSLI AVGF PADTTFALPLNMAAVQALAPQVRNLRAGGSAALHLAYVAA
GRLSAYTEVGLKPWDIAAGALLVEESGGKVTD TIGTPYQLSVNHVVASNGKIH DALTD
VLKEAKATGLE"

CDS complement(5187452..5188453)
/gene="uvrE"
/locus_tag="EFAGFIKM_04519"
/EC_number="3.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9RTE6"
/codon_start=1
/transl_table=11
/product="UV DNA damage endonuclease"
/db_xref="COG:COG4294"
/translation="MLVRFGYVAMSVLIENASPSRTMTMSSFNKIDDREAAIRKLERI
AAENLHNTLRLLRHNKGSHIHVYRFSSKLIPLATHEDLNDWDPFPALKQDFAAIGDFV
KENHMRVSFHPDHFTVLSTPREQVLHNSIRD LRHHVRMLNAMGLNATAKNNIHIGGAY
GDKPSAALRFEENFLKLRDIQERLTLEND DKTFNAPETLAVCQRLGLPMVLDIHHHW
VNNEGEQAWDLWPDILKTWQSPLAQADSPADQPLPPKIHVSSPKSEKDLRGHADGVEV
EPLLDFLRHIAADTPRLDVMIEAKRKDEALVQLMQKLAFYHEEGVEWVDESTVIIHP"

CDS complement(5188609..5188932)
/locus_tag="EFAGFIKM_04520"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGFQTEFNSVCKFKNEQELFELLEYGRGKMVKQGFRVFPTGQKV
IAYTPDNVAVAIVKIVVSIAEINFQGQEVTEVEMLLIRKLTEESRIQTALADEMFFG
EQAQE"

CDS complement(5188963..5190063)
/gene="ddl_2"
/locus_tag="EFAGFIKM_04521"
/EC_number="6.3.2.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P63892"
/codon_start=1
/transl_table=11
/product="D-alanine--D-alanine ligase"
/translation="MSMDKLKVGWVYGGKSGEHEVSLQTAFVNAFDYEKYELVPFY
ISKQGTWKKGPVMHAPFAQIEELKLEQSAGGTQDALNALFGRLYGGAEALDVMFPLLH
GTFGEDGTIQGMFEMADMPYVGAGVLASAGGMDKVVMMKKLFAQAGIDQCAFTYFNATQ
WKQTEHEMIVQVEDQLGYPCFIKPANLGSSVGISKARNRDELKTAVEFALRYDTKVI
EEFVEAREVEVSVLGNDEPMASVPGEIVSSGEYYDYAAKYIDGQSQMLIPAPLDPEAA
DRIREAALQAFRAIEGNGISRADFFIRKNDGALLINEVNTMPGFTPYSMYPLLWRETG
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CDS complement(5190202..5191200)
/locus_tag="EFAGFIKM_04522"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEREWKSALYTYVNQYNRCEIDYRPQTSERIVTDPDFVVERGER"

MARLEEWYRKRAVPLRSETSAKLVRTLMDGQEEAVVDVQLYSRLFYEKSGITHREDR
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RSSRQQSYRRDLAVAYADRWWNAGNPAFEEDVDCTNYVSQCLFAGGAPIHYTGRREA
GWWYKGYVNGSEMWSYSWAVSNSLERYLSGSSWGLTATEVERPEQLMLGDVILYDWDG
DGRFQHSTVVTAFDAGGMPLVNAHTVSSRHRFDYRDSYAWTERTVYRLFHIADEF"

CDS 5191583..5194297

/gene="citB"

/locus_tag="EFAGFIKM_04523"

/EC_number="4.2.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P09339"

/codon_start=1

/transl_table=11

/product="Aconitate/2-methylnaconitate hydratase"

/db_xref="COG:COG1048"

/translation="MSAKNHFSAARSLEVGGKSYRYSLDALQENGHGDLSRLPFSIK
VLLEAAIRQFDGRAITEEHVKQLTGWADGRDNNKEIPFIPARIVLQDFTGVPVVVDLA
AMRDTVKKAGGDPKQINPLVPVDLVIDHSVMVDAFGTNDALDYNIKVEFERNEERYRF
LRWAQTAFNNFRAVPPSTGIVHQVNLEYLASVAATKTVDGTVVFPDSLVTGDSHTTM
INGLGVVGWGVGGIEAEAGMLGQPLYFVTPDVIGFKLTGSLSEGATATDLALTVTQLL
RKKGVVGKFVEFYGPGLANMGLADRATVANMAPEYGATIGFFPVDSETLNYLRSTGRP
DEQVELVEAYYKAQGMFRTSSTVDPEFTDVIELDLGSVPSLAGPKRPQDRIELTQMK
ESFNSIIRTPVDKGGYGLSDEKIEQSVPVKHPNGSTSELKAGAVVIAAITSCTNTSNP
SVMVGAGLLAKKAVERGLTKPGYVKSSLTPGSLVVTEYLEKAGLITYLDKLGFNVAGY
GCATCIGNSGPLPDEVSEAIAENDMTVAAVLSGNRNFEGRVHAQVKANYLASPPLVVA
YALAGTVNIDFETDPIGYDTNNEPVFLKDLWPTSEEIKDTIASSLNAQMFRNKYENVF
TANERWNAISVPEGELYEWDPNSTYIQNPPFFQELGDKLNDIADIRSARVMALLADSV
TTDHISPAGNIAPSSPAGLYLKEHGVERKDFNSYGSRRGNHEVMMRGTANIRIRNQV
APGTEGGITKYLPTDEEMSIYDASMKYQDEGQNLIVAGKEYGTGSSRDWAAKGTFL
GVKAVIAESFERIHRSNLVGMGMPLQFQEGHGWSSLGLNGRETYDITGLSNDVKPGQ
ELKVTVTREDGTQFEFPVIARLDSMVDVDYYHNGGILQTVLRQMMKKA"

CDS complement(5194438..5194647)

/locus_tag="EFAGFIKM_04524"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIIMAVLFISAGLMFLVYPHKVTDASEKQITERVIMSRWVGGS
IALSCLFLIMGTIQLLDQASHHIGH"

CDS complement(5194661..5195221)

/locus_tag="EFAGFIKM_04525"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKHNNQKKSKHYILWTAVFIIYLLTKLILFKGSPVDFGIVKD
RLMAFLQQPDLIHTRTVNLTPFQEISRDWNSLSLHRPGTAIHLVGNILAFIPLGIFIP
VLTGNKLFSGVKVLLLSLLLSLGYEVTQVVTGMGIFDVDDLMLNTLGGLIGYIVFTMA
MGLKKVLVGGESRVTTKKLNSKESHV"

CDS complement(5195250..5196113)

/gene="vanY"
/locus_tag="EFAGFIKM_04526"
/EC_number="3.4.17.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37711"
/codon_start=1
/transl_table=11
/product="D-alanyl-D-alanine carboxypeptidase"
/translation="MKKWGFLICIVLIGYIVTQSPGWIQQKDELPIEQNTREN
PAGYTVSVTGNIQDQVHKGNLLLVLDKQYPVHPEGVKSDIVYVAHEDDLLRGYGILDQKIMLS
RQVAQEFQRMVEAAGEEGVRYFLVSSGYRDFTKQDELYREKGSYALPAGHSEHNLGL
SLDIGSSLAAMNEAPEGAWLEKNAWKYGFILRYPKDKVRITGIQYEPWHFRYVGLPHS
AVMYKNNLVLEEYLDMLKEKENITVEVEGEQYHIRYYRATRDTTVYIPEQGQTEISGD
NMDGVIVTVKK"

CDS complement(5196213..5197271)
/gene="sasA_17"
/locus_tag="EFAGFIKM_04527"
/EC_number="2.7.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01837"
/codon_start=1
/transl_table=11
/product="Adaptive-response sensory-kinase SasA"
/translation="MIMLLGLSMLASGAITYGIYKLLQAYYSGVRAEDQLAEYRHF
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SIGDIYFFLILFIPLAILFFFWFTKPYATYFKDISSGIRHLANGDFQHRVQISSKDEL
GTIAEDVNLASEKLREAVERGDAENSKDQLVVNLAHDLRTPLSVLGYLDLLMKDDQ
LTEEQVRHFTSIAFTKSQRLEKLIDDLFEITRMNYGMLPINKTQLDLSELLKQMNEEL
YPVFEKNQLVARLKIDTDLTVSGDGELLARVFENLLINAARHGKDGMVVDINGYRDAE
QVIIQVINYGGHIRPEELPHIFDMYYTGDRARTPQEGGTGLGLFIARNIVEQHDGTIS
AQSDVVRTQFEVSLPVFQ"

CDS complement(5197294..5197989)
/gene="walR_5"
/locus_tag="EFAGFIKM_04528"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9RDT5"
/codon_start=1
/transl_table=11
/product="Transcriptional regulatory protein WalR"
/db_xref="COG:COG0745"
/translation="MKRITILIADDEVEIADLVALHLQKEGYHTIKAFDQKAAVQAVQ
TQAIDLAILDIMPGMDGYEVTRKIREQHHLPIIFLSAKTSDMDKITGLVMGADDYMT
KPFNPMELVARVNSQLRRSLQFSQSAPVQRSILEKGGLIITPDQHRVTLYGKPVETP
KEFDILYLLASHPKQVFSAESIFEQVWGEAYYESGNTVMVHIRT LRKKLGEDVNKNKF
IKTIWGVGYTFND"

CDS 5198074..5199024
/locus_tag="EFAGFIKM_04529"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLERLLAIVVLLINRGRVQAKDLADMFEVSIRTIYRDIDTLGQ

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LSSIVPESKNDDFQANTNRFIVDYSTWTHPEALKIKLEIEQGMDQLRPVTFTYCSAE

GIHThRTADPHTIVLKKHSWYLYAFCHERNQFRMFKLVRMQDVTLANEHFERKVINPQ

DRPWQQEWSRPDNQARLTCLKFHARVRHIAEEWFGIENVMPDGTGYYSQVAFPEDGWL

YGFILGFGADVEVLEPQHIRDEICRIAEQIVQNYIPPTQT"

CDS 5199098..5199916

/locus_tag="EFAGFIKM_04530"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNVTVQCQSCGMPLTPAQFGTEADGSTTREYCIYCYKEGKFEQP

GMSLEGMTMCTAILKDEGMDEESARSMRLRNQLPFLKRWRNTTDDQHTESLAENSTAS

ANPGQVTTEHSFSAQPVRYVTLPGKRLAGVSAHTTNAIEVSGKGCIQGLWNNYFASEH

LPATEVARYGCYTDYTDGITGEYTLVGHEVSYDETLPEGLDDILLPPATYAVFTSRK

GPMAEVVGEAWGAWWAWDKQSDRTFTGDFELYDERSLNPESVQVDIYIAVRQNR"

CDS 5200383..5200550

/locus_tag="EFAGFIKM_04531"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIRMPIQQMIPYHHQYPRNTATTAPKKENENTQGLSFHEILQQK

MAKKTASPSLR"

CDS 5200729..5201415

/locus_tag="EFAGFIKM_04532"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MITIGCFHAHYSNIALIEETLAPYEVELVHYVDPGLDRLKHDAD
FSEVVIHEKVAQTLQWIAECHADAILVTCTLFATVLEQEALQVPVPVIGIDDPLLQEM
RRVAGDYIIAFTNPATIEGTMARMNQVLQQEVENGQLHVAKTSQTDVAVCIPGTFELIM
RGDQQGYLEAVSEGLQQIAEQYPGKTVVAAQLSMAPAAAQVAIDRGIPHIHSPLALLAM
YLEKNLGLAR"

CDS 5201514..5201681

/locus_tag="EFAGFIKM_04533"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRFLYIVILFIVGFSCSAFLYGGAPKLS DALLFVIAGILYKIWT
TNSHKANS DKG"

CDS complement(5201799..5203616)

/gene="thiC"
/locus_tag="EFAGFIKM_04534"
/EC_number="4.1.99.17"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P45740"
/codon_start=1
/transl_table=11
/product="Phosphomethylpyrimidine synthase"
/db_xref="COG:COG0422"
/translation="MSTENQTGQQPMEQQHNDQQVEKETGAAGRVQPFPGSRKVYIQG
SRPDIAVPEREIALHDTNTPQGVEHNEPLRVYDTSGPMTDPEFHADIRAGLPALRTRW
ITERGDVEAYQGRTVKPEDNGLKPGGKRPGAAEYPGLRGKPLRAQPGHCVTQMHYARQ
GVITAEMEFAAIREGVEPEFVRQELASGRAILPSNINHPES EPM LIGRHFHV KINANI
GNSAVSSSIEEEVEKMTWAVRWGSDTVMDLSTGKNIHTTREWIIRNSPVPIGTVPLYQ
ALEKVNGEAEALTWELYRDTLIEQAEQGVDFYTIHAGVLLRYIPMTAKRMTGIVSRGG"

SIMAAWCLAHHQENFLYTHFEEICEIMKRYDVAFSLGDGLRPGSIYDANDEAQMELA
TLGELTQIAWKHDVQVMIEGPGHVPMPHKIKENVDLQMEICKEAPFYTLGPLTTDIAPG
YDHITSIGAAMIGWFGTSMCLCYVTPKEHLGLPNKDDVREGVIAYKIAAHAADLAKGH
PRAQRRDDALSKARFEFRWRDQFNLSLDPERALSYPHDETLPAGEAKEAHFCSMCGPKF
CSMRITQDIRAFAADKGMSSENEAVAAGMQEKAEYRTRS"

CDS complement(5204267..5205010)

/gene="kipR"

/locus_tag="EFAGFIKM_04535"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42968"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator KipR"

/db_xref="COG:COG1414"

/translation="MEDRKLTVRAVERALDILLCFTTRSDLGLTEIASQIGLHKSTVH

RLMATLEDRGFVIRDAATEKYRLGIRIWELSAHMSRSDDPAIILLPAMERLRDRLGET

VSLYLRDGSERIRIQAVQSDQAIRRVAPVGVRLPLSVGASSKVLMAFATDDDREELMS

GPEWVPVFDPAVYLAQMGLDIRDNGYATSYEEREPEGAAVSVPIMDRRGNIAAALSVSG

PVSRLSQETLHEYAPVLKDAATQMGLMLS"

CDS 5205370..5206395

/gene="menH_3"

/locus_tag="EFAGFIKM_04536"

/EC_number="4.2.99.20"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01660"

/codon_start=1

/transl_table=11

/product="2-succinyl-6-hydroxy-2,

4-cyclohexadiene-1-carboxylate synthase"

/translation="MYQSSQSEAPLQTKVSDLPSSLSPLRIRFKHIIIVALLLSVVFFL

LFCFIALHGYIAWVLSNPTVAPVFSNPMQAKNMKYEDITFPAADGSRTMQGWYIPADN

AASKTIIFSHGYGANREETWVPMYDLAHYAHQLGFNVVMFDYGFASQVKNKAVATGGKA

ESQQLLGAIQFAKQRGAQELVWVGFSMGAGTALQTGLITQEVDAMILDSAFLLPEPTL
YHNIHNQIDLPRQPTLEIMNLLFPVLNGTGLQQIPYQEVKKEDYPFPIFFIHGTEDEK
APYPIAEQLAANQTNPYSDVWIVQDAHHELIFREHPKEYLRRVSTFLSHVTKTSSDDV
QNTNNGE"

CDS 5206546..5207826

/locus_tag="EFAGFIKM_04537"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNWYGYGHLLPLRTLEEIRFWKEQEKEHTLVIRALVPDLEPPYV
KLLIEWEVTFANSERVANQLLKQLLPATHPPAPYMVRCIDQLVLAARQQSREFIKQLY
VLLEQSAAVQAVPLAKVLILHFIRESEYFLGVLDTLGQPGILRETDSEPSLFLGDALH
RSVSGSIHRQASEAPTSLEGNVNAPAASAQIQSATVQPPSIGTTQATPSSTAPPVKEK
PVPIGGHTLPPLPYAYNALEPHIDELTMRIHHDKHHQSYVDGLNVAEKKLAESRKKN
FELIKHWERELAFNGAGHYLHTIFWTIMNPAGGGKPSGMLAEQIKRDFGSYEAFFKNQF
TEAANKVEGSGWAMLVWSPRAHRLEILQAEKHQNLSQSDIVPLLPLDVWEHAYYLKHQ
NERKKYIEDWWNVVYWPAVAERYETARKLLWPPY"

CDS complement(5207976..5208200)

/locus_tag="EFAGFIKM_04538"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDTLRYTYLYEVVSTGEKSEFSQMATSKEEAATLIVARIADLEF
TDESDIKLGDLSISKQVGDNYVACEGCAS"

CDS complement(5208271..5209125)

/locus_tag="EFAGFIKM_04539"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSVPSHSDQPVQPEKRLQADQQATLRLQIWETPLMRQGSSVLEA
FAWEEVMCRRVGAGHLPVAHIWRHPDAFVAGLRDRRLPQAVEAMERIRSQGTAVCVRP
SGGAAVPLNPGVNVSLILPNPGHAINIHDDFREMASIIAESLTPWSNQAQTGEVQGA
FCPGDYDVSVGGLKFCGIAQRRQAKAYIITAFIIVEGQGDQLAADVRQFYQHAAGGAS
EGYPDVQPGTMASLKELAGVPSAAAYTAALVRTLRNRYPPAETSRVLSVGSEEVRLTA
EQMKLRYD"

CDS complement(5209313..5209906)

/gene="folE"
/locus_tag="EFAGFIKM_04540"
/EC_number="3.5.4.16"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P19465"
/codon_start=1
/transl_table=11
/product="GTP cyclohydrolase 1"
/db_xref="COG:COG0302"
/translation="MAGVKDYLNKSVSDNREKIEYHVEQILKLIGEDSTREGLLETPA
RVTRMYEEIFGGYEVDPRDVLGVTFDENHEELVIVKDIVYYSQCEHHMAPFFGKVHIG
YVPSGKIVGLSKMARLVEAVTRRLQVQERITSQIADILTEAVEPHGVMVVVEGEHLCM
CSRGVKKPGSKTVTSAVRGSFRENPAQRAEFLSLVKD"

CDS complement(5209964..5210227)

/locus_tag="EFAGFIKM_04541"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDIVIPITLIVGLVGGFFIGVFYLRKQLEKMQSNPDMLQKMAK
QMGYNLNGKQMQRQQMMKNQQPGAKMPQPQQHPARKSSGRRK"

CDS complement(5210393..5211424)

/locus_tag="EFAGFIKM_04542"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MKYVNVESVEAGELLGKTVYSSNGTVLLSAGVQLTVYMVNTLKR
IGVTMLYIQDEAYKDVAEDILDETTKRAIINEMSVTLESIRSGKDWSRPRKVALSIEK
LLNDVLNGREMLVQLTDIRTKDNAQYVHAMNVCLLSSVIGLNMGLNYNQLKDLAVGAL
LHDIGKVGEPGSGSAANSSLHHTWRGFVVIKKNKREFSLLVAHTALQHHEHVDGTGMP
RGIKGSIDIHLFARIVSVANIYDNLINGLSKDSLMPHEACEEMMALSGTKLDRDILIEF
NKSVSVPNGTAVRLSTKETGVIVRQHRGLPGRPVIIRVARGSTRYSLDVVEIDLAQHT
TVFIEAVMT"

CDS complement(5211440..5213320)

/gene="queG"
/locus_tag="EFAGFIKM_04543"
/EC_number="1.17.99.6"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00916"
/codon_start=1
/transl_table=11
/product="Epoxyqueuosine reductase"
/translation="MTSVQTGAAQDASVWEKLEKQEIKAAGPGLGIDDIGFASADPFVS
LKSLLQSRDKGYASGFEEPDIKRVHPALKDGEPASLIAIAVAYPSKMVNPPKSEPG
AYRGIFARSAWGQDYHQVLRAAMDKLVNFIRERVPEAMIESMVDTGALVDRAVSQRAG
IGFSAKNCAIISPKFGSWIFLGELVTNIPFQPDTPVTEDCGECTKCIDACPTGALVGP
GQLNAQRCISFVTQTKGFVDEEFMLKIGNRLYGCDTCQIVCPKNRGKNWDHHPFHPD
PEIVKPLLLPLLDIGNREFKERFGQSSAAWRGKKPIQRNAVIALGNFKDKSAVPKLTE
VLKRDPPELRTAAWALSRRIGGEDAMRAIGEAAANEQDGNVLSMLQKAKERLSSSET
LPKQPQAGQVSEKQPEEQNNENNSLRALQQDLKMEAGIEPDSEQSAQPAKPEAAWKP
SAVTGLHGKPVYYDEVLTPIGTLTLCATDEGLCHIDFGAFHVREAHLQQWARIWIGEY
RYEKNEEKLSEAAKQLKEYFAGERKTFDLQLDRLGTPFQLQVWQVLSDISYGEASSHQ
QVAEIIGRPKAVRAVLDAISKNPPIIIPCHRISGKDGLVGYVGGLQTKEQLLALEQ
LS"

CDS complement(5213492..5214097)

/gene="sipP"

/locus_tag="EFAGFIKM_04544"
/EC_number="3.4.21.89"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37943"
/codon_start=1
/transl_table=11
/product="Signal peptidase I P"
/translation="MSSNNHSMEHVTSEQRNEPSKPEQLGKSWVVELWDWVKTIVVAF
VIMMLLNLFVFNLSMVKGQSMQPTLVERDRLFVNKIVYHLGTPSRSDVIVLRDPSEGV
EKKDFLVKRIVGLPGDTIEVRDHHLYVNGEQQAETYTDIEVQDPDFGPITLAPDHFFV
MGDNRHEGKSKDSRVFGSITSDQIVGKAEIFWPFSELKKL"

CDS complement(5214422..5214847)

/gene="ypeA"
/locus_tag="EFAGFIKM_04545"
/EC_number="2.3.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P76539"
/codon_start=1
/transl_table=11
/product="Acetyltransferase YpeA"
/db_xref="COG:COG0456"
/translation="MHVRSFQLSDASQMTELLQVALSEECYENTMGPFARQLSWDSDL
IMVAEEEGDLVGALIGTIDHNQGCIYRIAVHPDYRRRGVGKTLVEAMEQRFQQRKVSQ
VWVAGDEHNKVAMPLYEAMGYGANQIMSAFQTLSILSKA"

CDS 5215268..5215879

/gene="sodA"
/locus_tag="EFAGFIKM_04546"
/EC_number="1.15.1.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P00449"
/codon_start=1
/transl_table=11

/product="Superoxide dismutase [Mn]"
/translation="MTFQLPALPYANDALEPHIDAKTMEIHHRHHNTYVTNLNAALE
SAPELQEKSLEDLIANLDSVPEGIRTAVRNNGGGHANHSLFWIIGPNGGGAPTGDIA
AAIDSELGGFDKFKEDFAKAATTRFGSGWAWLVVGKDGKLSITSTPNQDSPLFEGLT
VLGLDVWEHAYYLNQNKRPDYIAAFWNVINWDEVNKRYASAK"

CDS complement(5216196..5217563)

/gene="nth_2"
/locus_tag="EFAGFIKM_04547"
/EC_number="4.2.99.18"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00942"
/codon_start=1
/transl_table=11
/product="Endonuclease III"
/translation="MGLQEQKQHFSVNLLDWYMVNRRDLPWRRHNNPYFTWWSEIMLQ
QTRVDTVIPYFNRFIGNFPTVQALAEAPEEDVLKNWEGLGYYSRARNLQAAARQVMEL
HGGEMPQDKPAVFALKGVGPYTAGAILSIAFNQPPAVDGNVMRVLSRYFLIDEDIMK
GRTRVLMEELAGELIPEGRARDFNQALMELGALVCTPKAPHCLTCPVMEQC SGRIAGR
ELTLPVKTKAKPPRPEQRLVAIVEGRGAHRGQVLVRQRPDTG LLARMWELPHVLAAPA
AASKKAAPLADEPAMALLAGSLWAEGFAARPEGLATHAEHVFSHIVWSLQVYKCTEQD
QSSELPLIAAEARAAYDAQAATREGTASSSTVSPESDTTHSSEPGTPNAQNISTSFND
GEMLMSSSDVSDLALSTPTLTGKGDGLTYRWIGPEDMDKMAFPNIFLKLISYFAGAY
DQVND"

CDS complement(5217593..5217949)

/gene="acpS"
/locus_tag="EFAGFIKM_04548"
/EC_number="2.7.8.7"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q81JG3"
/codon_start=1
/transl_table=11
/product="Holo-[acyl-carrier-protein] synthase"

/db_xref="COG:COG0736"

/translation="MRKLLSGRHAEAFIKRILTPAEREIAVRRGKRMTEFVSGRFAAK

EAVSKAFGCGIGGVMGFTDIEVLPGDTGRPVASLSSQAWERLQLPYDKQYDIHLSITH

QTELAFAIVEQMEK"

CDS 5218240..5219055

/locus_tag="EFAGFIKM_04549"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPITFELPTDVDAIIRGDDFFPAQQPAQGVILSHGYKGFKDWGM

FPYAASQLSQTHHVLTFNFSHNGIGEYLEQFSELEKFAVNTYSRELADLDLVLEHVAT

QPELNGLPVYLVGHSRGAGVSLVYALDHPEQVAGVISWNGVTNLDLFTAEQKEEMRTH

GRSHVVNGRTGQQMPLDVAILEDMDKHSERYAIIDRLASSPVRVALIQGTEDPQRLRD

GSAALVQVRPDIPWHQMPEGNHTFNTVHPFKETTPQLEQAITQTLQQIKDWNS"

CDS complement(5219182..5219991)

/gene="nadE"

/locus_tag="EFAGFIKM_04550"

/EC_number="6.3.1.5"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5DZX4"

/codon_start=1

/transl_table=11

/product="NH(3)-dependent NAD(+) synthetase"

/db_xref="COG:COG0171"

/translation="MSLQQQIIAELKVKPSINEEEVRKRVDLTKTYVKNAGAKGLLI

AISGGIDSAVATALCKKATDELTQENNQEYKTLGVFQPYGEQSDIDHSYAVAKAYDLK

HVVETNIEDAVNEIALEVEQGFKSLGSPRHMTHQGKGNVKARTRMVMQYALSFEENLL

VVGTDHASEAITGFYTKWGDGAVDITPLSTLNKRQVRQLAAYLNVPQAILDKAPSAGL

WEGQTDEDELGISYEANSDYLEGKQIDPAAQERLEAFYTRTHHKRNAIPGI"

CDS complement(5220131..5220565)

/locus_tag="EFAGFIKM_04551"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54170"

/note="UPF0403 protein YphP"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSMSFDQYMKDMVQPMRDDLTRLGIQELRTPEEVEASLPDAKGT

ALVVINSVCGCAAGQCRPGVSQALQHDITPDHLYTVFAGQDKEATAKAREFFAPYPPS

SPSIALMKDGELVHFIERHQVEDRSAEDIAADLKSAFDRYCR"

CDS complement(5220787..5222481)

/gene="sasA_18"

/locus_tag="EFAGFIKM_04552"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"

/codon_start=1

/transl_table=11

/product="Adaptive-response sensory-kinase SasA"

/translation="MVALKDMLLQVLLAGSAVFLIPLFRLVLSKRAIARMEHAGTVHT

SFVVTSVASMLLCLLFALYASPMAPISLSIVPVILVILYCKSTIGVTLSTILHILFYF

LFAHPYDLYGFLHTGILLYPIVWLSAKRFKHNTSPSRKMAILIILITMELIVTSLLWI

ASLQNESTYSATYMILTALGYTAGAIVAGSLSLWLERMKHYRGLEQHLSEVHHRYIA

ETEKLHQILNAVPLSIATVDKQGTVMFVNEMMEQTAREQLPCTSTPDLIGQPASQFVE

QGQADKMDKSIRRAIVHGEISGLTVRYGAHVFSRTVPIYAFSTESAREVTGAMLIQ

DITELEMLRSELDNVDRLSLVGQMAASITHEVRNPMVVRGFLQLMQEKSPDSLHYY

RIVLEELDRANSIINDFLSLAQNRIAEKEESQLHDIIHELSPLLWADANLRGQSIELM

LAHNVPKLHLNSKEIKQVVLNLARNGMEAMNEKGVLTLETRIVDDKVELCVRDTGPGL

PRVKKEKLFEPFYTTKAKGTGLGLSMCLSIVERHNGTITVESEEGQTTFKVAFER"

CDS 5222677..5223945

/locus_tag="EFAGFIKM_04553"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P44941"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/db_xref="COG:COG2081"
/translation="MYDVIVIGGGSAGLMACVAAAEHGASVLLLDKGDQLGRKLGISG
GGRCNVTNAKETDELIRHIPGNRFLYSSFQNLDNQGIMRFFENLGIALKEEDNGRMF
PVTDKAKTVVDALVGKIVSLGVEIRTKPEVKEIQNGQQIQGVKLISGKTILGRSVII
ATGGKSVPQTGSTGDGYPWAEAAAGHTITELYPTVPIVSGESWIQSKELQGLSLRDIA
LSVVDAGKKTIVISHRGDMIFTHFGVSGPVALRCSQFIRKVQMKSGNPQVIMSIDLFPE
LSPGALEAQVQQVLEQESRKAVKNILKTWVPERMIPLMMKRAEISDDLTFHHFPKGML
SILCGLMKAFTRADGTRSLKEAFVTGGGIHLKEIYPKTMESKLLPGLFFCGEVLDIH
GYTGGYNITAAFSTGYTAGMHAAEYKHAKL"

CDS complement(5224089..5224472)

/locus_tag="EFAGFIKM_04554"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MMDNSELQVHFSDDSALNAARATLEELGYKPYQSGPLELYIPTD
RQDPQSAVEIVQSHGGSVAVFASQTEELDQFQNISIPAHLVNEDWNEGYASGNQGSQTE
QGRHNYSDPTYDDSDADGFSGSVKA"

CDS complement(5224748..5225995)

/locus_tag="EFAGFIKM_04555"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="METSQRYTPLRLYRRRRKEHFKEQMKNLRLVVDWTVWVYLLVPG
LLYLIGWYTSWTKSLPAWATGLPLPVLTLGLIDVVMGTGGVLIFVEEADVLFKSRPL
WMRTLMRQGLYRSLQHLGKMILITALTAPLWSRVYEMSNLQIALMAVWFGAVASFQV
ITLHMTKVRHTGWRRWIQMIPLVIGMGYMTIHATSWMHGQTWKISFGIVIMLLLITV
GQMRLLMKGTFEQDVREDLRSRLQLTALMLSRAVSKPKAPRTRSIFRKPRKLLRNRS"

IANRTAEIAFKAFFRNSATMKLYLQLGGLSIAAVALPPFPVNVIVCALLIIMLTVMFY
RSWDVFATSDYVQLITYDSEALHLAGSMMVRMLFIPIGILMGFTLGLAWLGWMVGILT
AAGAVAFGLCVLSIAGWVRLTRA"

CDS complement(5226017..5226748)

/gene="ecsA_2"

/locus_tag="EFAGFIKM_04556"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P55339"

/codon_start=1

/transl_table=11

/product="ABC-type transporter ATP-binding protein EcsA"

/db_xref="COG:COG1131"

/translation="MGTEYKSTEVQESILDVHITEAGYEPGQSTIRNIRMNVARGELV

GIIGPNGAGKSTTIKTLGLLEHANYEVTIGGDGRYAYIPEQPVFYEYMTLWEHLDLA

AAAYEMEEEEAFGARAEELLVRFGMDHVRNDLPASFSKGMQRQKMMLMIGFLSSPDIYIV

DEPFIGLDPRATKDFLKLLDDERRRGAGVLMSTHVLDTAERICDRFILIASGRSAAEG

TLDEIREAAGLPGHSLFDCFDVLT"

CDS complement(5226844..5227011)

/locus_tag="EFAGFIKM_04557"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTRYLSIQEVIAINVAMIKRYSPEEQIGVKDSGLLESAAVVRAQS

SAFGNEAYPSI"

CDS complement(5227014..5227277)

/locus_tag="EFAGFIKM_04558"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNRVSEMERKVTKFGNSLGLTMTDAFKQIGLEQGDMVQIEVNQS

NGEIIKKSTKVNLPNGISSDFMDTLADVMGEYDQILKGLKDR"

CDS complement(5227427..5228728)

/locus_tag="EFAGFIKM_04559"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKVN RVWKLSVLSGTLVAGLLGASQATYADSYNNSSGNLDLN

AGLRLELGSLLSGHRDTGYGNHGSYGGSSSATGALNLDLGLNAGLSSESMNRYNDRSS

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AEGESASMAQSERNNSVKDGERTDNSSYASESRGALDLGLNAKAEGESATMAQSERNN

SVNDRERNTNSSYASDSRGALDLGLNAKTEGESATWTQSERTNSVNDRERNVNSSTAS

ESRGALDLGLNANAEGEGATMTQSERNNSVNDRERNVNSSTASESRGALDLGLNAKAE

GESATMAQSERTNSVKDGERNMNSSYASESRGALDLGLNVNAEGESATMAQSERNNSM

KDSERNDNSSYASESRGALDLNVDADAESATTSVVETNR"

CDS complement(5228778..5230127)

/locus_tag="EFAGFIKM_04560"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNVKLPKSIMRLGSIPLAILAGTLM LGFGSSHVYADEAQSSEK

PSSGLSLNLF SRDSDGGLNLTPSVSVSTPLLDVEVPSIKANESTGKLSVSELKVDTPL

GSAGTSEIGIDAKKGTVELPSVQADTPVIKADVSSSQVNLNDGTASLPGVTAEVPEVI

KAETSAVKTDLRQGKVELPSVKVDVPEVTSVNISSSRVDLSKGNVQLPSVKAEPVVD

VSAELNPDQEKVEIPSVKPERPVVTPEQPTVVKTPNVETSNTSALADPVSSQNNEEGQ

DALQVTGKVM EVTPESEVRPEQPVVPQALPVEGTDLTQSDVSAGLPDNELFLVDQPS

AEPSVTEQVQSNEEADLKQDDVDATSPLLPRTERPTSWSVAATSPGAANASAGTSSGS

SSVTGGGATAPAAA L PGATTGLVTPDYDFAFRMERLDGFSQWSQAPPGRPPQYTSFS"

CDS complement(5230335..5231666)

/gene="entS_4"

/locus_tag="EFAGFIKM_04561"

/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01436"
/codon_start=1
/transl_table=11
/product="Enterobactin exporter EntS"
/translation="MTSDLTFEGQRPLKNNRSFVTLMVAQAISNLGDWLHLLAILTLV
GIRWNATPWEITFVTLAALPILLTGPFAGTLADRLNRKWLMIADGARIIVGALIF
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LGGLLVAAFGITWCFVLDSASFLISGILLWIPGTRVIQTAIHNVTEVEEEPAGDVLN
RPKDSFWKETLEGIRMLASLPYVGTSILLASAILFLQFADSQTVVLFRLPGISSDL
LGWCVAASGAGTLIAAMSVRKWKHAGHVLKMGLGTILMGLVIGGAGVIVGIWPHAGLG
AILLVSLFALAGVGIGFAIVPFQILLQEQTPEAMTGRVFGTVGSMVTASNIMGPVVG
GFMVTSFGVVPFVCSGILMTLLGLIYLMKRSGEKADLTGSIEAKTMIAGD"

CDS 5232014..5232475

/gene="mhqR_3"
/locus_tag="EFAGFIKM_04562"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31672"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator MhqR"
/db_xref="COG:COG1846"
/translation="MLELQEIGTERSLHLYRTLAQTFKSVNEHAVSGSKVHGFNPTAY
GVLEVLYMKGAQPIQQVGAQLLLQSGNVTYVIDKLEQKGLLHRKHCPQDRRIIFVELT
EEGQRTMDDIYPGYALKIDRAVSGLSEEDKELLSELLGRLAHSADRLSASS"

CDS complement(5232944..5234467)

/gene="bmr3_2"
/locus_tag="EFAGFIKM_04563"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P96712"
/codon_start=1
/transl_table=11

/product="Multidrug resistance protein 3"
/translation="MNATGGLKRSFILTGLLLATFLSAIEGTVIGPAGPTIVSELGSV
QLLSWIFTAYLLTMAVSTPIFGKISDLYGRKPVFLIGCALFLLGSLCCLSQNMEQLI
IFRAIQGIGAGAVVPVFTTIIGDIYAIEERGKIQGWISSVWGISSLAGPLLGGYFVDN
LGWQWIFGFNVPFGLLAMWVFVRYLKEDISPRTAKIDYVGALTFTVGITALLFVLSAG
GQYYAWSSPLIVVLSVVAALFIILFFVVEKRAQAPMVPLHLFRIRDIRVANIAGLLTS
TLMIGLTSYLPLWVQGVRRGNATESGLLLAPMSVGWLIGSVMAGRLLMKIGSRLTALI
GLTGIAIGSGGLFLVGGTSPQAVLFVLTFIYGLGFGFAFTIFTIIAQSSVGKERGYSS
TALHTFMRTLGTIGAAAFTWLNRYRISTLSSEQNLAEGISENDLNELLAPHTDAAL
SDDKWALLRNVLEGLHSLFVIMFVIALVSWVTTLALRKRLIVPEDADAPPQPQGSK"

CDS complement(5234684..5235226)

/locus_tag="EFAGFIKM_04564"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:ISfinder:ISSpgl1"
/codon_start=1
/transl_table=11
/product="IS1595 family transposase ISSpgl1"
/translation="METARLRLRKMRRRDAAQMFAWSDREVTRYMNLAPMIGTSEAA
DMIGLLNQMAGEEDAIRWGIELKETGKLIGSCGFNTWQLEGAFRGEIGYELGRDYWRY
GYMTEAFSALLPFGYETMGLNRIEALVDPRNLASGEFLTNRGFTREGLLRQVQHTSTG
YKDMVMYSMLYDEFLRKKGK"

CDS complement(5235456..5235752)

/locus_tag="EFAGFIKM_04565"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MHAEVQNLVRIHLLHFAQNQDLNVSEALPLLEERGYRVEREI
KQELEHLTQENFLTAHGDQWSLTGTGIEEFKEITAVFGRVSELLGKGKKTSKA"

CDS 5235938..5236435

/gene="msrC"
/locus_tag="EFAGFIKM_04566"

/EC_number="1.8.4.14"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P76270"
/codon_start=1
/transl_table=11
/product="Free methionine-R-sulfoxide reductase"
/db_xref="COG:COG1956"
/translation="MFQAVSYEGTRSEQHTAVLGQLSALIRDEPSAIANLANAAALLN
VFMTDTNWVGFYLYDGKELVLGPFQGLPACIRIPLGRGVCGTSAAEKRTLVDVHAF
PGHIACDAASNSEIVVPIIKNGELYGVLDIDSPIKNRFDDEDRVFLEKAVSLLTEQLE
AT IPL"

CDS complement(5236587..5237399)

/gene="mta_3"
/locus_tag="EFAGFIKM_04567"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P71039"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator mta"
/db_xref="COG:COG0789"
/translation="MAYSMVDVSGMSGVSLNELSQYAETGLLNPAFGDVDADIYYEKQ
ELLRLQQILFCKEVMKENEIAPMLRDNPDVIRIMKQHRIDILGKALRLHGLIQTLD
KTISHLQGEQEIDEHDLYIGFVNKGRHQLLNESGSPVVNNDMNHVQTEGVQRSDIQS
SNSSTLPENQEMKSKEDYLD SQAKIDQVHDLQQAIEDGLEPGSAKVQQIIGRHLEWI
KGYTPTAEIYRDLANLYVEHKNFRQMYDGYHPRLAEFLRDGMMIKAHDLS"

CDS complement(5237769..5239193)

/gene="safD"
/locus_tag="EFAGFIKM_04568"
/EC_number="1.2.1.73"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q2BN77"
/codon_start=1

/transl_table=11
/product="Sulfoacetaldehyde dehydrogenase"
/db_xref="COG:COG1012"
/translation="MKKQHFLFIGGKPAESVDYKTLQAPYSGETLAEVSSASAEAEAA
VAAAVQAGKAMRQMPAHQRADILYKLSSMLEERKEEAARIIALEAAKPITAALAEVDR
TVETYRFAAEAAKRLTGETVPMDSAKGGEGRIGYTMRQPLGVIGAITPFNFPMNLVAH
KVGPALAAAGNTIVLKPAEQTPLSSYYIANLLQEAGLPD GALNVVSGDGKTIGDVLVEH
PRVAHITFTGSPAVGTSIRSKAGLKRVTLELGSNAAVIVDKDADLNKVVPRCVTGAFT
YQGQVCISLQRIYVHRDISEEFIRRF AEAAKQVVVG DPLSPDTVVSALITSKDVQRTL
DWIEEAKQAGAEVAAGGQAEGGVLRPTVLINVPRDAKVSCQEVFAPIWINTVDSVEE
GIEHVND SIYGLQAGVFTNDIHTALHAVDQIEAGGVMINDIPTFRVDHMPYGGVKQSG
IGREGVKYAVEEMTELKFVMFNKG"

CDS complement(5239435..5239857)

/locus_tag="EFAGFIKM_04569"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7A551"
/codon_start=1
/transl_table=11
/product="Putative universal stress protein"
/translation="MLKRILVAVDGSDHAHKALEQALILAEDMKQPPSLIVHVNPAI
SINEPALGVDLEARIAEEGQHIIPEVTRQLSGRDVPYETLLIAGDPVNEICRVARERD
CGMIVMGTGGKGMLAEMIVGSVSHGVLKHAECPVLTVK"

CDS complement(5239876..5241096)

/gene="yfmO"
/locus_tag="EFAGFIKM_04570"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O06473"
/codon_start=1
/transl_table=11
/product="Multidrug efflux protein YfmO"
/translation="MKREPSLPDELPSSRGGLLSQPRAWAVAFACIISFMGLGLVDP
ILPAIADQLHASKSQVSLFTSYNAVTVGAMLITGVVSSRIGVKWTLTSGILLIIVFS"

FLGGTSDTVGALVGYRGGWGLGNALFIATLSAIVGLSTSGTAKAILYEALGLGIA
VGPLLGGELGSISWRGPFYGVAVLMAIAFISITFMLPKMAKPKTRSSLSDPFKALSYP
SLKTLAITAFLYNFGFFTLMAYSPYVMNLDEHGLGYVFFGWGLMLAITSVFVAPRLQR
RFGSVPSMSVMLTLFAIDLVMVAVGTVMGSPTTVIVAVIVAGIFLGINNTLITTAVME
AAPVERSVASAAYSFVRFLGGALAPWLAGKLEWFLPETPFYFGALMVLVGWVLLVR
RHHLRDIDSAITSH"

CDS complement(5241327..5241779)

/gene="yfmP"

/locus_tag="EFAGFIKM_04571"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O06474"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator YfmP"

/db_xref="COG:COG0789"

/translation="MSLYKIDDVAKCEGLTKRTIRYEEIGVMPSQRTDGGTRLYTR
EDIDYLKKVRAKEVLGFSLQELHTYVATADALNEQRFDYQQTTEVRERIEKLTAMET
TLDGQLQLIEQKLQSIHAVQTELKELRERVRSIGIQLQAHDPPQGEDG"

CDS complement(5241972..5242328)

/locus_tag="EFAGFIKM_04572"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTGAVVGIIIGVCYFILGFMVFKKPPKMINGIYGYRTPRAMSNP
ELWDEAQSYSANLMMQFGVIITIFGIIGFWLTDVRALVLSLVATGFYTFRLFTRVEGR
LKQMQRAQQQQNEQNA"

CDS complement(5242613..5244967)

/gene="kdpB_1"

/locus_tag="EFAGFIKM_04573"

/EC_number="7.2.2.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00285"
/codon_start=1
/transl_table=11
/product="Potassium-transporting ATPase ATP-binding
subunit"
/translation="MGTGQEQVKRELLLDGLDCANCALKIENGVKKIKGINECSVNFV
TKTSLHTTSDMDEQVVEEAKRKVLRLEPHIRISEKGKHAVNGHVHTHTDTGSAAGAHN
HSHDHTGHDHGHSHSHGKHSHTHDHSDSEGHTHGHVHEHGHHAGHDHSHTHDDAHAGH
SHEHGAGQTKVLLARLAAGSVLLAAAIWSPLEGWAQFTLYALAYLIAGGDIVLQASKN
IIRGQVFDEYFLMSVATLGAFAGEYPEGVAVMLFYQLGELFQGMVNRSRKSIQSLM
DIRPDYANILTDSGDETRRVSPEDVRIGDRIVVKAGERVPLDGIVRAGRSMVDTsalt
GESVPRELEPGSDVLSGFVNKNGMLTIEVTKTFGESTVSKILDVQNASSRKAKTEHF
ISKFARYYTPVVILA AVIAFVPLILSGATFADWIYRALVFLVISCPCALVVSIPLG
FFGGIGAASRNGILVKGSNYLEALNDVKVWFDKTGTLTGKGVFKVTAIRPEGGRTEDE
LMELAAIAEANSNHPIAESIRAAWAKAIPTQGV EGYDEVAGHGIKVSVDGREVLAGNA
KLMKQAGISYTPDTAGTIVHVAEAGTYVGHLIIAEV KDDAAAAIQALKKLGI RRTV
MLTGDAKAVGEAVARELGVDEVYAELLPQDKVERLEQLEAAKSPKEKMMFVGDGINDT
PVLARADVGVAMGGLGSDAAIEADVIMTDEPSKLASAIRIAKRTRMIVWQNI AFAL
GVKAIFLLLG VFGIATMWEAVFSDVGVTVLAVLNAMRVLRVKNI"

CDS 5245196..5245567

/gene="ziaR"
/locus_tag="EFAGFIKM_04574"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q55940"
/codon_start=1
/transl_table=11
/product="Transcriptional repressor SmtB"
/translation="MEQPVKAPSECDAACSGTEADVQTIRTSLIDRETSSEMADWFKA
FSDPTRLRIIDALLQKELCVHDLTVLLDMGQSAISHQLRSLRNM RIVKRRKEGKTVYY
SLDDAHIEQIFLQTLQH IKHS"

CDS 5245700..5246017

/locus_tag="EFAGFIKM_04575"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAIKGQKYKTYSEKIKKEAIRLHTVEGWTYRKINEHLGIHDPGR

MKRWMRKHREQGEFGLMDQGRRRKEYLDQERYVQKLKRENELLKKCLVIWKEEANKKD

FRS"

CDS 5245966..5246850

/locus_tag="EFAGFIKM_04576"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISBth8"

/codon_start=1

/transl_table=11

/product="IS3 family transposase ISBth8"

/translation="MLGNLEGGSKQERFQIIEKVAAYGDIQKLCDFGVSRSGFYAYV

KRKRFD RDAKAKKQVLQTYQRYEGKYGYRQLQLFLWQDQGIWMNHKKVLRLMQMLGIQ

SRIRRKRRSNSSYAPAQRVAENRLKRDFS AEKPNQKWVTDITQYRVGERWIYLSAIKD

LFNNEIVAYEIGERNDNELVLR TFSKAFKQTDVTGLVHSDQGFQYTSHAYHDM LPK

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CDS complement(5246990..5248150)

/locus_tag="EFAGFIKM_04577"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEQPEQPRVWPERFKRFFLN NKFVLFLLILLVGLNVMVLT KVS

FVLHPLAVLIKTIVLPILSGILYLLNP IVDVMERWKIKRGWSILILYLAIGGILTV

VVLAVIPVVRNQIVGLIENFPTYSETVKQ QFEELTGSQ LFGQFQETVNLNSQDWWGTI

SQKATEILNSTWTKLGGFLGAFTETVLS IVTPFILFYLLKDGKKLP AKILSFLPIKS

RTGAMHVLEDINHQISSFIRGQIIVSFC IGILLYIGYMVIGLDYALILAIISFTSVV

PYLGPAIAITPALIVALVTSPVMLLKM VAVWTIVQLIEGKFISPQIMGKTLKIHPITI

IFVILTSGNLFGVVGILLAVPGYAVLKVCVSHIFNWFKDRSGLYDPNKNNLL"

CDS complement(5248461..5249495)

/locus_tag="EFAGFIKM_04578"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTTQNTASSHKEHINDVKLSILD LAPVVVGATPADALRNSLDLA

QHAERWGYHRYWVAEHHNMPGIASSATSVVIGYLAGGKTIRLGSGGIMLPNHAPLVI

AEQFGTLESLYPGRIDLGLGRAPGSDRRTSLALRKDLNSGEDFPELLAELRAYFDASA

TSYHAPVRAVPGEGLNIPIYLLGSSDFSARLAGQLGLPFAFASHFSPDYTRIALETYR

NNFQPSESLKEPHVIVGVNAVVDTEEAAWLGTMMQQQFLNIIRGTTGLVQPPAEME

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ELIAQLAGKA"

CDS complement(5249655..5249966)

/locus_tag="EFAGFIKM_04579"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEPILIFKALSNETRRQILLWLKNPEQHFPPELSQHPDGGKNG

ICVGTIQVKAGLAQSVISSYLLTMLKAGLLSERRGQWTYYRRNEETIRQFAEYVQNE

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CDS complement(5250080..5250661)

/gene="kefF_2"

/locus_tag="EFAGFIKM_04580"

/EC_number="1.6.5.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01414"

/codon_start=1

/transl_table=11

/product="Glutathione-regulated potassium-efflux system

ancillary protein KefF"

/translation="MKHLIVYAHPHTDSLNNAILNTAVEALEAQGHEVVVRDLYKLG
FQPVLTEADTVSMRAGQTPQDIATEQEFTVNAEAITFIYPIWWTGLPAIMKGYVDRVFA
YGFAYAAGEAGIEKLLTGKKGLIINTHGTPSEIYDQIGMTAGLKVTSDVGIFDFVGIE
AVDHLLFGSIGYLDAPAYQALLDQVKQTVTTKF"

CDS complement(5250828..5251265)

/locus_tag="EFAGFIKM_04581"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYNEVMPKYNAIALIARIRDHVNKRIVHELEQHEVTGIVPSHGD
VLMFLYREETLSIKMLAERVQRTQPTVTVLVNKLEKLGYVERSKSAEDSRVTMIRLTE
QGKRLEPIFHQVSEQINDIISGLSDEQSEQLESLLSIIVRKL"

CDS complement(5251449..5252126)

/gene="yfkO"

/locus_tag="EFAGFIKM_04582"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34475"

/codon_start=1

/transl_table=11

/product="Putative NAD(P)H nitroreductase YfkO"

/db_xref="COG:COG0778"

/translation="MEVTAKSKTKEDILKAYHFRHATKIFDDTRKISDEDFQFILETG
RLSPSSIGLEPWKFLIVQNPNLKRKLSEVSSGAQKQLATASHFVVILARSDASYN
SPYAEYMLKETKGMPNNVYELTSEAYGKFQNNQKILDNPRSLFDWASKQTYIALGNM
MTAA AQIEIDSCPIEGFSREGVHRIMEEEGLLENGAWGVSMMAAFGYRAEEPQREK
SRQSVE KITQWIN"

CDS complement(5252338..5254083)

/locus_tag="EFAGFIKM_04583"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSIQSKPKNKKGNKLNKMLTTTMMVIMTVISLIGLFTVFLIGIF
GMNEAKTGQGILYNDRFQHQTNVLELKSNFYNNRANYTKVLDNAEYTDKQYDQVQKGK
KSITDGLNEFSARTLDIKEKEIFADLAAKMDTTYQDIEQIMDTKKMSGTYDSEERGRI
NKSSTAIVETITLLSAHNEEESAKLYADTQEVIQQRALVLGSLVLLFSLAALILISFVW
IRSIRQRMKAITRYCEEITQGNLTASLDPRLTQGNNEISVIARAIRTMTDSTTNVIRG
VIQESHINQVSDLTNQNMAGLNERIREVSATVEELSAAMEEASAHTENMNHSAEMQ
QGAEYISEQTSKQAESAYVTSTKAELKQEARESSRAAIDMYDHTSKKMSEALERATA
VDQIGILSQSILDVTAQTNLLALNASIEAARAGEAGRGFAVVASEIRKLADDSRQAAD
QIQQVTEEVMQSVTNLSSNAKELLSFMFNQVGKDYKLLDTEAEQYYVDSL DHANAVKD
LNATSQQVTANIKILVGSIHIEIASASEQSAASSQEIAGHMASAAQSVEVVKQSDQVK
DSALNLNKLVQDFKI"

CDS complement(5254279..5254629)

/locus_tag="EFAGFIKM_04584"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVCPELLGGFSTPREPAEIIIGGTGKDVLAKTAKVIEKSGKDVTE
LYIKGAYQKLEWARELNVSCVVLKEFSPSCGTQMIYDGNFANHVKVTGEGVTSALLRQE
GYTVISENEWMEQL"

CDS complement(5254788..5256074)

/locus_tag="EFAGFIKM_04585"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRQKDEQWEKEIRKGPFASSPFTEDHKRVLQQVEWMKKSKEGS
KGDRPEESSRLSRPFRPQVNNVSHKLRPRRGPLVAGTGALVIAAGLFLWIWDDGQVLK
PVIEQVYPTAALQLSDGLNTNLLTDRMKRNVATTMRDDLKQKIKKVEDLPVSGRIY

VEAGNESEKEYAQIWLDATTGNLREVQMRREIQPNELEHRYLRQVPSLLQSIGSTPTL
KPASVQRFVSMKQGESEPISTTLALENDTGDGYGEIVWQQDKAVSITGDLRPDQVSQ
AALTDARNAIEALSGKANLNLVRASRSKDDDELGKDTVFFSFKDNYFVQMTEGKAGLG
TVGDANYEQQEIGNIEEMEAYHEKLYNIDESLLREKVGPIVKKIFSIDFDAYKLHRN
AEQLGIVTFELESSKDVFQVEYREDGRIKMITRGEL"

CDS complement(5256071..5256649)

/gene="sigW_5"

/locus_tag="EFAGFIKM_04586"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q45585"

/codon_start=1

/transl_table=11

/product="ECF RNA polymerase sigma factor SigW"

/db_xref="COG:COG1595"

/translation="MDDQLLAQAQTIDNYTLSSIMDDYGNDVWNYAYFLTKSAEQADE
MSQEVFIRAYSGIAHYRGECSLKTWLLTITRNTTFTYRKSRFFRSSLWGETLPIETER
GDSSQRVMVAEQPAHPSAEMEVMRKEHIHEIWDIVLALPKKFREILLNLKYELTSE
IAEMLKISSGTVKSRLSRGKDKVRKHWEERSK"

CDS complement(5256880..5257614)

/gene="cmoB"

/locus_tag="EFAGFIKM_04587"

/EC_number="2.5.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01590"

/codon_start=1

/transl_table=11

/product="tRNA U34 carboxymethyltransferase"

/translation="MKQNKYDEAEFFDNYSKMARSVQGLDAAGEWHELQTLLPDLKDK
RVLDLGCGFGWHCRYAREQQASSVIGVDLSENMLQRAREMTDDPQIQYEQLAIEDIDF
APGQFDVVISSLALHYIERLDTVYAKINDFLVEGGTFVLSSEHPIFTARAAQDWHYGP
TGEILHWPVDDYHDEGKRVANFLNQDVVKYHRTLATHLNELIKAGFAIQKVAESKPSP
EMIDQVPGMRDENRRPMFLMIAAVKV"

CDS 5257777..5259132

/gene="mepA_2"

/locus_tag="EFAGFIKM_04588"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A7N0"

/codon_start=1

/transl_table=11

/product="Multidrug export protein MepA"

/translation="MNTNWTHTPLEGQSVGKAFISYLVPSVLGMLVAFNFIIDGIMVG
HKLGSTAMAGIGIASPVYTLFVAMSLWIGMGGATLYSNAMGRKDITSAKQIFTKSIML
IMLVTVAIGYVAFTFKDKLVYSLGANTETFPFASDYMNIMLLFGFVFTIENALSIFVR
NDGNPNTSMYAQITFAVANIINIYITLYVLEWGVRGVALGTIVSASLALLVLFTHFFK
KTNNLTFTFRKWNNKLLASLLIGFPSFLAELGMSVFSVSHNISMMDRIAGTDGVASFT
VLNYIHGWVLLAFLGLASAAQPLISYYHGANQIKRVQQTIRLATKTALACGLLLLWVV
QIGAPYFVQIFGNFSSGVTDNAVYGLRIFTFAYVFMGVNFVMSTYFQSVGNAMAIWI
TAAREMIIMIALIALPSFFGVGTGVWLAVPLSEMLVLATIALYRKRSLTDRINALQS
E"

CDS complement(5259289..5259642)

/locus_tag="EFAGFIKM_04589"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNISSTASSTTSYISTSSSDNSSSLEKQKTKLEAQLEKVQSRN
DDEQTKETKTKLQQQIKQIETQIAQQSSQGAGTTATKEAPPAQPPSNGMGVATPKEI
ANATTDSDNGRFDIRI"

rRNA complement(5259919..5260030)

/locus_tag="EFAGFIKM_04590"

/product="5S ribosomal RNA"

rRNA complement(5260110..5263030)

/locus_tag="EFAGFIKM_04591"

/product="23S ribosomal RNA"

rRNA complement(5263339..5264889)

/locus_tag="EFAGFIKM_04592"

/product="16S ribosomal RNA"

CDS complement(5265430..5266650)

/locus_tag="EFAGFIKM_04593"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKNWKRMLLSLTISVGLLASAVPAMAAPQGTSVKVNDQAVKYAT

GAPILEKGTMMVPLRRTTLDAMDVKLTATDDTITAVVDGKTITLKSRLTRINGVTYAP

IRIVGDAAGYEVWRDAATRTVLLVSKGGATETAQTGGRGFMWEVESNGNTVYLVGSMH

IAESFYPLRPEFEEAFEAADYLGVEIDISKAADDEEQQLVLSLGSYQDGTTLKDHIS

SETYTKLGDVLKKNLEPNALDAFKPWWVESTLASLKSTTAGYEASAGVDLYFIQKAI

ERKLPVIELESYQSQLGMFNDFSQETQEETLKATIENFDVLDNSVKEMAEMWKTGNDQ

QLELTNSFSTNEEYNKAMLVDRNIGMADKIDGYLKNGKGEEYFIVVGAHLYLGDHGI

VKLEDKGYKVERK"

CDS complement(5266790..5268085)

/gene="yhaP"

/locus_tag="EFAGFIKM_04594"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07523"

/codon_start=1

/transl_table=11

/product="putative protein YhaP"

/db_xref="COG:COG1668"

/translation="MNKMGTITGFTFKNKVKTKSFMVTTIVLALLISIGLNVFYFITL

FNGGSIGGASSNPVNIGLLSTGQPEVSEKLESFSAAQGDQAYRFIASGDKDEAALAA

DVEAGLTDGYLKFEAVSGQEFPPILYSAEDVSPQIIASIEAALQSVKLDVVVKDVL

AEQKERITTPVKLTEQSLSTDESGAGTESEGAMSPINYIVVYLLIILLFTSTMMTGNM

IASEITAEEKSSRIMEILITSVSPLSQMFGKIIIGIFMVGMLQIGIFGAVVAGNILLPHN

RAVLGDFNMSVSDVNSAVIVYGLIFYLYAVLFAAIGSMVSRTEELGQAVLPIT

MLSLVSFYIAIFSISTPNILLKIASFIPFTSPTAILVRIGAGVAPTWEILTSAILI

VSIIIFGWLAAKIYRTGVLMYGKRPTFKELFKAMKAYKI"

CDS complement(5268078..5268980)

/locus_tag="EFAGFIKM_04595"

/EC_number="7.6.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O86311"

/codon_start=1

/transl_table=11

/product="Multidrug efflux system ATP-binding protein"

/db_xref="COG:COG1131"

/translation="MNRLELKQVVKQYADKTAVNGVTLNVKEGEIYGLLGANGAGKTT

TMRMVLGLIHPDGGNILYNGKPYNTELQQIMGYLPEERGLYPKVKVSEQINYLARLRG

MNGKDADQSLKYWLNRFVPEYYDKKIEELSKGNQQKMGFIAAVVHRPQILILDEAFS

GLDPVNVELLKSTVKELRDEGTALFSTHRMEHVEELCRQITILHRANTVVQGEIKEI

KSRYPREQVFLGTIGSVEGLEQLPGVKKVERNERGYLIHISQVEAAQEILRTAMTQTT

VEHFELKEPTLNQIFIREVGESNE"

CDS complement(5269001..5269897)

/gene="btuD_13"

/locus_tag="EFAGFIKM_04596"

/EC_number="7.6.2.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01005"

/codon_start=1

/transl_table=11

/product="Vitamin B12 import ATP-binding protein BtuD"

/translation="MEPIAIQLNGVSKMRKRRVIGPIDLTIPEGYIVAILGHNGSGKS

TLLNMLQQVVLDPAGQIIWFGQEHDGPLPIELRQQIGFVADNAGSEENRITAQDAAHF

RAYWYPRWDMKLFDRLIQDMEVPVDVKLNKMSKGERRKFEIAAAIAARPRLLLLDEPS

SGLDPFAWKVMVEQFRTFMAGGDTTILIATHIADEVKRLADYIVLMHRGQSLGMAEKD

MVLDQWKEVWYEGDLRPESIPGVVLESSLEEGGLVRVITTRVSEAQERLELSNNRVLKI

RNLELDEVLAFWIAGYAPVQWK"

CDS complement(5269913..5270311)

/gene="ytrA_4"

/locus_tag="EFAGFIKM_04597"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34712"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional repressor YtrA"

/db_xref="COG:COG1725"

/translation="MQDVKIPIQINENSAEPLYHQIENQLRSLIITGQLGEGTHLPSI
REFAGALNCSVITVRRVYQDLENEGLLRTKQGTGTFVAQVEAGDRENYRLKAAQEAMQ
AAVQSGKSVGCTEEEMESLFREVLKVIYVK"

CDS complement(5270392..5271078)

/locus_tag="EFAGFIKM_04598"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTRSQMSKDRLQWLWSALFMIYTGGMSGVMFLGQQQTDIINPVV
DSFFLIMLPFQGFMFCRRSFRYIQEDSYTHMLAYYRRIPPEQVVMWSRLQQSLMAFT
YNGIFFYGSlyVVNLHAEGFRWDQYLAFSLTCTGYGLLVTFYIYGEFLNSGKKYLLL
STLFIPFAIGISILIRISGSYGLRIVMDGSKSWGLLSPIMWISLVAGVAGLWLSSRFT
LKKLVHRDLN"

CDS 5271305..5271634

/locus_tag="EFAGFIKM_04599"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDWLVEIGFVLLFLIVVIWLVLRDEPHRHSSKKGRHRIRRNNGY
TDSASGYPVITGDDSYDRHSKHTPDHKHHDSDSSSDTHSHHNSDSGSSNDSSGDSGGG
DSGGGGD"

CDS complement(5271745..5272116)

/locus_tag="EFAGFIKM_04600"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKTVNVVSQTYPRLTVYSEENYRGRSRIYRGNTGLRNLDNILDG
VESLRFFSTSSNATLVVFTRPNFQGGFRVFRGNTNLRDLDDLIRGNDVESLISTNQRL
TLAQIRAIRRDRSLPSGYNLV"

CDS complement(5272259..5272723)

/locus_tag="EFAGFIKM_04601"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDMYFWLPTISTSFIVISAVLVGIGWVLIIRGKREAHQSAMVAG
AIAALIFFVIYMSRTVFGNTAWGGDPDLEIFYRIFLIFHIILATVAAIFGISTLVLG
FKKKFGTHRRWGKFTSMIWFGSALTGVVVVLLYLLYPGGHTRPVWEVILGV"

CDS complement(5272758..5273681)

/locus_tag="EFAGFIKM_04602"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLGLQYFSFNDLWSPLILAVFLIIAAAYLVLVGPLSEQIKDAEP
ATAAQKIMFITGLFVLYLAQAGPFNLLGHVMFSFHMVSMAFSYLVAPPLMMKGLPIWV
WRRIVRWLPTRQLSFLAHPIVA AVLFNGLFSLYHLPVHDYVMLNFTVHRLYYIALFI
TSMLMWWTLLNPLPEGRQASGLSKIGFIFLNMVLLTPACGLIIFAAEPLYQTYSNPAV
WAEAMRYCVSGDSTALLRSFGGPAFFNFLSSAKEDQQVGGIVMKFIQEGIFASMLAYV
FFQWYRKEKQEDDDDSYPAGGAGGPLNPAAK"

CDS complement(5273790..5274110)

/gene="caaD"

/locus_tag="EFAGFIKM_04603"

/EC_number="1.9.3.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q03440"

/codon_start=1

/transl_table=11

/product="Cytochrome c oxidase subunit 4B"

/translation="MSAQDKTDQQPVKHRHRTEGPQKHVVVFIFSIIILTIAFAAASA
GGVNTTFIIIIILLMAILQVFVQLGYWMHLKDKGHLMPILFMAFGFFVAFTCIIMALY
WVWWW"

CDS complement(5274114..5274740)

/gene="ctaE"

/locus_tag="EFAGFIKM_04604"

/EC_number="1.9.3.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q03439"

/codon_start=1

/transl_table=11

/product="Cytochrome c oxidase subunit 3"

/translation="MTTSHAEPVNDKLPHEPEKATLEGRNKLIAFWLFLGGETVLFGT
LFATFLALRGQTNDGPTANELFHLPLVAAATFILLVSSLTSVFAIQAMHKGKRDALAL
WLGITVVLGMGFLTLEIYEFYEVVKHKEFGMTTSAFSSAFYTLVGFGAHVAFGIVWI
GIIIGQLFKKGLTVVTAPKVYVSAMYWHFIDVWWVFIFTVVYLLGKVG"

CDS complement(5274737..5276626)

/gene="ctaD"

/locus_tag="EFAGFIKM_04605"

/EC_number="1.9.3.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P16262"

/codon_start=1

/transl_table=11

/product="Cytochrome c oxidase subunit 1"

/translation="MAHAHSVCRYRGLMDWITTVDHKKIAILYLVAGGFFFGIGGIEA
ILIRIQLMKPMNDFVSAQVFNELITMHGTTMIFLGVMPLIFAIMNAVVPLQIGARDVA
FPFLNALGFWTFLFGGLLLNSWVMGGAPDAGWTSYTPLSGSEYSGTHGVDFYTIGLQ
IAGLGTLIGGINFLATIITMRAPGMSYMRMPMFTWTTFITSAILFAFPAITVGLVLL
TFDRILGANFFDVAGGGNPVLWQHIFWIFGHPEVYILILPAFGIIEVIPTFSRKRLF
GYSSMVFATILIAFLGFMVWAHHMFTTGLGNVANALFSISTMLIAVPTGIKIFNWLFT
MWGGQIRFTAANLFAVGFVPTFVMGGVTGVMLASAPADFQFHDYFVVAHFHYVIVGG
LVLGLFSGLHYWWPKMFGRILSETLGKWTFTWTFMIGFQLTFFVQHFLGLMGMQRRIVT
YLPNQDFDLLNLVSSVGAFLMGVGVIMFLVNIVITMKKPAGAPNDPWEDGRTLEWSIP
SPPPEYNFKQTPLVRGIDAYWKEKMAGHTEMTPAEPVGSIHMP SATPLPFVMSVGIFI
AGLGLMFSNDEFGNAFMNVIFNNYIVVIIGLVITFGAMALRSLYDDHGWHIEPEDQDE
KGART"

CDS complement(5276659..5277711)

/gene="ctaC"

/locus_tag="EFAGFIKM_04606"

/EC_number="1.9.3.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q04441"

/codon_start=1

/transl_table=11

/product="Cytochrome c oxidase subunit 2"

/db_xref="COG:COG1622"

/translation="MMKQWQVAKRILPLLAVFSLLLSACGREDLSVMKPQGPVAQGQY
DLMKLSIAIMIVVLIIVFAIAAYVLIRFRRRAGQTEMPEQVEGNFKLEVIWTAIPLLL
VIVLAVPTVQTIFAQGEDLSNDKNALKVQVTSHQYWWFTYPQYDVTTAQDLIPTGT
KIAFELKTADVLHSFWVPSLAGKMDTNPDGTLNKFSSAPNEG VYRGKCAELCGRSHA
FMEFKVKAVSQESFDRWVNQMKAPAVLPEDTQLAEKFTNCLSCHAVGDQGGPVAPNL
TGIGGKESVAGILLNSREGQEEGSPVLDNMKEWLHDPQSVKPGNTMPNPKDLGLTDEE
IDGIAEYLANYKLDYE"

CDS complement(5278277..5279038)

/gene="map_2"

/locus_tag="EFAGFIKM_04607"

/EC_number="3.4.11.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P19994"

/codon_start=1

/transl_table=11

/product="Methionine aminopeptidase 1"

/db_xref="COG:COG0024"

/translation="MHVDPILKTKEEIGYMREAGRILWSCHQHIGQWMVPGITTAEIN
ERVEEFLAEHGATPEQKGYPYATCASVNEVCHGFPSDEVLASGDVVTIDMVVNK
DGWLADSAWTYGIGETSRISIRKLMRRTEKALERAIAQAVPGNTLGDIGSAIERTARLY
RYGIVKPLIGHGIGQYIHEPPNVLPGYKRRRTGTMTEGMVITIEPIFTKGSSGAVVWD
EDGWTVRTVDGSWGVQYEHTVAITGNGPLVLT DGT"

CDS complement(5279172..5279360)

/locus_tag="EFAGFIKM_04608"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MATKGHNEVKESLREMTRIFRPKDPKKFVKEYVRKYRITGGYEE
ELTSVVEHELVKMDSSVS"

CDS 5279760..5280035

/locus_tag="EFAGFIKM_04609"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDRKEQDMLPLSHEKVEVDGVYINEAGREEHLHRGQHFPADPVL
GKSEWKLTEYAYDNHHEGRTDERLVPKENDTDKMGKITNPRRQIEGG"

CDS 5280231..5280569

/locus_tag="EFAGFIKM_04610"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MSPMKSSSGLDENIAGMLCYLFTFVGGIVFLAVEKRSRFLFHA
LQSVTVFGIIMVGHVLSAFLPLFGPLVASLLSLLGVVWVLMVVTSLQGKWLKLPWVG
DFAEKQLRHL"

CDS complement(5280836..5282197)

/locus_tag="EFAGFIKM_04611"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A0A2A5JY22"
/codon_start=1
/transl_table=11
/product="Nucleobase transporter PlUacP"
/translation="MARERIFQRHRHPIKTFSLGLQHVLAMYAGAVVPLIVSNALGF
TQEQLTYLIAIDLLACGVATLLQVWGNKYFGVGLPVMGLGCAFQAVSPMILIGMNSGVS
AIYGAIIASGLFVLIFSGIFGKLIRLFPPVVTGSVVTIIGTLIPVAFHDLGGGQGSE
DFGSGVNLMLGFGVLLFIILMTRFTTGFIIRSISVLIGLLVGTIAAGFMGEVNFAPIRD
ASWFHVVPFYFGRPTFEIVPILTMILVAIVSVAESTGVFMALGKILDKDLSSKDLAR
GYRAEGLAIVLGGIFNSFPYTTYSQNVGLVQMTRVKTRDVIVVAGGILVIGFVPKIA
ALAQLVPGAVLGGAMVALFGMVVSSGIRIIGSQVDLNRHENLFVIACSVGMGLGVTVV
PELFAGAPAWAQIMLGNGIAGSFTAIFMNLNFNGLGTKETAAKMAEQQADAILGETD
KSA"

CDS complement(5282199..5282786)

/gene="xpt_2"
/locus_tag="EFAGFIKM_04612"
/EC_number="2.4.2.22"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42085"
/codon_start=1
/transl_table=11
/product="Xanthine phosphoribosyltransferase"
/db_xref="COG:COG0503"
/translation="MQLLKDKVRQEGIVLSEQVLKVDSFLNHQMDPVLMEVGKEFIR"

RFEGENITRVLTIESSGIAPGIMTALELNVPLIFARKQKSLTLTEDILVEKVYSFTKQ
ETNEITVAKKFMKPGDRVLIIDDFLANGAAFGGLARIVEQVGAEVVGIGIVIEKAFQP
GGRLLKEAGYRVESLVRIGALSDGQVTFADDEEGTN"

CDS 5283458..5283952

/gene="mscL"

/locus_tag="EFAGFIKM_04613"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A742"

/codon_start=1

/transl_table=11

/product="Large-conductance mechanosensitive channel"

/db_xref="COG:COG1970"

/translation="MKGVLNEFKEFAVRGNVIDLAVGVIIIGAAFGKIVTSLVNDIIMP

PVGKLLGGIDFSQKIFNLDRDMKTANGQEITTLAQANEAGATVIAYGQFINVMIDFLI

VAFCIFMLVKGINYLKSKEHKKPEPQKTTKACKYCLSEIPAAATRCSHCTSELEAEGT

GALA"

CDS complement(5284195..5284497)

/locus_tag="EFAGFIKM_04614"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MECIVHFQVIYPQPQERKSLRGLIFVGQGQEPANSQLSSMFKDM

GFNVRLDEAQLLFKPVDSANFEYIRVTELDTGEEVYKEDKDLKSILEHLLPRRF"

CDS 5284577..5285269

/gene="idi"

/locus_tag="EFAGFIKM_04615"

/EC_number="5.3.3.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00202"

/codon_start=1

/transl_table=11

/product="Isopentenyl-diphosphate Delta-isomerase"
/translation="MTPERFDIYDDKQNWIGTSLRSEVHAKGYWHRSFHCWIVRDKGE
QRRVLFQRRRDIKDTFPGCYDITAAGHLTAGEQLQDASRELEEELGVYTPFEALTYLL
TATQQLQGEVRGVPFIDREFSAVYGLCLNQPLEAYVLQPSEVDSLVEVPLDDLALFR
NEIDVIQATGVQTQPLTSPPHSIGHKDPLSDHAADEPERIVREIRATEFVPHGTAYYT
DVLEALYHVPKE"

CDS complement(5285539..5286372)

/locus_tag="EFAGFIKM_04616"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLTAWGDGNMDQLLHHLRHLGFTEMESKIMVELARQGSASGYEV
AKRLGVSRSNVYATLQRLEQRGFLRCSPGEPAKYSVLKPEEMTRMISDQMRTSLDYVQ
SSMPKSEPEKPVFYNVEGDKNVFENLSRELAEAQHEIVVDVWREEAELLRNDLQQAEA
RGVRLWSCDGGEGMLDQVPWPGLPMYGTGNRKFSLVDDRWCMLGMRGESCATQA
LVTEHPVMTGLLLNHFAQELVLYELEQDMGEELESRYGHRYEELSARYWSSPSGEGDQ
S"

CDS complement(5286419..5287234)

/locus_tag="EFAGFIKM_04617"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKLLQRIKDGANKATERAQHAVEIGKLNNQIVGLQQEQEVHFTD
MGRIFYEGYRAQDMTRAEMVDLSQLCDELQDEIDGLRNKIAQLKNERLCECGHVAS
LDANFCPKCGRKLGEKTAAPKVAAAGVAGATTAAARQEAAVAQTPTPEPDFYDAPPEL
ELEEDEPYHTVIPSIADLETESEYNSTEFTQEEKEAFDAEWERRRDEEMQRERERQQE
LDERIRYWKENNPIVNTVDVQTEVSREMVNCQICAAELPKGSKWCPRCGAEQI"

CDS 5287584..5290166

/gene="rep"
/locus_tag="EFAGFIKM_04618"

/EC_number="3.6.4.12"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01920"
/codon_start=1
/transl_table=11
/product="ATP-dependent DNA helicase Rep"
/translation="MLSPNSTFYPRPLGVTPAASLPQSPSAPLETSRQLVGNEQQDAF
YFRSLEEAGIKLNAPQISAVRHGRGPILTLAGAGCGKTTVLAARAGYLIEVSGVHAGS
ILLVTFTNKAATEMKDRIAALPGIRPAAARAVQARTFHSFALTLLRHYG VQEEIFGES
RAQHTVLKMLLRQNGMSEAFQPESLLAMLSAWKMQGSETDLPEKSQEERDAKRVLLG
YEAWKQDRGKMDFDILLRAAALLRDPVGLPLQKRFQYIMVDEFQDTNHLQYEIVQK
LASAHRNLMVVGDDDDQTIYTFNGARQESILEFDKVYPGARIVTLDINYRSDARILGLG
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AILHRTASSSRVFEQLVLKDVFPVQHGASPVFYDQSLIRPLMDHLRLSLDPRAMDAL
PSALGPLYVSRDAGLEWIQRCEQQQAKKYPLIHLVKWDKLKPFQQEQVKERIKLIKSL
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FADELSRRHREMESLRRRAQSDAVQLMTIHRAGLEFPCVYWIGASEGIVPHSTALRQ
DIPEDQKAALAMQQTDAELDMALEEERRLAYVAITRAKQYLYVTSPASHHGKPADVSR
FLLEAFGMEVPDKRKPREESRTSSQASYGKNGQYARSSGSGARSEGRDAAQRRRAISH
SDRRDFEVHNERDEDRLGERRGSGEIRNHKAFSTPGVSQTAASSSSSQSHTSGSGNAE
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RFGK"

CDS 5290413..5290781

/locus_tag="EFAGFIKM_04619"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MQDGKQHLYVSVTHNLIERTKNESTPFEVLVDDEQLGRLKDLMK
VLEDDDAYTLQRAPVPYKSADHDEATEQFSDGMTLLYTFLYDHGTPDTRQAIESMNVL
PRLQD TDYDDPGYENSPLNK"

CDS complement(5290872..5291942)

/gene="iolG_9"
/locus_tag="EFAGFIKM_04620"
/EC_number="1.1.1.18"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9WYP5"
/codon_start=1
/transl_table=11
/product="Myo-inositol 2-dehydrogenase"
/db_xref="COG:COG0673"
/translation="MSTKQMLHIGMIGTGSISDLHMRCYAKNEDAVIYAICDLNEERA
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TNVEDALRIEEAVKKSGRTFIVGFVRRYDNNMQMMHRFIDAGEFGELYAKASILRRH
GNPGGWFAKSRSGGGPLIDLGVHIIDQCWYLMGRPKPVS VSGNTYRKLGNRAHIEHL
SFYKAADYSAAVNDVEDMANALIRFENGASLAVDVSFTLHARGDESSVKLYGERGGFE
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ASTRMLCGIYESAEKGQEIRLD"

CDS complement(5291989..5292465)

/locus_tag="EFAGFIKM_04621"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSDMLVALYRLPEQESGLRALEESSIVIRRAIAPEKQLVLDWVR
SHFSQAWVDECDVAFARQPVSCYIAVEHGKMIGFACYEATCRNFFGPTGVSQDARGKG
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CDS 5292714..5293778

/locus_tag="EFAGFIKM_04622"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P43131"
/codon_start=1
/transl_table=11
/product="Protease inhibitor"

/translation="MNNNMKKVVSALMALSMALGGGAAYAATLDNTQPVHQTSVSADSN
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DVKTVTERGVITRISNQDKYKSIQIGGAGTDGIVLNLSDETKFISVEGKEIALDLAI
GMNVEAEHSLITRSLPPQTPTYKVTVLDDAAESQLKDVLTAGTIENV TSAEGSISQ
IEITGTRLTETAPDHVVLNIAKDTLIVNHEGETVKAEEELTKGAKVIGFYSPVLTRSLP
PIGTAWKVVVETPAAELEAK"

CDS complement(5294405..5294797)

/gene="rutC_2"
/locus_tag="EFAGFIKM_04623"
/EC_number="1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AFQ5"
/codon_start=1
/transl_table=11
/product="Putative aminoacylate peracid reductase RutC"
/db_xref="COG:COG0251"
/translation="MSRQQVFTGSPWEPLVGYCRAIRVGNRIEVAGTTAMQDGVVGA
GDPYAQTRFVLQTIENALKELGADMSHVVRTRMFVTDISRWEEVGKAHGEFFGQIQPV
ATMVEVSALIDPLLMEIEVEAIVEDEI"

CDS complement(5295030..5295998)

/locus_tag="EFAGFIKM_04624"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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SFDEPHEKRHRMRKEAAEALFKLFAKADGIELRAVSGYRSYQRQVSIYNNNVKTKGQ
EYTRVSSVPGRSEHQTLAIDVSSPSVGNVLEEFGTSKEGQWLAEHAAEYGYVIRY
LQGEEDTTGYVYEPWHIRYIGTDLAPDVAKSGLTLEEYFDEANIKL"

CDS complement(5296408..5297220)
/locus_tag="EFAGFIKM_04625"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSEKWKIELHMSPGGWTAENVNTVADADQEVSVSASAAEGKTGSA
AGMFTVTGTPARLSEAQREAVLAQLRKRPLTYALLRGGPASEELAGLLPAVQAPES
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WAEELAHDPSPGPGRAAETAGRPQVRGGEGGAAVGEWIAEAAAADGAMHQPGPGFGAVEV
RLAQPGKPPALPELTALMPGVPATAGLDLIRERVAARMWQAVQKKTDSPATK"

CDS complement(5297267..5300470)
/gene="rapA_2"
/locus_tag="EFAGFIKM_04626"
/EC_number="3.6.4.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01821"
/codon_start=1
/transl_table=11
/product="RNA polymerase-associated protein RapA"
/translation="MMQSLYGVWLGDVFFCFSGTSEPRVDAWSHVVRRLNFGDGGRL
FQPAALRLAELRWPNPLRNTAEAKNTKRRQLLGRTLGLAVSPKDAFRLLLQWDDRLL
NAAGIQVGEEMRYWIKAAQFTQELLLRGAIAPSAEFAAKTGARRRTGQETLTGVWRPR
LQQEEDIERFRDLAEAMPPIGLAAPGAYASLEPETREEAGAAVLFSFMSGMIHAVVTS
ELEGMDSELSRYRTPYRRGSSPVAELWWNSLISMFRPVTVQGPTDDMTAFIHTLQEVG
GTSMPIVGAEEMAPAEGQLKLVLRLEPPLGEHETIWGISFWVDSEQEPSLRLPARTIW
AHPERDLDRGKVLTSAAEQLLMALGQAAEMAPELETALLTARPEEIKLEQQGFFEFL
THAVPRLQKAGITVLMPSRWSRAGKRRAGRLQMLNRGTERLPGATSALGMEQLVAFK
AEPMLDGKPVTAEEAALAESTVPYVMFRGEWIEVDTKAIRQVLRMYMKKEEQYMPLS
EWLHLAADEGEDSAWKGLSVFGAESDGMLAFLLDGQVLRISIEPRQVPAELHGELRPYQ
ERGYQWLSAMRELGFGVCLADDMGLGKTIQVITCLLDRKHEERQAAAAEEARENELNG
SDDSFADQHTNEQPVHLPALIVCPTSLLGNWQRELKRFAPDLSLYIHHGGQRLHGND"

FQAEAQTHDIVLTTYHLAGRDGPDLASLHWSTIVLDEAQYIKNYRTKQAQSVMLSTL
HRIAMTGTVPENRLSELWSIFQFLNPGYLGTAASSFRQRYTGLGPSEENAASLRELHRL
VSPFMLRRLKSDPDIRKDLPEKLELKSYSCLTPEQTVLYQRVVDDLMMGLDGRNGIAR
KGIVLSSSLTKLKQICDHPVLADSNRKDHGKAEASGKMERLLELLDAIRDNGESALIFT
QYVAMGDLLVSRLKQRYEEEPYFLHGGVSKGQRDDMVETFQKGEGPSMFVLSLRAGGV
GLNLTRASHVVHYDRWWNPAVENQATDRVFRIGQNRNVQVHKLICQGTLEERIDELIE
SKKALSEQVVGSGENWLTEMSDDELRLISLQGETWL"

CDS complement(5300698..5301129)

/locus_tag="EFAGFIKM_04627"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDEGMQYINFSVGDQIFALRIDEVHEIIRMVQVTTVPFGSPEIR

GFASLYGKVVSVSLRVLLGMPDQEDTSSTRIIVVPYKGGFVPLIVDMVDSVWSYDRF

EEPAEEHRRFMLGVFDKIGFCEDHRAGILNLDVLLGSLIRS"

CDS complement(5301742..5302689)

/locus_tag="EFAGFIKM_04628"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKQRVEISKNVLTECLGLRSGENLVVVADDMKRDLAESIYEAG

KALGAESVLLIMEERSRSGEPPAPIAEAMIRADVAVCVTKYSLTHTQARKKAAASGT

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NGVPSTGMYLNPGESGNLPSGEAYIAPIEGKGEYSIVVDGSGVAGIGALREPMLLTVSE

GRLVSAEGPDGDQLLETLGEGDGRFLGEFGIGTNNKARITGVVLEDEKVYGTIHVAFG

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CDS complement(5302783..5304774)

/gene="menH_4"

/locus_tag="EFAGFIKM_04629"

/EC_number="4.2.99.20"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01660"

/codon_start=1

/transl_table=11

/product="2-succinyl-6-hydroxy-2,
4-cyclohexadiene-1-carboxylate synthase"

/translation="MIVHTNRVSNEENTAANSTNMNQVIRKSDITATTIFMTGSTGFI
GKETVKQLTQGDEQLLLLRSEQRARTVLEAYGVKDFDRITFIKGDLSMSGGLGLTAAD
RERALEANVIIHAGGTMDVTLERKVAEQIFMNGAREVAQLAQEIHRTHGLRHFHVVG
YMSPYGERNEQGNYLQVEHVDNNESEAYEEMKFHADLHIREHAEQHHYPLSVVNPSTVV
GPRPTGETEQTGGIGLLIQAIQKGLMPVPPGGSSYWLPLVENDIVAQTLVFLSREAAP
VGGTYPLLARKEDSPNMKELLQLLAQQLDVPKPKGAVPLPWIQWIMRSGGSRSISGVPA
ESVAFITNRSFPVEETEALFTRMGQSWPDIREQLPLVTADLDYRLRYTPLPEGFPTDY
IRSRRGNMAMLGWEGEGEPWIIVHGLLQSADEMLPLGQQLRDLTGNPVWLIDLAGFGR
SPVHQGDEAFEGQVDALLTALGEFEGPVKLVGHSIGAAIAAAQMRSGRTDIRLGLLQ
PVANNSNPVLRWVSRLPRGVIRSLRGRSEKSWNQMFSSHSGVGDSSVMADTMGKRI
RSSLQSPRIAGAHTDLLRWIHSGQRKGARSTLWAKMESQHYAKSVLVVWANQDQEYHY
PQDMNSQAKRIDVPYGHYFPTFQYKETAAILAEWADTLR"

CDS complement(5304835..5305440)

/locus_tag="EFAGFIKM_04630"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNTGPAKSKSSNPVNRTKAVEVAAQLFLRQGYSYVSMDEVVRVS
GVSKSNIYYHFKNKEELLQAVVQYWIAQYESELYLLLSQRERGVEERIYSFMALLSAG
IEGRNYEGSCPFVTLYMQTPDSAPQVKESISRFFREL RPMVEKLFQQGLDRGEFRKEI
EPGPAALLFIAALEGSLILAGTARDVGIIEQSARTFCQMLR"

CDS complement(5305836..5307134)

/gene="msmE_4"

/locus_tag="EFAGFIKM_04631"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q00749"

/codon_start=1

/transl_table=11

/product="Multiple sugar-binding protein"

/db_xref="COG:COG1653"

/translation="MKRMTKLTLLMLIAFSVMLAGCGNGDKSGSPVNTDAQGGGEAAA

GDKTIKIFQFKVEIAEALNRLKAEYESSHPGVKLDIQTVGGGSDYGAALKAKFAAGEQ

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YNKDLFQKAGITEIPTTLEQLDQAAQKLQAAGITPFSNGYQEWVVLGNHNVNVAFANQ

ADPVKFIQGLNESTEKIPGNQVFADWINLLDLTLKYSNKNPLTDDYNTQVTLFASGEA

AMMQQGNWTQVQIDGIDPDLNLGILPMPINNEPNDKLFVGVPNYWVWNKNSQVKPEAK

EFLEWLVTSDIGKQYMTKEFKFIPAFSSITASEEDLGLATDIMKYSQENKTLWNFN

RFPEGVPQEYGSTIQAYVAGKSDKAGLLDALQQNWDSLKK"

CDS complement(5307738..5308574)

/gene="melC_6"

/locus_tag="EFAGFIKM_04632"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34518"

/codon_start=1

/transl_table=11

/product="Melibiose/raffinose/stachyose import permease
protein MelC"

/db_xref="COG:COG0395"

/translation="METTKNYRFSTILTEIVMVLLGLLFLVPFYFLVNSVKTFGDLL

TNSAAWPEVFQWGNANAWEKINFPSALMNSLIVTVVSNLLLVLISSMAAYRMVRSMT

RFNRILFGMFIAAMVIPFQSIMIPLVTVTSNLGLIDSLGGLIICYLGFGAPMSVFLFH

GFVKSVPLEIEEAARVDGSSVYGVFFRIVFPLMKPMYVTIILNTLWIWNDYLLPSLI

LQSSNLRTIPIATFALFGQYTKQWDLALPALVLGIMPPIIFLLMQKYIIQGITAGSV

KG"

CDS complement(5308574..5309455)

/gene="melD_9"

/locus_tag="EFAGFIKM_04633"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34706"

/codon_start=1

/transl_table=11

/product="Melibiose/raffinose/stachyose import permease
protein MelD"

/db_xref="COG:COG1175"

/translation="MKHRKSSQLLQQLVFGPSIVFFILIIIVPFLGMOVVSFTDWNG
VSENINWVGFDNFVHVFANDPKFQTAFWFTVRFTVVGVLTVNIGFFLAYFLTKPLKT
RNILRTIFFMPNVIGLLLLGFIWQFIFVKGFSAVGDTVGSFFNLPWLGDEPTAFWGI
VIVFWQTAGYLMVIYISLTVNSPDLLEAAEIDGASRWQVLRSIILPLIMPGVTICL
FLAISWSFKMFDLNLSTKGGPFGSTESVALNIYNEAFVNNRYGIGTAKALVFFVIVA
IITMIQVRLTKSKEVEA"

CDS 5309599..5311428

/locus_tag="EFAGFIKM_04634"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKYYSIRTKLIAFMLIATTLPLLASISMTFIQTKTALREQAVE
ENKRLIYQASTNLNNYVDNVARASLAVYNDPNFLRNLAIPGDYRAVAEVYTTLTQIR
AAVPDVFQLYLHSFAANQSTLITNPFPKREERKQAYSGSLHGKTGGDSPDIWVESAHM
SHTYGFKAAASPDDPARTVITLHRVIKDIPSTERLGVLAIDLNMNTIAAICGRLYDPAK
EQIYVVDGQNQIIYQGRSEVNHTDALREETASELNIARSNAGTAQNVAGHFEQDRSMY
VYQQLGSTYADWTIVKQIPNETLYARATTLTWNNAMIAIALVLVIVATLFIIRITG
PLKQLMRYMNQIQAGRLHVDIHLSSRDEFGVLARHFRDMMDTVNNLILREYRLEIANK
TNQLKALQAQIHPHFLYNTLQSIGTLALQQGQRAYTLLSSLKMLRYSMRDQTCVTL
REEAEHARLYLELQQERFGDRLEVDLDFAEDTLSVEMPRMTLQPLIENYFKHGADIQP
GKGHISLSSRRINDHWIEIELNNNGPSIPEDKLEIRGWLHQSHTTTGLSTQESDESE
SIGLRNVIRRLQLNSHPGHSARLEINNQEPPNGVKITVKLYTGE"

CDS 5311434..5313062

/gene="rhaR_37"

/locus_tag="EFAGFIKM_04635"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01533"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaR"
/translation="MKALLVDDEKHVRDAIRLLGHWKEFGIDTLLEAADGDEAIAAIT
AHQPQIILSDMRMPGKDGMALLEWISAHTPHSKVLVISGYDDFELVRHAIRHGGMDYL
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SPSHMQRLQDELNLPCLIPVCSVAVTSLSHLDADCLAKYRSQPDLLVFSVLNICAEML
STPDEGVMFRQLDQPDEIVLLHWGPSTSLEHILDKVNQGLEQTIQRRLHFGISICESY
PGGIAAAYLEASSRLWRRNAVQIKQRIHTSVESNGNKIRRLTAHEEPLRMAAMSCRA
SIVSAAVAEWLDPITDLEVVS AEQIQQWIDELEWMLSRWLDDTAGSSFHEEEVTEEQS
IPFAELPLDAEGLLSFPLLRSLLEQRLLAAGKALTTHHHANPDPMSEIARYMDAHYQE
DLSLQQIAARFYLSREYISRKFKQQFGLNWSEYLGKLRINNAKLLLQNPSLRVAKISE
MVG FQDEKYFSKVFKKMEGITPAEYRKTLL EAGT"

CDS complement(5313423..5314388)

/locus_tag="EFAGFIKM_04636"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLTRETMEKQQTWSYIVALFVGAAIGLSNPAWGNVLHYTVSPVL
AVLLYSMFVQIPFLQLKESWSNLRFMVALLVANFIVVPVWVWLLTLVFPQSPGVLIGV
YLVLLTPCIDYVIVFTQLGRGNEKLMLAATPLLFVIQMILLPFYLVLLMGTEVAQIMQ
VGPFVEAFLFLIVIPLLLAVVTQVLSRGKVSGERVMNATAWLPVPMMALALIVVVASQ
IGKVYNDMAIIVDVIPIYIAFLIIMPWISRLIATWFGLNPGAGRALIFSSATRNSLVV
LPLALALPPEWATIAAAVIVTQTIVELAGELIYIRLVPAILRDR"

CDS 5314614..5315372

/locus_tag="EFAGFIKM_04637"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MSRNNPYKWLNAIGFIAVIIVNYLSNALPIGGKTNKEVSDMYPV
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QNLQTGLALLIIVLLLLCLIMLYVKTRTITVPTTAEIWLVLKLPFSIYLGWISVATIVN
AAVLLYKIGWDGFGISEPTWTIIMLIVGMVLAVLVSFYRDSIYPLVFTWAYIAIALK
QKDVTSVYYTAIIIAIVLAIYAVWLFFARNQDRD"

CDS complement(5315489..5315863)

/gene="tdcF"
/locus_tag="EFAGFIKM_04638"
/EC_number="3.5.4.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AGL2"
/codon_start=1
/transl_table=11
/product="Putative reactive intermediate deaminase TdcF"
/db_xref="COG:COG0251"
/translation="MKKPISTDQAPGAIGPYSQAVDAGDFIYTSQGQLGNPQTGEFGA
DVQEQTRLSLSNVKAILEAAGTSMKDIVKTTVFLKDMNDFVPVNEVYSTFFEQPYPAR
SAVEVARLPKDALVEIEVIALK"

CDS complement(5316012..5316692)

/locus_tag="EFAGFIKM_04639"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNRLERKAMVIGATGLVGELLVHNLLEHSAYSLVRVLVRRPLEL
QHPKLEQHVVDWGNLESQDHLFDGIDDLCCGLTTIKKAGSQDNFRQVDYHYPVRAAT
IAKQHGVSQMLVISSMGASAGSRVFYSRTKGEMEDALSDIGFPSLHIFRPSLILGDRN
EKRFGEQMAAYAMKFLDRWMKGRADKYRAVHAATIAQAMTNIAMVQTKGNHVPNDVI
HVLGVDGG"

CDS complement(5316823..5317857)

/locus_tag="EFAGFIKM_04640"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MQRIRSRKRMLLLFVGTHRILWSATGLIPFIFPKEWWVSVYIGV
YTVAFISNTIGGMIWTSIGDIVPAKVRGRYFGIRNTILNALGSVCLFAGGIVLDRYP
GEMGFLILFIPVWICAIAANTVIYFFYPDVPFERSTEKVFWRMFIKPFQDRSFLKATLF
LASWLLIQTLIVPLYSYVMLDLLNINYQTVSLITVVQTLVMMAGFYVWGNLNARFSNK
TLLFWTLPVIALSCLSWGLMSFMPVLIALFLSHIFLGIGVGGFNQLAFNFTIGDTPKS
ERPMFVAVYSALTGVTSFLGPLLGGWLYEKMETWSDALAWISAYGFQVGVGVMILIT
FTLGRRVLLK"

CDS complement(5318189..5319604)

/gene="rcsC_15"
/locus_tag="EFAGFIKM_04641"
/EC_number="2.7.13.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00979"
/codon_start=1
/transl_table=11
/product="Sensor histidine kinase RcsC"
/translation="MQFSKMFVLNMGMILITIAYLASVFYKYVVIRTSSRVKQVSSVLV
LIFAGWISTVFGFQLTDEVVFDLRYVPLIVAVLTyrQPYSVIIVGIGIGLSRLTFGIT
DATLA AVLNMSILGVICAGLNIWMRRSNYRLIIKGILVTVIVNVNSVNIAIVGVIPA
TYFFSHIMPYTLPTGILLSLIFAFILRDFQNEQNRILLIQSTNRLLSVQKEELQKAQI
VLEDRAKQLMIASQYKSEFLANMSHELRTPLNSVINFAQMISENADTMDQEDIVRFAN
MIDHSGQELLTLINDILDLSKVEAGRLDIVLEDISVAQLTEDAMSHFQLGAEEKGIQL
VLDKKQGLPETLWSDPQRVQQILRNLM SNAIKFTHRGKVTLT VSTKQIKNAGIQNRWL
IFSVQDTGIGISEDKHHSIFEAFQQADGSISRKFGGTGLGLSISRDLARLLGGSIELE
STEGKGSTFHLYLPLDREKMS"

CDS 5319845..5320498

/locus_tag="EFAGFIKM_04642"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQLLKSKSYWLSLSMLSLAVMGLFYDILNSPERGFVVLDSPLD
RIIPYVPGMSIPYLGWYPFVFGVLAYLCAKDRLTYRVLLSMNICVWICYLIYFNFQT
MVPRPELTGTGLGASVLGWLYSQDRPYNCFPSIHSLHSYLMRAVLSVPSIRKPIKIL
VAAGAATIIVSTLMIKQHVYDALGAVILGECVLTITGLALHRRRRRKESKWTEGIS"

CDS complement(5320503..5322014)

/locus_tag="EFAGFIKM_04643"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEAYRSFIFRLIRNYLIGSLAAVFVVGTVVMVSTLQIPNIQFVR
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IMGPHMLGFSLPAAGLTIWMISTGWLEFPYFYIVVAAACAFIAIMHALIEYYLTVRA
IRPLLEIRHRGKVQYGMESLGGRIIVSIQRKFQLSTALIGLFPLFLFFLATYIRLQ
YMDSEFAKEYILWGILIVVLGAGFALVGSWLLIRDVRDPVAELTHEMNRIQGGDLGRR
APDLYADEFSALISGFNMMINRLEMQRERNRQLQSYFSTLAAALDARDKYTAGHSMR
VAEYSLMIGKLSGMNEEQADLLYKSALLHDIGKIGIPDEVLLKDGKLSDEEFAIIRTH
PVQGESILLQIEPIDAMADFLPGVRSHHERYDGKGYPDGMAGDDIPLFGRIIIVADAF
DAMTSRDPYRNGMSHEKALTILEEGKGTQWDPYFAGLFIDEWRRQQHLQKPSK"

CDS complement(5322206..5323189)

/locus_tag="EFAGFIKM_04644"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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ALLLGVYTAQLQSKIDSLTQQAAGSSATQEQLVQAQAQNAQLQEQLASALKPAQGMQT
GEAVKLNPATQDIVAQGLATIVIDSKGTHLVVQAENLPNLEGNEAFQVWLIKGDTPQN
AGTFLSRDGTGAVYYTLDSANDYDTVAITLEPDAMGDEPRGTMILAAKIKG"

CDS complement(5323186..5323752)

/gene="sigK_2"

/locus_tag="EFAGFIKM_04645"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WGH7"

/codon_start=1

/transl_table=11

/product="ECF RNA polymerase sigma factor SigK"

/db_xref="COG:COG1595"

/translation="MRQIAERDASALELLYDRYERVVYSFAYRIVGDPMTAEETVQEL

FMRVWNNNAERYDASQGKLTWWMFAITRNIAMDMLRRKSKGAATTSVEHETLAAYADEH

TNTEEEVQRKWEGTRIKEALSQLNGDQQQVIESIYYAGLTQQEVSSRFGIPLGTVKSR

VRLAMRQLQKLLADAELHPDAGREGIHP"

CDS complement(5324972..5325283)

/locus_tag="EFAGFIKM_04646"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSEVKPNPNQGQGHVYGHMGGYEHMQGYQYTGHEMHGYGYGCGT

MPMGYGYGYGHANQAPMMHGYQQGCGVSYGHGGGSWGSMTILVLFILLVIISKTMF

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CDS complement(5325547..5325654)

/locus_tag="EFAGFIKM_04647"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSEVVGGAGYGGWTSTGAILVLFILLVIITKSFVV"

CDS complement(5325698..5325802)

/locus_tag="EFAGFIKM_04648"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSGVVGGYGGAWTSTGAILVLFILLVIISKAFLI"

CDS 5326246..5327370

/locus_tag="EFAGFIKM_04649"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKLITILALTLLTACGNSETNTTNSQASEASKATETVSTEA
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STGSINPEEYANNIVDYTTQSGSSIGISDYKKTSTYTNKPYKEYSAGVLEGAYKHSSGT
DVILVQYLIPTNTELYTMTLTAKDTYNQDEIKDILDSLSITASLEQTAPTATTGNSS
ATASAAFFNELTPYITEDTAFMEQASYDFFGKHNDVFPAITAELSKKVQGLVDSNVT
TRHLNKNVANYYNFVQVNGEVISVEEDSSLGATFSVVHVMDENGNDIIALYPAMTGD
LLDGDYATVIGAPITNFSFENVGGGYTNATLIGASLVVAD"

CDS complement(5327493..5327819)

/locus_tag="EFAGFIKM_04650"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAIAEVTVIPIGTGTTSLSSYVADMQKVLEHQRGITYQLTSMST
IIEGPLNEIFTAIAALHEAPFLSGAQRVSTSVKIDRRDKPDASSIQKLQSVQDKLTS
LQARPN"

CDS 5328589..5330907

/gene="nrdE"

/locus_tag="EFAGFIKM_04651"

/EC_number="1.17.4.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39452"
/codon_start=1
/transl_table=11
/product="Ribonucleoside-diphosphate reductase 2 subunit
alpha"
/db_xref="COG:COG0209"
/translation="MPQVVTKPNNRQLAFDDMRISVYADRTLEGLEMLDKERLVRGVN
SKLRRDEVTGDEISNAFIMSALELVTKEEPNWKFAAARSLTSLYKKAATNRRYKSYP
DEPYGAFHPLLVDLVKKGIYREELLECYTKEQIDELAECIDYRNDLLFDYIGLLTLAE
RYLAHDFDGKVMELPQERYMVIAMFLMHQEPAERRMDLVKEAYWAMSNMYMTAATPTM
SNAGKKVAGQLSSCFIDTVDDSLLEGIFDSNTDVARLSKMGGGIGVYLGKVRARGSDIR
GHQNTSSGVIPWIRQLNNTAVSVDQLGTRKGAIAYLDVFKDILAFDLKLNNNGDER
MRAHDVFHIGICLPDLFMERVSTRGEWSLFCPHETKKVMGWKDENGALGLEDFYDESF
GEGAFRDKYEEAVNHPLLSRITVQAIDIMKRVLKSQLETGTPYMFYRDTVNRSNPNRA
HGMVYSSNLCTEIMQNQSATVIEKEELVTKDGQTRIVISKVPGDFVVCNLNSIHLARA
IPHNVLRLVPIQVRMLDNVIDINNIEVLQAQYTNSQYRAVGLGTGFLHLLALEGIH
WESDEAVTYNDNLYEKINYLLVKSSMELSKEKGHYPKFKGSDWESGHYFDQREYTSGE
RVGEFVTTEQWKELQAEVRQNGVRNAWLFAIAPNGSTSIAGSTASIDPLYELLSYEE
KTTYKIANPAPDLSEKTSPPYQTAFQVDQHASINMAAARQRHVDQGGQSFNFYVRPDIK
ATEFLELHLHAWRAGMKSTYYVRSRALTIEES"

CDS 5331117..5332148

/gene="nrdB"
/locus_tag="EFAGFIKM_04652"
/EC_number="1.17.4.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9KFH7"
/codon_start=1
/transl_table=11
/product="Ribonucleoside-diphosphate reductase subunit
beta"

/db_xref="COG:COG0208"

/translation="MQVQKIFNTEAPNQSTRIIEGECGILNWNDIRMPHMYKLYKVL

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TFRDEPSPQTFQAMVADLVLEGIFFYSTFAFFYNLARDQKMMATSMISYIQRDENQ

HCYFFAEVYKQLLVDFPELNTPENMEYVYTTIHRAVELETNWAHYTLNVRGIDLNEL

EDYIKYIANKRLRLMGMEKAYEGVDVNCMPWIKPFSDDALNATKTDFFEAKSRNYGKV

GDDNGFDDL"

CDS 5332331..5333305

/locus_tag="EFAGFIKM_04653"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MERELLEQINLWHEQDQFSLIIEGIPVAERDYDLIGQLARA

YNNDARYREAVQHLLSVQEQGVSDPLWQYRLGYAYCYIANYEQALLAFERADELLPHD

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AQENHVSEPFDEEEILTIEKELGFKLPASYIQLMNTQNGGIPALTVFPTKEATSWAED

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CDS 5333327..5334361

/locus_tag="EFAGFIKM_04654"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTTRIYFGSNQLGEVAAVSLQDALNELDLGTLEDYRRTDKGVMG

QTLIRSSRGEYILKGNPLYAGQLQEEKFFVEQLAKHTSIPVPDPYLLHEDTHLLGWS

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VSFAGDYLDWLYGTIRHWLHDAEQYSVITDEDVQWVDEQFKNAEPAFRSRAVPCFVMG

DFKVENILIQNLDDRSSGWQISGLFDFTTAYFGDGTADLTKMSTRYVREGQPELAAQF

LRCYRDLVCAADVEKYQHFRTRLSMHLLYQRILWWGEAKATGQVTWAADLPFAQWAQQ

SINSIVALLD"

CDS complement(5334546..5336357)

/locus_tag="EFAGFIKM_04655"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIQFPKPDVEQYFQTYRISHFAVSADEKRLFMDSNLNGQPNIWA
MDLPGGYPTYLYLNQSSQFIKADPQGRHLLTAFDRDGDENYHLYALPPEGGVPLPVV
PAEPNDRCYFAELSEDGQRLYYVTSAGNPNYLNSRRIDLETGEDELLYSGEEVTSSLV
AVSPDEKSYVILKMYSNTYQTAHLYRNNEEMGILPASERHSQVSDLIFADDNRLLFIT
NDDSAAYVAEYRIDTREFRLLCKIEGEDVEFIRWHQASELYFWTLTGPERMYVLG
KNADEPRRIEMPLDTIEQVIVTKAGNVYILGRGAIQPHNIYRKIAGAESWEPLTANRV
TGLDPSDLVYPDVIRYNSYDGLEIEALLFKAKPEQANGYTVFWPHGGPQASEAKFFRP
MFQMMLAQGYHVFAPNFRGSTGYGAEFVKLVERDWGEGPRLDCVAGINWLFDDQGITSP
ERLFVVGGSYGGYMTLLLAGRHPELFRAAVDIFGPSNLFTFLESVPEDWKPMMDNWLG
DPVRDRERLTKDSPITYLDQMVNPMLVIQGANDPRVVKAESDQIVAALQSKGLDVEYI
VLDDEGHGFSRKTNEILVYRRMLEFLQKHQESPVAQA"

CDS complement(5336499..5336918)

/gene="fosB2"

/locus_tag="EFAGFIKM_04656"

/EC_number="2.5.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81W73"

/codon_start=1

/transl_table=11

/product="Metallothiol transferase FosB 2"

/db_xref="COG:COG0346"

/translation="MNIQGINHLCFSVSNLERAITFYEQALGAQIQVKGRKLAYFELA
GLWIALNQEDVIRNYTERTYTHIAFTVTEEEFDESQQQLRAAGADILPGRPRDRRDAL
SVYFTDPDGHLELHTGTMKQRLDYYREDKAHMTFYT"

CDS 5337074..5337973

/gene="ydaD_2"
/locus_tag="EFAGFIKM_04657"
/EC_number="1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P80873"
/codon_start=1
/transl_table=11
/product="General stress protein 39"
/translation="MNPVYPFYGEKTVCKEQKLAFPPQHQQPGLETLMVPEPISED
PAYIGSCKLQGKVAIITGGDSGIGRAAAITFAKEGADIVIAYLYERTDAERTRERIEE
LGQRCLLIEIDLRLKKNCEAVIRTTMETYGBKIDILVNNHGVQYVQPSIVDITEEQLYH
TFQTNVFAYFFLIQAALPHLCRGASIINTASITAYKGNTQLIDYSSTKGAVVSLTRVL
AQSLAAQGIRVNSVAPGPIWTPPLIPASFSAEDVQVFGTDTMGRAGQPYELAAAYVYL
ASRDSSYVTGECIHVNGGDMVTT"

CDS 5338098..5339708

/gene="ywrD_2"
/locus_tag="EFAGFIKM_04658"
/EC_number="2.3.2.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O05218"
/codon_start=1
/transl_table=11
/product="Glutathione hydrolase-like YwrD proenzyme"
/db_xref="COG:COG0405"
/translation="MNFDPLYQPYPYSYRVVPYAKQGMVATSQPLAAQAGLDVLKKGGN
AIDAAIATAAALTVEPTSNIGGGDAFALVWTEGKLHGLNASGPAPQGISIEALQAAG
HTEMPKLGVPVTPVPAGAWAELSRRFGRLLAEALEPAIRYAEEGYPLAPGLARHW
VRAAEIYARQGDAEAGRAWFETFAPGGRVPAAGEMWRSPDHAATLRQIGESEARDFYE
GELAERIHSFMAEHGGYLTREDLKAFQPEWVDPISVSYRGYDVWEIPPNGQGLIALAA
LNLLKGYDFDEKESVLAYHQQLEAMKLAFADGEKYITEERKMGVTV EELLSEAYAKEQ
RKLIGDTARAPEAGDPRASGTVYLATADGEGNMVSFIQSNYMGFGSGLVVPGTGIALQ
NRGHNFSLDPSHANALEPGKRTYHTIIPGFLTRGSEAVGPFVGMGGFMQPQGHVQVVM"

NTIDYHLNPQATLDSRWQWTKGKTLVEPGFPQHIAQALARKGHDIQVALDPSQFGR
GQIIWRNPDNGVLCGGTETRADGSIAAW"

CDS 5340076..5341083

/gene="tmpC_2"

/locus_tag="EFAGFIKM_04659"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29724"

/codon_start=1

/transl_table=11

/product="Membrane lipoprotein TmpC"

/db_xref="COG:COG1744"

/translation="MKTNKNRRAGLGLTIMMILTVLILGACSANNTTATDTRTKVGI

VLTEVGLGDRSFNDAAFDGLVQARNEKSIVFDYREPGDNAEAAFEFAQAKFDLVIGL

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VGFLGGIEIPVLRNFEQGFKQGVLAVKPNATVDVVYAGDFGNAELGEQLAAEMIQEKG

ADVIYVAAGLTGVGALTEIQKLGKYAIGVDTDQFFLAEKSILTSMLKNVDVSIYNAVN

TFVQNNHTFPQKEIVEGLAENAVGLTALHNITLSDEQQQTFEDLKAKISSGQIKITLD

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CDS 5341110..5342762

/locus_tag="EFAGFIKM_04660"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLQGKLILNALISLLLCLVLVAYIIMQLLNMNNAKNQNLVPAML

KVSELNANQIQTQQALDVYSFSMTAGNQDAVLRLLDEGQTMIQELTDGLLETDQQQLQL

IQSIETKLQALNQGATEAMSAMNSAEAKRYSTRVRGIQNDIYSLDEMTRDRYDQYTV

LEHDIQQTWQTALVGAIVLLVAVMLFNMYTSRQIAKRIRTLKDAAGQIADGDLTGQLP

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VAEQLRLAEVNRMAAEVEQTVRELEESAVRITMTAYVSEIAKQTTMLSLNASIEAA

RAGEAGRGFAVVAGEVNKLAEQSAQSVKHIYAAVGEITTSMDKVKNSVAQSMQLFGEQ

EQATGQTRESFSAIRESVERISTGIHQLAEDMQHSNELSTQVQQAIENISAITEQSAA

SSEETASTSEQQRSFADASIKVKSLRDISAEMHQELLRFRL"

CDS complement(5342939..5344618)

/gene="nnr"

/locus_tag="EFAGFIKM_04661"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9X024"

/codon_start=1

/transl_table=11

/product="Bifunctional NAD(P)H-hydrate repair enzyme Nnr"

/db_xref="COG:COG0062"

/translation="MFIVTAEQMRAVDEYTIHQLGIPAASLMENAGRAIAEEVIKLCR

EGQTEGRLVDSRQLGYSSKTDARRAHTGPGDRQGYGGDIIADPALVMERLGDQQWYML

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EAVDFSRCTGIVDALLGTGSRGAPRGAYAALIEAAKDSGKPVVSADVPSGLDADTGEV

YESCIQARVTVCLALLKRGLVQYPGASAAGRIVVRAIGIPARLAPEHGPSVRLTDEV

LRGALRVDTGRLRAPDGHKGTYGHVLLAAGSLPMSGAGLLSAKAALRAGCGLATWALP

AALLPHVIGTVPELMLAAASDGDSGEWNAASTDAVLRLAESRDVLATGPGLGRFKGDT

DWLRRLWQQSDRPLVIDADALNMLADAGPHGPRDWGQRSAATILTPHPGEMGRLLGMS

TQEVQRDRIGHAAKYTREQGVTLVLKGARTVIATPSGEAYINTTGHAGMATGGAGDVL

TGIIAGLLAQGLSAEQAATFGVYLHGQAAERAALLRGDPSSLLAGDIIDAL"

CDS complement(5344822..5345454)

/locus_tag="EFAGFIKM_04662"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKVAIFGATGAIGKMILWELMDRGHEVTAVVRDPSKVEMVHERL

RVEQGDLLNPDQVADFAAGQEVVVSAYGPKFGGEEEMLEVTRSLIEGVRRAKAGRLV

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CDS complement(5345718..5347475)

/locus_tag="EFAGFIKM_04663"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGYPFLTRMSV NKERTS MLLGYDDNTCEWCSLDDTGRMDSRQSL
SEHGTESDQHTQH IQFMGRNRVLVITQDKSEKWLHIYENEKQAILVQSLLVKFPFPVM
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NVGGFGRVYSYSEDILSSSEIPYTEYAYPVMDKQGDIAVSIPVEGGFQPGWIRQGED
RVHECSRDTQPFSELIRMQLDPHQQLVLCEGITCGRWQYVQYTLDRKRYELYDYPGI
LTQAVLSRDRQGLIGKYESIIRPPVPGIYRFSEQTRTITRFPVERDERIGNHPDKEPD
VIYGWVRYGHDMIPYMDMHPEGAEQVVIYLHGGPHNCLFDSFSPVISGLYQAGVRVIG
LNYPGSSGFGTDYRMRIQNDWGGVDADVIQFMREQMLSSYSNVSLYGVSYGAYLALLV
AGKSPALWSTVVACAPFTDLEGLYAGGGAKLRSFLETEIDELLHDQSALRDRSPIAYV
SGLSEVDIQLIHGQADQLCPVEQTERLYLDIMENKQMSGAVGRVELHIVQDMAHEVYS
ERIWAQKAVDFTYSRVST"

CDS complement(5347457..5348923)

/locus_tag="EFAGFIKM_04664"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MMPVSLESTDYHDLRSKWFRVSHEPGLFVVEGTSDAVKHEIHKL
RTHWQDKAIQIAVGDPYATLPLIYQLNPFQPIDDLVACKNALLRFQRSGWTPGNRKWV
LVEVSSYLHPADLGAIHYILYRQKL RGVSVV LFFHRYPTMASNPEDIPKLPVSIVRDT
PDQTRRLLEEHLQMVSKDKGKEKEVALALYNRLAWVLLSKSADPARYTSCFHFFDHNS
LFQQLSATQQAVLWFELGQLLTKN GKQYTEARHCYSKAREIIAHDELTETYRTGKWAA
LDNGEALIEMQEGNVERAITLEQQAGQRIRQLSDGPDQVFQIQTLN IAGLHLRAGH
YVEAGKTL LAAEKL CIDAYVDWLGHVLQLKMVLHQQLGEQE QEYELLIQLLRMKTNTI
HPKLLGRAVEIAGALITQGSEERASRVYRLLMMGLPVASLPQIRLIRETLGRLGTVTP
LDAYTQDQYIDKLESQLEGWEQLKHW NERRKSGWAIHS"

CDS complement(5348920..5349720)

/locus_tag="EFAGFIKM_04665"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MMLTSISDILPQCQQESGKAGDRYYAVEPGKDETLSSFMLIDQG
EGQYTMDLWSEAHSNLYWEDRMSSVLDTITWSSLYATAPASFPWEKLGYRADVLAHRY
QFFGKLKDVPPAMPNEDAVWMSAEGQADSLAHLQASDPTCPGWEAARQAIGDIYQG
VYGKLLKGSGLVELEGGKIGGCLLSDEFGSVLLAHIFTIPEAKRQGWARWLAAYGLHR
CSSDPDQRIKASLDAINRGSYQLMTALNLQQVPELIHVCITKESELS"

CDS complement(5349698..5352442)

/gene="ramC_2"
/locus_tag="EFAGFIKM_04666"
/EC_number="2.7.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O88037"
/codon_start=1
/transl_table=11
/product="putative SapB synthase"
/db_xref="COG:COG0515"
/translation="MKFASVTPKKDAFENALEHIIREL PQSIQWSNDGHWICFRPEEL
RLPAQGWKIHLVIPVEGAELLRRIAPVLTENDVQWKVSSGLKLIETSNNGSIPLPQT
GKCVTIYARDEEQFLKLELMHSCTSDLKGPAIPTDRAYLGSQCVFYRYGAFTDRFY
DRYSGAKVYAIQNPEGKLEEDRRTPGRYKPEWVNEPEELLGVQAMEKNRADSRHSDSN
NNEFGIRNIRVRRVLKKGSGGVFLISGTSYEQAVMKEAVYRMRVDGGGRSAHNYLDN
EYRVLDLMKDTGVTPRPLDLFSTENNRYLILEYFESISLREYIHRRHVAADYNRADMH
RMGIHILDMVQQCHDKGIVINDLTPNNIVVLTDGSVRLIDLELAYVRSDSQADPLTG
HTPGYVPRGREHSRRSSYAYDLYALGGVFYMASSIDPYLK YRQSHLEAAQAYLDYQS
NTQLRGLGSLGIEIMSGGHVELSEIRETLVALLEQQEVNSGGSM DVIEKDECNMEPEE
VLRQAERMVKTLYTSLDFNSPLQLFPENSMSKMFHPANFNFGWTGMIFGFNQLGQITQ
NRQYHQYAREVLEWILT NHPYVPDET PVALYFGYGAVPWALAETAERINDPSLLRAE
DLALEITWHEPVQTNISHGAAGLGLMLLEIYRIGGRPELLARAEELGVYILEQEEQTD

ESLSLWKVKDKSDKKGHHSLGFSHGIAGIGYYLLALAERTGKEAYYS AVKRIVDTLDR
TSHGGQNGVSLWPASSEKPD TLVWHWCNGSAGIGRFLMAAADILQDPLCTRLGLQAAD
AVAQATVFASFGQCHGIAGNGDFLL LANRKFPGRYETKLVEYTQSLYVLRSDPQEDIW
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CDS complement(5352561..5352698)
/locus_tag="EFAGFIKM_04667"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MENKEILSVQDLMALEVEEDNNMFEETSLCTVCSWTSSQTIVVE
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CDS complement(5352884..5354155)
/gene="entS_5"
/locus_tag="EFAGFIKM_04668"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01436"
/codon_start=1
/transl_table=11
/product="Enterobactin exporter EntS"
/translation="MKNEIRGDSYRAVLR LPSFVLLVGRLISGAGQILFSMATMWYI
LQLTESALAAALIPMLPYLIYAFLGIPLATISDRLPKKQLLIWTDILRAGIACILALL
FMTGSMPLPWHIYAANLLIAILGFLFN PATQTVIPAILPEPAKQLAPANALLNSSSKTV
ELLGYALGGILIALISVQSILFLYAVTFLLSAISIFFIRIPVTKVVKQKGISGFVKDS
MQGITFLFSRKILACCIIFGAIINFAGAPLHIFTPIFANMVLQAGPQGYGLLQSAFAA
GSIAGSLLSGKYAKRLSLAHWFLISY LISGTSLLLMPMFNLYIAIACS FLLMMGLAL
VNVPLVTSILLSTPEEKRGRVMNSMGV LMSGISNPLGLLLGGWFIETYNPSWVYMGIG
TFVICMGMASLFVRPFREERSKRTRQQTSM"

CDS complement(5354145..5354522)
/locus_tag="EFAGFIKM_04669"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MYNDQKAQFNQMVERSVEQANKNLSGAKGVVSVRLSQEEIDIID
QLVFLELAKNRSDATAMLIREGIRTHQTLLNEIREYTAELERVKAKIQQTIRDSGLVT
RLHRISDDESVMYEGEAREKDEK"

CDS complement(5354679..5355092)

/locus_tag="EFAGFIKM_04670"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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CDS 5355204..5356091

/locus_tag="EFAGFIKM_04671"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MFQRWIEDLTSRPGTVAVLFGVMALLLGIYIWSATEVRRSHERR
MRRIRDTLYISTALLGQLTIQENRNYERSEHEHDDLITAMLACKAASYLSPQLQDQIR
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GFLVADLIFRQRMLDVPVDSWDSILPWIRAIISLMIITIIYGYLLWASPRRDRSSTVTM
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VSTEMEGNTRRTSGTNTDE"

CDS complement(5356704..5359424)

/locus_tag="EFAGFIKM_04672"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MQAMRKPLKKSLALLMLSMVGPTFAEKSFAADQKIQFSDIKGH
WAEANIQAWGDEGLIRGYLDHSFKPNTYITRAEFMNLVNGAFGYSGQAKITFNDVSES
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SSIAAWSKGAVGGAAAAKIISGYADGTFKPLNSITRAEAVSALVKAVETDATTAAKPA
KPKGATGLNVNPPADEARLSAVKHGANAGDDTLKNIAETNPFIDILDGFDQVWSMNQ
ADWRDGTAAATKIGADGKNKYGDGSPYYDGFKNDPTVAVADQKTYANEEIRNKATWE
ANIKYVEKVTQNRTAEETLAAYYDDQRDKIYSVMEGFGPLANTYVDIIPKPTNVERTV
DEMNVLTEETVEDESQGIGDWEAKTELSDLVNLVLDLVRFKIPASSNPSKYFYSSPRP
WRMNSNGEVKEVVDSKGLPVWETLGEGEKNEVPLASGGTKSTGEKHYQQYETNVKLIP
ALTYVKRIAEDGRGKDGGFPSGHTSAAYLSVFPLAYATPERFAELLTRAAQLGENRVV
TGMHSPLDVIGGRIQSTAMAAALNKAENKDVLEKGYENAGEVFGAAAKEKNMSLYEY
AHTVTEDYTFKSAYDEHKWEDHDANKAFYREKMTYGLPQTGTKGLAPVVPQGAEALLE
TRQPYLTDEQRRQVLYTTSIDSGYPVLDESKGWGRIDLVTAADGYGAFLNNVTVDMDA
SKGRFNAQDWWRNDITGSGMLTKKGTGLTLTGKNSYTGGLLQAGTLVAESATAFGT
GDLYVENGTVVVDVGALNLRNFTMDNGTLELVVTDSSNSQLNVGRKLYIDGGSLKLD
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CDS 5359781..5362102

/gene="rhaR_38"
/locus_tag="EFAGFIKM_04673"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01533"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaR"
/translation="MHKPFQSVRSKMVLSYLAVVLVIALLFSGILYLFFSRQYSKEIR
INNQLSLKSTVNYIESSVIQKVNQVYLSLALGNAASIDLSLKGNHISKILDIEQSLKN
MVQNYSDLIEAIHVYDTKNHFIVSSVYGLLLYEDTPSSVDHTTDWITAMKETPESSLW
MKTRMVPQDVYIESREQGKMSPLISYVHSYPFQSSGQNSKAMIAIDIKESAISQIIKN
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PLKRIMNNIKSRMDSPTSLKQDEYRFIDTTFNLSLNKVDLSLEETLQANHSMIKHSIML

NMLNNRFTPEELTEQLQSVHISMAYSRFRCIVIDPVNEKWKDLQPRQLQHTLYTMIQQ
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GGWVENFTKIHTSYHQANTLIRYSYFFPEQSAIQDLNREASSLEIPESYLVNFEK
KLQTRDVQGTQVQAIQELVAIIKEGPYSAEYSRIILLKTVSIYAECINQVRLQPTTEASS
LNMYKQFSLFYNNRYSEWMIHLVTEFVMHMEKRSEVRSVDTISAVKAYIHEHLSGDL
TLDHVSEQVFISPKYLSKLFKEETGIVYSEYVTNQRMERARELMTQREITVEQVASTV
GYRTPAYFIKKFKEIHGCTPKNFMRNLMEQGS"

CDS 5362314..5363954

/gene="lipO_14"

/locus_tag="EFAGFIKM_04674"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37966"

/codon_start=1

/transl_table=11

/product="Lipoprotein LipO"

/db_xref="COG:COG1653"

/translation="MNINHLRTLCLLIATSILIGLMSGCTFLNREGSQVQQQEHLASA
EKDTAPQYTISWTMHQNIPVEDAEMIAYIEDRFDVDLEVWNLENKRYEELLDLELAQ
GKIPDLFRIRQPHDLLKYQMVGVLAEITPEVLEQYAPNIVQRIRDYDSRYLEYGKING
GLYGIPAINQTNIRTPVVYREDWLKQLGLEVPKTLDEFETVMYAFAGDPDNGNGKQD
TYGLSREGLNVVFGAFGQSVFTEQLYFNEKNNQLVIGALEPKMKKALAYMQKWYRDGI
IDPEFITGENKGGYKHLSHAFINGKIGMTSMGNYYHWNQEGDYNVLNENGQETPVGAS
FNVNELLQKNATAEVVFGSPVIGPNHSGSGKGNLLMNFIAIGAEAAKEPGKLEKILE
ILDYVSANPDPEEQIKMEYGLPGKHWNWSAEDSNSFHLLYPYNRMENYINMIGSSIGM
TVPGTPSDKREQWAASAGLTENGIYNRLEVATPALIQYSSELIRMRDRAYISIITGDQ
PVGYFDTFMEEFMDAGGQVLLLEANHWYKEHMETSRAQ"

CDS complement(5364052..5364291)

/locus_tag="EFAGFIKM_04675"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAKPLKVDEVWLDRIAGQLNDMEFGSLHIVVHEGQIVQMERTER
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CDS complement(5364448..5365323)

/gene="cysW_2"

/locus_tag="EFAGFIKM_04676"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AEB0"

/codon_start=1

/transl_table=11

/product="Sulfate transport system permease protein CysW"

/db_xref="COG:COG4208"

/translation="MAGSVPLSPVPPVKTGRGTNRATTEAPWVKWLLIGLASLVLIWL
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TKFQFKGKGLMITLIDLFPFSISPVVGGLIFVLVFGSNGWFGPWLSEHDIKIIFALPGI
VIATLFITFPFVARELIPLMEDQGTREEEAAVTLGASGWRIFWSVTLPNIKWGLLYGI
ILCNARAMGEFGAVSVVSGHIRGETNTLPLHVEILYNEYQFSASFAVASLLLILALAT
LLLKSWLGHKAVSEK"

CDS complement(5365391..5366227)

/gene="cysT_2"

/locus_tag="EFAGFIKM_04677"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P27367"

/codon_start=1

/transl_table=11

/product="Sulfate transport system permease protein CysT"

/db_xref="COG:COG0555"

/translation="MSKVVVARRRTLPGFGLTMGYSVFYLSLVVLIPLAALLFNSTGL
TWATMIEVATNPRVLASFQVSFLTAGAAALIDLVLGLLLAWWLVRYEFP GKRLFDAVI
DLPFALPTAVAGVALTAIYAGNGWIGQFVEPLGIKLAYSQAGITLALMFIGIPFVVRT
VQPVLEELEAEVEEAAAATLGAGRWRIFRTILLPDLIPPLLTGFALAFARGIGEYGSV
FISGNMPMKTEIAPLLIMAKLEQFDYAGATAVALLLLVSVFILLIINSLQRWSRKAG
RA"

CDS complement(5366315..5367394)
/gene="sbp"
/locus_tag="EFAGFIKM_04678"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P02906"
/codon_start=1
/transl_table=11
/product="Sulfate-binding protein"
/db_xref="COG:COG1613"
/translation="MKKRIHKGILVGLALVLTGVLTA
CGSDSGGSSAAGTSGGAEGGK
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TIKQSHGGSGKQSRVIDG
LDADVTLALGYDIDAIEDKGLINEGWQDKYEHNSAPYT
STIVFLVRKGNPKGIKDWD
DLIKGDTQVITPNPKTSGGARWNYLAAWGYALKHNNND
EEKAKEFVGELFKHAPVLDS
GARGSTTTFVERGIGDVLLAWENEAFLSVKELGPDKFD
IVPSVSILAEPVAIVDKN
ADKKGSRDVADAYLKYLYSEEGQTIAAENYYRPTLDS
VEEKFKDQFPALELFTLKDVF
GTWRDTQAKHFNDGGIFDQIYVPGS"

CDS complement(5367876..5369753)
/gene="yesW_2"
/locus_tag="EFAGFIKM_04679"
/EC_number="4.2.2.23"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31526"
/codon_start=1
/transl_table=11
/product="Rhamnogalacturonan endolyase YesW"
/translation="MGNRSSLWKRTLRTAGVSL
LSSALLVTSLGLGNTPVTHAAGARQ
MEYLDGRGVVAVKTGTGVFVSWRLLGTEGSNVSFNVY
RDGTKVNATPITNSTNLQDASG
TSSSKYTVRAVVGTEQAASAAASVWGNNYLSVPLSV
PAGGTTPDGVAYTYSANDASA
GDLDGDGEYELIVKWDPNSKDNSQSGYTGEVFIDAY
KLNGTRLWRISLGKNIRAGAH
YTQFMVYDLDDGDGKAEVAMKTADGTDGTGVVIGD
ASKDYRNSSGYVLSGPFLT VFN
GQTGKALSTVNYEPARGNVSSWGDNYGNRVDRFLAA
IAYLDGERPSLVMARGYYTRSV
LVAYNWRNGQLTKQWTFDSNTSGNSGYAGQGNHNLS
VADVDGDGKDEIVYGAMAVDDN"

GKGLYTTGLHHGDAMHLSDLDPDRPGLEVFQVHETPSNAGVEFRDAGTGQLIWGVKTT
KDIGRGMAADIDPRYKGAEVWADGSLYTAKGQKLGTTLPSSTNFGIWWDGDLLRELLD
SNRIDKWNYYTNSTTMNLLTASGVSSNNGTKSTPNLQADLFGDWREEVWVRTNDSSALR
IYTTTAVTDKRIYTLMHDPVYRLGVAWQNVAYNQPPHTGFYLGEGMSTPPVPNIRYAG
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CDS complement(5370079..5371134)

/gene="pgl_2"

/locus_tag="EFAGFIKM_04680"

/EC_number="3.1.1.31"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34499"

/codon_start=1

/transl_table=11

/product="6-phosphogluconolactonase"

/db_xref="COG:COG2706"

/translation="MEPVTTQETLFYTGTYASADEPGIFLCVLNTDTGEMRIVNHMDG

VDNPSYLALSPDGNCLYVASETDEGEVLVYRRDKATSELHLMDRKQTRGASPCYVSVS

KDGQWVFSSNYSSGSVNVFPVGDQGTLGEMSAWVEHTGSGINEERQEGPHAHSIQPDP

SGQYAVVCDLGLDQIIVYRLEEGRLVTHREMDQPPGAGPRHLVFHLNSKWAYVINELD

NTVTAFLYDERRGEFTTVQHISTLPEGHKGEGTAADIRISPCGRFLYASNRGDDSIVL

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NGFKLELPRPVCITPVV"

CDS 5371371..5372231

/gene="rhaS_38"

/locus_tag="EFAGFIKM_04681"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MQKLIVLPDSLLQETAAYPVTSGLYVTDIGYFHEAEHHYRDRPD

GCESHILMYCVQGTGWYTMDSKTYDVSPGNLVILPAYVPHVYGANSAEPWSIFWIHL

RGEHALPYIEPLLTHHITTMPPAKAQKWLELFHECYGALETGYSMQTM TYASQIIGYM
LGMLAYGPETTGTGGIVSSKRAAEQSVQYMLEHLENGITLKELAAHARLSVPHYSQL
FKQATGHSPIDYFLRLKIQHSCRYLDFTDWTVKQISSELGFKDPYYFSRLFSKMMGRS
PTDYRNKSKG"

CDS 5372378..5373061

/locus_tag="EFAGFIKM_04682"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKNILATLTAGALLTSLSAGPINAAQAQFTDIQGIVGADKIE

SLHKDGFIKGVSDSLFKPELELNTAQGIQLIADGLNLDLTIRFIKMPVPSDYFSTVK

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TDEQELTPEYQGAIQRSLVLKINELDADGNFNPQTITRAEAAVMMYNAIEYMESFHA

PQIPETPEK"

CDS complement(5373180..5373806)

/gene="yodC_3"

/locus_tag="EFAGFIKM_04683"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P81102"

/codon_start=1

/transl_table=11

/product="Putative NAD(P)H nitroreductase YodC"

/db_xref="COG:COG0778"

/translation="MSGIEKNETLRVISERHAVKKYEKGFELPEADLNAILTAAAEAP

SSWNLQHWRFVLIESEADKALLPVAYGQSQIVESSVTIAVLGDLEANRNTVIYDQAV

EAGALTAEVRDALVGQINGAYQSPQIARDEAIRNASFASQNIMLAARSLGYDTCPIGG

YNPQKLIETFNIPARFVPTLLITVGKAAQPARPSGRLPLSEVVVKGSF"

CDS complement(5373872..5374054)

/locus_tag="EFAGFIKM_04684"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVLHEYGLGLVRHGGQVTAWAYAPVKDPLMFSSDSGHNLTDEE
RSSALMLFSEGKSLVE"

CDS complement(5374070..5374534)

/gene="ywnA_3"
/locus_tag="EFAGFIKM_04685"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P71036"
/codon_start=1
/transl_table=11
/product="Putative HTH-type transcriptional regulator
YwnA"
/db_xref="COG:COG1959"
/translation="MNSEFTIAVHCLVFLSMRDECMANSEDLSQSVGTHPARVRKVLS
VLRKHGYLTTKEGAHHGGYLLSRPSEEIKLGELYRLVAGGSLGPNWCSESGSSCVVSS
NMQDVMGNIYNGGEEALSAYFDRISIQDVKERIGHGETMNLCLKGLSAKEKS"

CDS 5374965..5375696

/gene="yflN_4"
/locus_tag="EFAGFIKM_04686"
/EC_number="3.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34409"
/codon_start=1
/transl_table=11
/product="putative metallo-hydrolase YflN"
/db_xref="COG:COG0491"
/translation="MRITREFDVVQVTFLPKLFPVNVYLVEEEDGLTLIDAGIPFSK
GILATAQSLGKPITKIILTHAHS DHIGALDRLKETLPQAEVFISRRDARLLAGDTSLL
PGEPQTPVRGGV PKPQAVHTQPNHLLDDGDKIGSLVAIASPGHTPGHMSFMDTRSRVL
IAGDAYQLQGGLAISGRMRPLFPFPALATWNREAA LASAKRLAELEPSVLAVGHGRML"

RQPAAAMRAATADAQQRFLAGGQR"

CDS 5375693..5376265

/locus_tag="EFAGFIKM_04687"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSPRQGLDRGALLSAAQLADSDGFQALTLAALAQRLDVRSPSL
YNHISGLPGLRQEMALMSVQQLSRALTAAIADRTGDDAIQAIAAAYIGFVREHPGLYE
ASFHAPDREEPQLAAASTATLELLLHSLHPYPLTEAEALHAVRGLRSLCHGFASIEAQ
GGFGMNFDPPDESLRLTVSAFLHGLRHLHED"

CDS complement(5376352..5376885)

/locus_tag="EFAGFIKM_04688"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLKVIGVTITLLSNLWGVSVLDNEAIKELNRVTNFNIVPKAM
KSATHYEIKSPENLAPKIDYILINYFDENNRYVFGIRQLKNNNSIVEKELVTIDIKTGS
EKSKIIPYKVQLEPKGERVDINGNTGWVYSYIGKQPTGGILTWIQEDTYMEIDTSKLD
KNSVIEIAKTMEQVNGK"

CDS complement(5377301..5378431)

/locus_tag="EFAGFIKM_04689"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKSYRPATMWTLACFTVVSVLVVPWIMWQSQAPVPLNIMIID
KSRPDLSYQGHKGLVWLLNQQKIVQHTGEYYSYEDYYGYDLLDGLPRMKQLLPDEV
TDLIYLTANRSSLQAQKSEGKQGGIYEGLTIYDVQKIREAAYKGVTVAEYSALANT
ASKMTREQLYPILGVDSSGWQGKSVSNLQSIEEVPRWIRTNYEQEKKKWSFHGAGIL
LVHLDGQVIVLEKGPDVKTGNVQVAFQTQEGRDWSGITQDIHYNGWFDIIVPQKQDSIL

AWYKTDLTkAGKQKLGNAGIPAEFAALVRYDDYNRSYYMAGSFGEMKHYSFWRRIRGW
EVVRSKLTpDQKDIPDMFYWKVYVPMKHILQEVQEGRQQWP"

CDS complement(5378485..5379939)

/locus_tag="EFAGFIKM_04690"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDERWIEMLRSFVLACYEGIFIYLVLAIVMCSVLVAAARTLIR

RRDLDPQYHEMLDEELAPAVSLLVPVRNSEDIVQRISCLLDIQARYEVIINDGS

EDGTMPLIETYDLMPIRSKVHYSGLGQETAQIKCVYQSRLHHRLVIDKAYGGRMDS

LNAGLNISQYPYIASVGPWTVLERDALVKIMKPVMDALPGEEVACSGRVDLIPPRNT

DHTDLTDNSTRLMGSTLYVMQTIEYVRAFLIGGVGLVRYNINVLLFTAQVFGVFKKNR

VMEVGGYKRNDQVAHMELVMRLQKHKMRTREGRRIIYPDPICRVEVPGTWRQLRTQR

TRWYMQLASSLWAQRSMIFNPAYGWMGMVSIPYFILIELLGPVMELGAILLFISIGL

QLVDINLCIILALLLTLYGSLLSAGMVMFEVWCSRKYTSREVTRLLLYACSETFWFR

PLNNIFRMFGILQAVGLWRKKEKEKEKEIRNGLG"

CDS complement(5379920..5381056)

/locus_tag="EFAGFIKM_04691"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYIKLIGSHHRGWLAGNTDWLVHVVSVCASVLAFLLLVIYGIL

WMKYSSRRREKVKTALMHELLAEGSFLQRYLNEGEIGVDLLNMSGDQQIVLQQLLQR

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MLRVTSCPTPLRFIILRIYARTGYFRIVKELLRKQYVWSDSQYLQILLLLTDSSWIRL

KDHFKDVPYQVQSNIVHAIRIRDDQTDGAVVLEKLILGEDALLRTHAYQALAQVGRG

REDLLKGLLLVWNESGEERQSRSLTVTQLMGTVHADAFIPRLKLMMGDPSFQIRQEA

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CDS 5381292..5381777

/locus_tag="EFAGFIKM_04692"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAQISPYYLQIGATVGMLVMALLAIFIRMKASHRPVTIRKILIP
PLGMSTGFLMFVVPETHVPLLWAFIAFLVGWFLFSYPLIRSTRFERVGEEIFATRSRS
FAFILLGLLAIRLILHEVIQRYVSIPQTGGLFFLLAFGMIVRWRVYMYKHYKEVLVAE
H"

CDS complement(5381898..5382911)

/gene="yfmJ"
/locus_tag="EFAGFIKM_04693"
/EC_number="1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34812"
/codon_start=1
/transl_table=11
/product="Putative NADP-dependent oxidoreductase YfmJ"
/db_xref="COG:COG2130"
/translation="MSLNKQIVLASRPEGAPSRENFKFIDAPLPEPEAGQVLVRTLYL
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AVNTTDLSLIDTEEAPITAYLGALGLTGLTAYFGMEDIGPKDGETVVVSGAAGAVGM
IAGQIGKIVGARVVGIAGSDEKCAYLKDKLGFVVLNYKKEQDMSAAIERACPDGVDV
YFDNVGGDISDAVLRHINRNARIPLCGQISSYNLEKPDIGMRPQTLTNTALMKGFL
LGDYTKSFKEGRAKLAKWIEGHIQYEENIVDGFEQTPEAFMGLFSGDNLGKQLVKVA
DPE"

CDS complement(5383086..5383832)

/gene="map_3"
/locus_tag="EFAGFIKM_04694"
/EC_number="3.4.11.18"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P19994"
/codon_start=1

/transl_table=11
/product="Methionine aminopeptidase 1"
/db_xref="COG:COG0024"
/translation="MITLKTKEQIEYMKKAGEILAACHREIAKMIRPGITTQEIDQFA
EAFMKKNGATPEQKGYNGYQYATCASVNDVICHGFPKYALKDGDIVTIDMVVNLNGW
LADSAWSYAVGEVTPAQHLLDVTKNSLYKGIELAVVGNRIGDISNAIQVYAEEGELS
VVREFIGHGIGEKMHHEEPQVPHYGPPHRGPRLKEGMVITIEPMLNIGTFRSKLDSGDW
TARTMDGSLSAQYEHTIAITADGPVILTAQ"

CDS complement(5384470..5385291)

/gene="ybdM"
/locus_tag="EFAGFIKM_04695"
/EC_number="2.7.11.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31435"
/codon_start=1
/transl_table=11
/product="putative serine/threonine-protein kinase YbdM"
/db_xref="COG:COG0515"
/translation="MELRRSWQRLLGLWTDPRPRREGTTIAERYTIQELLGMGSYGLTY
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VTEYIRGQTLEDCEQGLRYTERECVELAGQLLAPVAHVHEQGYIHGDVRIPNVILR
EGTVHLIDFGLARRLGEPLLPELRRRMREVPEPEDEPATPDHDLQDIGHLLFMYLYSA
YVPEKGREPASWQEELKLTPELYQMLERLLGLRSGYEGGATELQAEIEKVLLKLQ"

CDS complement(5385427..5386119)

/locus_tag="EFAGFIKM_04696"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MMIEEAGATTETAKSLGIGASTLRKYAAALEEQGYRFERSANKS
RLFKSDDIECIERLMTREHNLPLADAVVTVLAPEVPVAVVEVEVDVPVVGIEGLSE
TECAATVMSSVFPEEPEIMGNLRSEGLGQLVSEVTYGAVEQQQDDRVQLLQQRVDEL"

ELTLQHLADTHMALQEQMEKQRLWMNEKLEEEERDRELVTNLRSFQGRKRKPKGVSLRM

LFGFLPKKHKEA"

CDS 5386667..5387620

/gene="ldh_1"

/locus_tag="EFAGFIKM_04697"

/EC_number="1.1.1.27"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:D8KFT1"

/codon_start=1

/transl_table=11

/product="L-lactate dehydrogenase"

/translation="MLGKSGKVAVIGAGLVGSSCAYSMINQSI CREIMMVDR TYDRAV

AQALDFSHCMDFTHNRTKVYAGTYADCGNMDVIILTAGANPKPGQTRL DILEEAESIA

KDIVVPIMNSGFNGIFVVAANPVDIVTYMVWKL SGLPREHVIGTGTSIDSSRLKTLLS

EVFSIDPRSVHGYALGEHGESQFVAWSHVTIGGKPIMHIMDQHKERFKHLDLEDIARK

TKDAGWEIFTRKGSTQFGIGNALAHITRSILNDEHKIIAVSAILDGEYEQHNV CVGVP

AIIGGNGIQEIIELNLDATEREKFNN SCEILSGNINRLTLV"

CDS complement(5387785..5390493)

/gene="rcsC_16"

/locus_tag="EFAGFIKM_04698"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00979"

/codon_start=1

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/product="Sensor histidine kinase RcsC"

/translation="MDINKTETLKRIIEGSSYQSLFFNHPDAIYVMDIHGNYIDANP

SVERISGYTLDDLIRMNQSEICPPDSENSRKQYIKEVLAGRSVSNPITFYHKD GSLKQ

AEITYVPITEGKEVVGIYGIKDVTDILEVQRELKEAQEKYQVLADHAQDLITTCATD

GELLYVSPSVYTLLGYKPEEVIGKSFKDYCYSGDYDPIDLSKIGNGCKMRVLHKKGH

YIWMETLAKPVAGEPGKSVQIVSISR DITQHKDADRRRLRESRQRYRSLFEHNPAAVYS

LNLEGKYSAVNSKLVQMLDIPRNKLIGQSFLSNLDKCEVQYGKHYFDMVKQGEPQYYE

TRIVNSSGRKIEVSVTNVPIIVDKEMVGVYGVSDITERKEYTERIQELSKQHELILN
TVTEGIYGLDADGITMFMNPAAASMFGEAKEFIGKNSHPHHTRADGSHLPQEECP
IHMTVLDBGQRRSIKEDVFWRKDGSSFLVQYQVTPHIEQQGIQGAVVVFNDVTGEREIV
RAKETAELAAQAKSEFLSMVSHEIRTPMNGIVGMTELLIGTDLSEEQREYAEIIRDSG
DALLNILNDILDFSKLESGKMALAYEPFALRKMLEQVAELFKPRADEKHLEIRYRLNP
SIPEFMVGDAIRIRQILVNLVGNALKFTDQGSIEVAVDIIKGRKPEDSVLDFAVQDTG
IGIPADKLDQLFQSFSQLHPVINRKYGGTGLGLVISKRLVEIMGGSISVESIEGEGST
FRFAVPAASVDASAEQTASQFHDRTRQSDKVAMRILVAEDHPVNRKILREYLEKLG
HADVCTNGVEAIDAISQNAYDIVLMDIHMPVMDGLKATDLLRRLIPQDRIPPIAVTG
NAKREDKEACLEMGRDFISKPVMLSELKRVLQQWGPREDPQLAPN"

CDS 5391173..5391733

/gene="lacA_2"

/locus_tag="EFAGFIKM_04699"

/EC_number="2.3.1.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P07464"

/codon_start=1

/transl_table=11

/product="Galactoside O-acetyltransferase"

/db_xref="COG:COG0110"

/translation="MLPNRVKIAYGKLRGLAIFGKIQPSMGLLPRIKGVYLNRLGDL

QVGKRLNIIGKPWGTQLTVVKGARLTIGDDVMINAGVGIAANVEVTIGNNVMIGPRTS

IFDSAYHRIDSLDDGSQTAKRIVIQDNAWIGTGALILPGVTIGRNAVVAAGSTVTKDV

PDNTLVAGAPAKIIRELTIHDGWVRH"

CDS complement(5391828..5392562)

/locus_tag="EFAGFIKM_04700"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSFATTYFRILSAERLKMKGKSPIWLLILLSPLIALLLIGLLSTPS

GNWQVLMTTMVFLHGLLLPMLTGVFTSFVCRFEHASGGWKQMLVLPTRSGVYAGKL

TTVLMLLAGTQVLLLLMSILLAGMIHGITMTVPWGFLVGKLLLGLLACVPLAALQMFVS
LVWSSFAAPLALNFALTIPNILIVNSATYGPYPWAQPMILMTPVDGAGFGAYNVPLM
TMLAVVGGSVIFIGIGMIYFAKKEI"

CDS complement(5392564..5393280)

/locus_tag="EFAGFIKM_04701"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTGRALSSDWLKIRGKGIWFLVFLAPLGLTAMQALNFGRLDYL

KEQYADNLWGGLLGNVVVFVPLSLMLGATILSSMIANVEHEQGSWKQLLAMPPIRPAV

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LELWLTMVNKNQALPVTLGIVLAITGMFSLSISPSFPLAWAQMAWNGPNPYLYAGMGA

GLGLLILLGGMVHFSRKDVA"

CDS complement(5393277..5394191)

/gene="bcrA_2"

/locus_tag="EFAGFIKM_04702"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5WNX0"

/codon_start=1

/transl_table=11

/product="Bacitracin transport ATP-binding protein BcrA"

/translation="MSENIIQTANLWKTYRDRAAVRELDLHIKKGDIYGLGPNAGAK

TTTIRMLLGLIKPTKGVIRVFDKDIRKDRMDILRRVGSLEVEYPSYYGHLNAVENLETL

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NGLDPAGIQEIRELIKRMPLHGHITVLVSSHLLSEVEQMASRVGIIREGKMVLQDTIA

SLHSQTGSSIRLTVSEPEEAMKLAKEQGQFGHQGAALTFPYMDNSSVALLVRRRIEQ

DHDVYRVEEQRQSLEDLFMRVIGEGASI"

CDS complement(5394272..5395783)

/gene="sasA_19"

/locus_tag="EFAGFIKM_04703"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01837"
/codon_start=1
/transl_table=11
/product="Adaptive-response sensory-kinase SasA"
/translation="MDQKQSGRRKLRFGRSLMSRYIILILAAVLFPVILPIMSVIYV
VVVNNTNTNQAAPYGDVTRISNLWSLEAENLDGASDEEIKARLEQLHGSYPKSSMYRV
NASGETLFILGSEDVTLLKSTSPDGRTDMTLRWSLDSGQTAETRIPAENANNTVQFM
KEASFRDPLTVVSYIGGGEKDRGQGFMIEVPRSLQINHSNGLLELLYLGIVMTIIF
LIFIMMSILFFARIRKRLRLQTAMMTTGKEGLPLPVDIRRSDEIGQLEEAFNQMVHQ
LSDSRHREREEQLRKRLIAGLSHDLRTPLTVIRGHMHALHKEELSEQGDRSLHRMEA
KMEDLGGLIDNMLSYNLLTSGKYTLKLEEKDILRIVRETAAAWYPVWEKEQFDIDIDL
PEEPLIWHMDEQGMRRVLDNLFQNVIRHAASGKYIGISTQEIQGETAIVIQDRGPGMQ
PNSDTKGTGLGLSIVDLLIREMGLRKQVDSSDTGVQTYIYSGKGKGNNKPLK"

CDS complement(5395828..5396511)

/gene="phoP_6"
/locus_tag="EFAGFIKM_04704"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P13792"
/codon_start=1
/transl_table=11
/product="Alkaline phosphatase synthesis transcriptional
regulatory protein PhoP"
/db_xref="COG:COG0745"
/translation="MKTLLYIEDDTEIATWVRADLEERGYEVVWLGSGEAAEAAVG
CSLIILDVMLPGLDGFTVGQRLKKEHPAVPIVMLSARTSIDDKLHGLDFADDYVTKPF
HPDELAARIEVQLRKAGTAVSSDTALKLDHLSIYEKDNRIVNEETGDEIILSGKQFHI
FAYLLRHMGMIRTKEQIYEAVWNEPYLDGDKTLMVHIRHLREKLELDPANPVVIQTVR
GVGYRVKKP"

CDS 5396734..5398488

/locus_tag="EFAGFIKM_04705"
/EC_number="3.2.1.54"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q08341"
/codon_start=1
/transl_table=11
/product="Cyclomaltodextrinase"
/translation="MLLEAIYHQPKRNWAYAYDQDTIHLRLRAKKNDLTEVHALTGDK
YAWDATKALVPLTKFTSDSMFDYFEGEVKPPYHRLKYSFLLKNGDEQIWMETDFQEE
EPDDPGRMFQFPYIHAGAVFTPPAWVKDAVFYQIFPERFANGNPDISPEKVEPWGGEP
TPFNFFGGDLQGVIDHLDYISDLGINAIYFTPIFEATTNHKYDTEDYLRVDLHFGDAD
TVKRLVELCHARGIRVLLDAVFNHSGKTFAPFVDVQKNGEQSKYKDWFHVHEYPLDVK
DGIPTYETFGFEAHMPKLNTEAEVKAYLLEVAEYWIKEVGADGWRLDVADEVDDAFW
RDFRRVKAANPDAYILGEVWNESSSWLQGDQFDASMNYPFTDAVNAFFVKNTMHAEQ
FANSIGRQLSRYPLQASEVAFNLLDSHDTPRLLTLCEGDQRKMKLAALFQFSYMGAPC
IYYGDEIGMDGEHDPGCRKCMEWDEAKQDRELDFYQKLISLRHAHPALRAEGTVRFL
QARPDGSQLVFERQNEEERILILFNRSEETAIVELEAGDEEWTELFGGNHRTAKEDGV
LAIELPAYGYAVLSTSLT"

CDS complement(5398623..5399135)

/locus_tag="EFAGFIKM_04706"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNTQHVILGILHNQPSSGYEIKQYFEEYFSFFFDASFGTIYPTL
AKMEKSGLLTKESVRQEGKPDKNVYSLTPEGAAQFHAYLMSPLEDEVFRSDFLMRLYF
GELADENTVTGWISTELKRKELLYDKLQRQMKEFGEHISPSQRLCMQVGLVQYEATIQ
LLKEQLDQPE"

CDS complement(5399190..5400404)

/locus_tag="EFAGFIKM_04707"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MKGIFQTSLFLKNGATIVGLITAVLFQVFFNIIWLSGYDQVNE
RMTQLAVTIVNEDGVAAEPVAKSLAAGLNFEIKPSESMQEARQMLTDRDVYMIIEIPS
GFMQQAENLSKPMTVKYVMNESNVATVKSVMQNVAAQVTATLNREVQENGIRGVLNQS
SMTADQSDALALGLSSRVEAEVERLNPVDNFAFSMVPMLIVTATFTGAMLLGMNLQKV
SGELSGRAGKWERFWARNIVNVGAAFIVSLVGSGMMHVMGVSSADGWLMLWLFQLLVT
ISFILMAQLSLLLLGNAGAWLNSALLPLLMLSSGSTIPRDVMSEFYQGIGHYLPATYA
VEGMTNLVLGGNGIGRDALFLGVIGVTTLTLGAFSIWIRRSNPAISEPRREKQPATVP
AALEASVSSSDH"

CDS complement(5400669..5401607)

/gene="sdhA_2"
/locus_tag="EFAGFIKM_04708"
/EC_number="4.3.1.17"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P33073"
/codon_start=1
/transl_table=11
/product="L-serine dehydratase, alpha chain"
/translation="MRFKHLHELNTICTAESKTIAQLMIEEQVQETNTPEADVVKQMS
EYYQVMKEAVRKGLTEDTTSRSLTGGDGKKMAEYIRKGETCSGDASALAMAYALCVS
EVNASMGRIVATPTAGSCGIIPGVFISSQERFGWTDEHLVNGLFCAGAIGYVIANNF
ISGAEGGCQAEVGSAGMAAGAMVELRGGTPEQVVHAVGLALKNTLGLICDPVAGLVE
IPCIVRNGLGAVTALAAADMALAGVRSAPSDVIDVMLEVGSAMPSRHRETAQGGLA
QTPTGRKMMQKLAKPKAKRAEPEPESPAENDVETKA"

CDS complement(5401597..5402286)

/gene="sdhB_2"
/locus_tag="EFAGFIKM_04709"
/EC_number="4.3.1.17"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P33074"
/codon_start=1
/transl_table=11
/product="L-serine dehydratase, beta chain"

/translation="MRFKDVFSIIGPSMTGPSSSHTAGAARLGRIARQWLGCTPDRAR
LTLYGSFADTYQGHGTDLALIGGLLDYVTDDPRIPDAEQYAAEAGMEVEFYTSGLPAP
HPNTVKIELWHGERACSLIGASIGGGSVSVHSMNDFRVQISGEFPTLVLRHADKAGVL
ASVTSTISSSGVNIGYMQVDRKARDGEALTAMEMDGVNPDMLKRLRELDHVLDIRVI
DLKRGVDSDAV"

CDS complement(5403017..5404048)

/locus_tag="EFAGFIKM_04710"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTSKEMLIITTDQMPYDHMAAQIIQNYTIEKPVVSYIRHNENLT
YHVVD EASGQKYLLRIHQAA YASMTGIQHTLPALEAEMNLLQELNATTALRVQHPVRN
ASGEWVT VWKSEAGKEICCTVLEWIEGRDIQQGERLTTEQIYDLGAQLQMLHQYGREQ
NQTDQTKVRPAYGNSHENLVMLGQLEEGVRLGIFTTEFDLLRETFENINEQLETYPQ
HAGTWGIIHGDITRNNLLITEQGISMIDFCLHGYGYLFDAGGAALMFNREERDIFLS
GYTKQIAPLTDRLMEGFMLIFTLGYYAFQMANESRHEWMKDRMPKLCSKYCRPYV
QNERIFYEL"

CDS complement(5404233..5404988)

/gene="pstB3_2"

/locus_tag="EFAGFIKM_04711"

/EC_number="7.3.2.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A2V9"

/codon_start=1

/transl_table=11

/product="Phosphate import ATP-binding protein PstB 3"

/db_xref="COG:COG1117"

/translation="MAIPFGTEQLSIYYGHFQAVKQISLTFPEASVTALIGPSGCGKS
TFLRSLNRMNDEIAGSRTEGHIWMDGNDLNEPGTDVIKLRQKIGMVWQKPNPFHKSIIY
NNIAFGPRYRGTKSKKALDEIVEKSLRRAALWDEVKDR LHESALSLSGGQQQLCIAR
ALSVEPQILLLDEPASALDPVSTGKVEELITELKKELRIVIVTHNMQQAARISDYTAY"

FYLGSMIEHGDTEHIFTNPDNRLTQEYIMGRFG"

CDS complement(5405001..5405894)

/gene="pstA"

/locus_tag="EFAGFIKM_04712"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P07654"

/codon_start=1

/transl_table=11

/product="Phosphate transport system permease protein

PstA"

/db_xref="COG:COG0581"

/translation="MKMKAKTVDKIATSVIVVLALFIVILLGLLGFIMYRGIGHISW

NFLTSAPELLKGGGIGPQLFNSVLLVLTIVTIPLGWGGGIYMAEYAKPGKITSFI

RLVVEVLSSFPSIVIGLFGLLLLVNQFGLGFSLISGALALAIENLPLMVRTTEQAFRA

VPKEQKEAGLALGLSKWKIITSILLPVALPSLITGTILASGRIFGEAALMFTAGMSS

PPLDFTDWNPTSPRSPLNPFPAETLAVHIWKVNSEGIGPDSKEVAAGASAVLVILVL

AFNLSARWIGRVVFRMTASK"

CDS complement(5405891..5406826)

/locus_tag="EFAGFIKM_04713"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEQTEGGTVMNNKLKPRRPLKEKHYYWEEWTGRIYTSICVVFLIV

VMFSIVYFVASKGLSTFFQNGISISEFLGGKTWNPTGEPAFYGALPFITGSFITLLA

ALIASPLGLCAALFMTEIVPGKGKKILQPAIELLSGIPSVVYGFGLSVIVPLRSIF

GGTGVGIAAGCLVLAVMILPTVTSIMADALSALPKGLRESSYALGATRWQTIYRVIIIP

TTLPALLTGVLGMARAFGEALAVQMVIGNAPHVPTSLLSASTLTSVITLSMGNTTM

GSVHNNALWSMALVLLVMTFVFVILVRLLERRNRV"

CDS complement(5406942..5407868)

/gene="pstS1"

/locus_tag="EFAGFIKM_04714"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8DPB1"

/codon_start=1

/transl_table=11

/product="Phosphate-binding protein PstS 1"

/db_xref="COG:COG0226"

/translation="MFKKLPIFILMTLTFVLVLAACGSKNDAGTEGAASNGSGEAATEL
SGNILAVGSTALLPLVEQAGQKFMAVDEYKNVTQVQGGGSGTGLTQVSDGQATIGNS
DVFAEEKLEDEAKVKELVDHQVAVVAMAPVSNKDAGVEDLTQQLVDIFSGKVTNWKD
VGGADQAIVIVNRPSSSGTRATFEKYALGEKMGDIQGSIQEDSSGNVRKLVAETPGAI
GYLALSYLDDSLQVLKYEGVEATVENVEAGTYPVWAYEHMYTKGEPDAATKAFLDYIL
SDEIQQNDVTELGYIPMSGMKVKRDAAGNVVE"

CDS complement(5408357..5410282)

/gene="fruA_2"

/locus_tag="EFAGFIKM_04715"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P71012"

/codon_start=1

/transl_table=11

/product="PTS system fructose-specific EIIABC component"

/db_xref="COG:COG1299"

/translation="MKISNVLPENIILDVTATTKAELIDELSQKLNDNGYLSDIEQF
KKDIWAREEQVPTEVGFIAIPHAKSTGVQSPAII MGRSLSGIEYTESCNLFFMIAV
DQSSSSEHLQTLKISTFLMDELFRAKLILARDQEEIVRLFQAEEQDAQALHSPKKY
AGKKVVGVTGCPTGIAHTFMAAEALKNAAKELGVHIKVQTNGSTGVGNQLTPEDIAEA
DGIIVAADV KVDMDVFGDRPVIKTSVKNGVHHAQELIEDAIVGKGVLNQGNSNLKEA
KEKTRLKQPKIYSHIMNGVSFMI PFVAGGILIALSFMFGIHAADPNSPDYNFAAFL
STAGGSAAFALMVPVLAGYIAYSIADRPGLAPGMIGGMLATIGGSGFLGGMLAGFIAG
YTILALKKLKVGIPDSLQSLSPVLILPLVGSFITALIMYFVINSPMAWINESLQGWLN
GLTGSNAILLGALLAGMMASDMGGPINKTASAFGLAMFANQIFEPSAALMVGGMPVPL
GIALATTLFKNKFSIEERNAGKAAYIMGASFITEAAIPFAANDPLRVIPSNIVGAAIG
GGMCMALGISLQAPHGGIFVIPIAASNPLLYIVCIVGSIITACMIGLLKKPVYQPKN"

NSSDSPDKKALTTMKSA"

CDS complement(5410298..5411176)

/gene="fba_1"

/locus_tag="EFAGFIKM_04716"

/EC_number="4.1.2.13"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q703I2"

/codon_start=1

/transl_table=11

/product="Fructose-bisphosphate aldolase"

/translation="MLINMKDLLKVAYENKFAVGSFNVANSEFVKVVITAAEEQNSPA
IMQIHPNEIDLVTGFIAYVREAASKSKVPFVIHLDHGATIKDITRSIRNGYTSVMMD
ASHLPFEENIAATKEAVELAHLDVSVVEGELGTIGSNESSEGGADEILYTNPEEAAI
FVEQTGIDTLAVAVGTSHGIYPQSKDHSIKIDRLKQIHEKVKIPLVLHGGSDNPDEEI
REAVKHGIAKINLSTDMKRAFYNQLRATLDANPNAYEPDQLMPEATKAATELVKKKMD
LFGSTGRASLYKLGEI"

CDS complement(5411194..5413059)

/gene="licR"

/locus_tag="EFAGFIKM_04717"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P46321"

/codon_start=1

/transl_table=11

/product="putative licABCH operon regulator"

/db_xref="COG:COG1762"

/translation="MRKRYIKLLEHLKQSEHDFVSGSELANLFDVTRTIRNDIKEMN
ENYLDKAMIIGNTRKGYKLVDLSSLYKNEDDDEERAFHIIKALLSQTDFITYEDLAR
TLYFSTQTIRKDVQKLVTQIAEKQNIIEAIIFQGIRLKGSEVEKRILLKKLVTTDC
LKHMPIDEALQYYFGDWFNESSIHFIYACIEEEVAKYNLLLSFQELFSICVNVLISLK
RVSLTQKITEQDMRLDHTSFEELKIAQSILIRLAQEMDIPFDEYEQYLYLLIALQI
LPKKNEEIGHEHVNEMEQQIKSVIQKVGEQYGFISYKNQELLDRLLAHITKSLYPLKY
YFPVENPFIAQIKSEYTNAYNVAVVLAKELQFCLNIKIPENEIGYLTLMHMGIIENSQ

DNRKRIAIYGKNLLVGKLLERKINLYFPNIRIDSLANHEIHLLPEGIETIITTSEI
AEQQQLNVQNIILVSEMITSDDMKNISIQLNRGLLKYYLSPDDVFFLNEDNPIDLLKK
LTELGDIQHLYTSIVEREKMSSTNIGNLVAMPHPFDCGDNKKLRVLVAINKQKMLWGD
QMAQIIFLFIPPKNQKVNNTKFFEEIYDVFQKQTNMTEKLLHITNYDEFLEWSSK"

CDS complement(5413367..5414659)

/gene="arsB_3"

/locus_tag="EFAGFIKM_04718"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AB93"

/codon_start=1

/transl_table=11

/product="Arsenical pump membrane protein"

/db_xref="COG:COG1055"

/translation="MVYVAILIFVVTITLVIWQPRGLGIGWTASGGALLALCGVVSL

NDASDVASIVWNATLAFVGIIMISLILDETGFFEWAALHMARLAGGDGRRLFFYSILL

GAAVSALFANDGAALITPIVLAMVRALKFDERMVLAFFMASGFIADTTSLPLVVSNL

VNIVSADFFGITFVEYAVRMIVPNLFSIVASTGMLFLFYRKSIPLRYDISAARDPKEA

IRDPRMFRIAWFMLGLLLWAYASSEFLPIPVSVIVGVSALLFALLARKSEAVDLKRVI

KEAPWSIVVFSVGMIVVYGLRNAGLTDHLRWLDAIAEHGLLAASLGMGIIAAVLSS

VMNNLPTVLINLLAIQGAHTEGIIQEALIYANVIGSDLGPKMTPIGSLATLLWLHVLS

RKGVKITWGYFFKAGIILTIPTLLFTLAGLALWLWILG"

CDS complement(5414846..5416933)

/gene="mcpB_4"

/locus_tag="EFAGFIKM_04719"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39215"

/codon_start=1

/transl_table=11

/product="Methyl-accepting chemotaxis protein McpB"

/db_xref="COG:COG0840"

/translation="MSETQDNKPMKAAKPAKPKHNQNKKKKKKGFWVNIRNKLLVSFL

AVLLLPSLAIGLITLMAEDGIQEQLVDSAMQSVSTANTIVESQVNYKIHDINYFADA

LDPSLIKGENDSPELQVKLEQYLGLHPDAMNIFVGTTDGV MVRGKPTASSTRGDAYDP
REREWYKLAMEKPGTAVVSAVSVNTDGVAVVFISKTLKDQSGVIGLSLDLTLQEAS
IKVGKEGYVIIMDANKNYVSPVADAGTPETSGLLDEMYEGSEGQFDYVFNDQPKMMI
FSTNEATGWKIAGTMLKSEVTNASKDIRMATFIVILAATFLTLLFIWFRSMLRPIK
RLQESARAVSKGDLTVKMETGRKDEVGELAKYFERMVDNLRMMILGVQETTEQVSASS
QELSASAEQTTKAIEHSTLAIQELAEGAEQQVNSVKDGGSGQMSRMAEDVRMMSERVQS
ITANMRHTSGAASSGNEAAGQAVEQMNSIQETVEQLGTVVQSLNARSVEIGSMVDVIA
SISKQTNLLALNASIEAARAGDAGRGFAVVAGEVRKLAEESGSSAAQIGEVVHNIRQD
MDAALIAMNAAQTRVGEGIQAVNTSGQSFAQIREAVEDAVHTLDDLSATTQKLESGAS
HVAKAMSDISNVTQESAANTESVSASSQEQLASVEEIASSSAHLNSMAEQLQGLLGMF
KMVEDTPKDKGKE"

CDS complement(5417102..5418160)

/locus_tag="EFAGFIKM_04720"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNCSGCSPYPIEGQGTLYLRPISPALLEALQTLGRLIETSDDM

MWMHFSNPETVQSLIEEFGEIEPTLRDSLTVQIMPIYEQANEESWISLTMQESRFKHA

ELVSIILEHQFSSHMQPIVDASEQIIGYEFLLRPAENGKSFSSYELFEVARETGLHSF

LDRLARITAIETSALFLPHGVKRFVNFLPSSIYNPEYCLTHTFEAIERLSLDPKDFVF

EVVETEIQIHMPILQQIFEVYRSRGMSVALDDVGAGYSTIELMNRLEPDFVKIDRS LI

ERCDQDSTKQQKILHIVEMSSRFGGQVLAEGIERMEEFEFCRSIGIELAQGYFFGKPS

AQPPGGPYCNTSSNSCNN"

CDS complement(5418373..5420646)

/gene="yfkN_2"

/locus_tag="EFAGFIKM_04721"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34313"

/codon_start=1

/transl_table=11

/product="Trifunctional nucleotide phosphoesterase protein

YfkN"

/db_xref="COG:COG0737"

/translation="MKMRKKVLSSLTAALVALNVLAVFPVPVSAADATKVKL RIMETT

DIHDNLINYDYYSKEDTQYGLAKTATLIKKARDEAKNSLLFDNGDLIQGNPLGDYVA

KIDPLKKGETHPVYKAMNLLDYDAGNIGNHEFNYGLDFLDMTLEGANFPYINANVYVD

DGDDDETNDKNYFTPYEILDKKVTDETGKEHTIKVGVIGFVPPQIMQWDSANLEGKVI

AKDIIATAKKFIPKMKAEGADIIVAIPHSGFEDIPQTDLMENSVLYLSQVEGINAILF

GHAHKVFPSADFAGKKGVDLEKGTINGVPAVEPGFWGDHLGIIDLDELVDGKWKVVD

SKTEARPIYDTANKKPLVDADQDIIDAVHEEHEGTLEYVRGPVGETTAPINSFFALVQ

DDPSIQIVTNAQKWYVEKHMQGT EYEKIPVLSAGAPFKAGGRSGASYTNIPKGTIAI

KNVADLYVYPNTVHAVMVNGAELKEWLEWSAGQFNQIDPAKGGQQQLINNDFPTYNFD

VIDGVTYQIDVTQPAKYDGKATVVNASASRIKDL SFNGKPIDPAQKFIVATNNYRASS

SKLANPDGKRIVLAAPDENRQVIIDYIRENKTINPAADGNWSLAPIKPSAGLTAAALN

DLEVVFASSPDAKGLVEANPAMSFIGNNEGFAEYGLKLTGEATTPETGAEPVPTPT

KPTKPTEPTPTKPTTKPQPEKPAGGKVYVVKGDNLYRIGLKYGVDWRKIVTFNVI

PDVHNLKVGQKIVIPAS"

CDS complement(5421124..5421540)

/gene="ydaG"

/locus_tag="EFAGFIKM_04722"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80238"

/codon_start=1

/transl_table=11

/product="General stress protein 26"

/db_xref="COG:COG3871"

/translation="MNQTELEQNIVKALENNPFCSFSTVEN GKPKSRYMALFNDGLNI

HLATNRRTHKVEELENPNVSLLLGYEAGGSKEVVEIEGTCEVTKNEGLREQVWNDEL

KAWFDGPNDPNYVILDITPARIEYTGKDHEHHVWEQ"

CDS complement(5421995..5422453)

/locus_tag="EFAGFIKM_04723"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MKPIRNSAKAVIVQDGRLLVIRLEDQYGTAYVFPGGGQEKGEEL
KDAVARECLEEIGQAVNVGELLHIREYIGKNHEFAEWDADIHQVEFYFACSLIDPAAT
IFEGSNPDDHQVAVEWIALEELSQIRLYPKTIGELLLKSDSSSIYLGDLN"

CDS complement(5422524..5423312)

/gene="pxpA"
/locus_tag="EFAGFIKM_04724"
/EC_number="3.5.2.9"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42963"
/codon_start=1
/transl_table=11
/product="5-oxoprolinase subunit A"
/db_xref="COG:COG1540"
/translation="MNTSKTLDINCDLGESYGIYRTLSDEAILPLITSANIACGFHAG
DPATMRLTVERALEHQVAIGAHPGLPDLQGFGRRRMDITPREAYDMVVYQMGALDAFV
RASGGRMHVHKPHGALYNMAAEDTKLAEIAEAIYRGQPDLYLYGLAGSELIRAADRI
GLRSVSEVFADRTYGADGKLTPRSQAGALIEESGQAIAQVLRMVKDGWVSTDGTLVP
IKAETVCIHGDGVNALAFAQEIRRVLESKGIKLSPHTTDDTPVQ"

CDS complement(5423312..5424343)

/gene="pxpC"
/locus_tag="EFAGFIKM_04725"
/EC_number="3.5.2.9"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7WY77"
/codon_start=1
/transl_table=11
/product="5-oxoprolinase subunit C"
/db_xref="COG:COG1984"
/translation="MSIEVIRPGLLSTVQDEGRTGYRRYGIHPGGVMDTFAARAANML
VGNSRHAHVLEMTMTGPELRFQESQLVSLCGADLTATVDHLPVPLWRPVLVRAGSVLK"

FGPCRHGLRGYLAAGGIAVPEVMGSRSTD LKTGLGGMDGRALRVGDLLSNGELSVEA
QGWMQRMEQVQVKESEWDHRILAPAWLLSERERPDYYGQP VIRVMESKDSLLFSETSLG
QFYAEKYVISSRSDRMGYRLQGSILELDQPLDRLSEAVTYGTVQVPPDGQPIILMADH
QTIGGYPVIAQVARVDMPILAQARPGTQISFQKITHDQAGQLYMEQEINMQLMDKLIR
RRMAGMGGA"

CDS complement(5424340..5425056)

/gene="pxpB"

/locus_tag="EFAGFIKM_04726"

/EC_number="3.5.2.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P60495"

/codon_start=1

/transl_table=11

/product="5-oxoprolinase subunit B"

/db_xref="COG:COG2049"

/translation="MTKQPYSWTEEILYPLGEAAVIIQCGDQLSDAVQRRVMSVCALL
EKSTLPAMIEWVPSYTSVTVFYDPFISPYPKLCRILLQQLNQMKESVQDKPRTVTIPV
CYGGEWGPDLDYVASEHGLTPEDVIAIHTSGDYLVHMIGFAPGFPYLGGLSEQIATPR
RATPRIRVEAGTVGIGAKQTGIYPVDTPGGWQCIGRTPLRLFRPDENVPSLLAAGDRV
RFEQITMQEYLALKRKEGER"

CDS complement(5425096..5425929)

/locus_tag="EFAGFIKM_04727"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDALTKQKLQHIQSSNHFIDHEEQPYELALHMMSHIGSTDRV L
RDELIYVTFATWIGQGVSFEDQLRHMLQLALDDQHLYGIGEQGTDSVFTRTFSVLLL
PPILNVDRQRPFLDKEDIAGIHHRLTTYLEREKDVRGYADNKGWAHAPAHAA DAVEDL
AQSPYLERTDLLELLHALAVKITESSVVIYHDEDQRIAHAVITILRRNLLEQKDITLW
IDSLHQGDQVWNRSLLTSHRSLNVRLFLQTLYLAI RTEEDEPFAVCSLV LQALERD
K"

CDS complement(5425933..5426523)
/gene="gpmB_2"
/locus_tag="EFAGFIKM_04728"
/EC_number="5.4.2.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01040"
/codon_start=1
/transl_table=11
/product="phosphoglycerate mutase GpmB"
/translation="MTQIALIRHGSTAWNKEKRSQGQTDNPLDQDGREQAVLLAARLA
EESWDIAIYASDLERASETAHIIGDRLGIQEIHLDPRLREMGGGQVEGTTEERIAKWG
ADWSTLDLGRELADAGTVRGSVLEDIVQQHPDGRVIVVSHGAVLRNTLRGLVPELDI
SVKLSNTSITRIAKNENAWQCELYNCSVHLDSPGES"

CDS complement(5426520..5427110)
/locus_tag="EFAGFIKM_04729"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDMNQVFLETAEKQFLYYKQLGEKAMAQLDSEQLFQSWNEDANS
IAVIVKHLWGNMLSRWTDVLTDDGEKPWRERDAEFVNDISSRELLSNWEEGWNCLE
AIRSFTPEQLSHIYIRNEGHTVMEAIIRQLAHYPYHVGQIVFAAKMLKETAWDSLSI
PRNGSAQYNGGKFAKPKARKHFTEDELHIEKGEEQQ"

CDS complement(5427180..5427509)
/locus_tag="EFAGFIKM_04730"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIYSIISRLWDQVSKGTEYAPDSLETGFIHCSTKEQIPWWAG
QYYAGRTDLLLSIDEKALKPELVYEDLYELNELYPHIYGELNLDVVRKVIPFEPNAD
GTFSFPE"

CDS complement(5427561..5428118)

/locus_tag="EFAGFIKM_04731"

/EC_number="2.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9HX72"

/codon_start=1

/transl_table=11

/product="Acetyltransferase"

/db_xref="COG:COG1670"

/translation="MNVEKLFAELPEFETQRLKLRRRLAMDDLDEYYAFASDPRVSQQS
LWNCHETVEDSIQYIQRVLDNYERKTVHIWAFILKETGTIGRGGIFHLNEPMQSDEL
GYAIASSQWGKGLAAEAMQPIVDYCFRELDNRLLEGKCNAGNIGSARVMEKLGMSYEG
LLRKQLKIKGVFTDQKVYSRIRDDL"

CDS complement(5428147..5428554)

/locus_tag="EFAGFIKM_04732"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKSVLIRDRLIYFFAVMMTMAAGLASRHFGERLPDWWHEHLGDA
CWAGMIYFGIRMVWPHRSLVWAMCLSCVFSWMIEFSQLIQTPWLIEIRSTVLGALILG
HGFLVIDLIRYTVGILCMFVIDRYFLRNKMAGS"

CDS complement(5428559..5429110)

/locus_tag="EFAGFIKM_04733"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKDPLQPENWPSWATESVEIAPANPNWDAQAQEEILQKRLLQQ
FNIQQFEHIGSTSIPGLPAKPIIDLMAEVQSWDDMDLIADQLNPVGWNYVPPELDGRE
YRRFWVRVKDGKRAVHLHLMRPGEEWRDRQIRFRDVLKRKPDLEAYAVLKTKLADEN
KEDRESYTAAKTQFILQVLDEGV"

CDS complement(5429325..5430431)
/locus_tag="EFAGFIKM_04734"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q086E4"
/codon_start=1
/transl_table=11
/product="Ice-binding protein 1"
/translation="MNRIKLALRGTLALIMALTILVPSLALAATGDVTSIEITNSSPQ
KMSVSETAALQVMATVEGFDNKQDVTGVTWSTSNAAVATMVKGKVKAVAAGEATIFA
EVDGSKAQLVVQVQEIKSIKASPKSYSFVKGSESTLPKVSITRANGKEEDVTSEIWW
SVSTSSAVLENGKIKGVTPGRVLLQGKYGTTIVKVPVAVTDEITKVEVTPATMQLNIK
KSKALKVIGTYANGKTINLSKQVIWTSSNTNVAIVKNGAVKLTGEGQATLTGTYQNQT
IKAETVVPLLKKLITGQKKLVLSPPQGSTTLVMAQYDTGKTTVTNSAVWSSTKPGV
ATVTNGKIVAVGKGKTSITAKWGNKKVTIPVTVK"

CDS complement(5430716..5431999)
/gene="serS_1"
/locus_tag="EFAGFIKM_04735"
/EC_number="6.1.1.11"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A8L1"
/codon_start=1
/transl_table=11
/product="Serine--tRNA ligase"
/db_xref="COG:COG0172"
/translation="MLEMKWIRAHAEVQAAADGKKIKINIRTLLERDEERRALLQES
EEGRRRLRNTLSADIGRLMQAGNREQAEGLRQVKQINEQLEQVEARLAPVQEEVTKLQ
WLVPNIVSPDTPNGLSDADNVELRRVGEVPTFEYNTKDHVELGELHDLIDIPRGVKIG
GTRSYVLKGAGLLLHRAVQQALDLLLLKHGFTPMVPLMVREDALVNTGFFPTGRDQV
YELEGENKWLVTSEVPLVSYADEIVDVQEPVKLAAVSTCFRSEVSGGRDVRGLYR
VHQFTKVEQVILCTPDAEESERMLQEITGHAEELLQLELPYRVVAVCTGDMSQKTYK
QYDIETWMPSRGAYGETHSSSNLHDFQARRSNIRCLDAEGKLAYCHTLNNTAVASPRI
LIPLLENHQEDGSIHIPAALRPYMGGAESLILPK"

CDS 5432387..5433622

/gene="glcP_2"

/locus_tag="EFAGFIKM_04736"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07563"

/codon_start=1

/transl_table=11

/product="Glucose/mannose transporter GlcP"

/db_xref="COG:COG0738"

/translation="MKKLLWIGCLSYFLIGLAHVVLGSILPVVALEHYGKDYSQGGTLI

FAQFAGFLGGVLLSPWLNRRFGKRGGLLIATALLCIAELSYMLLPPWGWMMFVIAPAAAG

FGFGMVEAVIGTIIIAIKDNTAVAMSRLEVLFGIGAMVMPLIASGLIAAGYWRLSFL

VVAICAALTFVFWAKGSFGELDKFLERQSSNHASVNTHSAGTSGEMNPASASTSSPTY

RGRNRTLLVLFVLFFFLYVGTEMSLANFMPAILIEKMNMKEAGAVLSVTCFWIAMSVG

RLFAGYIAEKFYRVVLYSCLASVLLLMIFFPTNQIWSAFLIILLGLAMSGIFSIA

LVFASKLLPGTEESTPSILIASGGVGGAILPTTGWSLDHLAVNQSAWMLAIFAVGLL

VISVITYQWQNKHIANSAT"

CDS complement(5434047..5434556)

/locus_tag="EFAGFIKM_04737"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRELPTSKKEQIIFGLMMCTGMVLVMMFFNLWHSGLLGKMSPLE

ILLQFILCFVIAFLVESFIVGPVARKIAFSLPFDKSNKILGVLVMSFFMVIGMVLIMS

MYGMISAYLADQLSGASLLRRTLHTIARNFSLALPYQLIILGPLVRYVFGKFIKDNGP

VMPVVNKSV"

CDS 5434730..5435116

/locus_tag="EFAGFIKM_04738"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MSFQKRIDHVGIVVRDLETLRFYTEIVGLELKDRVHTHTNGAIQ
LAFLGFNGSNETEIELIQGYSDKLPAEGTVHHFAIHVDNLDSEYNRIQATEAEFIDGE
IITLPNGYRYFFIYGPEKEWIEFFQR"

CDS 5435133..5435888

/gene="udh"
/locus_tag="EFAGFIKM_04739"
/EC_number="1.1.1.203"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q88NN6"
/codon_start=1
/transl_table=11
/product="Uronate dehydrogenase"
/db_xref="COG:COG0451"
/translation="MNIITGAAGKIGRDLSQHLSEAFHLRLTDLNIDRLHTYQGTGH
EIMTLDVTDPEACQHACEGMDVVHLAGDPSPNAGFYESLLDINIKGTFNVFRAAKDQ
GVQRVILASSAQTEGYPIDAQVYPDMPTRPRNLYGVSKCFGESLASFYAYTEGLQSV
AVRIGAYDDFQPDGPALEARDMSAYISPADLCDLMFKAITATDLEPFTILHGISNNRF
KRLNLETTQKQVGYPKSDAFALSQISLYDSPR"

CDS 5436452..5437492

/gene="thiY_2"
/locus_tag="EFAGFIKM_04740"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9K9G5"
/codon_start=1
/transl_table=11
/product="Formylaminopyrimidine-binding protein"
/db_xref="COG:COG0715"
/translation="MKWRKTMGLLLLCVLMVTVAACGGKEAAPAGQNGNTNTESSNEG
DTAALKDIKVLDWTPNTNHTGLYAAVDQGFYKAEGLNVEIVQPGAGGADTMVASNEV
PFGVSYQESVTQARTQGVPLVSIAAVIQHNTSGFAAPADRNIKSPKDFEGKTYGGWGS
PVEEAVMQSIMEGDGADVSKVKINMGDADFFTAVKRDIDFAWIFYAWTGIEAELRGE

PIDMLYVKDYSEALDYYPVLVTNEQTIQNDPELVKAFLKATSEGYQY AIDHPEDAAN
ILIKAVPDLDKDLVLASQKWLSPKYTDDAPRWGEQKQEVWQNYTDWMFSKKLLDEQID
VSKAYTNEFLPQ"

tRNA complement(5437542..5437617)

/locus_tag="EFAGFIKM_04741"

/product="tRNA-Glu"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Glu(ttc)"

CDS 5437747..5438037

/locus_tag="EFAGFIKM_04742"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MASTLLSIQVIPKTPNGENSYPYVDRAIEVIQQSGLKYQVNALD

TTMEGELEELLEVVRKMHEVLVEAGSPSIISQIKIAHSPAGFSMDTLTEKYR"

CDS 5438037..5438795

/gene="ribX_3"

/locus_tag="EFAGFIKM_04743"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A9WGD1"

/codon_start=1

/transl_table=11

/product="Riboflavin transport system permease protein

RibX"

/translation="MPAYFKSVWPPIVAVILFIAIWQGAVSLFHIEKWMLPAPSDIAR

EAATQAERLGMHASATIQLTLIGFAAGTAVGLLIAMVLHLPFLKSALYPLLILSQNI

PTIALAPLLLIWFGFGLLPKLITIILVCFFPVAVAAMDGLTRTDAAMMNYMRMAGAKR

HQIFWKLELPHALPFVFSGVKIAATYSVMGAIIAEWIGADKGIGYYMMLQKSAYRTDR

LFVAIMIIVALSLLLFLFIALLEKLLVRWRPQKR"

CDS 5438833..5439741

/gene="btuD_14"

/locus_tag="EFAGFIKM_04744"

/EC_number="7.6.2.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01005"

/codon_start=1

/transl_table=11

/product="Vitamin B12 import ATP-binding protein BtuD"

/translation="MNRQQDEQVQPGRGASVMEPTHDEKLHPATPDRPANTAPAPVSP
ALDWVDVHVSFRERRSKLPVLNGLSLTVEQGEFVAIVGPSGCGKSTLFHIIGGLLK PQ
EGQVLMNGQNVTGQRGKISYMPQQPALFPWRTIEDNVLLAGEVASSAPPRAEALSEAR
KWLSSVGLAGFEQAYPHMLSGGMQQRAAFLRALLSPQELMLLDEPFSALDALTRSDMQ
RWLLDIWEQNRRSVLFITHNIEEALLADR VYVLSNRPATVLHEVHVPFDRPRREEIT
EESAFLERKRQIAQWMREEQQKARLS"

CDS 5439847..5440653

/gene="ycfH_1"

/locus_tag="EFAGFIKM_04745"

/EC_number="3.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AFQ7"

/codon_start=1

/transl_table=11

/product="putative metal-dependent hydrolase YcfH"

/db_xref="COG:COG0084"

/translation="MHSQAFAPLIDAHIHFDQYTPDKQREMLLSFPSQQVEAVIAVSM
NLAS AQANLELAKQHPRTIYPAGFGHPEQELPPVAEMDLFFQWIKKHM GQAIAIGEVG
LPYYNRLEAEQAGQRF DQSGYIKLLERFIQLAKKH NKPLVLHAVYEDADIVCDLLEQY
QFRRAHFHWFKGSRQTIRRMADNGYFISFTPDIRYEEEEIRELARQYPSEQVMAETDGP
WPFEGPFQGRMTHPAMTRQVVQAWSEITGMGTERAARLFYQNTKRFYGLT"

CDS complement(5440937..5441680)

/gene="nfrA1"

/locus_tag="EFAGFIKM_04746"

/EC_number="1.5.1.38"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39605"

/codon_start=1

/transl_table=11

/product="FMN reductase (NADPH)"

/db_xref="COG:COG0778"

/translation="MNETIELMMKHRSVRKFKSDPVSEEQLAAIVAAGQMASSSSSVQ
AYTVIAVTDIEQKAKLAELAGNQAYVNECPVFLVWCADLYRLSDAAKRHLPEKESYAD
STENFMVATIDAALASQNAALAAESLGFGIVYIGGLRTRIEEVAELLGLPEGVFPVYG
MCIGVADQETGIRPRLPLDAVLHHNRYNAEQSIKGVEQYDETTTAYMKERTNGERTTP
WSELMAKRLTEPTRLQVRPFLEGKGFLKR"

CDS complement(5441673..5442272)

/locus_tag="EFAGFIKM_04747"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTEPELDIKTRILLAACKLFAQQGYDGTSVRQICDEAGANVSLV
SYHFGGKEKVFEALFEHFFPGHMMNSLAEESMSSPVEGIRRIIGEYVKFTMTDREMSD
IVQLEITLRTHRTATVFRFLDPVWTRVRDLLQEGKDQGLFQIESVSYAMLQVMGVALA
HKRAKNSRFGFDYQDMNTDELAQTIEFVLRGLGVNSHE"

CDS complement(5442428..5443588)

/locus_tag="EFAGFIKM_04748"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLQALRTLFFKKPPVIVGIVTALMFQVIFSVIWM TAYSGVNDRAK
ELTVAIVNEDGEMSKGIADSLAGTLPFHTVSNLSAAEALDQLNHHQVHMLDIPAGFN
ELLQTAGSTAEIKYTINEANPVTIKSMMQGVSVTNTINKQATAQGVQTVLTASGAP
ADQAAEAATNLTRVEGTTTSINPVNGMNNQMVPMMMVLASYVGAMIMGMNLQTAMGM
LSSTYSRLTLFGARVVINVGSAVVSLGSSLIVALGGQIAQGFVAFWLFQALFLCTF"

MFFSQFFLICFGPAGSLFNIISLSLQLVSSGAMVPRELLNSFYSGIGQYLPATYAVQG
ILSVQLGGPGVQSAAGSIVIVLLVAVALSLVVTLLKKQRMAMPSPAQANN"

CDS complement(5443939..5446479)

/gene="copA"

/locus_tag="EFAGFIKM_04749"

/EC_number="7.2.2.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32220"

/codon_start=1

/transl_table=11

/product="Copper-exporting P-type ATPase"

/db_xref="COG:COG2217"

/translation="MMDNSTNKPMDRSSEPTMPPMAEAPGLKATLHITGMTCAACST
RVEKGLSRMEGVHQANVNLAIEQATVSYDPKTTNVNALRDKVEALGYGTVESVDLNI
TGMTCAACSARIEKGLSRLPGVSQANVNLALETGHIEYAAGALKPSDITAKIKQMGYG
AELQLTQEETTSVRERELQRKKWKWMISALLSIPLWAMVGHFSFTSGIYVPDLFMNP
WFQLILATPVQFVIGWQFYVGAYKALRNRSANMDVLVALGTSAAFFYSLYTLSSGYL
PSATMDHGAMGTSTAAMPSELYYETSAILITLILLGKWFEAVAKGRSSQAIKSLIEL
APREARVIRDGQEVMPAAYVAVGDLILVKPGDSIPVDGIVEEGQSSVDESMLSGESL
PVDKKPGDAVTGATLNKNGVLRRLRATRVGSDTALSQIIKVVEQAQGSKAPIQRIADVI
SGIFVPIVVGIAALTFLIWYLFASPGDFAGSLEKAI AVLVIACPCALGLATPTSVMAG
SGRAAEYGILFKGGEHLESAQQIQTVVLDKTGTVTQGKPVLTDVITAPNWTESDLLEQ
VGAAEQSSEHPLAEAIVAGIHAKGLELPPTENFENIPGYGVRASAKGLEILVGTRRL
ADAQVNVSEATVQQMNRLEEQGR TAMLVAVDGQWAGIVAVADTIKDSREAIGRLQAM
GIDVIMITGDNERTARAVAEQAGIGKVLAEVLPEGKAAEVKKLQESGLKVAMVGDGIN
DAPALATADIGMAIGTGTDVAMEAADITLMRGDLNSIADAIEMSRRTMGNIKQNLFWA
LGYNVIGIPIAAVGFLAPWLAGAAMAFSSVS VVLNSLRLQRMKLKRND"

CDS complement(5446642..5446842)

/gene="copZ"

/locus_tag="EFAGFIKM_04750"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A3E5"

/codon_start=1
/transl_table=11
/product="Copper chaperone CopZ"
/translation="MSNVTLNVTGMSCNHCVKSVEEAVKNTGASGKVDLAAGTVAVEY
DEQKVNVDQIKAAIEDQGYDVV"

CDS complement(5446902..5447300)

/locus_tag="EFAGFIKM_04751"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEHQSHPEEPMQSSISDSTEASVTVQEAVSCHAEGSDGKHVRKS
HHSQEMKSNLVSRLNRVEGQIRGIKGLIEKDTYCDDVLTQIAAAQSALNSVGKLLLEG
HMKSCIVERIQAGEHEVVDELLVTMRKLMK"

CDS complement(5447400..5448665)

/locus_tag="EFAGFIKM_04752"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKGMR SINEKEQLGQNSILQSTEDVEYLVRSVQKLLEEDTVIQ
CWEVESINPGLLNFTTSGIYRIRGTATVVGASLSWSLILKCIKPD SAEKEDVTYHNYW
KREAEIFSSGLLDHLPGR IAPRCFAIQDRPDQTIGLWMEDVSGQSKCDHVWSLDDWG
WIAECLGEFHGAYLTGTSQPQ QEWICPYWLKSWVSGCRQYAPSIQEPKLESGFGDDDT
GARGRHIGVGG SERYA IAGSIQEQAHSIWQWFNQYSGQMEKVINS LDPLPRVLSHQDL
AQGNIFLP SERLDDSVLTLIDWQFMSISGVGEELGKLFGVNASFGHIAAEDIFAAKEE
VFDRYVHGLRTAGWIGDERLARYGYCVA VAARSMWEVPEWLKWVDQSCTASDSNEELD
RKISTRARIITIQKEMSFEAAELAHALFT"

CDS complement(5448717..5449205)

/locus_tag="EFAGFIKM_04753"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTGTINIRKAEMRDYSGVSLLMDELHQMHEARPDYRALETR
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DTKHRGQGTGKQLLQAFIELGRELQADSVELSVSTFNSGAQAFYEQMGLVVRSSRMEY
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CDS complement(5449327..5449515)

/locus_tag="EFAGFIKM_04754"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMTQNNQPQDEAEIRNKLDEDEGDSLMEKKKILSGVDIEPQADEW
AAKPSPVAFNEGNASSKK"

CDS complement(5449615..5449902)

/locus_tag="EFAGFIKM_04755"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEDFGEIFNQFKALRMESIGNLVIYNSKEYKRLSQESDRLFMEL
CEYVKPEGMALFLDYCNVITLLQGTAESVMYEQGF RDGFSLIKLMFNSNNT"

CDS 5450038..5450223

/locus_tag="EFAGFIKM_04756"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MATDKRVFTLRLREKNFEKIKVIADKNKRSIAMQIEYLIEQHIE
EFEKEQGVISPDTHNDV"

CDS complement(5450289..5450900)

/locus_tag="EFAGFIKM_04757"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGWSELREIPNEYSDEVQRIDEQLLKLVAARKDITGAVQYQPPQ

NTIDEWVSLDMKEEDIRYVLRVQMPQQRHYFPSEPLQLTSVVPIMKKMIKDSCEYM

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ISFRVVPALPSSLENVRFSLIPSIPEMEYKVEEIIILDKQVDFD"

CDS complement(5451156..5451914)

/gene="deoD_2"

/locus_tag="EFAGFIKM_04758"

/EC_number="2.4.2.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01627"

/codon_start=1

/transl_table=11

/product="Purine nucleoside phosphorylase DeoD-type"

/translation="MLMPILQIHSEDIPAYAIVCGDPARAEKISRKLEQARELAFSRE

YRTFVGLYEGVQIAVVSHGVGSPGAAVCFEELIRAGVTTLIRVGTAGSYTADYPAGSV

IVSTAAVRTDGLTRQLVPDGFPAVADIGVTQALIEAAREQESADAATFAGKVGVGITV

TLD AFFAGVEEIPHRKYKQAGALAAEMEIAALYIVSTLRGARAGAIVAIDGFADSDLA

AEYDPHTDAVGQAVEREINAALRALVALARKDQA"

CDS complement(5451916..5452587)

/gene="msrP_1"

/locus_tag="EFAGFIKM_04759"

/EC_number="1.8.5.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01206"

/codon_start=1

/transl_table=11

/product="Protein-methionine-sulfoxide reductase catalytic

subunit MsrP"

/translation="MHNKAERLKKSKTPAPKTGNDHGDRLPPGQMLTEKFPILHEGEV
PEYDLSTWDLKVFGEVEEEKVFSLAELQAMPQVNTVSDIHCVTRWSKFDTPWEGIRFS
DFVKLLGVKPEAKYVMIHADHDYETNPLEELMHDDVLLAFKYNGEPLTPKHGFPLRM
VVPQLYFWKS AKWIRGLEFMTEDRNGFWEVNGFHHFADPFKEQRFSGEDLPIPEDEWT
KKEFD"

CDS complement(5452635..5453558)

/locus_tag="EFAGFIKM_04760"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQQLFDAAMFGSTLRIMTPILLAALGGALCSRVLFNVGLEGLV
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ALQFYLFKSVSGFRLRSVGENPIAAQSIGIKVRGIQYGAVLMCGVLCALAGAQLSLGQ
VTMFTEGMTAGRGFIALVATMLGQANPLGVMGSSVLFGFMEALSIRLQGFSLPTHFTL
MLPYIVTLVAMFFFKDRTYAQDALKAGGSSR"

CDS complement(5453542..5454609)

/locus_tag="EFAGFIKM_04761"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNRVKETLRGLVQPLLAVFIGLIAGAVAILVGGNVVDTYAEMW
KGAFGNFYFFTNTLARSTPIILAGLGVALAFRAGFFNMGAEGQMILGGLSAALTALYL
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PFKDRTGSAAMAQTPMIDQSIWLPKLFQGMGLHAGFIIAIVAAILIYWFTHKTVTGYE
IRMLGSNPSFATYGGVRRIRMMMLSMVISGGLAGLAGAGEVLGTQYRFLDGSLSASY
AWSGIMATLLARSHPLGTAVAAILLAALQTGAMGMERNTDVPLEVGSVIQAVLTLFVS
AQIGYSFLKRRKEKKS NATTV"

CDS complement(5454606..5456105)

/gene="rbsA_3"

/locus_tag="EFAGFIKM_04762"
/EC_number="7.5.2.7"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P04983"
/codon_start=1
/transl_table=11
/product="Ribose import ATP-binding protein RbsA"
/db_xref="COG:COG1129"
/translation="MLLEMEQITKKYGGFTANRDIRFNLREGEIHALVGENGAGKTTL
MRMLYGMEQPTSGTIKVRGREVSFATPSQAMASGIGMVHQHFMLFPSFTVAENIVIGR
EPAKAGAFDRKKAAAQVNELGRQYGMPVDPWKKVSECPLGMQQRVEILKVLHQGADII
ILDEPSAVLTPLEVKELLANMKSLAKLGKTFVLITHKLQEVMDVADRITVLRDGGQVTG
TLEAKDTHVEELSRLMVGRELVRMDKQPSVPAEAVLQVEGVNLSGAKDRSALKDIHME
VRKGEVVGIAGISGNGQSELIQIIAGLRKADSGRVVLSGQDTTNWPVRRIREHGLAHI
PEDRYMWGAAKDASVRENGLMGHHHRLQSRGIKAKAARAMVESWIQQFSIKTGS AET
KAQFLSGGNLQKLIAAREFAQDTPFLIAAEPTRGVDIGAMETIHAELLRKLSEGAGIL
LISSELS EILQLSDRIIVMYEGE IAGELRAEEATEEQISLLMAGGKERI"

CDS complement(5456220..5457275)

/gene="tmpC_3"
/locus_tag="EFAGFIKM_04763"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P29724"
/codon_start=1
/transl_table=11
/product="Membrane lipoprotein TmpC"
/db_xref="COG:COG1744"
/translation="MLKRGIFKMKRGLSFVLSIIMLAILLAACGNSASKDEQSAQGSD
SEKSLRMALVLPEKIGVNPFFVQMDEGFKKAGEEFKVDTKTIESTDPAAFEQNLRAAV
AENYDLIITATFQAEDALKKVA AENPDKSFAIVDTTVDLPNVRSVGFREYEGAYLLGA
AAGLSTKTDKVGMI AAMDVPLIKKYTEGFKAGLESVNPGA EFLVNYVGGFNDPAKAKE
LALVQFGKGADFIAGASAVGDLGVFEAAKEKGFYTS GQDTRTVEDPEHIVLSQLKST
DTVAYETVKDFVEGNFKAGAVNYGLKEDGVGLTYVTRDSESPLNAFVGQEVIDKVKAI"

KDDIVSGKIVVKDPLQQ"

CDS complement(5457285..5457416)

/locus_tag="EFAGFIKM_04764"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTKKGLIQNGFQSLVESELSIIFYLSVYAQRFIDKDRQYPLG"

CDS 5457528..5458949

/locus_tag="EFAGFIKM_04765"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKITQITLAALLAAPVTLGSLSLPASASAASATPAKPATSQSV

KGPVAQAPVYTESAADFAQFLQAKYNIQLPQQITKGDIFIQIAAITEAIQASDSEAK

APVFTDLSSGDSSYDAAVSLYNNGVLTGTEVRAKDHLSTYAAVFIKVAAGFKELAYT

YPAEKTAKALAKVGISPNRVQQGAAQELAAIDTGLIPESLYPALLKGGVASKDFANT

LLGRVLVSQGKYKHEIGRSGDADIYSKLYAAYRTADLIESPELRKIVDQALRDDLVGT

YNLKDSRFDSNFIDELTLTYGHDNIQHAVQLVGLLRSEGIDADVQFQPKTSAFIYLKE

WGEPKETPDYKVTQIENGNYIASAKEYDIQLEFNNVADKVRFNDIVLKYAKKNSDSTS

PLILSSWWQPLYYSPTALANYPVISNNKIALGNYYAQSFSLKENAKSIREGFLKLAPD

ADITTYDFWVDQPFFNYLNGGSE"

CDS 5459192..5459782

/locus_tag="EFAGFIKM_04766"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVYDGILLGLIVGFFRGGRLRHGLNQFAALKLRSGWIFPVLLLQV

FFIFYLQERFEWVASINGYLFAAVYITGLAFLWLNRRHTGFMLIWIGVFLNFAVMAVN

GGRMPVSVEASAVLGPYYVDMLREGGAVSKHFMMDVSTRLPFLGDIPLSSPYPRQV

ISIGDVVMNVGIFLFIQYMMVNRDKKVQPAKTHQA"

CDS 5459821..5459925

/locus_tag="EFAGFIKM_04767"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKFEGVKYSRIVINAIIVASVVVALTSGYKLGG"

CDS 5460093..5461925

/locus_tag="EFAGFIKM_04768"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNFIRNLIHKADRSSMYVILLSCTGIGVFLYMNKWSYLHLTTAD

WVMVYTMLGAALILDYFTFQIPPKGNQQSMDSSVYLACIFMFGGAFSLSVLLPVSIIL

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NTITLGLFFHFSTKDALQQMKRAVTESELLVYLCTLILALVLTILVVHNGVLGLLLYL

SLSILLSHAFRQLFVMYQTIEEKANTDQRTGLFNHSYFESMLENELTTARTQGTPLCCL

GLIDIDDFKKYNDRFGHLQGDSLLALLGDFLMRKTEGTPVTAFRYGGEEFTLLMPGME

LDESYRFMNKLRKQLNDTPFEGVEVFPHGCLSFSAGVAPYQVDMYNKSQLVDQADKAL

YYAKKQGKNNVHRHGSNDGMEHEIDLVDVRDIEQQLNLFYKDMDTFKHSKRVIKYA

LDISELLALDNAEKRRFVLGALIHDIKLEIPWSILNKKDKLTAEEWETIKGHVTWGK

KMVITNDRFADLIPYIELHHERYDGKGYPYGLKGKEIPRLCRMLTVIDSFDAMTTERP

YQETKNVEEAIRELRACSGSQFDELAELFIQYIEKRQAQQLLQ"

CDS complement(5462059..5462226)

/locus_tag="EFAGFIKM_04769"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSQEVLERSELLKKNIHQMLVQDNQHGISRQDNMFLQQMIKEL

HQTSHELNTKS"

CDS 5462532..5463362

/locus_tag="EFAGFIKM_04770"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSYKQIKWMILLIPTFTVGIWEYIRHQFLMPYLSMDAGNWLTPV
IVYLVSVTLLSRLFHMLEGARAALEQERAAKAALEARDQLARELHDGISQSLFLLSVK
TDKAGRSLAGSGHEHEIQEIQKTVHEVNTYVRQAIAQLRFVPSSTVTSEIISLHAQVE
VLVKETVPGAQIHWDLRGVTFSAKEQVELLACIREGLLNVRKHAQATRVQVHAEGNPI
AWFIYIQDNGNGLSGDPLHLKDRYGLRITKERAEMGWSFTLDSRPGHTRMTIGKEHA
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CDS 5463364..5464020

/gene="degU_2"

/locus_tag="EFAGFIKM_04771"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P13800"

/codon_start=1

/transl_table=11

/product="Transcriptional regulatory protein DegU"

/db_xref="COG:COG2197"

/translation="MEHVRVLVDDHAHAREAICSILSEDSLFEVIGTASNGQEALEL
TGQWMPDLILMDVQMPDMDGLEATRQIKLRFPYVIVVMVTVSDDVTFLFEALKQGAQG
YLLKNLTPSTWLEYLRAIVSDDAPLSKELAYRILQEFPAPRSEDVQDNPLTARELEIL
QWVSAGYTNREIADQLGISDQTVKNHLKNILQKLQLENRVQLTRYALESGLAGRLRK
"

CDS 5464229..5465944

/gene="ycnJ"

/locus_tag="EFAGFIKM_04772"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SP95"

/codon_start=1
/transl_table=11
/product="Copper transport protein YcnJ"
/db_xref="COG:COG1276"
/translation="MILTRFTLKWGKRHWALVTCLLLVCCLVMPQWASAHAYIVKASP
GENEILVAAPERLTMEFNESLQTAFYDIKVTGPDGNQADDGNVQIDVDRPHILETGLQ
AGLGNGTYAVNWKAVSADGHPIQGAYVFHIGEPSGSPAGLSDLTSGSGSTGGPLKWIV
SLTDWVQYLGLSVILGTAFLLRIAPTSMTREPM DVPGSYRLLWISYAAASFAALVS
LPLNTLYESGVALNELSWRLIGSALKLTSFGQIWMLQILIVMLLAVTILSGYDRDRSI
RARIWSSYGSLLVLGWLFTHAMTGHPAAADQRALAIAMDFVHLIGAAFWIGALTAMA
ICLPPLADKLPSKVRGEVYWVAIRRFTAWGIGAVAALVATGIYSSLIILPAPVLTSLF
TTAYGLVLIGKIVLLIVMVLFAWRHARLARAATGSRLSGSLKAELATGAVILALAAVL
THLSPGQPAAVGPYQETKTTEGSAITLQVSPNVTGENQFEVDVKRADGSIVNDLEQI
TSLTHLDMMDMGIYEITIPKNDTGVYKAEDYISMPGRWNIKVHLLTKTLDALDAEFEI
DTAKP"

CDS 5466409..5467170

/locus_tag="EFAGFIKM_04773"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKTSWISKLTSTIATGTAAFMLFAGFASAHVTVSPSVAQTS AW
QTYTIKIPSEKELPTTKITMKVPEGVAFKQYQPLAGWKITTEKNDSNEVTSITWEIDG
DNEGILAGQFQQFNFVAQNPTAEAEVAWDAFQYYS DGSIVEWTGQPSDANPHSITTIS
EDPAAADNAAAGGGHDSAGTEGATGDNAATDDSKANDDTTLGDALNDTVTGEPNNTDT
DPGTLKLQQATLIVSILALILSFLGIALATRRKKR"

CDS complement(5467395..5467667)

/locus_tag="EFAGFIKM_04774"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MGGQLLVELNDLRIA EKELTQLLARLQADEQE ARALYSRLNDWK
GQSADHTRQQIEEFFAGLSRRIQSIEQQKKSLLQYIEIMIQT DQER"

CDS complement(5467719..5469059)

/locus_tag="EFAGFIKM_04775"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSNGSNIDDETYKTMSDLAYQDQKAGDKLTE L PGWEVLEGTESN
KFSGFDAVTFYNPETKEAVIAYRGTEGSASLDRSVPDFVMDGRIGGGELIRKGQQEAG
NFVNNLTPDWLDKGVEGVKDFTGISKVEDWAGDRVRDVENWTGDRVKDIEKTVSPTGW
ANQMYQSEDYANHMQNKHKDLNFSMTGHSLGGGNAQYASAYTGIPAVTFSAPSVMGNL
TPEMRRRAESGAFDGQVVNYANPSDLVASGTLGGYDRHVGSTYYINS DYDSANDGVSI
IDKAKNSFGGENYHSLDQYDFKNGYISNDLYDPITGERIRYSPRLMDHMGPF SKNFGP
LRKSGGGGGMASAAAASGLIQVTPEELKSVASRWKQNAQQCNAELNQVRSRMAQYLH
TSRSRRLEPIVTQLDASIQELSTWHMKHTSQFLNFIDEKADAFRQADESPVHFN"

CDS complement(5469075..5469356)

/locus_tag="EFAGFIKM_04776"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNASEKEALYQEA EATVIQHFKQKFELDVVITSKELLPEMAVSQ
IGLKGHVKD HEDQSFGISYDYKKKVTKNLVISPEIEEVMMAKGHN PYDK"

CDS complement(5469708..5470964)

/locus_tag="EFAGFIKM_04777"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAKPKQTKKAAAWSLVVMGAGFAASLPFQGV PVGKLLVGSFEAG
LVGGGLADWF AVTALFRHPLGIPIPTALLPKNRDKMTEGLVSAVENNLLNKDSITEKI"

ADFKAAETVLDLTRELHSDGIKIMIDTLCKRILAGLPLEQIAPLVAREIKSQAGAFD
LGPILERAHHQMTERGYDAKALDYGLKQAEWLKPKETIMFLGESGMKAISGIQMNGL
MQFAMNAFLGYMNEERLGGILQGYLFDRVEDMKREGSALRYKVLDMMVRTQTVRLAMSE
AMQDGINSWKNNMLEGWNAEETVLNKLTELKALAAAMEDGQYVDTYALPAIERVLVD
LRADDELMTGMNAKIVNGVTTLLEKNHSGKIGKLVRENVKMDNATLVSMIEDKVGQDL
QWIRINGAVTGFVIGIALTALQMALA"

CDS 5471298..5472125

/gene="ytbE_1"
/locus_tag="EFAGFIKM_04778"
/EC_number="1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34678"
/codon_start=1
/transl_table=11
/product="putative oxidoreductase YtbE"
/db_xref="COG:COG0656"
/translation="MKHVQDTTTLNGVKMPWLGFVFKVKGDEVVHAVKTAIQAGY
RSIDTAKAYNNETGVAQGIRESGVAREDLFITTKVWNSDQGYESTLAAFEASMERLEL
EYLDLYLIHWPVKGYKDTWRALEKLHKEGRIRAIQVSQFQIHLEDLMIDATIKPAV
NQVELHPLLIQSELREYCNKHQIQIEAWSPLGQGHLMHPLLKDIAAKYSKSPAHVIL
RWDLQNGIVTIPKSVTPERIYANADLYDFELTSEEIEQINGLNENKRFSGSDPDNFNF"

CDS 5472401..5472919

/gene="sigV_4"
/locus_tag="EFAGFIKM_04779"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O05404"
/codon_start=1
/transl_table=11
/product="RNA polymerase sigma factor SigV"
/db_xref="COG:COG1595"
/translation="MIRLNHRKTKEEQFSEKITEIQNKLYRLAYCYVKNEQEALDIVS
EAVYKGYIAYGKMESMTYFDSWMSRIVINTAIDHIRRNQRVTYMEDHAQEFVAPERGA

SVEEKMDLYDALDRLVPEDRAYIILMFFGNMRFREIAEVLSLSENTVKSKFYRIINKL

KMDLIEGEVGDL"

CDS 5472916..5473770

/locus_tag="EFAGFIKM_04780"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTGKERYENIEIPAQLTDVIRQAQQKAAARKSSSRIIRYTSILA

ACAAFLFIVNIPTVANAMVKIPVVGTVQLQFGDGGKITDGVTVGSEATENKLKINF

STDEHDQTNDAAPHYNVVHKEAPNRILFTFSGARYMDIEKVKADFMQPLVKDVYGSMI

LDDSSVGFVVVLKEGVQYAVTEFKNPGYLEVKLTSDGKLVTPRKVYSLRTESMPFGES

MGIKESYPDEDISFLKTSTGEFTAVIGEYLTAEAEQKLKELAQQPDYHEEFYVDSW

MSNDNPSD"

CDS complement(5473929..5474387)

/locus_tag="EFAGFIKM_04781"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTTHELSPLVAALNMQPHVEGGWYKEEWKASYQIPQSVLPDTYS

GPRFSASSTYFLLHAHEISEWHTVLSDELWLWHSGSPVELKLGGNGENPENEEVLVLG

MDIAAGQSPQVLVPAGVWQTARPLGDEPVLVTCVVAPGFHFDDFKLVSKG"

CDS 5474588..5475439

/gene="rhaR_39"

/locus_tag="EFAGFIKM_04782"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MSLIEDRIGPKYRIGEHSFTIEHMRRHDGNGMPQPHAHPFYELY

YLLEGERVYSMNGQILSARKGDFILINPHDVHTTSKGSIPGFERILIGFSPAFATGME
LGICGLLPFNCSRLLRLPEAEQPEMERILWQMLQECKERRPHYEIAVRSLLAQLLIRI
HRVEENIRQSCPGPLHPMQDKISEIVTVNKNYTEPLTLEGAANRFYISPSYLSRMFS
RFTGFRFSEYLRVVRVREAQRRLTTQERVQMIAEKVGFEHTAHFNKTFKQVTGTTPL
RYSRKEHR"

CDS complement(5475592..5477202)

/locus_tag="EFAGFIKM_04783"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNTYHSPMSRASAQSDVRAYEANLPVIPVQDFQLTDYGAVGDGV

TDNTEMFRLAIASCAEAGGGRIIPAGVWLTGPVIMRSRIELHVEAGALVTFSRDFDQ

YPLIASSFEGWQVVRQCSPIDGDQLEDIAITGEGIWDGGGEAWRPVKRSKMTTSQWNQ

LVASGGVVEQSGGDEEIWWPTAALEGGTIANRLHQEQVRDVAAYEEVRDFLRPNMVS

LRRCNRVLLDGPTFQNSPAWNLHPWASEHVTIRNVSVRNPWFSQNGDGLDVESCRHV

VEKSVFDVGDDAICLKSGKDAEGRELGLPSEYITIRDCTVYHGHGGFVIGSEMSGGVR

HVRVSDCTFIGTDIGLRFKSARGRGGVVEDIQIERIYMKDIIMEAISFSFFYANQEGS

ARGSDLSQEISEETPVFRDIRISDVVCAGADTALLVSGLPDGVIIQRYHVQARS

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CDS 5477683..5478411

/gene="glnQ_4"

/locus_tag="EFAGFIKM_04784"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34677"

/codon_start=1

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/product="Glutamine transport ATP-binding protein GlnQ"

/db_xref="COG:COG1126"

/translation="MIEFRGVQKHFGHFHVLKDIHLHIEEGEVVVIIGPSGSGKSTLL

RCINRLETITEGELVVSGIPLHQKKVDINLFRRDIGMVFQHFNLYPHKKVIDNITLAP
IKVRKQPKEQAAATAMKYLTRVGIADKADSYPSQLSGGQQQRVAIARGLAMEPKIMLF
DEPTSALDPEMIGEVLDMRSLAHNGMTMVVVTHEMGFAREVADRVIFMDEGRIVEEA
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CDS 5478451..5479281

/gene="glnH"

/locus_tag="EFAGFIKM_04785"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34563"

/codon_start=1

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/product="ABC transporter glutamine-binding protein GlnH"

/db_xref="COG:COG0834"

/translation="MKKLLKWPSFMLVLILSLVLSGCSTGTDTPSASGGGDAAKGTI
ERIKERGKLIAGVKYDTKLFGLKDPASGNVEGFDIDIAKALAKQILGDETKIELKEVT
SKTRIPMLQNGDIDIIATMTITDERKEQVDFSDVYFEAGQSLLVKND SAITGLESLS
GVKVLAVKGSTSAQNIREKAPDAEVLEFDNYQDAFTALKAGKGEALTNDNIILIGMQQ
TDNSFQLVGGNFTSEPYGMAIRKGD TAFVEEVNTLLKSMKDSGEYDTLHEKWLGAKPE
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CDS 5479383..5480105

/gene="glnM"

/locus_tag="EFAGFIKM_04786"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34671"

/codon_start=1

/transl_table=11

/product="putative glutamine ABC transporter permease
protein GlnM"

/db_xref="COG:COG0765"

/translation="MGTLD FSVLMRHSDRFLEGLNTIQVSIMALIGSFILGAILAIF
RISPVKPLNWIGTAFVEFIRNIPLLLVFFFYLGLPALGISLDGFVSGTLGLTIYTAA
FIAEAIRAGIQTVPRGQLEAARSSGLSYVQAMNLIILPQAIKIVLPSIGNQFINLVKN

SSILAVVAGMDLMYFADLVNSDTFQPLSVYTIVALFYLVLTPLSFLVHYMERRFGQS

DAEARSTKGKPKKNKPAGQVTM"

CDS 5480215..5480865

/gene="glnP"

/locus_tag="EFAGFIKM_04787"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34606"

/codon_start=1

/transl_table=11

/product="putative glutamine ABC transporter permease

protein GlnP"

/db_xref="COG:COG0765"

/translation="MDFSGAYAWPNLRFLQGFLLITLQVAGLSIIFSFLVLTGTIR

FTRIPFLSQIVAVIVDTIRNLPLLLIFFIHMVLPQLGIKMSVFWSTVVGSLFEGAM

IAEIVRSGLKSVERGQVEAARSSGLSYMQTLGGIIMPQALRRMSPPMVSQFISLLKDT

SLAIIISLPELMHNVQILGGQSFQDIIPALLAAVLYFVINYALSIVARRLEARMN"

CDS complement(5481114..5482469)

/locus_tag="EFAGFIKM_04788"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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PYHPAIFQVAAEMLQEAGVRLLLHSFVDEVVVVDDRVEAVRVTNKSGRKEFQANVTV

DASGDADLAYLAGASVAKGRDGDHQSQPMTMKFRMRGVDLGRVKQYMLEHPEDFYVKT

PFAELDSIPLTGVSQWKKAGVPINRDQVLFFTGPAEDEVLINCTRVQGLDATDA

EDLTSAEQEGRKQVLMIAEFLQRDVPGFERASISAVAPQIGIRESRRIIGHYALTQVD

VVAGRKFDDVIARSGYPIDIHDPGQGVAAFIIEGDGAYDIPYRCLISRNIRNLLAAG

RCISTTHEAHATTRLTPSCMATGEAAGTAAALTVKMKLDPVDLPIELLQAGLRHNGAA

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CDS complement(5482511..5483365)

/gene="araQ_29"
/locus_tag="EFAGFIKM_04789"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94530"
/codon_start=1
/transl_table=11
/product="L-arabinose transport system permease protein
AraQ"

/db_xref="COG:COG0395"
/translation="MKAMPSPSGRKIGSTLGTYLLLALISLIMIVPFIWMISTSFKEP
QSIFTYPPQWIPETFRFQNYIDVFQLIPFHRFYWNSIYISALVVLGTVFFASLAGYAF
AKIPFKGRNVVFLILLSAMMIPHEVTAIPMFLFMRQLGWIDTHLPLILLPIFGAGGVF
GIFVMRQFFITVPTLEEEAAMMDGCNRFRIYARIMLPIAKPGMATLTIFTFVTIWNEF
FDPLIFINSRDLMTLPLGLSLFTDEVGTAWQYLSATVMATLPLLIVFFLAQRRFIEG
VAMTGLKE"

CDS complement(5483349..5484263)

/gene="lacF_10"
/locus_tag="EFAGFIKM_04790"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P29823"
/codon_start=1
/transl_table=11
/product="Lactose transport system permease protein LacF"
/translation="MTHSRKRKRGGPLAREAQIAGWLFVSPMVLGFTLLLLFPMGLAL
YMSLTDWPLLGDHHFIGLENYRDIMTDAMFWKVLANTVYFTAGLVPLNIVLALLLALL
LSRNLRGIGIFRTAIFVPVMTSLIVWAIWVKLMYATESGLINQLLLMLGIKPAWLYN
PDLAMPAAIVTSVLKNVGLNMVLFIAAIQQVPRSLYEAATLDGAGRRGTFFHVTLPMI
TPTVFLTVVMTVIGSLKVFGQIYVMTQGGPSNSTKVLVYYIWEKAFKLFQFGYASALA
YVLFFIVLILTLLQWQLRKRWWVFNEGDA"

CDS complement(5484503..5485213)

/locus_tag="EFAGFIKM_04791"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGKFKELLEQKPLSLVVSLPENDIALARAAMEEGADALKVHYNV
GHRASGNHFGPLDMYAEVFRAIRSEFGGPLGVVPSGSIDGARREDVERLSGLGDFDYS
YAHHLPSFMLNDLGLDPTFAINEEYDASLVTSAAHFGFTALEASIVPGKEYGTPLSF
ADVLKYRRLLVLAQPLVLPVSQRKLPEDVRVLRDTGVKAIMLGAVVTGNTEEQLRRA
VNGFRNAVDSL NHPDYIS"

CDS complement(5485244..5486539)

/locus_tag="EFAGFIKM_04792"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKAGLILVFILMMASIACTSSNSNSESGSASGENGEVELKFM
MWGNQAHMDVYNKLIDDFTKENPGIKVTMESVPFAEYQQKISVLAAGGSLPD LAWVSE
RMVPQFKSNHILADVSEFKDDAQFKLDDYIPSTLDLFRDGD ELLGLPFSTPPVVMFY N
KTLFDQAGLTDPNTLATQGQWTWEQFEESAKAITSKDATNRVYGANFFRDWKTWAVLS
SYSWSNGSGPFDEGMTTFTWNDAYGVQTFELLERMMFTDESHPKAGEQVSFDAGNVGM
FFDNYSYVSKAREITDFEWSIAPMPSGSQGSVPMLGQAGYAMFDDSKHPEETKLLKY
FASEQGIQATATYFVPPRTSVLNSDAFILQPNNPSKEHIVQAVIDEMPKARLIPGHIR
WQDIDNAVLQGFDR LFAKTATAEDNLNQMQEEIQSVLQP"

CDS complement(5486643..5487410)

/locus_tag="EFAGFIKM_04793"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q5HJF7"
/codon_start=1
/transl_table=11
/product="putative response regulatory protein"
/db_xref="COG:COG4753"
/translation="MYKVLLVEDET VIRQGLRELIVQVSSQFQVTGEASSGTEALDFL
RCEVPDVLITDIRMREMDGLTLVSKARDMYPELLMLIISGYGEFEYARRAMEFGVLNY

LLKPIDRYELALCIQKIQLLLDRRYGISTLSIPEPSGKTEHAGGDTRKIIRDVKEHIK
QHPDGDRLRLQTIADLVNLNPTYLSQLFKNEIGINYSEYITEARMERAKWLLINTGLKI
YDVARLSGHQSPKHFMLVFKQQVGWTAGEYRDRFSIS"

CDS complement(5487416..5489239)

/locus_tag="EFAGFIKM_04794"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMDKVRIFFGKNVNLRTKLLLLFLALTLLPLSLQGVMNYKHFSQ

TMDRKTEQFTIELVRQINANLNRLLKDFERLSLLPLYDQMVLGILGKYNASMGSGAWA

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SNLNIEQDASLMIVDSKQRLLFERTSTGGMSAYDQLLMNGQLQNYVGNQKVVLAGQSY

LYVQHHSSYSGLSVISLTPIAVIQKESGEMLTFTIWFVAVLCMAAAILAVLLSYRITR

PLIRLKHHMIRVEQGDFSQRVAHFSSDEFGQISRGFNRMMEIHRLFNEVFLLGIQER

EAELSALQSQMNPFIYNTLESINMMAIRQKHAEVSDMVTALGKLLRYTIDKVDRMVP

LGEELAFVQSYVRIQQVRYDGKLEIYDIEEAITEYLIPKLVLQPLVENAVYHGIEGQ

ENGGVIWVSALKFDHELLISVRDNGKGMTQAKIDELNESISKQPSNEALRCHAGDSL

LNIAQRLRLIYEGGSLSIDGSPGQGLVVTISIQLLPKGD"

CDS complement(5489482..5489724)

/locus_tag="EFAGFIKM_04795"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNFLAMYPKMLYKEGVHAVSEPVQITDKIERNRQELSRLAENHG

MQDNQVLRQSMVLDELINENRFKYKSHLRNRQPIA"

CDS complement(5489861..5490130)

/locus_tag="EFAGFIKM_04796"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MKSKMISLVALICSLILFVIGFQFIAQSTDWGMDKAMLVLAEQ
NVKSDTSDIFGSFINSEIWSYKIEGILLIFLGMLMLYLANSLRSK"

CDS complement(5490302..5491201)

/locus_tag="EFAGFIKM_04797"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MIKSYTNECIKLIKHPFSIWATVIFLVFVIYTYLSVGSNFGNSF
QAFMNNSGYSLEQTYQFIRGSDTSSSSLSAMLFILSPKMAIAYSLASVNALGPVVISI
IGALIFGIEYRSFTLRQLWVQGLTRLEVLLTKVMAIFTFILLFMLLTMLVGIMFSYVT
PAVFNLPMDLVNTKIITIKDYTLQILGSIISLLLWGMFAGCITVLSKSLMAGIIVGFI
YPTIESSVFHSWFIGQYLPLFIQKSMLPILFRDTAYGGIVSFYDMPDIYSVTTSMLFT
LAYTMFFLLVTWIALKKQRTLMP"

CDS complement(5491194..5492093)

/gene="btuD_15"
/locus_tag="EFAGFIKM_04798"
/EC_number="7.6.2.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01005"
/codon_start=1
/transl_table=11

/product="Vitamin B12 import ATP-binding protein BtuD"
/translation="MNRILKVDNLKIKFKNDLILNNISLSLNAGDVYALVGINGSKGT
TLLSSLAGLLSPTSGNVFIEEKLSQFNQTSMSFQPTSFYAHLTGNDNVRLSPDPQRA
LKILKKLDLTPQIMKKKVKTLSFGQKQRLGIAIALSKNAKVYLLDEPTNGLDNYSYN
RLVEVIQDMSNQECCEFVIASHEWDVIEHCCNRLGMMINGRIEKELDISDYNNGLQPKL
IQIKVNAEFSTNELLELDGVLKANRLDRFSWKITLDKNCTFESFQDSLQKNVSINW
MSLNHVQEWESIYNQLVEGGNHD"

CDS complement(5492193..5492708)

/locus_tag="EFAGFIKM_04799"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKISFLKMLSVAVMSTGLAFGSVAPSFAAENVEIPDTSIIGSE

SYVAPVPGANNDGFSTFATISTHSWQKSYKNLYGITVATQEAFQWTWNDGKITNFGN

LWQNNSTAPLYGFKDEENKWNKYKTSTGQTNQGVLFESGIPTPWGHAGGSEFTSRILI

NVSSTGSSTAQ"

CDS complement(5493191..5493370)

/locus_tag="EFAGFIKM_04800"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRERSILKDQIEQGRQELSRLVDQYGIPSVKVLEQSMALDELIN

EYNRFTSGMNMNIKK"

CDS complement(5493850..5495208)

/locus_tag="EFAGFIKM_04801"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSNIRSYIESHLKNKGYKLQQFSEMADINVGTLSAIKGTRLMS

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KTLSKYDNLNAAVKFESYIDKLNEEVQLDAIKDLANVYNTIHLWDFKVDWARELERKA

EFQLKIQSRRRKSNNRRLTAYPLFTYAAYANLLISSVYDTRKEYDEAINYLQKYMELI

EIENPTEEDQKIIDLFFKKWGEGNQYAFRILLGQEEVIFPYLGYLENNPEEILTGLLNI

LEAANQYGFNIGHALKKFEYPINLFNTDFHNKGGYTDQMIDHGYRVFYELAKYQINQ

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CDS complement(5495239..5496609)
/locus_tag="EFAGFIKM_04802"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MELVPKIRVHIEKYMREQNLKLQHFSDITGINVGTL SAILKGNR
PMSMNQLNQITSMGLEKGYFYESYGVESFIESSPHWRRLEPYLYECAELCKLDCIQQ
VITHVTDDRSYIEELFDVAESFFARGLKEVALILYECVADSEKYQH SERLALCQYRIF
LLHKT LNKFN LNA AVKFEPFIEKLNEEVQLDAIKDLANLYGAINLWDKVFELANELI
QRTEFQVQLQSMRRNRKPRIASYPLFTYKAYANLLMANVSEERKQYMKALEYTDVYED
IMDGIKNPTEEEQELIDRFKGWAEGNRYLYKILSGDFEGLNRYLNYLDVNHAEILTAL
AYIIQAA NQYSFNIDHALNRFQNHIDQIKAARHVKG IYNEQASNFRYIRLFYELAKYR
LNQNQIEQGIEHLITSLERSSSCNEDLMCIKCIDLYGKYRDRASKTQEEQYTKLIDKL
SVPTFR"

CDS complement(5496768..5496899)
/locus_tag="EFAGFIKM_04803"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKKKIYYIILLSIMIINVSQ LANFNSDGIIQIMGITHGVGKL"

CDS complement(5496862..5498247)
/locus_tag="EFAGFIKM_04804"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MEPTTTIRSYIEDYIRKQGYTLQYFADISGVNAGTLSAIIKGTR
PIAMAQLDLITQGMKLEEGYFYEIYGAECFVESAPHWRRLEPFLQRCAELDKLECIHK
VIQEVTD DRSYISELFEMAEGMLERGQTKAARMLYECVAECEKYQH SERLALCQYRIF
TSLGQNQH DNLRAAVHFEPYINRLDEERQLDAIKDLANTYASLRYWEKVFNLAEEEL

QKTKILQSYTKKKIDKIDRLTAYPLFVYRAYSNLLKSSVCEKQGRYEEALVYTEFYAK
LANVSEPDEEDQIFIDNFAGWAEANTYLYKLMMGDHSVLPAYMEFIEENEEEILPAII
NILEAANKFDRNIDDILYKFSDRINSEINCLKGYTEQMKNEIYAAFLLESLYHLNRH
EYPEGLKQLIHCLRESVRFNNQTDIIHCVSLYEKYKNMGTEIEHQYKLIMMEVQKSY
EKKENLLYNFA"

CDS 5498512..5499636

/gene="limB"

/locus_tag="EFAGFIKM_04805"

/EC_number="1.14.13.107"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9EUT9"

/codon_start=1

/transl_table=11

/product="Limonene 1,2-monooxygenase"

/translation="MKFALFSLMMNLPNAVLTGEALTTQKFHNILEQAKLAERLGFDA

YGIGERHGAFLSSSPVVLTAIAAATTRIRLLTTVTLSILDPVRVAEDYATLDQLS

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GVTTWPRPLQQSIPIWHGSASSTVSTELAAKYGEPLFTSNSFHPQAKYKALIDHYRER

LDYYGHDPQQAVIGSGAGSLYLADTGEEAIRRYKPYEAFHATAAAQHNQSPFSDLED

NIARGPALIGSPEQVIEKILDYHAAYEHQVLSISVDGLTHSEQLEQVERFAKEVAPVL

RRELPSVWNEPPVLTQHSSVLSSNVTDWPTAISPIFQV"

CDS complement(5499737..5500315)

/locus_tag="EFAGFIKM_04806"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WMD1"

/codon_start=1

/transl_table=11

/product="putative HTH-type transcriptional regulator"

/translation="MTAKRGRPRNMQNAILTASYELLLEHGFVVTIEKIAERAQV

SKATYKWWPNKGAVIMDGYMSAATARLPVPDTGSVLEDIRIHASNLRFLTSREGKV

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PVFYRMLVTGEAMDDAFVDVMLRSLFEGIQSE"

CDS 5500596..5501807

/gene="sotB_4"

/locus_tag="EFAGFIKM_04807"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00517"

/codon_start=1

/transl_table=11

/product="sugar efflux transporter"

/translation="MMDMRQQVKKAPVPTWIIFFLLASACGLIVANLYYAQTVIGPISM
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 TAVVFLTASLFIGIGSVVAQILVPYATYLTSEEQRGRVVGNVMSGLLLGI MLARPVAS
 FITSLFGWQTVFVFSIAIVITLLMLLLSRALPARQPEPTLKYGQLIVSLGTLFRTMPLL
 RRRAFYQASLFGAFSLFWTTVPLRLANDFDMSQQGIAWFALAGVGGAIAAPIAGRLAD
 RGLTRILTGAAMVIAVASFGLAYVFQSHSTFALILLVIVAITLDMAVSGNLVLGQRII
 YSLGSEARGRVNGIFMSIFFVGGAGSSLGWSYANGGWSLTTLIGLIMPLLALVYYF
 TEKKA AVVSNG"

CDS complement(5501871..5502326)

/locus_tag="EFAGFIKM_04808"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGMFYTKYTEGEYSHMKRIAILDKNLEPGAAANVAALLMGQAA
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 TGQSLNNAFEQYAVEIASMELEATKVVGIVWGEDDQVRAATKKFSVMK"

CDS complement(5502278..5502841)

/locus_tag="EFAGFIKM_04809"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEIVKEKYAILGTLGDDEGFLTCSMHIAKKLGNSERIKPYPEFE"

AAAEDLRLGIISCLLVPGAYPKLNSFIMDSELAVSESFVEKIPALVLSGFHAVCPDQI
DIIYHHPATTYLLSELDTTYRENSTVSSNPEACRKVMHNTEKSIALTNQLCADHYGLV
TYKVLREGINMPWVCFTQNTQRVNTVI"

CDS 5503059..5504300

/gene="rizA"

/locus_tag="EFAGFIKM_04810"

/EC_number="6.3.2.48"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:B5UAT8"

/codon_start=1

/transl_table=11

/product="L-arginine-specific L-amino acid ligase"

/translation="MKTIVYISDFRLPTGLNFVKPLQKLADHKKILIIERHNLHHDEV

LRDFFDEIRYVDHLESVDAIREHMOVQIRESHSISALLTPGENAIEIGGQLRSEFGIPG

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SINTFKLSSMDELVHYLHHTRQAQQRDLLEEFIHGTEFHCDIVSKGKVVFASVSQYL

YNCLDIATKQKPPASITFPEGTKADFIHHIKELNEQVIAALGINQSVTHAELFLTPEG

EVVFGEIGARIGGSHVMPPCIKNTHGVDFFEAVTDLEVGIYEFKKQETSQKFTGMICF

PSRAGVIQHISGREYADIPGIVEFNVSQVVGQRAGDVNDTMTRSGYAIVEGDSFEEL

RQTLDDMYDRFKIEVTVAETV"

CDS 5504367..5505653

/locus_tag="EFAGFIKM_04811"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSLFKTYAGLSRDIYYLCLARTINSTGDFVFSLLTLVLTLMGM

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VGYLLIAVMFFISITRPAYNALIIQLCTEEKERKSAFSLMYLGANLGAIGPLVAGFF

IKDHVNIVFISIGTVFLISTFIIINQVKIGTRKELASTNSEHAGQQEQQRSSQPPSP

LFRLLLKNPLVAFFIVVSFLNYFIYMQYSFSLPLQMNHSFGENGAAYYGSVMTINAIS

VIIITTVILSATRKLTAALNSIATGALFYGIGFGALNLLGTFPHFSIVALSTVLWTIGE

ILVQTNINLYIASRVPDTHQGRFNGLLLFVGCLGYTLSPYLTGIFIKSMDMESVWIII

LAVSLFYALSMIILWYIEKSSTRKSEMNPDLHHSKI"

CDS complement(5505695..5506756)

/gene="nemA_2"

/locus_tag="EFAGFIKM_04812"

/EC_number="1.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77258"

/codon_start=1

/transl_table=11

/product="N-ethylmaleimide reductase"

/db_xref="COG:COG1902"

/translation="MDNLNTRSVLLSPVKIHQWQLRNRIVMAPLTRGFADDQEGNVTD
EMVAYYEQRARDGVGLIITEGINPNLAGKGTYGIPGLYTDEQTTSWKRVTDVHRHGG
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FQTAARNAVLAGFDGIELHAAHGYLIDQFINEKTNHRTDKYGGDTAGRLRFLRDIIVA
MKKEIPVDRISVRFSEKKDDDASYAWADKAGMIDAYLNLFRETGITLHPSTAQYTKA
WDGELTFHQRRSQWDGIIIGVGDLDVQTAEHAIGKGSIDLAAFGRPFIANPDLVQRL
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CDS 5506913..5507776

/gene="gltR_4"

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/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94501"

/codon_start=1

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/db_xref="COG:COG0583"

/translation="MELSDIDIVLAVARSGKISQAAKELNYAQSNVTTRIKKLEQEYQ
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SRFMEILNEYQITYPKVSISLVNATSPKVLRRKKIQDDEIDGAFISGACVKEGLKVEYE
MQDTVHIISKQMDTPPESLCQVSWVVFPEGCPYREMTTEFLQEEGLSARNIIEVSTME

NLLSCVESGIAFTIMPCSVIHKKPDDFSVFDLADRYHTTTTTFVRGEDRYVSSALDQF

MKLLNQKCITF"

CDS 5507840..5509423

/gene="rhaS_39"

/locus_tag="EFAGFIKM_04814"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MKLTNLIYRLIDARRVDNNAEQVSFSPRPHHTLLVVIKGSITVK

VEDKIISLCAPQVLSVPPSHTCIAITEVQPDFECVTLTYNVYNEELDGNMQRVIDPHL

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AVRQSQKYINTHYQDNFTREKLAEMAGLSVNRYSRLFKKMIGQGPIEYLNVRIREAG

DLLLASDNTIKQTARQVGYEDEYFSRKFKATTGLSPMVYIKKHSVTRIASLAHPYT

GHLLALGIEPYAALINPVHRTSYEFKNVIQVGRDQPDLELLMNAHPELIIGYEGTDYE

EPKKAELFRHIASTCTVSFAGDWRKQMYSIAQSVGKITAGEEWLERYDLSVKQKISSI

LHAMDDRPVAVAQYEDGKFRVYGNRNLGTVLYDDLQLSVPQALHRVSHSRLMSLEQLV

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HNLFLNRVSQLFLSQTSMH"

CDS 5509436..5510401

/gene="yfmC_2"

/locus_tag="EFAGFIKM_04815"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34348"

/codon_start=1

/transl_table=11

/product="Fe(3+)-citrate-binding protein YfmC"

/db_xref="COG:COG4594"

/translation="MDYDLECTYNYFDNDNQNLKGVYNVSLPNNQRFSTFFKSGRFL

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QAEPDLILASKTLNEANYEQLSKIAPTILFDNEEKGDWERFIETATVLGKEKEAQAVK
DAYDAKVTQTHDELAVKAKDETVAYMRVQDKQLQLIKPDDNFTLFGALGLTPASVDSV
DFQGSWNVAISEEILPELNPDRLFILRPGEENKVVLNNIMDTSI"

CDS 5510537..5511106

/gene="ydjA_4"

/locus_tag="EFAGFIKM_04816"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ACY1"

/codon_start=1

/transl_table=11

/product="Putative NAD(P)H nitroreductase YdjA"

/db_xref="COG:COG0778"

/translation="MKPKTSLRQTVIERRTIQEFNGLPIPLETIHEILED AIWAPFHS

KKEPWRFILFMNEGRIEFASAVLSTRNPEFIAKYGQQIRAA YCAQTPVHLVVVMTANL

PSKAWEEAFAATSALIQNIQLLAWEQHIGVVWKTSTFNENPLFCEAIGVTSEEKIVGT

LHMGYFNAEDQPM PKPRTPLPQLLHLIDH"

CDS complement(5511223..5513289)

/locus_tag="EFAGFIKM_04817"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGKRKGVGHKIKNMSLKIKLPFMISVLVVLVLLGATTTSYMISS

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KESIQGKSFISDAVVSKTGKKLIIVFSEPITDEEGNNLGV LAMSVDSSFFLGQLGDIK

INGQGRVEVLSRSGIIMYDSLDP SVVGKTL EEDKDAMGII EARATDKVKITSMDREDT

YYRINQIPGADLSVLIIDDYADIKRPIEDMQRQMVIVILIGIALAIGVGLLISRSITR

PIIRLSGLFQQLAQGNLTVKANGKYNSEFKDLAESFNGMVEQNRNLITDMNSSIHVLQ

ASTQELEETSRQTARSIDETSATSMGIAKAMEAQSEDTEQIAGKFNSFGDKVAAMNSS

AQDVKARADEIETVFHNGNEVVNELMRINEVNEREVEKISEITVKLQTSSGSISQITE

AISQIAKQTNLLALNASIEASRAGEHGRGFAVVAEEIRNLAEQSSRQSKEISSIEQN
LADVAENNQSVAEIHTISSRQDELVLQTRQAFDVILEKVTVINQQIATMAGQMQEMLQ
NKDDVLESAHSLSASGEQVSASVEEVATMMEQSSTVQQLANMVDTIDQLTQKLAESA
ARFKVE"

CDS complement(5513520..5514626)
/gene="ldh_2"
/locus_tag="EFAGFIKM_04818"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P13154"
/codon_start=1
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/translation="MSWFEAMEHHDYEELVLCQDRNSGLKAIHDTTLGPALGGTR
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AAKEAFGTDLLEGKTIQVQGVGNVAMHLCKYLYEEGAHLIVTDIHKDSVKQAVDRFGA
TAVDPADITSVECDIYAPCALGGTINDDTLRTLKAKVVAGCANNQLLETRHGDQLYDM
GIVYAPDYVINAGGVINIADELNGYNADRAWISKIGEIYSNLEKIFESSRTEGIATYVA
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CDS complement(5514914..5515540)
/gene="cdaS"
/locus_tag="EFAGFIKM_04819"
/EC_number="2.7.7.85"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:D5TM67"
/codon_start=1
/transl_table=11
/product="Diadenylate cyclase CdaS"
/translation="MTQQADCDSSSMRQKLKADLHRVAERMNLTLSQFDNDSACLLGQ
FAEIRAEIKQIEVLASSFYLD CYLSPFTEKFAELTSSVQHLSDRRYGALIVIEREIP
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KIGTRHRAALGLSELTDAAVVLVVSEETGQASFAVDGDLHPINVVETLP"

CDS complement(5515753..5517318)

/locus_tag="EFAGFIKM_04820"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKALWQHWIGAFILVFIMMATAALLGPGSQSPVQAAAPLTVSQAI

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LPDGTGKKVLFDNTHAQTAGAADWIIDGAFSDFANGLRNAGFAVDQLERSIPYTFGEQ

AITYNKLKDYHVFVIGEANVPFKATEQAALVQYVQNGGSIFFISDHYNADRKNRWD

SEVFNGYRRGAFLNPAKGMSSAEAEAPAMQSVTSSDWLATNFGVRFRYNALGDVNASD

IVAPAQSFGITAGVNSVAMHAGSTIAIDPNKAKGLVYVPSGVSKWGNVAVDQGVYNGG

GRAEGAYAAIAKVGAGKAAFIGDSSPVEDATPKYLREETGATKKTYDGFKEVDDATFL

VNTVKWLAVKESYTSIAQVPGTLTDTATSLPIEAPAASTEPQLEPWAAPAAGYKWYD

PTTFKTGSYGKAQ"

CDS 5517495..5517785

/locus_tag="EFAGFIKM_04821"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLVFLLLLLIVPLIMAYVALRSRMVRRLFHILALLCFYSAATV

IAGDVYATNAHMTTFTTEIHHFLLNGWFLYPSAYLGVIPIYVLWMSLFSEKS"

CDS 5517939..5518094

/locus_tag="EFAGFIKM_04822"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNTTLQKADLQLDDYLDLLNLATNLGDTRWQKEIRKLAYTYPA

VQCKQPQ"

CDS 5518369..5518929

/locus_tag="EFAGFIKM_04823"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMQLETDRLIIRDILETDWERIHAYTSMPEVTQHTAWGPNTTED

TRAYVQFVLDTQQAHPREGFELAICLKSDGTLGGVGIVHMEKTNAEIGYVLNPAYQG

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SFHDSVIYSILAKEYAGEQLQRNTKS"

CDS complement(5518971..5519666)

/locus_tag="EFAGFIKM_04824"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISBth8"

/codon_start=1

/transl_table=11

/product="IS3 family transposase ISBth8"

/translation="MMAIHFANREFGYPRMTTALWEAGLNVNHKKVWRIMRELSIQSV

IRKKRKKSSYTPSVIYPNRLKRQFHATAPQQKMVTDITYISDGSFAFVYLSVIQDLFNN

EIVAWQLSKRNDVQLVLDTVEQWTQKRDVSEAVLHSDQGFQYTSQAYNSRLEAFGVKG

SHSRKATCLDNACIESFFSHLKTEKLYLNQCNSEAEIRQAVEDYMYNRYRRFQAKLK

QRAPIEYRCALAA"

CDS complement(5519831..5520175)

/locus_tag="EFAGFIKM_04825"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MILGGDIFMAKKGQTFQTYTEEFKLNAVRSYVEGSSSYKVAER

EGIRNCSQLKVWVKWKNGEAFDERKNSVPNPLKGRPRTAFGSVEEERDYLQAQVDYL

KKRYPNLVKEKR"

CDS complement(5520399..5521175)

/gene="fnr_3"

/locus_tag="EFAGFIKM_04826"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P46908"

/codon_start=1

/transl_table=11

/product="Anaerobic regulatory protein"

/db_xref="COG:COG0664"

/translation="MGTVFVERTTQRAEQKQTEAGKMTRETGGILSFVTSEQWGLIEA
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 GIGGLNHSYSAEMAIEKGELAIISLSDLESILSKHGDALALKFLQWMALSQRITQSRFRD
 LLLYGKAGALASTLIRASNSYGRVTPDGIVLDMKLNHTDLAEMIGATRESVTRMLGAW
 KEQGTLDMMDGKLMIRDLAALRCMCGCPTFPSCPVELCRL"

CDS 5521552..5521983

/locus_tag="EFAGFIKM_04827"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHDELPSGIQEMIDGLRLNTSSDFCGLACLNGTMLRWKYTSGAS
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 QEGSVPGAVLLVGSRLPCTFSPDMIRQTEQIALHLQPHVYG"

CDS 5522199..5523809

/gene="rhaS_40"

/locus_tag="EFAGFIKM_04828"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MFVLTNASVIPWESTQHNSAISIKTPSLVTCTATVNYRYGNEHG"

VLHKGQLLFLHSQCSLELIHIPPSAFTLYHIGFQDYALTEESPDKR VYQLTSVHLPSH
GSKTGASPQVLRMLAI IQELSETRTGSAQTEEARSHYLLSELLELFKLAIKPSTEMVD
SIIREALRYINH HYDSHLTRKELARLTGFNASYFSRFFQKEVGRSFQAHLTRVRMDKT
KQYLLSTHATLNEIALLVGYS DGLYLSRKFKQFTGISPSEYRLQPRARRIATVQYTG D
LLALGVQPIAASFLPWAMSPLIQDELHDVLDLDQYGV EeilRTEPPDLITPDYLYYL
PHKLEQLEQIAPVMVLPWDKLNRL ETVQLIGRIIGREQAAEDWIRHYTALVSSGAERL
GAAIQPDETVGLYELWEDGTICIWNV TARAAYNVYYGLNLT PPPSILRDVLEPNNHQF
IQEDQLTEYAANHMFLVLSSHEGGLYHDAQVKLRERPHWNKIMNNGNSRIYPLKLEQF
WCNDALALEKQLQLMVDILIRENGEKNR"

CDS 5523927..5524925

/gene="yxeB_1"

/locus_tag="EFAGFIKM_04829"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54941"

/codon_start=1

/transl_table=11

/product="Iron(3+)-hydroxamate-binding protein YxeB"

/db_xref="COG:COG0614"

/translation="MTGVKSKWWTGLMFLVLVIGIIGCSSQVEETTENKPSSPVATEE
QPADSAAKTQIISTVNGDVEIPANPQRIVTQGYLADFLALGIKPVGAPDYELESPYVL
DLVEGVADIGRIDGGSVEKILSLEPD LIVTVGGDEKLNEQYRKIAPT LIIPYGTYDNV
HEEITAFGEILNKQKEAADWLSQFEVKVKSAKDSIQGLVQEGTTFSNFSLFGKDWYIN
GDGVNRGGQAIYQQLGLKAPDIVQKELIDQDKDTVTVSEEKLADYAGDYIFLDLSNGG
SLDETSPVWSSLD AVKNNRVFKLDGERFWPYDPLAVEAQVQEIANMIQERFSQTEH"

CDS 5525047..5525697

/gene="nreC"

/locus_tag="EFAGFIKM_04830"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7WZY4"

/codon_start=1

/transl_table=11

/product="Oxygen regulatory protein NreC"

/db_xref="COG:COG2197"

/translation="MIQLLVDDHVVVRSGLIALLLEGKNDIHIVGDAADGDEAIAKAQ
ELKPDVWLMDFSMPPGKDGLTATAELKKLMPDVSILILTMHDDEEYLFRAIHAGASGY
ILKSAPHEELLAAIRSVAEGSAYLYPSATKRLMSEYLDKAKQENAGPYDTLSEREKEI
LSWIAKGYANKEIAEHLIISVKTVESHSNLMKGLRLTRPELVKFAMKKGLLNFE"

CDS 5525690..5526805

/locus_tag="EFAGFIKM_04831"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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KNLWDTISSGKVWNGEILNRARDGSHYVWNTTIVPFLDNDGEPYQYLAVRSEVTKLKS
VEAELQKMMSQVMNIQEEERRRISRELHDGIGQSLFSLVIQMDRLLADQPHPGVEALR
KQVTGIMEDVRGMAWELRPSVLDDLGVVPAIRTYIENYTRHYGIEVDLECNLRKRLEM
NREIAIYRIIQEALTNVAKYADVAEARVTIEDAENMTMVIIEDQGAGFSEAIAGNGVG
LFSMEERARGAGGTLRVSSPEGEGTTVTL LLPKTAQV"

CDS 5527077..5527571

/gene="asnC"

/locus_tag="EFAGFIKM_04832"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ACI6"

/codon_start=1

/transl_table=11

/product="Regulatory protein AsnC"

/db_xref="COG:COG1522"

/translation="MSEKRSSKGGEIPQMYNLDEM DRKIIAALHHNSRISYTD LGTQI
GLSRVAVQARINALSEKGIIFRTVINPGKVGLQVSAFFNVDVEPPFLDEVAEKLDE
EPAVTSLYHMTGPSTLHMHGIFSDMEEMEQFLLEKLYKMPGIVKVESQLLLKRYKSRM
GMRL"

CDS 5527584..5528171

/locus_tag="EFAGFIKM_04833"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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IHPGIVIAVFLGYGVFHLDIVQRFKSKGKSDKGVS"

CDS 5528174..5528719

/gene="srpC"
/locus_tag="EFAGFIKM_04834"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q55027"
/codon_start=1
/transl_table=11
/product="putative chromate transport protein"
/db_xref="COG:COG2059"
/translation="MLQTTWELFWGFFVANILGYGGGPASIPLMQEEIVNHYQWMTTE
QFGDVLAIAGNALPGPIATKIAAFVGYHVAGWFGAFIASFATIVPSATALIILLRLLNK
HRTSPKVKGMTLLVQPVIAVLMILLTWEFGQLSTDSIGIWQTLIIAGISLWVMTKTKL
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CDS complement(5528877..5531249)

/locus_tag="EFAGFIKM_04835"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MLKPRLTKYVMMLVLMLSISNVGLAAAADKELSKIVVSKNEMS
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SDEKVATVVNGKVTGQSAGTAVITAKVGSQSVTVDVNVEVVKRVDVDKQQVNLLLNKS"

ESVKVTATYPDGTTKDVTDLAEWTSNEKVADVLKGEITGYSAGSAKITAKYGTKSVS
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ATVFKGQITAISAGSTTIKATYSGKTVEIAVDVDTARYLDIKDVNDKLAMSVTGDNKS
KTLVANAHEYIDASTENVTSKATWTSSNPDVVYVSNGDLIAYKSGTATITVAYGGKTVK
FTVNVDVADKYEMDKKKASVAVGGTTSKVLALYGETSKDVSEDATWSSSSDKIAEVD
SKGVITGVAIGKVTITAKIEGKTLTLPVEVGMAASGLEADVNFVVLSTKETQTILLTGT
DEDGNTLDVTSEATWKSSNARVADVKKGVITGNSSGKANITAEYGSKKVTIQVEVDVI
TRIEASEPVLSLKSGDTADLTVTAFLSDGSERDVTDKAEWKTNYSYKVAQVTKGKVKAT
GSGKAKITAKYGSKSVTIAVDVDTLKYLQTDKVTLTMPGKVTVAATATYADGSEAN
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CDS 5531461..5532066

/locus_tag="EFAGFIKM_04836"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVQPFDIYGYWEETYRSGETSGRGSYGVLAEFKAEVVNGLIQRE

GIHRVIEFGCGDGNQLQHMNYEDYLGVDVAASSVKRCASQFAKDSSKSFMLYTPGLWI

NRGFLQADLTVCLDVLYHITDEDFRNTLYDILHSSTAWVLYTRLKENGNGPIDTIQ

DRNLFEYLFDYPDFKVEIIPQRYPDQSSADVFILRRTPSK"

CDS complement(5532451..5533587)

/gene="ugt_3"

/locus_tag="EFAGFIKM_04837"

/EC_number="3.2.1.179"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9RC92"

/codon_start=1

/transl_table=11

/product="Unsaturated glucuronyl hydrolase"

/translation="MNTSTSVKWLEEAQQGATKTIRNAKRIKDTFPHTAPQGTYDRN

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SMMNLPLLYWASEQSGDPRFRWLAEAHADTVAREFIRADGSICHVVEFDPHTGQKLRE
HGGQGHAPGSAWARGTAWALHGFALSFRTYGEARYLETAERAADFFLAMLGEEIVPMW
DFRAPAEHQVAWDSSAAAIAASGLLELAKLSPREETYAAAGERIVRGLHEHYSSGDSA
AEEGLIMQGTVHYPEGRGLNVPIIYGDYFYMEALAKLRGHAGLF"

CDS complement(5533777..5535744)

/locus_tag="EFAGFIKM_04838"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKYTSASTYPWKDELERYRTLAEQAGRPPADGWNRRERKLALVE

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MNNPNRMINWNAIMISGEYLRWHEQLASEDTTWMDRYLEAYHVPRFTALGLYQDGPLD

RPNCPFSYDIATRYHLGVMLEAGYEGATADRLREQLRDGAFSSLLSLPLGEIPPRGR

SSQHQWNEAAAAYVCSTHATQALEAGDPMAGAFARAANRCFAAVERWKMDDGRLKIV

RNEYAPEDRHGYEITYNHTCYNLWTAALAHACLSDPGDDVSEVYLPSELGSRVLQTD

GWFETVIASVPGQQLVLHTAMNDPYTIPGLVRIQQTGLPGLIGPSAASHVQAGFTEFA

EGAVRPLSYCPAWKTPDGVVHSLAEGIPSGGAYDRDVGLDPAQGGGSIVYEKVDHDTR

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CDS complement(5535737..5537728)

/locus_tag="EFAGFIKM_04839"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEDSIHEVENENINQRGTESRALSSLSADRILLEKLSRPELATLY

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RLDRLVIERIRSEAERRIFIPLYREQRKFHWQTADHNWSAVCGGCCGMAALLLLEDEF

TLQESISHTVSCMNAFLSGYGEDGGCAEGIGYWVYGFGYFTYYAEMLRQYSEGELDLL
TGSKITAIAAFPLRVHLSGGTFVNYSDSAEEIPPGLLSLLASRVGLQIDLPLHIPL
LTDDSCHRWAHLLRNVMWSDPPVYGDEGASGQAERGFIFQNLGWMIAKGLFDSPDTKH
ANGAPLHVAISIKGGHNDEPHNHNDLGQFIIHCGGENILCDPGAGLYTQAYFAPGREQ
LFHISSSGHNVPLIEGQEQCSGRQAQAHVLEAKLAEGGCELNATMDLTSAYSGAASLA
RYTRQFHWKMASGGSRDRAELRLTDRFQWKS RMVSSAERFSSVDDSDAGCSSVVERWM
SRVQPEVVKSGNLRWQGVHGTVMHTYDANQWQILTEKLDTVHDNVPVTFYRTSLSWT
GVIDETDVRIESSNPLETVCEVRFIIEPKMGETEVSMRE"

CDS complement(5538033..5538689)

/gene="axe2_2"

/locus_tag="EFAGFIKM_04840"

/EC_number="3.1.1.72"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q09LX1"

/codon_start=1

/transl_table=11

/product="Acetylxylan esterase"

/translation="MSTSPSVILFQGDSITDGGRSRNDDPNHFLGHGYAYLISSKLGM

ELAGKQKTFYNRGISGDRASDLYARWNEDTISLKPDLISILIGVNDAWRTMNGEPSGV

TDRFGRAYRHLLLEETREVMPTGLILMEPFILRTGATAEKWEAWEEYIGQYQKLAQGL

AEEFGAVWVPLQQTENDALKQADAAYWLWDGVHPTAAGHELIARQWLSVQNSPLGIV

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CDS complement(5538823..5539152)

/locus_tag="EFAGFIKM_04841"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEVRWDVFWIIMGSALLTFIPRVLPMLFSKIQIPMWLLRWLEY

VPVAVMAALIGQELFMSDNQLVPITHNAALWASLPTIAVAIWTRSLLGTVLVGIVAMM

ILRYWIG"

CDS complement(5539143..5539949)

/locus_tag="EFAGFIKM_04842"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDLHPYISVYGDRNWRGVVRQLDQSTLQISGQENMEEVRDQATF
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GSAIAIMFTIFFVNLRHLLLSAAVSPYFRHLTPLKNMWIGSLLTDESFGVAMTRAIGR
ERLSERWMHGLNITAYLNWFVANMAGAYFGRWITNPERLGLDYALPAMFIGLVVLQLV
HRKNKKIHISVAIIAVVCVIFASMASLGSM SVIVA AVIAATMGVFMERWK"

CDS 5540294..5542294

/gene="mcpB_5"
/locus_tag="EFAGFIKM_04843"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39215"
/codon_start=1
/transl_table=11
/product="Methyl-accepting chemotaxis protein McpB"
/db_xref="COG:COG0840"
/translation="MKKNRKQGVKRTMQMREKLILSFAIVLLIPTISLGIISFQTADA
KVEEKMYENAISSVTVLNQTIDQIIGATRKNVDFLASQLDAGNVGPNQGDETD TIRTL
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PYLSSNTGNVVASVAQTSADGHGVVSVLSLEALSKTVNSTKIGEEKGYIYIIDNANKI
IVHPTKEPGTEGTMAPYKDIFAQKNGSLTYTLNGNQEHAFFSTNETTGWTVVGVIDSG
EVTASVRPILYTTLIVVAIAIAVSSIIIFWIVQSITKPLNRLVKASDEISNGNLTIEV
AVLGQDEFGLSTSFNKMSSESLRTVIQDVRHTADELTASSTQLAVNSSETTKATEQVA
LITEESAAGLEKQTSSLKHTALQMNELAGGVGQVTNSTQQVSEAMQASELADKGNAT
MQTAVSEMSSVS RFVQGMADTAGRLEQHSTSIGEMSVITDIAAQTNLLALNASIEAA
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CDS complement(5542488..5543684)

/locus_tag="EFAGFIKM_04844"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKSSEPWLQTASLEEIKHGYMEEGPAYICVCCGYRTEAGIIYPE
DGVLYEAARYMRVHIEKVHGSVFYLLLEQDKSVTGLSDVQRGLLSQFYEGKKDAEVQK
TLGIGSASTIRNHRFVLKEKERQAKIFLALMELLKSKDTQAPAEWVAPVTRHEHTIHP
NSFDITEQDREKVLNKYFPEGTVGRLLTFHMQQKHKYIVLTEIAKRFETERKYSEKQV
NELLKEVHDDYVEIRRYLIDYGLLEREPDGSQYWLGSHTDQQSAKVGKQERKEKGEQE
KMNRRKELQEQAKEVKTEAGVYQIRNERNKGKVIDSTLNLKTINGQRFMLQMGSHLNR
RLQAEWNEYGENAFVIEVLETLKQDDNPYNPKDALAKCLNRWFEQLEPYGDQGYHGD
IKQSAE"

CDS complement(5543903..5545876)

/gene="mcpB_6"
/locus_tag="EFAGFIKM_04845"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39215"
/codon_start=1
/transl_table=11
/product="Methyl-accepting chemotaxis protein McpB"
/db_xref="COG:COG0840"
/translation="MKKRIRNWFTLTVKKRLIAALLLFLIVPSITVGWLSYQKAADQV
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WVVTAAVKLADGKGVFGANVSLNHLKESVDQIRIGKEGKLYMLDNGGKFLFHYNIESG
TQSDEAYINEMYTKESGTVKYTYDGHEVEAVYFTNPVTGWKIVGEMVPSEATETVMPI
LIRSITIVASALVIGLILLVFIIRSIHRPLLQTLQAASKVSAGDLTVRVGLQRKDEFG
LLGESFDTMTTSLRNVLGEVHDTSSQLAASSEELMASSEQTSKATEQVAELMQDAAAG
TTLQNNSLAATGQLVGEMSIGVKEISSAEDTARIALDASTKSEAGMVTVEEAVTHIQ
QVNDESKAMSVVIEDLRAKNEEILVIVAEITAIKQTNILALNASIEASRAGEQGRGF
AVVANEVKTLAHSSGASAERINVLMEHMQEKTNAVQSTFARTGEGMVKSSQMVTEAGE"

AFNNIRTAVQLVAAQAGEVSAASRQIDGGMSHINKAVSDTMVLSDRIASGTEDGSAAA
QEQLATMEEVAASSAALSMAEDLQSMIERFKL"

CDS 5546144..5547544

/gene="dap_4"

/locus_tag="EFAGFIKM_04846"

/EC_number="3.4.11.19"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01960"

/codon_start=1

/transl_table=11

/product="D-aminopeptidase"

/translation="MFRILLALILCAGPILGQAGITASAAQATQAVHIEVNGEQQSWK

NTPLIIKGSTFVPLRDVVTSVKGTCLKWDNRKTATITVGRDKLIHQAGSNSIKVKNKVD

LATGVNSRTVNGTLMVPVRAMANAIAKADIKVQRTATGQMSVNMFTDQVSLLNSEVASV

DTYLREINYPGMALIARDGEVLLKQGYGLADEQTLNRPDQKTRIASLSKSFTAASILS

LVEDGKINVQDPISKYISGIPKGDQITLHMLLSQTSGLPSAFGRGEGTSMEETVEEIR

HKTLKFEPGSAYLYSNSGYVLLAYVVEQVSGMSYADYVQQTILKPLGMKNSGEASRKV

HTISGFVQEDNAWVTAPYYVSQSGSGTIYSTVDDMLKWDRALYTDKILSQDTIEQMYE

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LLDEVEAQAKALLQ"

CDS complement(5547731..5549431)

/gene="nagZ_4"

/locus_tag="EFAGFIKM_04847"

/EC_number="3.2.1.52"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40406"

/codon_start=1

/transl_table=11

/product="Beta-hexosaminidase"

/db_xref="COG:COG1472"

/translation="MSGPKELYQSRLKQMTLREKVGQMLLCGFHGTAAAGDVESFLRK

YPIGGVIYFARNVESPEQVERLSSGLQQIAKSSGNVPLWISIDQEGGMVARITEGITL

MPGPMAIAAAGSIDDAYQAAYISGLELKSMGINMNFAPVLDVNNNAANPVIGVRSFGE
SPQSVAEYGAKTIAGIQDAGIAATAKHFPBGHGD TDTDSHLDLPIITHDRERVERLELI
PFRAAIAEGVDAMMSAHYFPALEPERLPVTL SQTVLSGLLRQELGYEGMIVTDCMEM
DAIAVNYGTVDAAVMAVEAGADLVLSHTAKLQAEAFEALLAAVRSGQISERRIDESV
NRLLMYKAKRGLLESETGGAGDEKVNIVVSNASLPKASNAPALSSGSERNSSLHQEVA
RRISENSITLVRDQLNMLPLKPERTLVITVATSVTTIADEQLTQTFTLGSALSTYGLD
VVDLTVTPEEVAIRSARLLQAAEADDIRQIVVGTYNAGSPSGDPQCRLIGWIQQLGKP
LAVVALRSPYDLLALPDAQVYVAAYESRPLAVDSVAQALMGCIPFAGKLPVTLKQTDD
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CDS complement(5549463..5550659)

/locus_tag="EFAGFIKM_04848"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGQLNGTEQIPAVKTGVDLLSRGLSHPWITGNRIGLITNPTGIT

AD FVSTIDVCAGLANTEL T ALYACEHGLYGELQAGVRFGDMLHPRLDIPVFSLYGDYK

KPTPAMLAGVDTVLFDIQDVGIRYYTYASTLFHMMDACAGAGKRMLILDRPNPLGGNV

VEGGVLNAGYESLVGAWRVPVRTGLTVGELALMVNSEMDVPCELDVVSMEGWQRSMEF

ADCGLPWMLPSPNMPTLDSVRVYAGTCLFEGTNVSEGRGTTRPFEWVGAPWVEGERLA

ERFGEYKLEGVHVHPVYMSPTFSKHAGELCGGVRI FVTDSRKFRAVETGLVLLHELVS

LYPEQFCWLEPPEPGSRYFIDLLAGGKEVRETIHDRAEFVRLMEAWDVQAAEWKERRK

PFLLYQ"

CDS complement(5550659..5551369)

/locus_tag="EFAGFIKM_04849"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRKLSEVLIKSGAEIYRDIIPVALYSVSSIVLVPILMFAPLPI

AVLLLALIYMPILFGVCYAVHHRLEKQRRNGLKDIWAGTLKGII PGGS LGVLF AVL G

FILWSTWWYYGGQG GITGTAVSAFQTFVLMALMSQFYTWQLVLQKNMGIVQAMGESV

KLFFRHPGYTMGACFQAMCLTALLMLTVVGFGALFGGMFAIQHKVALNVLEPEEEPV
VTGGNDHQHTGWISQGNV"

CDS complement(5551418..5552527)

/gene="msmX_1"

/locus_tag="EFAGFIKM_04850"

/EC_number="7.5.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94360"

/codon_start=1

/transl_table=11

/product="Oligosaccharides import ATP-binding protein

MsmX"

/db_xref="COG:COG3839"

/translation="MARVEFRQVRKEFKDDHKGTFTAVAGSDFVIEDKEFVVVVGPSG

CGKTTSLRMIAGLEKQTSGDIVIGDRLVNDLHPKDRDIAMVFQDYALPHMTIRENLS

FGLKNLKKPKSYIDEQVQNAASILGLEAMLERKPRELSGGQRQRVAVGRAIVRDPQVF

LFDEPLSNLDAKLRVQMRVELGELHKRLGATIVVTHDQVEAMTLGERIVVMNHGDIQ

QVASPKELYASPRNMFVAGFIGSPAMNFI DARIEGTQVVVDGASFTLPEDVLARLQSH

QGKPVIMGLRPEHIFGDDVAPNIPTDHMLQARVQVVEHLGSENLVYFHSGARTVTAKV

HPETHAYVGMDKNFVLDLRKAHFFDPETELAIGRE"

CDS complement(5552571..5553404)

/gene="araQ_30"

/locus_tag="EFAGFIKM_04851"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MKSTQKKILLVVASILLVWVALVTVIPMYWMLVGSVQDSAMSAS

FKPQMIPEQLSLSPYERFFAKTDAWRWLYNSLLISIILTVTNVFFASLAGYAFKLF

PGSQAVFWTLLGTMMIPAQVTLIPLYILMVNVFDLGDYTAIILPAAVSVGNIFLMKQ
FMSTLPTSLIHAARIDACSEFGIFWKVILPMAKPGIAVLAIFTFVASWNEFFWPFLIT
NSNEMRTIQVGLASFVFAESTDFGAMMAGATIGALPMIILFFSLQRYFLQGITIGAVK
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CDS complement(5553443..5554366)

/gene="lacF_11"

/locus_tag="EFAGFIKM_04852"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29823"

/codon_start=1

/transl_table=11

/product="Lactose transport system permease protein LacF"

/translation="MQTALAPKPSVPRTSRVARFWRDYGWAYLFILAPVLLFLIFTLY

PVLTALVMSFQKYNIMNSTWWGLDNYERLVKDETFWKSINKTVIFTVGTVPVNILITF

VLSYFIYQMKSKWQTFKATMYLPAVASGVTISIVWLAIFDPTDSGLLNRFGLFGLD

PVIWLGQSGTALFSLILMNWLGSHGAGIILYAAMGGIPKSLYEAADIDHASGWTQFS

KITWPLLKPTTLYLLVTGVITSFQVFISVYLMTQGGPNFATTTIAYLIYETAFKFYEF

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CDS complement(5554422..5555774)

/locus_tag="EFAGFIKM_04853"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKKGLVWTMLLMVWVTACGNSGGAASDDPNADDTVTWVWTPV

HGTYEDELKDLISDFNKEHPNITVKTEMLSWAEGPKKFDVALNAGNPPDLYFHSDGT

YVNTGLALELDSYLTPEIKDDYLPGLDLGQIQGKQYGLPLYQFQWAWGGNKRILEEA

GIDWKSIIQQNGWTWSEFNDAALKTKLDGGAKQYALVTDGTSLDFIEMLSRNNGMID

VLDKDGTFQWNDGRILDTLSFIKNLMDQGYMPKETAALAPAKRTDMFYAGETAIISKA

IPYYDVMIQNRNKIDDDGKVQGEKIDFVLLPVPHNDDQPAATTMGGEQYVAFKQKKDK

GEQHAKNTFLVMEALSGAKAGNSANELALPFVRQSQVDLFKGKELGQPDNLAAAKVMA

ENIAMPVVLELDIDKASQQKQFKEQVVKPNIQVLFSGEKSPEQIAEDFKSKGQQMFGQ

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CDS 5556131..5557093

/gene="murK"

/locus_tag="EFAGFIKM_04854"

/EC_number="2.7.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q97ML3"

/codon_start=1

/transl_table=11

/product="N-acetylmuramic acid/N-acetylglucosamine kinase"

/db_xref="COG:COG2971"

/translation="MRVYGGIDGGGTNTDAAIISSEGEILARLSGGPTNPHSVSTEQA
ISELQRVLEQLFNLISDLSTNCEGICLMSGVDTIQERQLIAEAVNNYMKSRNRQASE
GCPIWVWSEGEIALMASLGHTHGVLCSGTGSIVYGFTREGERYRAGGWGHLLGDEGS
GYRIGQRALQVVMQSYDGVLPPTCLTPLLLKKLNLRDISELKTRVYQTDWGKTETASI
ARLAIEAAELGDEAARALIIDEASQLADTAKALIARHPEFASTPVVLSGSMFRYAALF
RSTFIQKLSEYEELDLVYREDAPAPAVGAAQLARRRCSLNEF"

CDS 5557116..5558021

/gene="murQ"

/locus_tag="EFAGFIKM_04855"

/EC_number="4.2.1.126"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P44862"

/codon_start=1

/transl_table=11

/product="N-acetylmuramic acid 6-phosphate etherase"

/db_xref="COG:COG2103"

/translation="MNHMLNSLVTEQPNPLTDHIDELPSAEIMELINKEDQRIELIQ
PLIPVVAQAADRILEAFQSGGRLFYVGAGTSGRLGILDASECPPTYGTPPSMVQGIIA
GGFRAVKDPVEGAEDNEELGAADLDEHGLDKNDVVVGIAASGRTPYVLGAMRHAKEIG
ATVISLSNNSGTPMTLLADVSIEAVVGPEVVMGSTRMKAGSAQKMILNMLTTTAMIRL
GKVYRNFMVLDLNPSNEKLVHRAKRMihLATGANEEDIEEAFNGADGHVKTAVMLMAG

VDATEAQHRLDLADGFVRSIAGPS"

CDS complement(5558170..5559018)

/gene="ybbH_3"

/locus_tag="EFAGFIKM_04856"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q45581"

/codon_start=1

/transl_table=11

/product="putative HTH-type transcriptional regulator

YbbH"

/db_xref="COG:COG1737"

/translation="MEGMKGGLVRLRALMDDLTPSERKIGAYILDHPQETVQSSVAQL

SERSGGSPAIIRLCKSLGVTGFQELKLKIAGDLQTSEPYQYTEIRPQDSMESIIQHV

SANNIQSVKDTVHILDPRLVEKAVDVLHQANRIFYGVGASNLIALDAHYKFMIRINRT

SFSFADPHMQISSATTLREDDAVVCISYSGETSNVISCLKHAHDGGAATISITKWGSN

TLSSMADVPLMITSTESDIRSGATSSRIAQLNVIDILYLAIASRDYNQSVEYLEKSRQ

AILEHK"

CDS complement(5559135..5560364)

/gene="anmK"

/locus_tag="EFAGFIKM_04857"

/EC_number="2.7.1.170"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8EHB5"

/codon_start=1

/transl_table=11

/product="Anhydro-N-acetylmuramic acid kinase"

/db_xref="COG:COG2377"

/translation="MDTGSYPMWEKYRLKQEHLVIGLMSGTSLDGTDAALVRIQTDMS

GALQQIELVDFVCVPYSNGLRDVLIRLCSPGTARVDELTAAHFGVSEWYAHSVTELIQ

SAGISTQQVDVISMHGQTVWHAPVATSFPGPTGASIDVVSTLQIGECAVVRERTGLPV

IGNLRARDMAAGGEGAPLTPYADALMFGSPTEGRLVQNIGGIGNVTLPSESFTEGIS

AFDTGPGNMVMDAIVRQATDGRQHYDPNGSIAAQGKVDQGLVDLCLEDEYFKRLPPKS

TGREVYGAAYAVRLMEMAAERSLSLEDTLATATCLTAETIVRAVKDFILPKAQISAML
ACGGGTSNATLMEMIRQLRPEDIRLERTADYGIPDDAREAIGFALLGHEALMGRNTL
PAVTGAKYAVISGNLTL"

CDS 5560647..5562059

/locus_tag="EFAGFIKM_04858"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKTILLFLSLFLLVLLPNQGNAAASTKIFMDGEELVLPSPDV

QVTIINKNVMIPIRVVAENLKFVDWNQQAHTVKIQDQQTISLTVDQKQAMVADKQV

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SSSTAQVTDIQFANNQLVLSTDGAVQPVVTLKYPDRLVVDLPGATFGDISQPLDQGL

NGKLDVSGYPNVTEVRYSLFKREPAQVRIVVELNNVKNVQYSHNVIADKLIVDLNVAG

DNVTPAPVTPVGDSGRKVVIDPGHGGSDPGTISITNKPEKEYNLIAHKVQALLNE

PNIELVMTREGDTPTRPERVQLANQLNADVFSIHGNSVKSAPQATGTETYYYQRSN

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VVQMKAQAIAADGIKEYLGL"

CDS 5562085..5562645

/locus_tag="EFAGFIKM_04859"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKKLGCALILSCLILIGVGCVQKPVSQSGSNEPAVQGGQAQAP

NPSETEVDLGMTNTQVVDVYLADSQVLELEKTEQEIEYKDDSEKYEKTFALQTNTDS

ELVSLWEQVELLSIQYAEGTVTLDVHIPAEANLGTSGELLALEALTTMFQFDELNSL

DILVDGEAVDSLGMGHSELEHPIHREP"

CDS complement(5562726..5564342)

/locus_tag="EFAGFIKM_04860"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MIKLNWGGAGEHGRSAYLLSGSNVRLLLDCGVKKEGTGEYPLI
DPKIVPQLDAVLLSHAHEDHSVAIPLLYKRGYQGEVWTTRETRAQLRITYFANWCRFVE
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GKRIFYSGDYTSESMLLQEDCPAEAFWQTSMLRENPVSDAPSSEQWGAEELIVMNSGK
KAGEFITSQDQTSVASEASSRTLVAIMEIPMKQGNFTSNGADRAVRANIANIANIANIA
DVAGAAPISSVGLVDLAIVDAAYGTDQDAQADKLEQLERAIRQTIAQGGKVLLPMPVV
GRGQEILWAQQQFPAVPIVVEQGLVDGMKQLMHVPYWLREKGEHVIGSSLKDEIDCF
LTGRGWDLPNTNTQEREQLLEHHAASLWFIPDGM MQSSLARWYYSQLSDREENLILLTG
HVAHGT FADKLLRVPDKYGVCDVRKIRYKVHQGWKDVERMLHQIPARHTVLVHAYRAE
TDRLKEGLLRNSPSPGTVIHSLSAGDELYV"

CDS complement(5564339..5566024)

/locus_tag="EFAGFIKM_04861"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKPVGMDNNRIFRRVGVILALFLTISIGVPLLLIFWQSVYPDG
QWDWVAPIRTITGHHLSGVLLNSVWLGCVVAVTTLLALPLAWMMAKTRMGEHRWVDV
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LYLLLRDALIRIGGNLEEAGAVHGARAGYRFRRIILPLLSSYGMGIMLVFKTIAEF
GTPATFGRKIGYYVMTSEIHKYISSWPIDFGKATSLASVLLSVCLVMWYMQSAMS RKF
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FDNLTL DHYKELLSWGSVSMKAIGNSLGLSLAASTVAVIIGTG FALAIGRSSSFMQRV
IDLFSLLPNTVPGIVMVVGLILFWNSPWMPVTLYNTYGMVVLTYVVLFLPYTVQYVKS
SFTQIDGTLFQAGQVFGGKPLYILRRILPLILPGMLAGWIMTFTIATRELVGSLIL
PPSMQTSATYIFAQFEQQVSLGMAMAVTVGMTVLMLLGIELLNSKRKWNAS"

CDS complement(5566218..5567291)

/locus_tag="EFAGFIKM_04862"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MLGMNTRKKSVMLLLTAVMSISLFGCSTGNSTTGNAAQPAGEGN
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IVYNTKLVSTPPTSWAELATPAWKDAVNIPDPTLSGSALDFITGYLSANGEKGWDLLS
AYKANGVAMAGANQEALDPVITGAKSIVAAGVDY MAYSSKAKGEPLDIVYPEEGTVIS
PRPAAILKSSPNVENAKAFIDYLLSDEAQKL VADAYLIPGRE DIEATNRANVKDIPQL
KVDWNWMSEHGEETAARFSETFK"

CDS complement(5567362..5568384)

/gene="btuD_16"
/locus_tag="EFAGFIKM_04863"
/EC_number="7.6.2.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01005"
/codon_start=1
/transl_table=11
/product="Vitamin B12 import ATP-binding protein BtuD"
/translation="MLMKLEMTGIQKSFNQTPALLPTDLTLEHGKFTTLLGPSGCGKT
TLLRMLAGLEQPDAGEIRADGQCIYSAKRIDIPTHKRNLGMVVFQDFALWPHMTVYEN
VAFGLKAGKQKSDLRQKVNEALGMVRLQGMEDRYPHQLSGGQQQRVAFARAVAVRPGV
ILFDEPLSALDAVLREEMRIEMMSLVRDIGLTALYVTHDQIEAMSMSDEIVVMQKGRI
LQKGSPETIYSAPSDPYVASFIGKSNWLTPNQSMVRPEHVTWNKTGHDDLCYPGTVLS
VSYVGERYEV RVQMEGLGVWTAYMNQRARVGERVQLYVTPERICRMDGYDHPSVKQNE
AIAVAY"

CDS 5568746..5569654

/gene="cmpR_6"
/locus_tag="EFAGFIKM_04864"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q55459"
/codon_start=1
/transl_table=11

/product="HTH-type transcriptional activator CmpR"
/translation="MNLIKLQIVELIDKHHHMTSVAELLGKQPTVTFHMKSL EEEMG
VRLFESRSGKTFLTEAGQALLHYSVKINALTQEARRVVKEYDSL YRGT LHIGASYVPA
TYLLPTILNTFSQEFPGIRIVLSVKPSPVIREMLIRHQIDLGVISSEPFVGPALQAET
LCEDDLVLICSPQHGLAQKDTLIPDHIAQIPFALHG NESSTRRLTNQWLAQHDIRLRS
TVEMDSLEAIKQLVLIGGHVSFMSRMAVQWEEQHGLIQVLP IPGEQAPRHIYTVHNKD
RHPSVQVNRKF EVLREVSHGFPIFHG"

CDS 5569795..5570661

/locus_tag="EFAGFIKM_04865"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVLKKWKKV TASLMLSIVTLGSGMTFLGAPQASAAANAVPAYEV
KFLAKPELVLNTDGT PRSEVIQTLGLSSTPKNINVEYFDTNALGLDQQGWNVRFRKKD
DKNNYELTYKKRYPVINGDINAALT LANQEGFDKSDDN YEAEIDWGYGKQTL SFSNTK
KVDTQATGVQLPSQQEALNMLLDKLPGLKNWTSSNWGKQQLTQSRAYGPITFQRYEG
TWNGQELTLEVWPIRDAAGTG IENIVEVSFKTDDTVAVSGLRTQLLQ LLENNNNWLIPA
DGLKTQTILERY"

CDS complement(5570912..5571337)

/locus_tag="EFAGFIKM_04866"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MWFILGFILVSIFGIRTRSRSNKLKQQFGSRLHAVGIHQSGLP
QVAEGRRVDVLIGNGNLYIQSGQQTFELSLRKIGSAGYPKRTGSSNSRNYLVIHYEMN
GRVRPIVLRFMKPAHAKAFLWEIEGQLFTRNSSDGIIRL"

CDS 5571484..5573166

/gene="btr_6"
/locus_tag="EFAGFIKM_04867"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40408"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator Btr"

/db_xref="COG:COG0614"

/translation="MTLQVFPLISNGDHTRDLYARFKTSEVLDQASFLPPFVLTDShL
LLICTGGEANIRIGHRQNHATLGKMYLILPGTAIEYTTDEVHPLQGIAIYFDMLKPIS
DINKTISGSTVMEVYQKGLLRSSYADELPHELFQECTKIASQLHECISVPQENRPFRI
QTLMHELLTHVYAPPKESAIGDSEHTSALDQTLELIELGYAEHLSREVLAVAGMSVW
HYSRVFKNRTGISPMYVNSIRMDRAKEMLLVPGQTIKHASQVGFQDEFYFSRKFKK
YVGVSPSTYQRQKRSKIAALSFGTTGHLLALQIIPHAALIDNRRDQHGNLFFSNIPYH
LGRSKRMNPHIWQTNVELLMQASPDILCNEYEAHTLKRTLQRIAPTIVIPWKGLSWR
EHFVHVASIVGQQQEAQQWLEQYDDKVTHAKEMLSHLIGKDTVSIHIMMGHLLIYGR
RNGGAVLYNDLGVSPSYDLLPGQVYRALDEQELPQMVGDRMLLIVDQDSESQQRWHKL
KHTQLWQHLMPVQNQHVVYLLDEMPWLDYSPYAHDQIIDETLKLFGSTQHINP"

CDS 5573264..5574310

/gene="yfiY_7"

/locus_tag="EFAGFIKM_04868"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31567"

/codon_start=1

/transl_table=11

/product="putative siderophore-binding lipoprotein YfiY"

/db_xref="COG:COG0614"

/translation="MYKQHYVKITGILFILAMLLVACGQTPASTSQPSTDGVKSAAGT
DGDSSTESATKTVESASGSKEIPAHPERIVSINMEDILLSLEVPLVLATPIGRQDYLN
EQLEAQGVTVEPINESVNFEAVVSANPDIIANAGLDAKILEQLEKIAPTITYDRRNW
QESIVQVATALDIEERAELLQKNKDQVTEAQKLAADITKTKPTAAFLRLEEKDMRLF
FSSIPSTPPASNYVGAGYEVGFTPDALVTKLEAENPERMNASISVELLPEIKADYLF
IVSISSDGSALQKTKDELNEIQQLQVWKS LPAVQNGHVYVLNAKKWLIDGPIAESL
KRNEMLEVLGLPAP"

CDS complement(5574524..5575129)

/locus_tag="EFAGFIKM_04869"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKRALVIGGNGTLGKAVVAKLRDYSVEVITAGRQSGDVQVDMTS
TESITTLFETVRNIDYVIVAAGQTHYAKLEELTPENNMISVQGKLLGQVNIVLIGQHY
INDNGSFTLVSGIIQDHPIEKGASSAMVNGAIDSFACAAAFELPRGIRLNSVSPNLFV
ESAEKYKDFFIGFNPVPVEKVANTFIQSALGIETAQNFKIY"

tRNA complement(5575314..5575384)
/locus_tag="EFAGFIKM_04870"
/product="tRNA-Gly"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Gly(tcc)"

tRNA complement(5575396..5575471)
/locus_tag="EFAGFIKM_04871"
/product="tRNA-Pro"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Pro(tgg)"

tRNA complement(5575487..5575563)
/locus_tag="EFAGFIKM_04872"
/product="tRNA-Arg"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Arg(acg)"

tRNA complement(5575570..5575644)
/locus_tag="EFAGFIKM_04873"
/product="tRNA-Gly"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Gly(gcc)"

tRNA complement(5575653..5575739)
/locus_tag="EFAGFIKM_04874"
/product="tRNA-Leu"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Leu(cag)"

tRNA complement(5575749..5575824)

/locus_tag="EFAGFIKM_04875"

/product="tRNA-Lys"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Lys(ttt)"

tRNA complement(5575834..5575908)

/locus_tag="EFAGFIKM_04876"

/product="tRNA-Gln"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Gln(ttg)"

tRNA complement(5575920..5575995)

/locus_tag="EFAGFIKM_04877"

/product="tRNA-His"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-His(gtg)"

tRNA complement(5576093..5576168)

/locus_tag="EFAGFIKM_04878"

/product="tRNA-Thr"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Thr(tgt)"

tRNA complement(5576192..5576269)

/locus_tag="EFAGFIKM_04879"

/product="tRNA-Asp"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Asp(gtc)"

tRNA complement(5576296..5576369)

/locus_tag="EFAGFIKM_04880"

/product="tRNA-Met"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Met(cat)"

tRNA complement(5576387..5576462)
/locus_tag="EFAGFIKM_04881"
/product="tRNA-Val"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Val(tac)"

tRNA complement(5576469..5576540)
/locus_tag="EFAGFIKM_04882"
/product="tRNA-Glu"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Glu(ttc)"

tRNA complement(5576559..5576650)
/locus_tag="EFAGFIKM_04883"
/product="tRNA-Ser"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Ser(gga)"

tRNA complement(5576654..5576729)
/locus_tag="EFAGFIKM_04884"
/product="tRNA-Asn"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Asn(gtt)"

tRNA complement(5576731..5576806)
/locus_tag="EFAGFIKM_04885"
/product="tRNA-Ala"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Ala(tgc)"

tRNA complement(5576841..5576914)
/locus_tag="EFAGFIKM_04886"
/product="tRNA-Ile"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Ile(gat)"

rRNA complement(5576977..5577088)
/locus_tag="EFAGFIKM_04887"

/product="5S ribosomal RNA"

rRNA complement(5577237..5580157)

/locus_tag="EFAGFIKM_04888"

/product="23S ribosomal RNA"

rRNA complement(5580532..5582082)

/locus_tag="EFAGFIKM_04889"

/product="16S ribosomal RNA"

CDS complement(5582690..5583655)

/gene="rocF"

/locus_tag="EFAGFIKM_04890"

/EC_number="3.5.3.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39138"

/codon_start=1

/transl_table=11

/product="Arginase"

/db_xref="COG:COG0010"

/translation="MKNDDDVHGGIKDTSIDTSQTSVRRNIAIHKVPFGLGGARGGAE

LGPDELITAGLKREIASLGLVLSKEVRVDCPSEPAAPIERNRVKHLNEVRQVSEKVCS

EVSGAVEEGAFPLVLGGDHSVAIGTFAGLTVHYSNLGVIWFDAHADLNTTEERSLSGNM

HGMSVAASLGHTAFNLSHIAGAGAFIDPSNLVYIGLRDLDEYEKEQIKGLGIRAFTH

DIDRMGIQQVIEQAVATAGKGTGDIHVSFDMDCCLDPREAPGVGTPVPGGLNYREAHYA

LEILASTNQVTSMEVNVNPLFDHNRHTARLGVELIASLLGKRIL"

CDS complement(5583645..5584865)

/gene="rocD"

/locus_tag="EFAGFIKM_04891"

/EC_number="2.6.1.13"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P38021"

/codon_start=1

/transl_table=11

/product="Ornithine aminotransferase"

/db_xref="COG:COG4992"

/translation="MSDSKMLIDWSERYAAPNYHPLPIVIEQAEGVWVEDPEGRRYMD
MLSAYSALNHGHRHPVIIQALKDQADQVLTSTRAFHSSSASLFYQKLSQFTGKSKILA
MNTGAEAVETAVKAVRRWAYRCKGVPENQAEIIVCSGNFHGRTLTVTSFSSSAEYKKD
FGPFTPGFRIIPYGDIEALKKAITPNTAGFLVEPIQGEAGIVIPPDGYLAFAFALCKS
QQVLTVSDEIQTGFGRTRRFASDWEGVEPDIWIMGKALGGGVMPISAIADAIEILD
FEPGSHGSTFGGNPLACAVAVAALKVLEDEKLAERSERLGNYFMKRLRDIRSSAIRD
RGKGLFIGVELHEPARPYCERLMSTGLLCKETHETTIRFAPPLTIKESIDWALERIE
QVLINNEGADLHEK"

CDS complement(5585007..5585663)

/gene="yecS_2"

/locus_tag="EFAGFIKM_04892"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AFT2"

/codon_start=1

/transl_table=11

/product="L-cystine transport system permease protein

YecS"

/db_xref="COG:COG0765"

/translation="MNLDFSFLLEHWQDYARSAWVTELSFLGVLFGTLLGVIMALMR
ISRIWPIKFVASAYIELIRGTPMLVQILIIHYGLTVIGVNLPAFMSGVVAlTMNSSAY
MAEVFRAGIQAIKQGTEASRSLGMTNGMTLRYIILPQAFRNMLPAIGNEFIIIKDS
SLVSMIGIAEIIYTARTIQGVTFQPLAPLLVAAGLYFIITFTLANLLSWLERRLSTSR
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CDS complement(5585687..5586508)

/gene="artP"

/locus_tag="EFAGFIKM_04893"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54535"

/codon_start=1

/transl_table=11

/product="Arginine-binding extracellular protein ArtP"

/db_xref="COG:COG0834"
/translation="MKKVLLPMMLLLWVFMSSACGQEKTTGTGSDATSSSGSSSAEKE
VIVLGTSADYAPYEFHKKIDGKDTIVGFDIEIAKAIAADLGAEKIEDMDFDGLLMAL
GTDKVDFVISGLTPTEERKKNVDFTDIYYAEQAVLVRRGGEDTALKSIDDLSGKQVGV
QKSSIQEGIAQEIEGAKLTSLAKIPELILELQTGRVDALILEKPVAEQYVKNQEGLVV
AGVEVEQAEDEGGSAIAVKKGNQKLLDQINTTLEKLTNGDIERFVVEANEMLGE"

CDS 5586831..5587475

/gene="rspR_3"
/locus_tag="EFAGFIKM_04894"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0ACM2"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional repressor RspR"
/db_xref="COG:COG1802"
/translation="MEVPKYRSLKDHVYDYIAQKIQDGTLLPNQKINEAEICKKLDIS
RTPREALFQLASDNLLQYIPRRGFIVTPFDAGKKLEFSQAIGVLEALAATLAADHLR
PSELMEMETLVVRMEEDISQLDLAAYNKNQYQFHNLYIQRCGNATVIEMLNTLKNSEI
RQSYVSDNPKPLSEVLLEVNEEHRQILSAFRAKDKNQLEALLKHHWRIIDNDML"

CDS complement(5587534..5588268)

/gene="COQ5_5"
/locus_tag="EFAGFIKM_04895"
/EC_number="2.1.1.163"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01813"
/codon_start=1
/transl_table=11
/product="2-methoxy-6-polyprenyl-1,4-benzoquinol
methylase, mitochondrial"
/translation="MDYHDMLARLGECSAHPGGFLATLKLLDNLSLPVGSCHILEIGCG
TGRTACYLAKSGYRVTAIDLHRNMLDKAVRRARRERVDVRFVQADVTSLPFPENHFDV
VFVESVTIFTPWRSALAEYRRVLKPGGLLDREMLVSGQKTELMCRRLKQFYGIRTLV"

TATAWRKRLKQCGFTKVEVKEHSRSMGKWGADHDPHREIDMNWFEDERMQRMSQTNDR

LLAKYGKKLGAVFAARAPLEVEKEK"

CDS 5588433..5588780

/locus_tag="EFAGFIKM_04896"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYRINRVCEETVSPHVGRSVCLVMNDGKHMYGTLSQCRDGKIYL

NGCFEGPRLCSVKSKQQLVKSSKKNVATKKVKSSAYGRYGYGGYGGGYGYGAGIDLA

LVATLFLLPFLFI"

CDS complement(5589025..5589252)

/locus_tag="EFAGFIKM_04897"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYNRKKPLEEIPQADAAIWECTSDTCKGWMRDNFAFDNVPTCPI

CASEMVSTRMLPLENSNSNLKTMPKGNNRI"

CDS complement(5589441..5589641)

/gene="cspD_2"

/locus_tag="EFAGFIKM_04898"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P51777"

/codon_start=1

/transl_table=11

/product="Cold shock protein CspD"

/db_xref="COG:COG1278"

/translation="MQNGTVKWFNADKGFGFIEVEGGEDVFVHFSAITGDGFKTLDEG

QRVQFKIVQGNRGPQAEVVKL"

CDS complement(5590035..5590271)

/locus_tag="EFAGFIKM_04899"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEKTAQGVAEWMVQEIKFTGLHQEAAIVYKTHFGEEFVFMNE
NGNSSLSKEVKKAFRKLHRGQIAWDRDAFMWAWT"

CDS complement(5590422..5591210)

/locus_tag="EFAGFIKM_04900"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MINARSKPKHSFSERKPVLTVIIELFLLLAVFAAGAIATIKQL
DYTSPVLISFTPIAIVLMIYLTLLRRKWGETGFRSLRSIPAGHAKYYIPLLLVLGTLAL
KGFGELSLSRVAFFIFFTLLVAFVEETIYRGLIFKTLQKSAVSAVTSSILFSITHL
LNALSGQDMTDIIQLIYALLLGAVLALLMLKNGNIVPLILFHFHNLIQFLGNDLED
TGTLPYDLFILAVLIAYCAWLWWSIRTSSIPSKGSEQANTVVH"

CDS 5591514..5592185

/locus_tag="EFAGFIKM_04901"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKAFFQRWGHLLAILCIPLQGSIVFLGSNTGSDVFYNYAWIDT
QIPFLKEFIYPYISWMPILYLGFLYLGLTNKSLFWRTLITYNVGVMAANVCFAVFPTH
VPRPEIGGTDLSSVLVQFIYTDAPFNCFPSVHVLTSYLLFIVINRHLNFKPLARISW
SVWLWLIISTVFVKQHSLLDIAGGILFAEAAWTVHVFALRLGQVRKKGKQPLTASN
PSSHV"

CDS complement(5592163..5592267)

/locus_tag="EFAGFIKM_04902"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MSTKKEGLGPLLLYSMIILPVTYINVVIHDCLG"

CDS complement(5592320..5593099)

/gene="rhaR_40"
/locus_tag="EFAGFIKM_04903"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01533"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaR"
/translation="MVTPLVRHINGVGWYEEAVQSQETWRLSLVTYGKCVYWVNGDK
QIMEKGELLIPGGTPYYGKSIPTVTHTQIVQLQRDHTETLPALERYEALRHKPGCY
ELIHQRMSAIYQQWQERPSYYVMMSQALLMEVLIYMNRELDRGVIPPERHNNHVERMKR
YIERHYREKVTKEELGDEINKTPNYAAALFKSMTNQTSQYVHDQRMKRAIYLLTESQ
LSIQEIAEFLGYRDLSEFYRIFKRITGSPPSDLLHERPPIA"

CDS 5593212..5594627

/gene="pyk_2"
/locus_tag="EFAGFIKM_04904"
/EC_number="2.7.1.40"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P80885"
/codon_start=1
/transl_table=11
/product="Pyruvate kinase"
/db_xref="COG:COG0469"
/translation="MLKTKIICTMGPAACDSIELLKVMIQEGMTVARLNMAHGELEDHV
TRINNIRKAASELNTYIPIMMDIKGPEVRIGKLKEASCHLQAGKELITTEEILGDAE
RISVNYPELNLVVKPGDRILIDDGLVDLTVLSVEGSDIHCKIISGGILKPRKGVNLP
G
IKTTLPGVTERDVMHIGFGIENDIEIIAASFVRKGDDIREIRSILKERGVDPVQIISK
IENQEGMTNLDDIIEASDGIMVARGDLGVEVPIEDVPMQKEMIDKCNRAGKPVIVAT
HMLESMQVNPRPTRSEVSDVANAVLQGADVVMLSGESAAGKYPVQSVRTMAAVARRAE"

TMIDYKEQFAQKSAQQIADITEVISQGAVSSSLVLNAKAITSTESGFTARMISKYRP
KAPIIAVTQHEEVLAKICLLSGVIPVMGDKVTTTDEMFEATRNAIKTGYIEKGDIIV
LSAGVPIGQSGNTNLIKVVQV"

CDS complement(5594768..5596297)

/locus_tag="EFAGFIKM_04905"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFRKRTESTKHLRTDAHQNLLSESRKLVANAEGDYDAWIEDGI

EFQDTDEIASNIKKAVHMMKAQNEAVEMRLRMLNQAMNVGLWESKIVAGDPLDNNNIV

AFSNEFRQMLGFHNAKDYPDSFASWAKSIYPDDRPQLVQEIMKHVNDTRATTAYNVIS

RMITKSGEIRWFRCLGQVIRNQAGVPVKLLGIMFDIHEEKSXSDEALVTRYDLVNR

ALVEAPWDMTVVAGDVVNPNEFWWSPQFRKELGFKDEQDFPNVFSSWSSRLHPEDHD

RTINEFARHMNDYSGRTPYDLDYRLQRKDGGEYRWYHAGGETIRDQDGVPLRVAGTIRD

VTHEKNKEQIVEAMNLKTKQLSESIGEMVRGINSITDQAQDLVTAQELSADAAIQVKS

SADDTKNITVFIREIASQTNLLGLNAAIEAARAGELGLGFGVVAGEVRKLADHSSEAT

VNIEDSMQMKMTLIDQILEHIGNMSTLTQNQAALTQQVNASMDEINTMSQDLVNYSRN

L"

CDS complement(5596473..5596922)

/locus_tag="EFAGFIKM_04906"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MELKYEYINAGLEEVWNALISPDGTRNSFFGSELRTNFQPGQP

FAYVGPGNDGAETVHVYGDILEFEPLSRLSYQEHPGPSYHANHAELQSRVVFQLETVG

ECTKLTLLINDQFTDNHPSIANAQSSWWMLSSIKTWVETGKTLNFGW"

CDS 5597180..5597917

/gene="tagA_1"

/locus_tag="EFAGFIKM_04907"

/EC_number="2.4.1.187"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P27620"

/codon_start=1

/transl_table=11

/product="N-acetylglucosaminyldiphosphoundecaprenol

N-acetyl-beta-D-mannosaminyltransferase"

/db_xref="COG:COG1922"

/translation="MSQSTNIMGIPFPNVTMDQTVAILDKVVDQESNELFHVITGNPE

IVMSYQKNASLRKVVDQAGLVTADGAGIVMVSFRGGQLTERVTGCDLLFRLLEEGNQ

KHWSFYMLGAEESVSEEAVKVIAQRYPGVVVKGRHHGYFQTDEEQQIVEEICTAQPDF

LIVALGAPHAHEHWINKYRHQLNARVAIGVGGSLDIVAGKTKRAPAIWQKLNLEWLYRL

LSQPSRWRRQLILPRFAVRALLFREPK"

CDS 5597946..5598785

/locus_tag="EFAGFIKM_04908"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKQVEQGDRPSMGLLNLEGDHXYQLTRHAPSEALRPFVKHYWI

VSWDLTGLEPYYPQHVPNPCVNLVVERNNTFFFGPSGRKFSYLVSGKGRVFGVKFNPG

GFYPFLRVPVSSLYGQPMNVSNILDVTAESLEDRLGAGVDADKTSYIDQLLCAHLPA

EDVQARMVHDIVQQIEQNREMLRVDDLSSYWNMHTKRLQRLFNQDVGIGPKTVIKLYR

LQNAAEWMDRGLHCDLIKLSQDLGYHDQSHFIRDFKSIIGSTPEEYLHSHKHPNGERRG

LIN"

CDS complement(5598802..5599335)

/gene="yuaD"

/locus_tag="EFAGFIKM_04909"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32079"

/codon_start=1

/transl_table=11

/product="Putative metal-sulfur cluster biosynthesis

proteins YuaD"

/translation="MGTVQFVMLADDPSTFVTRVVPFIDIELAGIPGDRHYGLLRPAD
SRQKIYKRGTPIANRRQISIVSEEECALIAEKMNIPEVRPEWLGANILVRGIDRTEL
PAGTRLLFPNGTGLICEGENLPCVHPGKMIEQFYEQDGLRKKFVPAARKKRGIVCSVE
REGVIHTGDTIEVINLS"

CDS 5599602..5599958

/locus_tag="EFAGFIKM_04910"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MISIIFVALVAVEHFYIMVMEMFMWTRPRTMKTFNLTPEFAKST
KSLAANQGLYNGFLAAGLIWGLVYPDAAVGQHIQIFFLACVIAALYGGATSSRSIII
KQGLPAIIALLLVFL"

CDS 5600074..5600874

/locus_tag="EFAGFIKM_04911"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGLFDKLRRRKKEKVPAGGAVESTNYSETIVGFVLLERDDCDFD
LFIRNMSNEWNIEIERPEEGNLFFEVNGMQVCAHIPAPVPDREVEENAKLNILWRE
AEQVTSRHQSQIIVSVLNATNAIDGHVLTQTASALLQLDHALAIYMAPLVVEASQYV
ETSRGIKHDELPVSLWIFIGLFQNAEGASAYTYGLRNFGKEEMEIMQSSESLSDFEM
MFMTTTYVVENDVTLHDGETLGFSAEQKLSISLSKGVATEGNSLKIGF"

CDS 5601136..5601495

/locus_tag="EFAGFIKM_04912"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSVRRLDSTKPIIEIIEWEGIVSPEHVEQANSEIQRIAEQLGSSF"

DVLVDMRNMKAFFPQDTKEKIVEHQLLTQWGMKRASVAVGGAIKMLNRISKESAHQ

TEFQWETYDEALAFLLK"

CDS complement(5601644..5602153)

/gene="mshD_4"

/locus_tag="EFAGFIKM_04913"

/EC_number="2.3.1.189"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01698"

/codon_start=1

/transl_table=11

/product="Mycothiol acetyltransferase"

/translation="MTIITNYYVRPIEEQDIPFLWEMLYASLHRREGDEPFPIESIHT

PGLSKYVEDWGREGDFGYVAVDQQGKRLGSITLRFYTDQNAGYGYVNAATPEMGMMAVT

EDARGKGVGSLLLQTALDEVERRGIAAVSLSVDPDNQAIRLYKRLGFVEECLNGTSVT

MVRVSKLES"

CDS complement(5602150..5602746)

/locus_tag="EFAGFIKM_04914"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLYWNISIITNLYVLCRSREGIGMSRQIKMIMGIVMIIVFLAIA

VRMYTSGQYTKYIPSKHTTFRAEVTDHMTMLDTLDRILTIRKISDNEPYNEDDEITITD

PKEIRDMLKLLKDVDLKRLEFDVSERNPHYIEWRLTINKEGRFTDGFGLTFYNEKSI

SIYSEAKTRDKFQDYEITNEFNLNEMDRLFELKKEEQT"

CDS complement(5603007..5604014)

/gene="degA_7"

/locus_tag="EFAGFIKM_04915"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37947"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator DegA"
/db_xref="COG:COG1609"
/translation="MKATYDIAREAGVSIATVSQVINGKGKISEKRRAEIMEIMERL
HYQPSAIAAALTGKQTYTLGLLVPDISNPYFAELARAVEDRSRQLGYSVVICSTDNKD
ERVERYLNLLQQKRVGDGMMIGTGIDNAEILSPLLQQSIPVALIARHMPSLSVHTVTID
DILGGALAAEHLLELGHTRVAVLSEPSKVSSSQERVGRGFRETLIKAGHTLEPNQIRES
AADLSSAKKEALLLLGEKDHPTGLFCCNDIQAIGALQAAKELGLRVPEDVSIIGFDNT
ILASVTSPPLTTVAQPIEELGYRAVDLLIEELKDEQKEPQKIVLKPELVIREASAGRVL
S"

CDS complement(5604143..5604949)

/gene="iolB"
/locus_tag="EFAGFIKM_04916"
/EC_number="5.3.1.30"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42413"
/codon_start=1
/transl_table=11
/product="5-deoxy-glucuronate isomerase"
/db_xref="COG:COG3718"
/translation="MSERIVKPVVNPEGDGTLINVTPESAGWEYVGFQVAKLAEGETL
TRESGDQELCVLLSGFANVSTREHTWDNIGKRMSVFEEKIPPYSVYVSTSDQVQITAR
TELEIAICVAPGKGTHPARLIAPEDVGVEARGYGNLERQIHNILPEQKEADSLLVVEV
FTPDGHWSSYPPhKHDRDALPDESLLLEETYYFRVQPEQGFAIQRIYTDDRSVDETLAV
KNGEVVLVPDGYHPVGAPPGYEVYYLNV MAGPTRTWKFHNDPDHEWLMKK"

CDS complement(5605058..5606110)

/gene="iolG_10"
/locus_tag="EFAGFIKM_04917"
/EC_number="1.1.1.18"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9WYP5"
/codon_start=1
/transl_table=11

/product="Myo-inositol 2-dehydrogenase"
/db_xref="COG:COG0673"
/translation="MGKDKVRIGIIGAGRIGKIHADNLLRNPHAEIVGISDLFAGPEL
EAWASSRGIPVVTNNSSELISMPNVDAVLICSSTDTHVPLIEQAAQAGKHIFCEKPV
MDLAQTQAATAVAVQKAGVKLQIGFNRRFDHNFRRIRAHVQDGTIGDPHIKITSRDPS
PPPAEYIRVSGGIFMDMMIHDFDMARYLSGSEVEEVYAQGNVLINPVFAEHGDDVDTAI
VTMTFANGAIGVIDNSRQAVYGYDQRVEVFGSMGSAAAANDHPNTAEISTAAGLMRD
PLHFFLERYNEAYVQETALFIDAILHDTPIVVDGHDVQAERIALAAKLSMERGRPVK
LSEVPGVSLESQTATP"

CDS complement(5606180..5607655)

/gene="iolA"
/locus_tag="EFAGFIKM_04918"
/EC_number="1.2.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42412"
/codon_start=1
/transl_table=11
/product="Malonate-semialdehyde dehydrogenase"
/db_xref="COG:COG1012"
/translation="MGKGISEASATATMVQNWIGGAWVTPASTRTEPVVNPATEEVIA
HVPLSEQADVDLAVQTAREAFKSWSSSTPVPRRARILFRYQQLLVEHWHEELARLVLEN
GKSYAEAYGEVLRGIECVEFAAGAPNLMMGKQLPDATGLESGLMYRYPVIGVIGGITPF
NFPMMVPCWMFPLAIACGNTFVLKPSERTPLLAGRLAELFKEAGLPDGVNLIVHGAHD
VVNGLLEHKDVQAISFVGSQPVAEYVYTTASKHGKRVQALAGAKNHSIVMPDADLDT
VKEITSAAFGSAGERCMACAVVAVGDVADELVQKLVEAADRISIGNMDEGVFLGPV
IRGPHKERTLSYIEAGEQEGAALIRDGRKDQATGESGYFVGPTVFDQVDSNMKIWQDE
IFAPVLSVARVSTLEEAVELANRSDFANGACLFTRSGASMRQFRETIDAGMLGINLGV
PAPMAFFPFSGWKKSFYGDLHANGTDGVEFYTRKKMVTARW"

CDS complement(5607755..5608765)

/gene="iolC"
/locus_tag="EFAGFIKM_04919"
/EC_number="2.7.1.92"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42414"

/codon_start=1

/transl_table=11

/product="5-dehydro-2-deoxygluconokinase"

/db_xref="COG:COG0524"

/translation="MTYVSFPVSRKKDFTAIGRLCIDLNANEINRPMEETMTFTKYVG
GSPANITIGMSRLGMETAFIGKIAGDQMGRFIQSYLEKNGIDTSNVVKDDTGAVTGLA
FTEIKSPTDCSILMYRDNVADLLLQAQEVQEQLIADSKVLLISGTALAQSPSREAVLQ
ALTYAEKHGTVIVFDLDYRPYTWTSDEETAVYYNLAAEKCDIILGTREEFDMMETFDH
NPDHSDQVTAQKWFDIFSANIVVIKHGKEGSIAYTREGLSHRADSYPAKVVKTFGAGDS
YAAGFLYGLMQGWTIERSMAYGSGAASIVISSHSCSDAMPTVEQVNDYIERCNRGEIT
VS"

CDS complement(5608965..5609867)

/gene="iolE_2"

/locus_tag="EFAGFIKM_04920"

/EC_number="4.2.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42416"

/codon_start=1

/transl_table=11

/product="Inosose dehydratase"

/db_xref="COG:COG1082"

/translation="MSKLPFQLGIHPINWVGEDVKEHGDATTCAQILDDIQRGLTGT
EMGRKYPTDPAILREELSQRNIKLVSQWKSFLSDPAYRQSELDYRRHAEFLQSMGS
KVISTAIEVGGSLHFDPRRTPNEKEVLRLESESEWHILAEGLNEAGAIAREHGLKLTYYH
HGGTVVEQPDEIDRLMELTDPSTVYLLYDTGHAYYGGADPLELLRKHYDRIAYIHLKD
IRPHVLDEARAEQSDFVGCIRKGVFTVPGDGCIDFAPILQELITRGYDGWAMLEGEQD
PAIHNPYIYAKQSLNYMESLYQHS"

CDS complement(5609921..5611786)

/gene="iolD"

/locus_tag="EFAGFIKM_04921"

/EC_number="3.7.1.22"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42415"

/codon_start=1

/transl_table=11

/product="3D-(3,5/4)-trihydroxycyclohexane-1,2-dione
hydrolase"

/db_xref="COG:COG3962"

/translation="MKTIRLTMAQALLRYLDQQYISVDGVETKFKGIIIGIFGHGNVT
GIGEALERSPGSLTYMQGKNEQGMVHTAAAYAKQKNRRQIYACTTSIGPGALNMITAA
ATATVNRIPVLLLPGDNFATREPDPVLQQLEVSSDYTISATDPFKAVSKYWDRIVRPE
QLMIAVTQAMRVLTDPAETGAVTLALPQDVQAEAYDYPESFFARKVHYLDRRPPVQAA
IERATEQIARGSKPLLVAGGGVLYSEASVQLVEFAEAFGIPIAETQAGKSAVSWDHPL
NVGAIGVTGSLAANRLARDADVIGVGTRFSDFTTASRSFQHPEASFININLNGMDA
AKLGGEAILADAREGLQALQKELQERQYRSAYGASEIADLRAEWNAEVDRLYAAQHEA
GLAQTTAVGIVNRTIDPSSVIVCAAGSLPGDLHRLWRAAEPKTYHMEYGFSCMGYEVS
GAFGAALAEPDREYAMVGDGSYMLHSEFVTSLQEQQKMTILLFNNNGFQCIHNLQR
EHGSDGFGNEFRYRESESGRLTGDYMPMDFAAHARSMGAKSYRAETAEQLEQALRDAK
NETVSTLIEIPVVPGTNAGGYESWWNVGVPEVSAEEKVVHAHQTMQANRIKARPI"

tRNA complement(5612180..5612250)

/locus_tag="EFAGFIKM_04922"

/product="tRNA-Gly"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Gly(tcc)"

tRNA complement(5612261..5612334)

/locus_tag="EFAGFIKM_04923"

/product="tRNA-Pro"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Pro(tgg)"

tRNA complement(5612341..5612421)

/locus_tag="EFAGFIKM_04924"

/product="tRNA-Leu"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Leu(caa)"

tRNA complement(5612438..5612514)

/locus_tag="EFAGFIKM_04925"

/product="tRNA-Arg"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Arg(acg)"

tRNA complement(5612522..5612596)

/locus_tag="EFAGFIKM_04926"

/product="tRNA-Gly"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Gly(gcc)"

tRNA complement(5612604..5612688)

/locus_tag="EFAGFIKM_04927"

/product="tRNA-Leu"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Leu(tag)"

tRNA complement(5612694..5612769)

/locus_tag="EFAGFIKM_04928"

/product="tRNA-Lys"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Lys(ttt)"

tRNA complement(5612780..5612865)

/locus_tag="EFAGFIKM_04929"

/product="tRNA-Tyr"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Tyr(gta)"

tRNA complement(5612875..5612950)

/locus_tag="EFAGFIKM_04930"

/product="tRNA-Thr"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Thr(tgt)"

tRNA complement(5612971..5613046)
/locus_tag="EFAGFIKM_04931"
/product="tRNA-Phe"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Phe(gaa)"

tRNA complement(5613065..5613142)
/locus_tag="EFAGFIKM_04932"
/product="tRNA-Asp"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Asp(gtc)"

tRNA complement(5613169..5613242)
/locus_tag="EFAGFIKM_04933"
/product="tRNA-Met"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Met(cat)"

tRNA complement(5613259..5613334)
/locus_tag="EFAGFIKM_04934"
/product="tRNA-Val"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Val(tac)"

tRNA complement(5613341..5613412)
/locus_tag="EFAGFIKM_04935"
/product="tRNA-Glu"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Glu(ttc)"

tRNA complement(5613417..5613492)
/locus_tag="EFAGFIKM_04936"
/product="tRNA-Asn"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Asn(gtt)"

tRNA complement(5613494..5613569)
/locus_tag="EFAGFIKM_04937"

/product="tRNA-Ala"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Ala(tgc)"

tRNA complement(5613604..5613677)
/locus_tag="EFAGFIKM_04938"
/product="tRNA-Ile"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Ile(gat)"

rRNA complement(5613719..5613830)
/locus_tag="EFAGFIKM_04939"
/product="5S ribosomal RNA"

rRNA complement(5613913..5616834)
/locus_tag="EFAGFIKM_04940"
/product="23S ribosomal RNA"

rRNA complement(5617142..5618692)
/locus_tag="EFAGFIKM_04941"
/product="16S ribosomal RNA"

CDS complement(5619325..5619873)
/gene="aaaT"
/locus_tag="EFAGFIKM_04942"
/EC_number="2.3.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P46854"
/codon_start=1
/transl_table=11
/product="L-amino acid N-acetyltransferase AaaT"
/db_xref="COG:COG0454"
/translation="MMIDQQEYYIKGLSYSIRSAAEEKDAEALPSLRVQIDGETENMDR
EKGEAYIDATGFRRIIHLDEKSRNLFLVAVVAGEVVGYSRCEGTVLKRCHKVEFGV
CVAREFWGHGIGKNLLEKSIEWADQTGVEKITLNVLASNEKAIELYQKSGFEIEGILK
KDRRHADGQYYDTIVMGRFREL"

CDS complement(5619925..5621529)

/gene="rssB_10"
/locus_tag="EFAGFIKM_04943"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00958"
/codon_start=1
/transl_table=11
/product="Regulator of RpoS"
/translation="MMKTIMLVDDDPHIVKALTDHIDWPSLGLSIAGTASNGLDALEL
FHRMHPDVVMTDVYLPGMTGLEITQTLRRDHPHLPPIIILSGYDEFENARAAMRWGVNH
FLLKPAEVEEIESVLREVLLEQDVRERHERLEQTYKQEVGRVLPYLRKQFLHELLTTR
YRADELPKERMDYIGIHMSSQTRAIQLNRPVFLTRMKERDWQLLRYGAADIQETV
KEQAARMNGQVEIVDYSQVFLVLLLGDKDHLEECPLVERMIDQIFTYKVEVSAGI
GRSKSHPCVIDSYLESREAVETAEFQGGSRITYHYEASKETEPSVTDYSLLLRQWNEA
WADIRPDLAEEVWHHICLLLKEGKCVGIQDVQVAVSLFDTLMHSWNRLHPMLTPPLA
MSDFLREIQSKYALPDLVSWMDRIICDWLEQIRKEMGEKSNKLIEQVKQYVELHYAE
EISFEAIAKGLFVHPKYLSQLFKRVTGENFVSYLNGYRIQRALELLQSGHYMVVEVSE
MTGFRNATYFSQVFKMLTGKSPSEVG"

CDS complement(5621526..5623394)

/locus_tag="EFAGFIKM_04944"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGKGRWFSEFIKQLQSKLSTLMVTCFITNLLLVSVVWVWLAYQ
SFSTVTFAEISKARLALLNESTRRGDFDITGVTGTSYALASNRELSSLLEMADTGRLA
QIHQRREVSRILDHTMVVSEGITSIELYTDVFNEVTVTMADRIFPVDITIAHDSWFATL
EKADAAWVPLRENESGQSLVGYAQRIFDSRGGTVAYVLIRLSRADIVRRFADVPMVLD
GKVLLVDTAGNVVMQMGRVDPAREKERVDIRNEASTVQETGEAVNSSSSIIDSAWIQE
HVQHGADGYEVVSGQPGGAQLVLYSRPAMLQWRLVQTIPVYTLLSPLRQAGWQILGIA
VLGLLCSAVLAYLFVRQIIRPLRQLIKRMRQLEKGFDFTRVQLSFTEEYAHLAYGFNH
MASQLTTLMEQVKDENRAKREAQTGLLEAQIKPHFLYNTLDMIHWRALDYEAKDISRM
IVQLSKLLRIGLSGGRLFIRVRDELEHARCYVNIQSERLPFSIQYQEIDPHIRGCYI

PKIILQPFIENSVMHGHPEEGTLRIQVHMHEVEGQHQDIVIRITDNGRGLPEGWRLEE
TCGIGVRNVHQRIQLYCGKRYGVQLSDRESGGVEVTITLPRIETDEQLNLWLDGEK"

CDS complement(5623423..5624271)

/gene="dasC_8"

/locus_tag="EFAGFIKM_04945"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9K489"

/codon_start=1

/transl_table=11

/product="Diacetylchitobiose uptake system permease
protein DasC"

/db_xref="COG:COG0395"

/translation="MIGQRNSTAWVVSKHVLISGIAFVMLYPILWMLGSSFKPGHMIF

TETWFWPQEWNWQNYTNGWSGIQGNPFARFLTNSVILSLGAVLGNVISCSMAAYAFAR

LNFRFKAICFGLMLMTIMLPHHVTLIPQYILFNHLEWVNTYLPLVVPKWLATDAFFIF

LMVQFFRGLPKELDEAATIDGCGPVKIYTKIIIPALVTTMIFTFLWTWDDFFSQ

LIYLSDEVSKYTVPLGLRLFLDSSSQSDWGPMFAMSVLSLVPCFIVFIVCQKYFVEGIA

TSGLKG"

CDS complement(5624268..5625218)

/gene="lacF_12"

/locus_tag="EFAGFIKM_04946"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29823"

/codon_start=1

/transl_table=11

/product="Lactose transport system permease protein LacF"

/translation="MNTSEVSQARIERVTTTRRVKRRYAHNGAALLFLAPWLVGLLFLT

LGPMLVSLYISFTDYSILAAPSWVGLDNYTTMFTSDKLFTQSLKVTFTYVAVSVPVKL

IFALLVAMLLNKGIRGLGIYRTVYYIPTLLGGSVAIAMLWRKMLGGDGLLNSVLAMVG

IKAPDWVANPKYALYSIVLLSVWQFGSSMIIFLAGLKQIPPEYDEASVDGAGPLRRF

FYITLPILSPVIFFNLVMQLITSFQSFTQAFVISNGSGGPVNSTLMYSLYLYKKGFSF

FQMGYASAMAWVLVILIGVFTLLVFRSSKLWVHYEDGGKS"

CDS complement(5625266..5626606)

/gene="yesO_4"

/locus_tag="EFAGFIKM_04947"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31518"

/codon_start=1

/transl_table=11

/product="Putative ABC transporter substrate-binding protein YesO"

/db_xref="COG:COG1653"

/translation="MMITKKWVTLFCLSLLLFATACSGGATDTPSSSGEASGSEGDSS
GKIELRMTWWGSQTRHDLTTKVIQLFEEKHPGITIKPEYSGWDGYFDKLTQVAGSNA
PDIIQMDYAFLTDFARRGALLDLTPFAESKELRTEDHDQSMITAGSIDDKLYAITLGV
NAPGVIYDATVFQELGIEEPQESWTWKDFGDIATKIAAAKGEGFYGSADISGTTNMFE
VFIRQSGKGLFDGGTMTATSEELQQWFDMWALRENGGVTTAEITASTTNALETRPIS
LGTAAMDFAWSNQLLTFQQVNKNQDHLGLIQVLPHGVGEKQIGEYLPKGQFLSGYGKT
KHPKEVAMFIDFMVNDPEATAILGSERGVVPVNSSIREQMQPTLPEAEQTIFQFIDTVS
KNSSEIDPPYPQGFAEVDTSFKSASEQIAFGQGDTDPDVIAQFIEGAKATLGSSQ"

CDS complement(5626878..5629121)

/locus_tag="EFAGFIKM_04948"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTTYFSEPQSMYYRFGEDQDQVLKVLAEYIGANAQADFVYRVF
QKSGILQNEKGLYDLNLGKRFPDTPKDHISYAAALVWGDEDRNLDVLRVRCYGPVRFYF
NEQMVYRSTVMDEISPDATVKLSIDIKPGWNTIWLEMKNTPAGFGCQFGSDEGKVRIL
NVFAPFQERQQAGWVFSQPNPATSKQPDLLGKESDYSLNWLPETGWSDEDKTKPALE
RIYEHLPGRHVYAWTHLNNNDSTGNAVRLSGQSSGSLSIWISGKPVAQLKEAGPFEVD
VPASFGRSDLLVRSECTETAGPWHFNLNATVSGKPLSLELPQRVHGASGESWLYVGP
ESEVEPDLADLTRTDRVYQTGQGQTYWRLDRPDWIRPYENAMLSNKWTVGSVTNYG
RWDYPLGVTVYGLLRTGRYLQRPDITRYAAEHVQACTQMYEYSLWDREYGFPAVNQQ"

LVMLKMLDNCGSFGSAMLEAYSECHEPTFLPIAERIADFMLSRLERQEDGAFYRTCVG
EYAENTMWADDLYMSTPFLVRYARVTGNSAALDEAARQFSLYRKYLFMPEFKIMSHVY
DFKYGQATQIPWGRGNGWTLFSLTEVLEALPVEHPERPALIDFFNELCEGYAALQGES
GLWHQVLNVPQTYEEASCTAMFAYGFARGVRFGWFKDPEVYVTAAERAWKGLICKAID
RQGNVHGVCSGSRYAFTA EYYDQDLRTVTNDNHGIGIMMLAGTEVAKMKKHLAEHRVS
SPAVSHS"

CDS 5629492..5630319

/gene="yfmS_1"

/locus_tag="EFAGFIKM_04949"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O06477"

/codon_start=1

/transl_table=11

/product="Putative sensory transducer protein YfmS"

/db_xref="COG:COG0840"

/translation="MNTLESLVNAMPFVSQMFRDDISISINDHEKVLVFSEAKSLEIG
VKVGDELHDDYKHFKMLTNRDSRTVARM PGDLQGRPFDA ILIPIKENDQVVGILGVNY
ALDSHMTLET LIRENETTINALVGGIQQIAAHSEELSATSEEILRNSKKASENSVSVS
KVTTVIREVSEQTNLLGLNAMIEAARVGDQGAGFGVVASEVRKLS DHTKQAAADIESS
LGSVQDSMKHMEQEIGQITTATVDQAKLVTEFMESIEQLSETSANLKKFVHQMLALE"

CDS complement(5630481..5631299)

/gene="mapP"

/locus_tag="EFAGFIKM_04950"

/EC_number="3.1.3.90"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:E6ENP9"

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KGQWELTESKLAPYMDQPLYIMGDFNNVAEVRDEGYDYMMSKGWNDLYTTALQKDEGA

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CDS 5631580..5633358

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/inference="ab initio prediction:Prodigal:002006"

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MLQPIEKDAPELLLPFYHQAVERYIGQKNRDGYKAAVKLLKRLSKIYKKMKQEAHWEQ

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CDS 5633355..5636384

/gene="rapA_3"

/locus_tag="EFAGFIKM_04952"

/EC_number="3.6.4.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01821"

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/product="RNA polymerase-associated protein RapA"

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SVLGNWQKEISRFAPSINVSLHYGARRLSGEEFREQTEQVDIIITSFATATLDQEMLQ
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PEELPEDGALTSAYDVYSPQDMAMLSRSKLERLMELVRELDEGERCLIFTQYIGM
GQMLQQVLRQELQEPVLYLHGGTSKTGRDRMIEEFQSRTLPEDKQPSVFILSIKAGGV
GLNLTAANHVFHFDRWWNPAVENQATDRAYRMGQTKDVQVHKFISLGTLEERIDEMLE
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CDS complement(5636496..5636960)

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/inference="ab initio prediction:Prodigal:002006"

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CDS 5637344..5638027

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TNEEETLAQQTEYVPFLLEDALRERAAQYDKAAAFSSYVTTDGRVVTGQNPQSSKAVA
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CDS complement(5638132..5639091)

/gene="kdgT_1"

/locus_tag="EFAGFIKM_04955"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P50847"

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/translation="MNILGRIKKIPGGLLIVPMLAAVINTVFPSFFQIGDPTTALFT

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CDS complement(5639098..5640555)

/gene="bglH_11"

/locus_tag="EFAGFIKM_04956"

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/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40740"

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/db_xref="COG:COG2723"

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RKLIDLYVNYCDVLFNRYKGKVYWWTFNEINMSVKASAKTLGIIDYDAPNYEEMLFQ

GLHHQFVAASRATKMAHEIDPNNQIGSMVAYFTTYPYTCKPEDALQMQQDDQMKNQFY

LDVLNKGEYPYYSKTYFKNKEIQLNIEDGDLESIRAHTADFGMSYYNSMISSSDTEQ

LELTAGNVHVSYKNPHLPANEWGWDPIGLRYTLNLVYDRYQKPVFILENSSGFYDK
LNEDGTINDPYRIDFLSKHIEQMGLAIADGVEVLGYTMWGPIDMISSGTSEMSKRYGF
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CDS complement(5640649..5642577)

/gene="bglF_11"

/locus_tag="EFAGFIKM_04957"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P08722"

/codon_start=1

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/product="PTS system beta-glucoside-specific EIIBC
A component"

/db_xref="COG:COG1263"

/translation="MNNKDLAKNVLDLVGGEQNI
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NVVLETIAGIFTPVLPALVGC
GMIKCLATVITAMGYLEGSGFLT
IINMIGDCIFYFMP
FFLAVSAANRFKTNPYLAVALAAGLMHPT
ILNGAAQIAETGVNSIDFLGMPILLMKYS
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LLTPMIVLFIMIPLELIVLGPVGSYIGD
WLTNGINSLFSTAGVLGAILGFFKPI
MVMFGMHYAIMPIQVQVATLGATVLLPTAL
AANLAQAGAAFGVFVLTKNKTMKSAA
SSGFTALFGITEPAIYGVTLKYKRPFFAGCL
AGGLVGGFYSLVHTTANAISLPGVLAIGTY
TSDRYMYVVGCVAAVVLGFVFTLLAGI
KEDTDV
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VEDQAF
AQELMGK
GIAIVPTDGKVYAPFDGVVEALYRTKHAIGL
KAANGVEILIHIGV
DTVSLK
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NIITSIVVTNMQQYGDVLT
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CDS complement(5642716..5643552)

/gene="licT_8"

/locus_tag="EFAGFIKM_04958"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39805"

/codon_start=1

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/db_xref="COG:COG3711"

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QVGSSEMTDTTKVTTVTGEILSVIKYALKIDFQEDSIHFMRFATHIRYFIMRQMSGKS
LKDENESLFLMVKEKFPKELACVEKIADFLKNNYGWTCSDDEKLYLILHIQRLISNEP
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CDS 5643875..5644507

/gene="udk"

/locus_tag="EFAGFIKM_04959"

/EC_number="2.7.1.48"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P67411"

/codon_start=1

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/product="Uridine kinase"

/translation="MLIIGIAGGTGSGKTTVARSVIDRLGSGKVTFISQDNYYKDQSQ
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HIVIVEGLHVLIDEHLRSLMDIKVFVDTS DVRILRRVLRDIEERGRTIQSVYKQYLE
TVKPMHDAFIEPSKKYADIIIEGGHNEVGIQMLSILTEKYLTGENWNGA"

CDS 5644617..5644946

/gene="csaA"

/locus_tag="EFAGFIKM_04960"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37584"

/codon_start=1

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/product="putative chaperone CsaA"

/db_xref="COG:COG0073"

/translation="MATFEEFMQHDIRVGTVEAEFPKARIPAUKMTIDFGPLGLKR
SSAQITQRYTPDMIIGKQVVAVVNFPPRRIAGFVSEVLVLGGVPGEGDVILLTPDSPL

PNGTPIA"

CDS 5645279..5646559

/locus_tag="EFAGFIKM_04961"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MRKMMISCVTVLALLTGGIVGFGGVGSSVEAAQATTKFKDVPAT
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DVTNTVPAKEYFTGKLASGQKNAVAVALGTGLMSVANDKTFGVDRITTTAEVAVLIA
RYAAVAKTKPADFQGLNELRAVGLTGTNLNVIAPSYKKTPEKKVNPNDYDSVTEDFS
KIRNKNLVTLTNYSDLKIHNWIVVSPYAVGAKRSIYYPVFVDEGVITTLRGAYHSFVE
FELNIKSSSMNQLQAGSLLNSSAVDPLLSPKTKTSASFGIPTNIEFLKSKGVFTVKDP
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CDS 5646567..5649941

/locus_tag="EFAGFIKM_04962"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

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VDEFDGLSTKFQMIGGAIAPTASREYNPPKWSADYIFRTDLYWKALAEITKEINLTA
GGQLNLNQSKQLNATVKTNGDGNFGAETNVNTGSGGTTTWESSNPGVATVNNSGLVQ
AVSRGTTTTITVLWEKDDFQLTTTTNIGVEENPGTGEGDGNGGGGGGCTPTIGPPSAGT
IMSMNDLDPNANGVIKSDNRDNETFNLKGIPTSESLYTNAFADNYLFKQAWAKMSGK
VTYNCNVTISYDREWTVPGPEECDDDGCTPGPPVPANDTVPKPYNFQITRDYSYWKIN
NLEVYKIAKATMNNYALPGETVTMNPTGYTPPTLESKNDESVEHVPRGQTTSISYTP
PKLTGGLNQPPSVDDTSRLKGMAESNTPQSKVNNDLVKFNNTPIMNDVEATKDGPTP
SNIPNPTTIGRDVLYKPGNMISNSLLNKANTTSSGEIYYDLLPGNVNGGSNKILPING"

INTVTVHTPVVNYAWVSDDQPHNQKTVDPDPTSAALILERPFIVRIPTSGQHLDAAASP
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VFRKRLGSPEPTGYSYWTGMNSIDGDPRGNLAPFALPIRPGSHPVQGFANATVKTGYH
FKFDLKTGKNMFGKQDGIRITPTFAFVSKDGSSRQEVDLYYHRGQERLIRIGSAQDLE
KRFVVLNSRLRNVPGETELGDTARYQYTYELTAEERNQRTLAEHMOVRLVDQTS HQKTWV
GRYDWMILSAPIRTLIGPKTDIPSGVNVDRANAAIQRWYGEYSLPADVYAVPKGTDLE
PLARQNQLDEKSNVFLKNGYIVVNFNMESLRNGNTEAPHLQYIHAPLMNQWQMEGFNK
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CDS complement(5650924..5651751)

/gene="araC_8"

/locus_tag="EFAGFIKM_04963"

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/inference="similar to AA sequence:UniProtKB:P0A9E0"

/codon_start=1

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HYIHEGRGTVYMGDQEYKLTQGQGFVILPDTLIHYEADPQEPWTYSWFGFKGVQAKAF

MQRAQLSPERPIYDAHDTNTMEQLYTEMVQAFTRPGGDVMNQSLLYRLMAELISSPV

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CDS 5651956..5653257

/gene="melA_3"

/locus_tag="EFAGFIKM_04964"

/EC_number="3.2.1.22"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34645"

/codon_start=1

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/product="Alpha-galactosidase"

/db_xref="COG:COG1486"

/translation="MNKITFLGAGSTVFVKNVLGDVMMTEALQDFELALFDIDAERLS
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GLRQTIADTLGIGGIFRNLRITPVMLDFARDMQEVCPDAWFLNYTNPMAVLTNVMNVH
GRIKTVGLCHSVQVCVPHLFDALGIDQTGVVAKIAGINHMAWLLEVTKDGDLYPEIK
RLAKEKQKEQHDDMVRFELMQRFGYYVTESSEHNAEYHPYFIKQNYPELIERFNIPLD
EYPRRCVNQIEGWKEMRTKLFASENIEHTRSREYASHIMEAMETNNPYKIGGNVMNNG
LITNLPREACVEVPCLVDGSGISPTYIGDLPPQLAALNRTNINTQLLTIEAAITGKKE
HIYHAAMLDPHTAAELSIDDIVAMCDELIEAHGDWLPKYTS"

CDS complement(5653373..5654074)

/gene="kdpE"

/locus_tag="EFAGFIKM_04965"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P21866"

/codon_start=1

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/product="KDP operon transcriptional regulatory protein

KdpE"

/db_xref="COG:COG0745"

/translation="MNAPLGARILVIDDEPQIRKLLKVTLQAHQFELHECGDGEEGVI
QASIVHPDLIILDGLPGMSGMEVLRRIREWSQVPIIVLTAKDQEGDKIAALDGGADD
YVTKPFGMGELVARIRVALRHVAKTTDEPILRFGSLTIDLAQRQVELEGLTVKLTPT
YEMLKVLASNAGKIITQRQLLQQVWGGHHHESDSHYLRVYVGHLRKKLNEDPTNPRYI
QTEPGIGYRFLPAE"

CDS complement(5654076..5655674)

/gene="kdpD"

/locus_tag="EFAGFIKM_04966"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P21865"

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/db_xref="COG:COG2205"

/translation="MSEQIKKETRAAHGKRVPAYAYVWVTLGVTLLTLLHTIGMSGD

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LTLGKPAAVYLPNGQGDLVTSSSAPASEWEKDGWGDGESEIAIAKWVYNHGHIAKG

SSTLRESLGLYVPLRTEEQIHGVLAVSMDAGEVHEQQEQLRLLLEACGGLAAGAIARVK

LAEEARLAQITAESERIRTALLDSVSHELRTPLTAIGSATGLENLFTLPEDRREL

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QVELPDAPAFIYGDEVILLEQVLNIVSNAIKYSPDESLIVITVSDKSPSQTIVVAD

QGIGIPEAERLRIFDKFYRSESTQHVTGTGLGLAICKGIVEVHGGTIVAEPNPGGGTR

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CDS complement(5655682..5658021)

/locus_tag="EFAGFIKM_04967"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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PGSVRQKRYEDILLNAGISVITTMNVQHLESLNDAVEHITGVRVRETVPDRIIQMA

DEVQLIDVAPQALRQRMREGKIYATAKVEQALANFFKIGNLIALRELALRELADDVDE

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CDS complement(5658110..5658670)

/gene="kdpC"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94606"
/codon_start=1
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/product="Potassium-transporting ATPase KdpC subunit"
/db_xref="COG:COG2156"
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QQENPGLKQIPADLVTGSGSGLDPDLSPEAAEAQIPRISEATGLSEQQLVQLVNEHMQ
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CDS complement(5658732..5660873)

/gene="kdpB_2"
/locus_tag="EFAGFIKM_04969"
/EC_number="7.2.2.6"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P03960"
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subunit"
/db_xref="COG:COG2216"
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CDS complement(5660941..5662620)

/gene="kdpA"

/locus_tag="EFAGFIKM_04970"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32327"

/codon_start=1

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/product="Potassium-transporting ATPase potassium-binding
subunit"

/db_xref="COG:COG2060"

/translation="MGIGVVQVAVTLLIILLVKPMGKYVVKVFDGQRTGLDRVFGGP
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RRDELGNFYVDLVRISITRIFLPLSFIVALFLVFQGVQPQLAGAVNATTLEGAQQTISR
GLVASLESIKHIGTNGGGWFGTNAAHPFENPTALSNLVHIVCMMLLPTALVYAFGLRV
NNRKQGWALFAAMSFLFLVMLTTVFVSEYRGVPALDAAGLQGNMEGKEVRFIPESAL
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CGLMVGRTPFLGKKIEGKEVKLASIALLIHPLIILGPTAIALMRPEAIAISISNGGMH
GLTEVLYAFASGAANNNGSAFAGLNANTDFYNIAIGIVMMLLGRYVSMIAMLAAGSLAT
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CDS complement(5663082..5664278)

/locus_tag="EFAGFIKM_04971"

/inference="ab initio prediction:Prodigal:002006"

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CDS complement(5664355..5664894)

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CDS 5665311..5666165

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CDS complement(5666268..5666696)

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/inference="ab initio prediction:Prodigal:002006"

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CDS complement(5666864..5667457)

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CDS complement(5667504..5667731)

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CDS 5667909..5668784

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CDS 5668781..5669563

/locus_tag="EFAGFIKM_04978"

/inference="ab initio prediction:Prodigal:002006"

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CDS complement(5669612..5670484)

/gene="iolE_3"

/locus_tag="EFAGFIKM_04979"

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CDS complement(5670497..5671372)

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CDS complement(5671411..5674557)

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CDS complement(5674554..5676866)

/locus_tag="EFAGFIKM_04982"

/EC_number="3.2.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:T2KMH0"

/codon_start=1

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/product="Beta-xylosidase"

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TRGKRYLEMDLAPQYPFGYGLSYTEFKYENVRVIPDVIGPDDEAQVMVEVTNTGAVSG

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CDS complement(5676912..5679131)

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/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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CDS complement(5679307..5680944)

/gene="lipO_15"

/locus_tag="EFAGFIKM_04984"

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/inference="similar to AA sequence:UniProtKB:P37966"

/codon_start=1

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CDS complement(5681074..5681982)

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CDS complement(5681998..5682975)

/gene="yteP_34"
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/inference="similar to AA sequence:UniProtKB:C0SPB3"
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permease YteP"
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CDS complement(5683473..5684885)

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CDS complement(5685382..5686440)

/gene="iolG_11"
/locus_tag="EFAGFIKM_04988"
/EC_number="1.1.1.369"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01671"
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CDS complement(5686693..5687559)

/gene="iolE_4"
/locus_tag="EFAGFIKM_04989"
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CDS complement(5687826..5689607)

/gene="bga"
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/EC_number="3.2.1.23"
/inference="ab initio prediction:Prodigal:002006"
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CDS complement(5689609..5691069)

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/inference="ab initio prediction:Prodigal:002006"

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CDS complement(5691143..5691865)

/gene="cutC"
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/inference="similar to AA sequence:UniProtKB:P67825"

/codon_start=1
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CDS complement(5692697..5695480)

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CDS complement(5695937..5697025)

/locus_tag="EFAGFIKM_04994"

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KSILFAAFTSIFVIAIWWQYFDNVEKKVSKEIQTAGQAIYGHFLFIYISMSMIAASIQ
LLYQNQLNYVFM LGFVFGSTLLYFLSTSLVFHRYRHAHLRLRPFLAVMVGLLVAFVL
VDLIYRVPGYVIMGEEMLFFLVYAKLTT"

CDS complement(5697267..5698223)

/gene="mhqO_2"

/locus_tag="EFAGFIKM_04995"
/EC_number="1.13.11.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P96693"
/codon_start=1
/transl_table=11
/product="Putative ring-cleaving dioxygenase MhqO"
/db_xref="COG:COG0346"
/translation="MTIQTAGIHHITAFAGDPQANVDFYAGVLGLRLVKKTINFDAPD
VYHLYFGDEHGSPGTIITFFPSAGSPRGKIGGGQVGITSYVIPPGSIGFWQNRLEQYN
IEVTKTSRFNEDLLQFEDGEGLRLELVEREEGATSTWAHEGIPTDKAIKGGGAVLFS
VNPQRTMDALEKILGFVRVSENEEYARFRSSGDIGNVVDVPVTRIPLGMGGAGTVHHI
AWRAKDDEEHAQWSEAVRDYGYQPTPVRDRQYFNAIYFREAGGILFEIATDPPGFAKD
EPADSLGQKLMLPEWFKEYRPQIEDNLQPIEVRTLVPATAAN"

CDS complement(5698356..5698586)

/locus_tag="EFAGFIKM_04996"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31818"
/note="UPF0291 protein YnzC"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIIPTLTRINELSRKAKEGGLTEMEKEEQVRLRQEYLQTFRGSV
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CDS complement(5698834..5699877)

/locus_tag="EFAGFIKM_04997"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGFFRNQFSNVVEEFRDDMIFWKWSNREIKKGSKLIIRSGQD
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WGTQSPVLIPTPQLPGGMPIRANGTFNFKVSDYVTLIDKIAGIKQSYLVEDVKIRITS
VLDQLLMKWISREGKDMFNLQANASDIAGIQEDLDMQMMDIGIGITGFQVMSFNYPK
EIQDMITKTASHEMIGNLQKYQQVSMTDGISSGKVQGGGAASDMAGMMMGMNMANEMM
KNMNQNQGQNQNNNANSSSNQNADQKPAGNSNGNSNTSSSTEGNKKPNFCPNCGAKNE
GANFCPNCGQKLG"

CDS complement(5699955..5700755)

/locus_tag="EFAGFIKM_04998"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRKRTPLAVMAALILLMITLVAPSIPMSSASAAESKNLIYDEAN

LLSEQEISELNLLANQYGAERQTDFVIYTSNNEEHKSEILLTEDFYDHQGFYDKTHG

NAVILTIDMYNRKMYLAGFYKGEEYIDNGRAAKITAKIASDVSDGNYRLAFEKYLELS

YEYMDLKPGVNPDNILFKTWFLAVSVAIGGIVVGVMTHRSGGRVTVNRATYEDSSNS

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CDS complement(5700752..5701783)

/locus_tag="EFAGFIKM_04999"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPVIEYKCPNCGSGMIFDSVSGALSCPSCGRQDNIEQIPDPLKR

QVFTENEVKEYHCNSCGADIVTEPETSATTCSECGAAVVLSDRLTGNLAPAMVIPFSI

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YLAGYIAEKYSYTDEELFPRAKDKTRSYIDSYIASTVSGYSSVSYTDKQIDTTLKNAD

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SWMMGGGFL"

CDS complement(5701820..5702524)

/gene="ydjF_3"

/locus_tag="EFAGFIKM_05000"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54617"

/codon_start=1

/transl_table=11

/product="Phage shock protein A"

/db_xref="COG:COG1842"

/translation="MGILSRFRDVMKANVNHMLSRAEDPEKSVNEYMRSLSSDLGKVK
AETAAVLSDESKRALDECSAEVKKLQRYAEKSAELGDEDKARGFLEKKVKLADKMN
ELQAAYERASAKAKMMKHMNDKLVDLGQLEARHAELKGRIADAKAQQQANERNASAG
RADAAFKAMEDKANQALNEAEALAE LRAGA QEDDLDELIAQLERDMNADAGNNESASP
SAEEELAAIQEKLKNK"

CDS complement(5702729..5703682)

/locus_tag="EFAGFIKM_05001"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRIVLKRLGYGALAILGVMLMCIVISFTNHTIKLKSELSILSPP
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YGFSETAEVSRDIDTILEETRTALTLAGQNPYPVLFPHSMGIEALYWAQRYPTEVKA
IIGLDPAIPEVYEAYPLPSECMMSLTGLGARMGITRFFPGIVDSSAAIKENHLSPQEE
ELYRALFYKNTQTSNMNDEVNMIKQNAAKVATQGIPDVPMYFFISNGEELPVENWKTY
LITYIESVKMGQYQILDGGHYIHNTDSDRIA EKSVLFIKGL"

CDS 5703801..5705600

/locus_tag="EFAGFIKM_05002"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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LIKKA VTIPVIDVQLSGYDMIRSLTLASQFNGQTAIVGFSNITSGAQSIIIDLMDLPLK

VYTIHSSSEDVARLLLLLELKASGYRQIVGDVITVNTAKTYGLEGLLIQSGQESILRAMED
AQLVYRYLSKNHAISIILNDLVTREHPNLLILNERNEVVFENLTDFGKNPLTDNHIYL
TNTSLEFHQSQIQNVFMVDDYQLTVNAYETTLDNKNYKVYMLEKGQPYAFAQFGITTF
TDASMEPIVAESPAMQAVLQNIRALYENHEPIYLRGEADSGKSFLVKHIHQMYSGGGL
LLQMDLSQVPPGHLHKIPLAKVRNVEINHMETRMEDPELLAFIQSCLQNQIGVFILGE
QILNPQWSLDLELNTIMMPNLADRPEDLAPLMQHFLTDYYHKYGTAVRIKEDALQLI
QDQITHMNVNQLKHLIKQAALNEQDYVITTATLSRLLDQQPSSSPMKLNGTLKEIEKE
VIQFVLQEENNNQSKAAERLGINRATLWRKLD"

CDS 5705768..5706754

/gene="kdgT_2"

/locus_tag="EFAGFIKM_05003"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P50847"

/codon_start=1

/transl_table=11

/product="2-keto-3-deoxygluconate permease"

/translation="MNIKATLDRIPGGMMVVPLLLGATINTFFPNALRIGGFTEALFV

NSASTLIALFLFIAGTQITFKTAGSSVGKGLTLLTFKWVIGAALGFIAILFADSNGLF

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GFANGMFSPMAFVAVLLPLIVGVIIIGNLDRNLGEWLHKGSDKLVPPFAFALGMNISFS

SIIQGGLSGILLGVLTVLLTGGIGFLLFKAIGWNPIVGASEGSTAGNAVGTAAIVAA

NASFGPIAEIATVQIAASVTTAILLPIFIGFLSKRLEKSGGVEKYNQRPTT"

CDS 5706850..5708145

/gene="dtnK"

/locus_tag="EFAGFIKM_05004"

/EC_number="2.7.1.219"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8ZRS5"

/codon_start=1

/transl_table=11

/product="D-threonate kinase"

/db_xref="COG:COG3395"

/translation="MKLAIADDLTGANDSGVQLARHGLKTSVLFNIDEGPLTRYDAV
VFDTDSRSISSQEAYDRVYQAAELLTNNGFETIFKKMDSTMRGNIGIEIDAVYDVVKP
DFMMIAPGYPKNNRTILEGIHYLNGVPLADTEIAHDPKTPVTISYLPDLLKQQTKEYE
GEITVADLEAGQNHTRTKLEQLKTNNIPYVMVDSTEERHLELILQMTRELEYTFTWAG
SAGIANYLPAHYELESRAASLDIPENSGPILTVVGSVNKNSREQLHRLMRNSRVASVS
FHSFKAVSATADRAEEMERVYNEVRDKALEGQDVVLYSTAEQVDIELARATGEIRGLN
HTEVSNEIVLAMGEICARLLEEGLFKGVSMGTGGDTAKQICLKWNISGFELLDELEIGV
PISKFIGIDDLHVITKAGGFGKPDVFIHAIQKLKGGILV"

CDS 5708142..5709143

/gene="pdxA2"
/locus_tag="EFAGFIKM_05005"
/EC_number="1.1.1.408"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q0K4F5"
/codon_start=1
/transl_table=11
/product="D-threonate 4-phosphate dehydrogenase"
/db_xref="COG:COG1995"
/translation="MKPTIGITMGDAAGIGPEIIMKALGHQEMYDQCNPLVIGDAKIL
ERVLPIVGSSLNVNAIQEPSEAKYEFGTVDVIDLNLVPADLEYGKVSAMAGDAAFQFL
AKAIDLAKKQQIHSICTAPLNKEALHQGGHLYPGHTEILADLTDQDFSMMLTTPNLR
VIHLTTHMGLIDAIASINPERTYTVVKLAHDTLKKAGFENPRVAVCGINPHAGENGLF
GNGEEREEKLQPGIERAQQEGINVVGPLPADTLFFRAGRQDFDIVVACYHDQGHAPIKV
MGIEEGVNITVGLKGGIIRTSVDHGTAFDIAGKNIADDKSMLAAIRSAIELAPKDQG"

CDS 5709450..5710016

/locus_tag="EFAGFIKM_05006"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGRKQSFTETELLDTTKKLVLEHGYDGFHLKLLSQHLSGARSTI
YQYYSNKEEIVAACMKRSISTVLENSLAIDETDPMDALEQLLLIYAEESTLHQLLGDA

SKINTTNSSAAARDIEFIEKAHMTLKIQLSRLFERAQDQALRQDIPLPVLVGVFFNL

INTPNMMNIPTPDWGKLLFQMWVGGAKS"

CDS 5710139..5711260

/locus_tag="EFAGFIKM_05007"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WG17"

/codon_start=1

/transl_table=11

/product="putative ABC transporter permease"

/db_xref="COG:COG0577"

/translation="MFLAMKELMHSKMFKLMIIFVLMAWLVFILSGLGNGLSTLAA

STFKTMKADYVIFEEGAQSSMSKSLSDQLVAEAEKLPNVDAAPMGSTMATAALKENS

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GTTESLTIIGYVENQTYNHVASVFTPMAEWRKIAFAAPSSDKGIAGPVNAIMLQGENI

DPEAINKELSSTDVTTRSEAVPGMPGYKEENGITLMMLAFLLAISAFVLGVFFYVITM

QKTNQFGIMKAIGASNRFLGKAIISQVFLALTSIVVGILLTYGTAAIMPKGMPFKLK

TSLVFNYSVILLVIAMLSLVSVRKITKIDPLKALGRVE"

CDS 5711260..5711943

/gene="hrtA_2"

/locus_tag="EFAGFIKM_05008"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q99RR8"

/codon_start=1

/transl_table=11

/product="Putative hemin import ATP-binding protein HrtA"

/db_xref="COG:COG1136"

/translation="MSKGLHMREVTMYAEGNNRITALDHVSISVEPGEFVAVVGPSG

SGKSTFLSIAGAMLKASEGDIQLNGNHISKLTEKELSNIRLQEVGFIMQSSNLVPYLN

VLDQLLVVKRMAGTIKKEDKVFATKLLEELGLGLKLKSFPEELSGGEKQRTAIARALM

NNPNIILADEPTASLDTKRAHEVVSIAQEVKSRQKAAIMVTHDERMLEYCDRVYRMV

DGGLSLAES"

CDS complement(5712067..5713008)

/gene="rhaS_41"

/locus_tag="EFAGFIKM_05009"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MTPSVLAYEQGYAIHVNQPGDSLFIHLDDYDERSHELNMEFQHFIH

DFYEICILLDRTAHHIEGSLYEIQPLDIVLLRPSLLHKTQYPKGAPPKRLMITFAMP

RHIPGLESgyTELFsIFDKPVIFRfTEERRKEVLAPINDIFAISQQPSALQSVMIHS

KFVEFLCALHRYSPENGYVREETGSTMSRRMYAIASYIHSHYQQDLSLDEVSKRFYVS

AHHLsrQFNKVTGFTfTEYVQMTRIRNAQQMLLNSSEKITDIAAQCgFTSFSQFNRI

NKQNGMSPSAYRRSRHSQSEREVMLVGERPEPIGSLE"

CDS 5713208..5716381

/locus_tag="EFAGFIKM_05010"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKMNSLYTRIHTIVKHLERARLTskTYIPELYHKESGYHSWELV

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QVSDLYYDLKAALDAADLLREDDLERLKLVEHLNKAVNLLDLRQENSAEFHVSVLEAR

RYLQDHVYGDIRPAGDHIPTVHCIGHTHIDVAWLWTLTDTREKVIRSFASVLYLMDKF

PEYTFMSSQPQLYAYLKADYPSLYEKIKEKVAEGRWEAEGSMWLEADCNLISGESMIR

QIIYGKRFFKEEFGVENRVLWLPDVFYGSAAMPQIMRKSGIDYFMTTKIAWNDTNQIP

NDTMYWRGIDGSEVLTHFITATDYDKHPDFRQRRFETTYNGRFNASQVKGTWQRYQNK

NINADVLQCFGFGDGGGGPTEEMLEHGRRLDVGLPGVPAVKRTFVREFFEKLEQNLAD

VPSVPRWSGELYLEYHRGTYTSMARNKRYNRHSEFALADAELYAMIHRQANAQAAYPT

DALEHAWKLTMLNQFHDILPGSSIEQVYVDSKEQYEEVLRVTDELKDSALNGIASQIT

SDGEAIVVFNTTGfVRTDVVELPAFARKVTYDGDPRVPSQRTPEGGLVFLAENVPAS

GYKSFRITPDLTDELVAGVSVAQWEADRRHIHTPWYDIHLNESAEFTSVWDKLEGREL
LQSGKRGNVLQVFEDRPAEYEAOWNIDDYEQHMWEINDLQSLEWVESGPVRSVLQVTR
QFLDSVVEQTIIFYAHTRRIDFRTFVDWKQEHLKAAFLDIWSEKAVYEIQYGNVE
RATHRNSTWDQARFEVCGQKWADLAENGYGAALLNDCKYGYDIHNSVMRLSLIKSATY
PNENADKEQHVFYALYPHQGDFREGRVIQAAYDLNRPLVAREVSPQTGTLPGTWSLA
SVDQDNVWLEVIKKAENDDMIIRLYEAHGRRSRASLQLPEGAGATTYACDLLENNEA
ECAVENGRVSFDIKPYEILTRIPAGQ"

CDS complement(5716498..5717352)

/gene="dkgB"

/locus_tag="EFAGFIKM_05011"

/EC_number="1.1.1.274"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P15339"

/codon_start=1

/transl_table=11

/product="2,5-diketo-D-gluconic acid reductase B"

/translation="MNHQIPEYTLNDGLKVPAIGFGTYSKGEEGVKSIASAMDAGYR

LIDTAYNYENEATVGRAIKQSSIAREELLISSKLPGRYHAHDKALVAIQESLYRADLD

YYDLYLIHWPNNPKKDMYVEAWQALIEAKKRGYIRSIGVSNFLPEHNERLIKETGIAPS

LNQIELHPFFDQADQREQDTKHGIVNESWSPIGRGNDVQDILKDENILRIAETHGKT

PTQIILRWHVQLGSIPIPKAGSLQHQQENIDIFDFELSTEEMQVISAFNRPDGRLWDQ

DPSEYEEF"

CDS complement(5717518..5718765)

/gene="tylCV_2"

/locus_tag="EFAGFIKM_05012"

/EC_number="2.4.1.318"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9XC67"

/codon_start=1

/transl_table=11

/product="Demethylactenocin mycarosyltransferase"

/translation="MARVLVMMMPAEGHINPSLGLIKELIESGDEVVYCCTEKYRTKI

EALGAQFKAYSFNEATLLNNPNMKPFEIKHPYQFLYMILKKITQRFIPDVLNLIENET
YDYLIFDSLIGWGGQILGEKLGIP TICSTSTFVFVEPLGSGSYNLKDDNEEVQELYNG
IMEMSQQLASRFNVAAPSLAELSGHPGQLKIVYTSSYFQPMGDKLDDSFVFTGPSIIP
RKDAPAFANESLHALYKQAVYISMGTILNKDLEFYKLCFTA FRDLPVQFILSSGKDTD
LEPIAELIPDNFIIRPYVPQLEVLQCVDAFLTHAGMNSTSEALYYDVPLIMLPLTSDQ
PRVAGRVQELGAGVIVDKNNLTPDVL RNAVLEVLGNASYKEHAEVIGKTLRDAGGYKQ
AAMA IKNFIGNQPISATPISSFE"

CDS complement(5718950..5719399)

/locus_tag="EFAGFIKM_05013"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKTLYS AIMVTLLSGSIVGTALADNYESNDTLSSAYKIPTQTV

ATPYGPAYWGGS AWSYLSSPTDVDYFTFRGHGKSVVLGSPSGYDYDLYAYDSAGNLVA

SSTNTSGADTVLVDYNNVYFKVVSKDGRYSDDAYS VTFYKRDVWVP"

CDS complement(5719780..5721033)

/gene="ybdG"

/locus_tag="EFAGFIKM_05014"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AAT4"

/codon_start=1

/transl_table=11

/product="Miniconductance mechanosensitive channel YbdG"

/db_xref="COG:COG0668"

/translation="MDFIRNQLEELGMSGPSIGYLSNIIMIIFI AVISILANVIAKRV

VLKTVHRIVSNNRFBKWHIVVQKNLFQKLSHLVP AIIYY SAYIFSPYQAII EK SAMT

YMIVIMITVLNALLNVFDDIYRTYEVSKIRPIKSYIQVAKIVLFIIGGIIVISSLIGQ

NPLIILSGLGALS AVLMLVFKDSILGLVAGVQLSSNDMVRVGDWIE MPKYNADGDVID

ITLNTVKVMNFDKTITMIPSYALISDSFRNWRGMQVSGGRRIKRSIYIDISSIRFCTE

EMVAEFEKIHYLT DYVTAKLKEIQAYNMEHQVNTESNVNGRQLTNVGVFREYIHQYLR

NHPKINKDMT MIVRQLAPEDRGLPLEIYAFSNDINWGVYENVQADIFDHIFAVASTFG

LRAFQNPTGHDIVQLKEDKQYAREY"

CDS complement(5721150..5723954)

/gene="recD2"

/locus_tag="EFAGFIKM_05015"

/EC_number="3.6.4.12"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01488"

/codon_start=1

/transl_table=11

/product="ATP-dependent RecD-like DNA helicase"

/translation="MDLDKIMIIKKGKEKTEEVSYKVGPSGVQIIYRDLDEYNYRN

QDVLIFQEPYIQEPGDNIAIYHDDVPFNNVKRVWDFGVKIRICFENASMRVYDKDRIR

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VLGQIIQKNPIKQEKMLTVDPVFPFSFNLSQKKALEHALTSNISIIEGPPGTGKTQTI

LNIIANLAIMQGKKVAVVSSNNAAVLNVQEKLERKGYHFFVASLGNQENKKKFFVNLP

KVNMSDWDVDISEAECDRINHFDRLHRLMEMDREKAQCKQKLSAYLLEQEHFEHYF

ARQDVSHIEKLSFYKQTPNKILEFMKDSFLAVEIKKKYKLFYPFKLFFKHGFTDFKKL

KKQGLDVILNYQRQFYILRIEELSNQILKIEEELKSYNYQDLLDDHQHCSENLFRLKL

HKKYHNRSVIQSNEKSYIHLNLFKDFIENYPVVLSTTHSLRNCVPPNYMFDYCIIDES

SQVDLLTGALALSCCKHAIIVGDTKQLPHIVDLKIKEKLKNSLYPDMSSAYDYFEHNV

LSSLLALYGDTLPSVILREHYRCHPAIEFCNRKYYNGDLITFTDPQMSDSPLMIYRT

AMGNHMRKLTHGKKGRFNSRELEVIEQEILQAELDVVDIPSNI GFTTPYRKQLEKAVQ

HFTVDIESDTIHRYQGREKDTMIMSTVLDRTKLGNMGMKFNPNPNLINVAVSRAQRQF

ILVTDHSAFHRYGNEVGDLRMRYMEYSTLDDNVVESEIVSIFDILLYREYSEKLREFRNR

ASHYNNNSRYKSENLMALLTQILEEPQFKDFTLSSQVYLMNIFVDLDRLNEEERKFIK

HFSSVDFAIYHKLDRSLALAIEVDGFEFHENKPDQIKRDEIKEAIFRKFGTLARFKT

NESGEEQKIINLLNGMIDPE"

CDS complement(5724087..5724728)

/locus_tag="EFAGFIKM_05016"

/EC_number="3.5.1.104"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81AF4"

/codon_start=1
/transl_table=11
/product="Peptidoglycan-N-acetylglucosamine deacetylase"
/db_xref="COG:COG0726"
/translation="MVNIVMVEQESVREKVVAFTFDDGPHPVYTPQVLEIFRRAGGRT
TFFMIGQEMENHPEIAVEVHREGHEIANHTYTHPDLTKLTLEEVGEELQRAENLVQEV
TGQPVRCFRPPYFGVNDLILSLAAERGYRTIGAVNGDARDWDNPGVEHILEHTRSAVK
PGSVLIFHDGYGDRSQTVEAVRVLVEELVAEGYRLVTVTELLGISREQDEKIT"

CDS complement(5724911..5725786)

/gene="ngcG_8"
/locus_tag="EFAGFIKM_05017"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O50501"

/codon_start=1
/transl_table=11
/product="Diacetylchitobiose uptake system permease
protein NgcG"
/db_xref="COG:COG0395"
/translation="MSTVEVMLQKKPKSRSISGPIGKVFLQAFLILVAIVQIYPLIWL
ALFSLKDNSEIFSGDVAGLPKAFLWSNYTKAMSDGHVLTTFMNSVLVTTASIVLVLIL
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VAFGIPMAVFILGSFFKGIPREMEESAVIDGCGIYRTFFSILPLVTPAISTVAIFTF
LSCWNELMFAVTFINNTAYQTLTVGMMSMVGTIYITQWGIIAGLMITTVPTVVIYLLL
NKQVQKSMIAGAIKG"

CDS complement(5725802..5726671)

/gene="ngcF_4"
/locus_tag="EFAGFIKM_05018"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O50500"

/codon_start=1
/transl_table=11
/product="Diacetylchitobiose uptake system permease

protein NgcF"

/db_xref="COG:COG1175"

/translation="MNSVFSNKGTIAVFVLPTLLFCGIVLIPIFVSSYSSLLDWNGV
GRGTFIGLDNYVEMFKDSRVLNSIKNSLLFAGASVFIQLPISLVLALILASNVKGEFG
YRTVYFIPVLISTVVIAQLWSKIYNADYGLLNVLLQSIGLSSLAQDWLGQKDTALAAS
FIPTLWQYVGYHMLLMYAGAKSVSQDVLEAARMGDGASRIRTAWSIMIPLMKPILKVSL
VFSVIGAFKVFDLIYVLTGGGPFYTTTEVPSTLMYATIFDTFRYGYGSAISVFIIVECL
VCTILINSLFKTE"

CDS complement(5726878..5728191)

/gene="msmE_5"

/locus_tag="EFAGFIKM_05019"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q00749"

/codon_start=1

/transl_table=11

/product="Multiple sugar-binding protein"

/db_xref="COG:COG1653"

/translation="MKALLKKSASLILALGIVSSLAACSSGSSGGTQGESDGKIKLTL
WDQSVGNTPSAKLLPEIVEKWNSEHPDIQVERTGTTGEQYKTKVKTSIAAGEAPDLF
YGMGGGSFMQPYIKSGNVLEISSYLTDDIKERMGPGMAEAINMDGKIYTLPVYTHIAN
LYVNTELFQAGAKIPTTYNELLDVSKLKAAGITPAVIGEKRWPGRMYWYDIAMRQ
AGNAAVMEAFKDPKWDSPDFVAAATKMQQLAQAGAFNSSMFSMSYDEMLGAFNAGNG
AMMFQANWVNAGIEDPSSAVKGKVKVIPFPVFEDGKGNTNTEIFGGAVDGFYINQNTKH
SKEAVEFLMYLSEQLTGQFLAGAGLPSWKTDALDTSSLSSLDLSAADIMKTATSFIA
WWDNILPAESAEAHKNLIAQLLAGDVTPEEFCKQMAQLKPTLSL"

CDS complement(5728379..5730136)

/gene="cheB_15"

/locus_tag="EFAGFIKM_05020"

/EC_number="3.5.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00099"

/codon_start=1

/transl_table=11
/product="Protein-glutamate
methylesterase/protein-glutamine glutaminase"
/translation="MELTVEPLKVLIVDDEYLIRNLLRMRIDWEQQGMTIIGEASDAE
EALDQVELLRPDIVFTDIYMPKMDGIELSGILMERYPNMKIVVVTGHDEFEYARQSVK
LGISDFILKPIRASSELLQVTAKLRAAIEQEMGREYELMKLREEMKQSLPYLRERFVNQ
WLSDVMPEDDELQEKARFFGIPISSGEPGSRIAVMEVKVAVPQAKIAAPEVYQHLSEPY
HPTPQTAEHRGPQQQHGGPQLSQHQTEAHRQPAEEIHILLRMVGMKQVQAFYPQDSQ
TIIVMDPHNRIVLSLGADTEFANQVQQQLQEELQHTLKLEGGEVDVTVGIGQWQSRWE
KACVGYREACRALDYQAFVGKNQVICFEDLVIEGGKRPYHSDAQLLQQLQFYVSVGAG
EEAVLLLERMLSQVFSEVSQFLMAAMDVVTECQRAAIEQQLEGEHALNKEAVAAIFTA
DHLPELKSMLEQHVRMVSDVIQAKRQAKEGNLIDRVKAYLEEKMGNAEVGLSSTAAAF
YVSSGHLGRLMKKETGQTFVEYLTQLRMKKAEMLLKQTDMMKGYEIGEQVGIPDPHYFS
VLFKKHIGRSMNEYRNVKT"

CDS complement(5730127..5732259)

/locus_tag="EFAGFIKM_05021"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKNRAKNVTTEAEETVEEDATTEVKTTATASDVETNAETNENTK
ANTRATSSAMKKKWTPRFKAFIQRKPRTLAFKIPFAYFVILLTVAFSALVLNRISEN
DAQRKINEASLQTITSIETNVNLMIEENVNNYSKMIFSDPNLQNLLRQGNVYSNLQTQS
KVSAYLTNLMQAVPIIDSVYIYDNSGHRFSVGTQEWPTFMEANVKEAPWHEQALKHNG
RYLLRLNSGNNDSGVSATGENDGHEVVSFIRLIRDLDDTSPLGFLVMNIKGASIAQAY
ANLSAPDSFQVAILNEHQVVIATNATDGKKGVPAVSDASMSAASGQEGMYEMLDANQA
KLKQTLQEQQSGFITLQSGGQEYAVTYRSAGDDQWKFISMSPYQATDTRNKSMVLLAL
ILLAVNGTVFFVSSFIISRSVIKPIHKLLRSMQKAPSGNFRKVTVELNSYEFAQLYGG
YNQMIEQIDQMLKRRIIEQQTIRRAELNTLQAQIKPHFLYNTLDSITSLAMSGMNDKV
CELLEALGSYYRLSVSKGRELITLHEEVEIVRNYLTIQQVRYPGVFEVQYDIESGCER
VMIPKLVQLPLVENSLEYHGIRPKGSPGKIRIQARRSKEGVLLTITDDGVGMSEEEIQQ
VHRKEINSSNRSDSTNSSNPSNSINLSNTSNPTYNSKHNPSTFGLWGTMERLRIFYDRE

DGLKLQSEVGKGTIIITIPKGADESWN"

CDS complement(5732822..5733097)

/locus_tag="EFAGFIKM_05022"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEYLETVLTQADLGEVDGCDLGSRVADPKEYVMNIFCVTDEDR

SIALIKKVLRESRLDYTRIQIATMPYGIEGSYTLKYASKKGVTEFSL"

CDS complement(5733293..5734000)

/locus_tag="EFAGFIKM_05023"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSETQQQIREFVAGVQAYVSPVNVINPWKDYVTGYDIGPEAVKI

RSEHLVRYLEPRMSKARYIFIAEAVGYQGARFSGVPLTSERMVTGNHSLVNHQMIFSG

EPGVRTSLPNIAKPNRSQALYGFAEPTASIIWGEVISSSRWKPTDFIFWNIYPFHPYQ

SSENRMNTNRTPTLAELEDGVVFARQLMQLNPDAQIVAIGRKSADTLSSHLIKHHHVP

PANGRAVQFQKAVRSMI"

CDS complement(5734214..5734786)

/locus_tag="EFAGFIKM_05024"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSEIRPVMTVFAGTNGAGKSTLSMQMREWLGEVDPDQIARELK

PENPRSADLSAGREAVIRIRSLIKSGVNFAIETTLSGSFVLKHMEIAKENSYEIVVYY

IGLEDVQMHIDRVASRVEQGGHWIAEEDIRYRYGESLKNLKPALAIADRVIIIDNTYE

PLIVAEIIQSNLIYCAESIPAWANPVLVGY"

CDS complement(5734779..5734976)

/locus_tag="EFAGFIKM_05025"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFENREQLQEILKKANQHARKQAKELGASIYYIKNNKRVREDAE

GNKFEIIFDATGKRQEFHEYHE"

tmRNA complement(5735068..5735429)

/gene="ssrA"

/locus_tag="EFAGFIKM_05026"

/product="transfer-messenger RNA, SsrA"

/inference="COORDINATES:profile:Aragorn:001002"

CDS complement(5736007..5736489)

/gene="smpB"

/locus_tag="EFAGFIKM_05027"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32230"

/codon_start=1

/transl_table=11

/product="SsrA-binding protein"

/db_xref="COG:COG0691"

/translation="MGKNAGQSKVLAQNKKASHDYFIEDTYEAGMVLGTGTEIKSLRNG

RANIGDAFATIRNGEIHNMHISPFEQGNRRNNPLDPTTRKLLMHKVQIHKLLGLSK

QDGYSIVPLKIYIRNGYAKLLLGLGKGKKQYDKRETAQRDIQRVLREKQKVAR

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CDS complement(5736751..5739549)

/gene="rnr"

/locus_tag="EFAGFIKM_05028"

/EC_number="3.1.13.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32231"

/codon_start=1

/transl_table=11

/product="Ribonuclease R"
/db_xref="COG:COG0557"
/translation="MITEQQLLDFMRETAYKPMTYQEQHFAIEDAADFKAFLIMLN
TLEESGKVLLTRNNRYGMPERMDLVRGRLQAHAKGFAFLIPEDREHPDVYIHANDMKS
AMNGDTVLVKVTSQGPSGGRLEGEIVRIVTRAVTQVVGVFQSHEVYGFVIPDDKRINR
DIFIPRTNFAGAVDGQKVVAKIVSYPEGRAAAEGEVIEILGHKDEPGIDILSVIRKHQ
LPEAFPDEVVEEA EKAPDSITDEEIVQQGRRDLRGLNIVTIDGEDAKDLDDAVNVEKL
PNGNYRLGVHIADVGYVYVQENSKLDQEAYNRGCSVYLVDRVIPMLPQRLSNGICSLNP
QVDRLTLSCEMEFNDQMKVVKHDIFTSVIKTKERMTYSNVRKILEGEEPELLERYKDL
VDDFHLMKEIALKL RAMRMRRGAVDFDFEESKIIVDAECKPIDIVKRERSIAEQIIEE
FMLAANETVAEHFHWLKVPIYRVHEDPDQEKLNFLAFAANFGHQVKGRGNAIHPRA
LQSLLEDIKETKEQTVISTMMLRSMKQAKYDSEMSGHFGLAAEFYSHFTSPIRRYPDL
VIHRVIREVIENNGALPENRQEYLAARMSDIAQQSSERERVAVEAERDTEKMKKA EYM
LDKVGEEFEGMISSVTSFGMFIELENTVEGLIRLSALTDDYYHFDDQH MALIGERTSK
VFRIGDEVKIRVARVSMEEYTIDFEMVDMKPRAERPGGFGGGRGGKGRPPGSGGGHS
GTKGGPGGFSGSRGGKGSSTGAGASRGGRSTEESKGGRGGRSGAASAGAGAGSSGGY
AGKGGGKPKGERRASDAGGSTGRGKGAVSFGFGSGKGGYGSTSGGSDSSSTGGQG SGL
NSGSGRGEFSFKSGKGGGKGGKGGSGRKNTSPSGVFIGENATPGGAQEGGAPRRKRKK
SNGAAGNGTAA FVRKKKK"

CDS complement(5740110..5740343)

/gene="secG"
/locus_tag="EFAGFIKM_05029"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32233"
/codon_start=1
/transl_table=11
/product="putative protein-export membrane protein SecG"
/db_xref="COG:COG1314"
/translation="MDIALKLLL VVFSIGLITVLLQHGKSAGLAGAISGGA EHLFGK
TKARGLDLFLQRATVVLGAGFMILSIIVTVASK"

CDS complement(5740557..5741843)

/gene="eno"

/locus_tag="EFAGFIKM_05030"
/EC_number="4.2.1.11"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37869"
/codon_start=1
/transl_table=11
/product="Enolase"
/db_xref="COG:COG0148"

/translation="MTIISDVYAREVLDSRGNPTVEVEVYLES GAIGRAIVPSGASTG
AHEAVELRDGDKSRYLGKGV LQAVKNVNETIAPEVIGMDALDQLGIDKLMITLDGTPN
KGKLGANAILAVSMAVARAAADALDPLYVYLGGFNAKALPVPMMNIINGGEHADNNI
DVQEFMVLPVGAPSFKEALRVGAEIFHNLKSVLSSKGLNTAVGDEGGFAPNLGSNEEA
ITTIIEAIEKAGYKPGVDVFLGMDVASTEFYKDGKYTLAGEGKSYTSAEYVDLLASWV
EKYPIITIEDGMSEDDWDGWKLLTEKLGDKVQLVGDDLFTNTERLGRGINEGIGNSI
LIKVNQIGTLTETFDAIEMAKRAGYTAVISHRSGESEDSTIADIAVATNAGQIKTGAP
SRTDRIAKYNQLLRIEDQLGELAQYNGGLKGFYNLKK"

CDS complement(5742083..5743627)

/gene="gpml"
/locus_tag="EFAGFIKM_05031"
/EC_number="5.4.2.12"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39773"
/codon_start=1
/transl_table=11
/product="2,3-bisphosphoglycerate-independent
phosphoglycerate mutase"
/db_xref="COG:COG0696"
/translation="MTAPKPVALIIMDGFGLRNTVEGNAVAQAKKPNYDRFMSQFPHT
TLTACGEAVGLPEGQMGNSEVGHLNIGAGRIVYQDLTRISK SIRDGEFYDNETLVKAV
REAKQSGKKLHLYGLLSDGGVHSHIDHLFAMLDLAKKEGMNDVYIHAFMDGRDVM PDS
GKDFMQKLIKIEEVGVGKIATVQGRYYAMDRDKRWERVEKSYRAIVYGDGPKYTDPL
KAVEESYEKSVFDEFVEPTVIVKADGEPVGLVESGDSVIFLNFRPDRAIQLSQVFTNQ"

DFRGFERGPKFPVGLHFVCLTLFSETVEGYVAYSPKNLDNTLGEVLVQNNKKQLRIAE
TEKYPHVTFFFSGGRDVELPGETRVLINSPKVATYDLQPEMSAYEVADACVREIEADK
HDAIILNFANPDMVGHSGLVPTIKAVEVTDECMGRVVDVLAKGGVVLITADHGNAD
MVFDEKGRPFTAHTTNVPFIVTDANVTLRGAILADIAPTILDLMQLPKPAEMTGTS
VIATRK"

CDS complement(5743629..5744381)

/gene="tpiA"

/locus_tag="EFAGFIKM_05032"

/EC_number="5.3.1.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P27876"

/codon_start=1

/transl_table=11

/product="Triosephosphate isomerase"

/db_xref="COG:COG0149"

/translation="MRTPIIAGNWKMFKTVSESNDFIQEVKGKAEVEGVETVICAPFT
NLPSLVEAVKGNTNIKIGAQNLFEDNGAFTGEISGVMLKDLGVDYVIIGHSESRQYFA
ETDETVNKKLHAAFRHGLTPIFCLGETLEEREANQTKDICKVQTVAAFAGLSAEQAAQ
VVIAYEPIWAIGTGKSSTSQDANEVIAYIRTLVKDLYNETVANAVRIQYGGSVKPELV
TEYLGQSDIDGALVGGASLQPASFIALVEGAK"

CDS complement(5744418..5745599)

/gene="pgk"

/locus_tag="EFAGFIKM_05033"

/EC_number="2.7.2.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81X75"

/codon_start=1

/transl_table=11

/product="Phosphoglycerate kinase"

/db_xref="COG:COG0126"

/translation="MNKKSVRDIELTGKRAFVRVDFNVPLEDGKITDDKRIRATLPTI
NFLIEKGAKVILASHMGRPNGEVVESLRLTPAAERLSELLGKTVMKADGSGVDAVKAQ

IAELNNGDVLLLENVRFHAGEEKNDPELAKQFAELADVFNDAFGAAHRAHASTEGIA
HLLPAVSGLLMEKELEVLGKAISNPERPFTAIIGGSKVKDKIDVIDNLLNIADNVIIG
GGLTYTFLKAQGHEIGQSLDDSKLDVALGFIEKAKKLGKNFYLPVDIVVSDDFSAKA
NTQIVDIDGIPADWEGIDIGPKTREIYADVIKNSKLVVWNGPMGVFEIEPFSHGTRAV
AEACAETEAYTVIGGGDSAAAAEKFKLADKMNHISTGGGASLEFMEGKVLPGVVALND
K"

CDS complement(5745751..5746758)
/gene="gap"
/locus_tag="EFAGFIKM_05034"
/EC_number="1.2.1.12"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q59309"
/codon_start=1
/transl_table=11
/product="Glyceraldehyde-3-phosphate dehydrogenase"
/translation="MIKVGINGFGRIGRLAFRRIQNVAGIEVVAINDLTDAKMLAHL
KYDTTQGRFDGDVEVHDGFFKVNGKEVKVLANRNPEELPWGDLGVDIVLECTGFFTTK
EAAEKHLKGGAKKVVISAPATGDMKTIVYNNVNEILDGTETVISGASCTTNCLAPMAK
TLQDKFGIVQGLMTTIHAYTGDQNTLDAPHPKGD FRRARAAAENIIPNTTGAAKAIGL
VIPQLQGILDGAAQRPVATGSLTELVTVLNKKVTAAEVNAAMQEASDPETFGYTEDE
IVSSDIQGITFGSLFDATQTKVLTVG DQQLVKTVAWYDNEMSYTAQLVRTLEHFAKMI
K"

CDS complement(5746867..5747892)
/gene="cggR"
/locus_tag="EFAGFIKM_05035"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32253"
/codon_start=1
/transl_table=11
/product="Central glycolytic genes regulator"
/db_xref="COG:COG2390"
/translation="MRTILEVQKQLLPDLMDILKKRYTILQQIMLSDVIGRRTLANS

QMTERVLRAETDLLKAQGLIEIDSAGMKISEAGYDLLQQLEPVAKELFGLSELEERIK
QAYGLQKVVVVPGDSVSPFAKRELGRAGAKALGNIMSDNDVVAVTGGSTTAEVAEQL
NPPTSLKGVWFVPARGGLGESLEIQANTIASTMAKRVGAQYKLLHVPDLLSDHAYESL
IQDPSVQEILQLIRQSRIVIHGIGDAVEMAKRRKLATEIIDELQEQGAVSESFGYYFN
DQGKVVHTMLTGMRLQDIERTDVVIGIAGGKSKAAAIHSLRFGQEDILIIDEEAAAE
VIVAEME"

tRNA 5748319..5748393

/locus_tag="EFAGFIKM_05036"

/product="tRNA-Arg"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Arg(ccg)"

CDS 5748570..5749166

/gene="clpP_3"

/locus_tag="EFAGFIKM_05037"

/EC_number="3.4.21.92"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80244"

/codon_start=1

/transl_table=11

/product="ATP-dependent Clp protease proteolytic subunit"

/db_xref="COG:COG0740"

/translation="MSFIPMVVEQSNRGERAYDIYSRLKDRIFLGSDVNDVVANAI

MAQMLFLAAEDPEKDIHLYINSPGGSITAGMAIYDTMQFIKPDVSTICVGMAASMGAF

LLNAGAKGKRFALPNSEIMIHQPLGGAQQQASDIEIRARRILKMRDTLNRIISERSGQ

PLERIEKDTDRDYFMSAAEAADYGIIIDKVIENVGSQGI"

CDS complement(5749335..5750432)

/locus_tag="EFAGFIKM_05038"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTSWKKWTSALLAAGIIVGSGSVWQDSSVQAASVSSKVTTPTPEV

TLKSGGKTLTQKGLLQGGSTWVSLTAVKDVAGGTLKYDAKTKEYALTAANNTMTISLL
DGEPSVRINNYYPQVEAKLIQGRLYIPFSAMRDYLGVQGNWDGKTKTLTLSKVQNNV
KIKSATVNVTVKNAEVDVQYPQVSGLASKEAAINKVLKDEVDAYVADFKKQTSEFG
GATANRPYAFESSYVVITYNEKGVLGLITQRYEDYAGAHGMTYRTGHTFALDTGKELTL
DDVLQNNKTMRETLSSKKVGEQLKARGGYLDGYKGLNKDQDYVPTGVVFFQLYEYT
AYAEGFPEMPFTYKELLPKGTEPFSNVTGTK"

CDS complement(5750820..5751572)

/locus_tag="EFAGFIKM_05039"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q44642"

/codon_start=1

/transl_table=11

/product="26 kDa periplasmic immunogenic protein"

/db_xref="COG:COG2968"

/translation="MGKQWMKPFGAVLVASTLLVGGTAWVAPGNAYAAEVQGVQQNV
INVVGKGEIQVKPDIAYLSIGVNSTAETAASAQKANAQKVQKVSNLLKNTWKISADDI
QTSQFSVQPNYTYSEKDGGQIKGYTAHHTLTVTYRQMDKIGELDAASGAGANNIENV
RFTVENPESYESQVIEKAVANADVKAGAIKAVKRQLGAVLSVSQGDANVPVYASEA
LMSKAQDTAGGTEIETGQVKVSTILNITYEMK"

CDS complement(5751729..5751998)

/gene="crh"

/locus_tag="EFAGFIKM_05040"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O06976"

/codon_start=1

/transl_table=11

/product="HPr-like protein Crh"

/db_xref="COG:COG1925"

/translation="MTKHPVVRLKTGLHARPAALFVQEANKYSSEVFVEKDDKKVNA
KSIMGIMSLAISTGTEIQISAEGADAEQAVNALVSLVSKEELENQ"

CDS complement(5752254..5753192)

/gene="whiA"

/locus_tag="EFAGFIKM_05041"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O06975"
/codon_start=1
/transl_table=11
/product="putative cell division protein WhiA"
/db_xref="COG:COG1481"
/translation="MSFAAQTKKELTMIIESEPCCEKAELSALIRMLGAVQLSNRKVIL
DISTENAAIARRAYSLLKKQFQVHTELLVRKKMRLKKNNVYIVRIPTMVQEILNSLHI
VSEGFLFTPgistelfQQNCCKRAYLRGAFLAGGSVNNPEGSSYHLEIASMYEEHCQA
LVDLANEFHLNARCIERKKGFILYIKEGEKIIELLSIIGAHQALFKFEDVRIMRDMRN
SVNRIVNCETANLNKTIGAAVRQIDNIRLLQKEVGLESLPEKLREVAEVRLAHPDINL
KEVGELLKGTVSKSGVNHRLRKIDELAEKVRTERYG"

CDS complement(5753199..5754185)

/locus_tag="EFAGFIKM_05042"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9K706"
/codon_start=1
/transl_table=11
/product="Gluconeogenesis factor"
/db_xref="COG:COG0391"
/translation="MKEAGPRRERPRIVVMGGGTGLSVMLRGLKEKPLDITAIVTVAD
DGGSSGILRNELQMPPPGDIRNVLTALADVEPLLSDMLKYRFNTGAGLAGHSLGNLIL
AAMTDISGDFVTAVRELSRVFAVRGEVLPAAGQAVVLHAEMEDGTIITGESKIP EAGG
RIKRVFLEPDHVEPLPEAVEAIRQADAILIGPGSLYTSILPNLLVPKLAEAVVEADAV
KMFICNVMTQPGETDNYTVSDHLKAVHEHIGHQLFDYVIVNNGDIPLQVQNKYAEKGA
KPVVLD MNVLESAGYQVVADTLVLFKTYLRHDADKLSHHIYQLVQNWMLRKR"

CDS complement(5754199..5755098)

/gene="yvcJ"
/locus_tag="EFAGFIKM_05043"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O06973"

/codon_start=1
/transl_table=11
/product="Nucleotide-binding protein YvcJ"
/db_xref="COG:COG1660"
/translation="MLEGEGSPGTGATLIITGMSGAGKTIAVQSLEDLGFFCVDNLP
PVLIPKFAELIEQSNGKIGKVALVIDLRGREFFTALSES LNYIKDHFTIHCEILFLDA
TDSVLVQRYKESRRRHPLAPEGMPLDGIRLERKMLEELKNSATQVLNTSTMKPAQLKE
RIISRFSHLESQMLSVNITSFGFKYGIPIDADLVFDVRFLPNPHYIDHLRPNTGQNSD
VYEYVMKWPETQAFLTKLLDMLHFLIPQYRKEGKSQVIIGIGCTGGKHRSVAISEYLG
KMLGSSETEAVTVSHRDADRDRH"

CDS complement(5755150..5756100)

/gene="glcK_2"
/locus_tag="EFAGFIKM_05044"
/EC_number="2.7.1.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54495"
/codon_start=1
/transl_table=11
/product="Glucokinase"
/db_xref="COG:COG1940"
/translation="MSEKIYVGVDLGGTAIKVGICDEQGQLMHTYEGPTEVDKGVDTV
IANIEKYVRHIVAESPYSWEQLEGVGAGVAGFTNVREGIIVHAPNIGFRNVAIRSILE
ERLGKPIKIDNDANVAALGEVWAGAGKGV DNCVCYTLGTGVGGGLILNGNIYQGFSGM
AGELGHISVVPDLEAIKCGCGKMGCVETVSSATGIIRMAKDAVERGDHTSLALVDKIA
AKEVFDAAKAGDEVAQRIVNRAAFYLGKSMATVAVINPEMFIIGGGVSKAGNFLFDE
IRTVFAKLTPEPLQDGVQILEATLGNNAGIVGAAGLLLR"

CDS complement(5756546..5757481)

/locus_tag="EFAGFIKM_05045"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MILLFLVTVVMNRLQHFITGGLNRLFPINYKVVVILLYMIVIA
VIVLGISRYSRIVDQVVQLTNEIMKFLDSADGDNFASKIAGYLQSFDIKNYTNDALK
YIFALSKWLEFILLVILSLFFLLQKQEISKFTSKFKTSKIGWIFYNEVAYLGDKFVSS
FGKVIEAQLLIAVFNTVLTILGLWILGFPYLFALTILVFMLSLVPVAGVIISLVPLCL
IGYQMGGGLKLSIIVIIMIIVHALEYFLNPKLMAHKTCLPMFYTFIVLILSQHFLGI
WGLIIGIPIFVFLLDILDVNKMEKTEEPVRVETKL"

CDS complement(5757740..5758699)

/gene="trxB_3"
/locus_tag="EFAGFIKM_05046"
/EC_number="1.8.1.9"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P9WHH1"
/codon_start=1
/transl_table=11
/product="Thioredoxin reductase"
/db_xref="COG:COG0492"
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TEVENFPGFPQGIMGPELMDNMRKQAERFGAEFKNGWVEEVDFSKPPFKVKVGGIGEL
EAESIIISTGASARYLGIPGEQENVGRGVSTCATCDGFFFRGKKIVVVGGSAMEEA
SFLTRFATDVTLVHRRDELRAKIMQDRARSNEKVKWALNRTPLEVVPEALGVKGLKV
RNNETGQEELLEADGVFVAIGHTPNTGFLGNAIALDEHGYVVVKPGTTETNIPGVFAC
GDVQDTKYRQAITAAGSGCMAAMDCEKFLEGSIVHDWSETLDK"

CDS complement(5758871..5760604)

/gene="bepA"
/locus_tag="EFAGFIKM_05047"
/EC_number="3.4.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00997"
/codon_start=1
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/product="Beta-barrel assembly-enhancing protease"
/translation="MKGKLVRAEGHLANIPIHLASFFFERAVRSLDRNHVDKALKY"

FRKAVEYEPENPVNHCNMAGILSEKGDYEASNAILANVLEVVDPSMTECYFYMANNYA
NMDRFEEAEQALVTYLEEDTQGQFMTEAEEMMELLYYELDRPTKLNRIKSRKGVVEHD
QARELLEEGKFAQAAELEGMSDDYPDYLAARNNLALAYYMGFLPKAKETIAEVLEQ
EPGNLHALCNLAIFHQENRADQVLLLIKLRVIVPFQHEQVYKLATTMGILGQHDTA
YVHFRRLLKDEETAADPALAHYAAYAAYNTERYDAAERLWHHVSKLDPGSEVSRYYLS
GLEAVKQGEQEPEKLSYHYHLPFDEQFRQWENYGSIGPEEMKNDPLIRSSFFWALRHG
DRATKLQVIHALGMIGDYEYVQQALQSFIEEPGEEKDLLEAAQTVLNGLKSAEHEDRNS
QVVRPFSPVALKSIGKVPSTSGQSDTGSTSHWQAVVDRALQMSEAKAELQQEMERLWT
DYVSRVHPEVPGTKQIEGWAAGLEYLAACKNHSRPVTYQSAERYGISASTVSKYAKQI
HSVCNSKPPLV"

CDS 5761037..5761489

/locus_tag="EFAGFIKM_05048"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRISKIKPLIFILICLFALNGCSKDIENIENKFTLEDVLRALLES

QELDLVSFGITGYPLKLNDVVPEVYSVEVPVEEPEYSPEFIHFYIFNSEKDRINGTKK

FNKHMESAQFTTFPLYEKGNVLIVYWSKTKDDPLFTKPIETALEQLK"

CDS complement(5761629..5763380)

/locus_tag="EFAGFIKM_05049"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYKQLVDSNDRAVERGISRQMLDPESRYGGTIDPFTGVAWVNH

TTGTPTDMCYWGAALSNPDSIYYRDESLNRLLLATEFVLRQFHEDGSISPGWTNYHS

PPDTAFVVGYSQLYQLLLQWEPLQPVLLNMRLFLERTIPTMLTGGCHTPNHRWVL

CAALGFLHEIFDLEEAQRAEQWMDEGMDITPDGEWTERSNGIYSAVSDIMLIHAARL

LNRPELLEPVRLNLHMMVYLVHPTGEIVTDYSGRQDLGSVHDLSPYYLPYAILARLDG

DPLFAGMAAWAGDTLTDPGVCSVNTLIRLMLEPELQQTNNGTRDALPEQYEVMLNEHFV

RGEYLEQMDSVGHGHRISHSRMHTDFGAPVARIRDGATSVTMTEVPSFFALRHGKVR

LLAVQLASYFNPGYVPMQQMTRLSEGYRLTGEQKKGGYGPPIAKMLPESAASAIWPY
LLPHQSRQLTHEQTFRVGAELQPTKNGWNMHLSGQEPEDIMMQLSFVFGSEGELICED
AIETSEGHYLVKGGTLRYTCGEDWLEITGGELGHLAATVREAKLLDKCKVVLVNFMTF
FDKTIQISLSPSMASKI"

CDS complement(5763636..5764586)

/locus_tag="EFAGFIKM_05050"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQHIDKGIYSFSTCWNIRKHDVGEDMIREIADLGFRRELNYNV

TKEMLTIEPMIERGEIGISSVHNTFPHDPDPDYGTDSILLGFEDVKKRAIELLVE

SAEYAQRYGGEAVVVHPGEVFPEDISKDLGKIYNEEGPDSPKYRSKWELMERREAL

SSGYVEKIIASLDEVNRAAAKGLDVRFGIETRSRPQQIPTLAETIITALKGAPVG

IWYDTGHAIMMDRMGLYDSVGEMQGLMDDIVGVHIIHETLGLSDHWCPYVHSDMNFDY

VYLPIMIRRAQVKVYELKSACKAEIIESHDLLMKKLGVTE"

CDS complement(5764636..5765508)

/gene="araQ_31"

/locus_tag="EFAGFIKM_05051"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MSERTSNRIFDIVNISFITLFVIFCLAPFLHTIAISFSSNRAIT

SGEVTIFPKEFNWDAYIQVFSDQSMIYSLGYTTVLTIAITVLCMVFTLAAAYPLTKKK

LKGRKLFMYVIIIITMFFSGGIPEYLLIRDLNLLNSVWALILPGLVSPFNLIILISFF

RGIPESLEESAIEDGSSHVHTLFKIILPLSMPVLATLALFYAVGRWNGFQDSLMIYIND

PKLYPLQLKLFQMVMQNNMVSELTQMEGANRTPLTPESLKAATVIFATVPILLVYPWLQ

KYFVSGAMLGAVKG"

CDS complement(5765579..5766478)

/gene="yteP_35"

/locus_tag="EFAGFIKM_05052"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system
permease YteP"

/db_xref="COG:COG4209"

/translation="MTTTYLKRYWQLYALISLPIIYFLIFRYGPMYGVQIAFKDFNLF
QGISGSEWIGFDAFREVFGRDFYTTLRNTFMLNFLDLVVSFPAPIILAIMLYEVRFK
WFKKISQTILYIPHFISWVIIGGIVYQLFGNQSGMVNGVLESMGLNSIPFLTEKNPWL
VTYLFTGVWQSAGWGTILYLAALTGVNKELEAAEIDGASRLKRIWHITLPSIKPTIV
TLLILNLGHMVSIGFDRPYIIGNTAVREYSDVLSTFVYRVGLESGQYTLATVVGLFQA
VVGLIFVLGSNYISKKATGEGIL"

CDS complement(5766593..5768263)

/locus_tag="EFAGFIKM_05053"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTEKCEILWASFKHSRKAKGDDKMRSKATKGSLLKKWMGLALTMV
MGVSLLAGCSSASKESAEGGTSGNGERVTLKVEIFDRGNSSPYTITNNYLSKMIQEK
FGDPNNIDVQFVPVQRSEEVTKLNVLMASNTDVPDIVFYDSSVFYRYAQQGGLTDVG
ELIDQHGPNNLKKFLGEDTLKFGQVEGQQFAVPGKRAITGRYSSYIRQDWLDKGLPAP
KTTDELYTTLKAFKDKDPGGLGSKNIPMGMALAPAQFETLIYSFIKPVSGDLTYGQRY
ELPLHEGFKESMQFLNKLYNEGLSKDFSLDEDKTQLGKDIQNGNVGYWSEDVDAMFY
GDGTLNHLHKNVSGSEVL PVDVYTNPNADNKHISRYGTNGMYIMIPKSSKRSVEAIK
YLDWMASDNNLIDIYSGVEGENYDLVDGIPVVKEDASQEAQDRLFNAGDTAISNGKN
IGDQATNEKAWIMGFPQNNQEMLKQSIDIANTDTVGPIIFDKPIEAEMKYSTALKDKL
NVIIVKTAMAKPAEFDVYEKEMADFMSLGGTELKKELEEAVQALPAN"

CDS complement(5768643..5770904)

/gene="rhaR_41"

/locus_tag="EFAGFIKM_05054"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MSRNWYYRLLFSYFPIFFLTVTILIFIAFVINDISKEETKKAD
RISSSYMIDTVDRITRDIELSILETVQSQQAYKLYFNNTNLTSSDTVYIAIAQNIRELS
NSSSWIQSIYLYDKRNKHVLTVSGSREVEGFSDKAWIDQMGNSSIGSGWQPVREFDAD
SVQRTPIRVLTVNKDMPLPFGSQGTLVINIKMSSIEQSVDSMVNGQLSFLTITDRDGK
VVYNAHSDQEGSIDGQELNRLALERLGWTISSGIKAGNLFGWVSVISYVWVIAIVT
ICAIVYIVYITRRNYKPIQIIMNRIESHQIRAFEHSGARTDEMKMIDGVLENLINHMM
DYDKKSRENVLMQRSKLFNALLHGEHMENAAEQLKELSPLNDVHDSSRFVWVGEINR
YEKGFQERYTRGEQNTLKFALMNVLQELSRNTGVQCWTEWISVDRIALFVFKEQNDN
NLDMSGQIRVVAEECKSWVEQNLRISLSFGIGPIAQGIGTIRDSYAAAEAVMQRKLLM
NGDVGQADCGETQHPLLDITYTYLQMIADFVKRFRMSSGQWREQLEEIFTAFEQNKLPD
DEIRSLIQAMLQMLSREVAMMSEGLQEELSEENINRWLSAVEEAETLTDVKSLLFDGL
TDLFRTYVAVTETKSYKAMVNEMKNYIEEQFANPDLSLKHLSDRFQITGKHASYLFKT
EFNMKFVDFVTELRMKETEQLLLNTDYSLQDIALKVG YANGITLGRVFKRVTGITPGD
YRRLKREHREPEE"

CDS complement(5771159..5772106)

/gene="prs_1"

/locus_tag="EFAGFIKM_05055"

/EC_number="2.7.6.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P14193"

/codon_start=1

/transl_table=11

/product="Ribose-phosphate pyrophosphokinase"

/db_xref="COG:COG0462"

/translation="MQHSLRIFSGSSNPKLAEQVCDKLGVLGKIKLSRFKSGEIYVH
YEETIRNCDVFLVQSLSHPINELFVELLMIDAAKRASARTVNIIVPYYGYARQERKS
APREPISAKMVADVLTAGANRVVTIDLHAAAIQGFFNIPVDHMTSLDLISDYLLSKG
IKNPVVVSPDAGRASMAEKLANRLDSPFAIMIKRPSHNESVITHVIGDVEGRTPIII
EDLIDTGTILNVVEGLKERGSKNVYVCATHGLFSDGAVSKLNHPSIEEVVVTDSIAL
PDDHPECFKVLVPAPMLARAVRIIVDGGSMATLFKDSGI"

CDS complement(5772187..5773047)

/gene="hisK_2"

/locus_tag="EFAGFIKM_05056"

/EC_number="3.1.3.15"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34411"

/codon_start=1

/transl_table=11

/product="Histidinol-phosphatase"

/db_xref="COG:COG1387"

/translation="MNGLAAIKEASFVRIDYHTHHERCGHAVGKLEEVVQRGVEIGLS
QIGLSDHMPLLHVDPAQYYPEMAMPMDDELPRYVEECFSLKERYRGQIDVRVGLEGDYI
EGWETEIRAIERYPWDYVIGSVHFLGEWDITDFRQTHHWEGKDILEVYRQYYDAVSK
AAATGMYDIMGHTDVIKRFGYVPSTEQTEERISLENAALQAIKSGCAMELNASGISK
PCAEMFPSRRMLTEAIRLGIPLTMGSDAHDPLKLG DYLP EAEALLHELGCTEVAVFEG
RHRSFIPLNV"

CDS complement(5773025..5773759)

/gene="hisI"

/locus_tag="EFAGFIKM_05057"

/EC_number="3.5.4.19"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01019"

/codon_start=1

/transl_table=11

/product="Histidine biosynthesis bifunctional protein

HisIE"

/translation="MTKVSDEIKEQLSLEQVVEHIRWSEGLVPAIVQDVDTREVLMMAYMNRESLKLLESGETWFWRSRQELWHKGATSGNVQTITSLKYDCDGD TLLVEVKPNGPACHTGAVTCFHNEIIGLPEKSADKASDEAGAASASASSGSES RFEVLAELSVIAERERERPEGAYTTYLFDKGVDKILKKIGEEASETIIAAKNKDND ELRLEVSDLMYHLLVLLQERKLPLDDIMSELSRRHERPRRD"

CDS complement(5773752..5774513)

/gene="hisF"

/locus_tag="EFAGFIKM_05058"

/EC_number="4.3.2.10"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WMM3"

/codon_start=1

/transl_table=11

/product="Imidazole glycerol phosphate synthase subunit

HisF"

/db_xref="COG:COG0107"

/translation="MLAKRIIPCLDVKDGRVVKGVNFVNLRDAGDPVELAALYDREGA
DELVFLDISASVEGRETMEEVVRQTAGEIAIPFTVGGGISKVEDMKRILRAGADKIAV
NTAAVLNPQLIADGARRFGSQCIVVAIDAKYNEAWGEWEVYTHGGRKPSGIKALEWVK
QAESLGAGEILLTSMADGTDGFDLKLTAAVSESVRIPVIASGGAGKESHFYDVFTT
GKADAGLAATIFHYKEIAIPALKQHLREQGVEIRD"

CDS complement(5774544..5775278)

/gene="hisA"

/locus_tag="EFAGFIKM_05059"

/EC_number="5.3.1.16"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A1R562"

/codon_start=1

/transl_table=11

/product="1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]
imidazole-4-carboxamide isomerase"

/db_xref="COG:COG0106"

/translation="MSSFILYPADIRDGKCVRLVQGDYNQETVYNDDPVQVALSWEK

QGGTYVHLVDLDGAKAGHPVNDELIGRIASAVNVPVQVGGGLRTVADVERLLGLGVSR

LIIGTAAIEDRAFTEEVLGRYGDKVAIGIDARNGYVATRGWLETSEVQAEVLAKELAA

YGAETFIFTDISRDGMMQGPNEAIVSLAKASGRTVIASGGVSVMDLLRLSRHADDG

VGGAIVGKALYTGSIDLSEAVRAVVK"

CDS complement(5775341..5775967)

/gene="hisH"

/locus_tag="EFAGFIKM_05060"

/EC_number="4.3.2.10"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9KSX0"

/codon_start=1

/transl_table=11

/product="Imidazole glycerol phosphate synthase subunit

HisH"

/db_xref="COG:COG0118"

/translation="MAIAIVDYGMGNLHSGKAVERLGYEALVTGDREEILGADGVIL

PGVGAFGDAMVHLRESGLDKVVKEAAVGSKPLLIGICLGMQLLFSSEEHGEHEGLDIL

PGKVVRFAPGELKVPHMGWNRLEFLHAENPLFTGLEAGHVYFVHSYHALTENRDDL

VTDYGHPVTAIVGRGSNFGMQFHPEKSGELGMKLLGNFLALTGAPVQR"

CDS complement(5775971..5776600)

/gene="hisB"

/locus_tag="EFAGFIKM_05061"

/EC_number="4.2.1.19"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0QX83"

/codon_start=1

/transl_table=11

/product="Imidazoleglycerol-phosphate dehydratase"

/db_xref="COG:COG0131"

/translation="MDKQNGVELENKGAVRQAEVDRKTNETNIQLAFNVDGTGQSTI

ETDVPFLNHMLDLFTKHGQFDLNVQARGDIDDDHHTVEDIGICLGQTLREALGDKRG
IKRYASVFVPMDEALAQVIIDVSNRPHFEYRAEYPSQQVGSFSTELVHEFLWKLALAE
RITLHVIVHYGQNTHHMIEAIFKALGRALDEATMIDPRVTGVPSTKGVL"

CDS complement(5776593..5777897)

/gene="hisD"

/locus_tag="EFAGFIKM_05062"

/EC_number="1.1.1.23"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q606Q2"

/codon_start=1

/transl_table=11

/product="Histidinol dehydrogenase"

/db_xref="COG:COG0141"

/translation="MKIVPAREFDLKREVEYGTPEQNETVRRIVSDLRREGDAALLRY

TEQLDRTKLTAELRVPQEELQAAYSAVEPSFVTAIRQAAANIRAFHEKQKRNSWMDW

QPDGSLLGQVIRPLKRVGVYVPGGKAAYPSSVLMNVIPAQVAGVPEIVLVTPPSTNGG

EGINPYILVAAAEAGVSEMYRVGGAQAIAALAYGTESIAPVDKICGPGNIYVALAKRE

VYGAVDIDSIAGPSEIVVLADDTANPVVYAADLLSQAEHDEMASAILVTNSATLAEAV

QGEVQRQLEVLPRRDIAAASVEQYGAIIVVDSIDEGIDVVNRLAPEHLEIMVQEPMA

YAGRIENAGAIFLGPYSSEPVGDYFAGPNHIIPTNGTARFSSPVDVDDFIKKSSLIYYS

KEALLKNGAAIIELARHEGLEGHARAI AVRLEQEGKAESDNG"

CDS complement(5778080..5778739)

/gene="hisG"

/locus_tag="EFAGFIKM_05063"

/EC_number="2.4.2.17"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34520"

/codon_start=1

/transl_table=11

/product="ATP phosphoribosyltransferase"

/db_xref="COG:COG0040"

/translation="MSDILKVAMPKGRIYKKASKLFREAGLDIPEDVDDTRRLVIEVP

EAGMEFIMAKPVDVPTYVEYGVADIGIVGKDVLLLEEDRDVYELNLGIAQCRMSVIGL
PDWKPGIQQRVATKYPRIASQYFREQQQQVEVIKLNGSIELAPLIGLADRIVDLVETG
QTLRENGLVEMTGILDITSRLIANRVSYRMKNARIQALCDALQEVIPASNEISAGSLR
G"

CDS complement(5778741..5779940)

/gene="hisZ"

/locus_tag="EFAGFIKM_05064"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9K6Z0"

/codon_start=1

/transl_table=11

/product="ATP phosphoribosyltransferase regulatory
subunit"

/db_xref="COG:COG3705"

/translation="MSKPKGFEKPTGFRDYTPHVSKLRTIERNVLECMERWGYRQII
TPTIEYYDTVGVASSTSDRKLFKLLNSRGTTLVLRSDLTAPIARVVSSMLKDEQLPLR
LSYHANVFRSIEEEAGREAEFFQTGVELVGDDSPEDAEEVVALAIASLQAAGVSSFKI
AMGHMGFLNGLLEEVIPGQTAEQEQLKEGELLGRDYVGYRQSIEALNLEPKLKEQLEAI
LRLRGGKEVCTHAVESSSAEAAQSIHLCAVFEVLEAYGVSEHVLIDLTMIGDFSYY
TGMTFEGYAAELGSPVCSGGRYDNLLQQFGRSLPATGFALKTNRIIDGVHGITIEEKK
PVLIQYTPKRRAEALTEAARLRSMGQNVVTL LLPEDGAGASAVSVEARTAQAQEVITY
GSEEGGR"

CDS complement(5780345..5780887)

/gene="dapH"

/locus_tag="EFAGFIKM_05065"

/EC_number="2.3.1.89"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01691"

/codon_start=1

/transl_table=11

/product="2,3,4,5-tetrahydropyridine-2,6-dicarboxylate
N-acetyltransferase"

/translation="MRKVTRYPVEDQNALWHIYKTVSPWKGVRNFIWIQLSRYCPILS
VKNWIFRRMLGMKVGKHTAFGLMVMVDVFFPEKITVGENSVIGYNTTILAHEYLIKEY
RLGEVIIGENVLIGANTTILPGVTIGDGAVVAAGAVVHKDVAPGAFVGGNPLRDLSRA
AASTEETVFNTDGSSQGSVH"

CDS complement(5780884..5781540)

/gene="ppaX"

/locus_tag="EFAGFIKM_05066"

/EC_number="3.6.1.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9JMQ2"

/codon_start=1

/transl_table=11

/product="Pyrophosphatase PpaX"

/db_xref="COG:COG0546"

/translation="MIDTVLFDLDGTIIDTNELIISSFQHVMGGWEHSAPWTREQIIP
HMGGTLEQQMRTFSGQEEVSEYVKGYRAYNDIHHEAMVRPFPHPHVIEWVEALHQAGIVM
GVVTTKIRPSTLKVLERFDLLKYMKTIVTVDVTNPKPHAEPVLKAMTELSADPAKTL
MVGDSPVDIQSAQNAGALSAGVAWSLKGETILNGYGPDHMLHDMRDLLKLIRIETGRS
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CDS complement(5781547..5782572)

/gene="lgt"

/locus_tag="EFAGFIKM_05067"

/EC_number="2.5.1.145"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34752"

/codon_start=1

/transl_table=11

/product="Phosphatidylglycerol--prolipoprotein
diacylglyceryl transferase"

/db_xref="COG:COG0682"

/translation="MDTLLLLNPIAFSIGALKVHWYGLILGAAALIGLLLVIKRGKRY
NIPQEVFMDMVLLGVPSAIIIGARIYYVAFKWEDYKDNFWDVFKIWNGGIAIYGALIGA

IICAVIFFRRKGYNFWRMADICAPGLLVGQLIGRWGNFVNQEAYGGPVEESFLRDKLH
LPDFIVNQMNVEGVFHHPAFLYESMWSLVGLVLLLVLRRQKFLRSGELFMSYFIWYSI
GRFFIEALRTDSLGFQAPQWVASLVNGLWSPMTAMGFEQGYLDPAYGNVRISQLLAIG
IIIVAVVFIVRRVTGKADVRYSDPIVSSKVTSDMEHTGTVAGKENKVTPPAKDESK
QVDDKKE"

CDS complement(5782694..5783632)

/gene="hprK"

/locus_tag="EFAGFIKM_05068"

/EC_number="2.7.11.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34483"

/codon_start=1

/transl_table=11

/product="HPr kinase/phosphorylase"

/db_xref="COG:COG1493"

/translation="MAKKVKVSELVQQFQLEVSGSHGLKRVITVDDLNRPGLEMAGY
FEYHPQERVQLLGRTELAFFAMLPEQERRDRMQRLCTEETPCIVVTRGLEVPQELIDI
SEEQNLAVLRSNMATTILSSRITGFLEKKLAPTATIHGVLCDVYGVGMLITGSSGIGK
SETALELVKRGHRLIADDAVEIRQTSDFQLHGTAPELIRHLLERGVGIINVMTLFGA
GAVRNNKRITLVVRLEAWQQDKQYDRLGLDEETTRIIDTDVPLVTIPVRPGRNLAVII
EVAGMNYRLKQMGLNAALQFTNKLATISED MEDMD"

CDS complement(5784051..5785178)

/gene="msmX_2"

/locus_tag="EFAGFIKM_05069"

/EC_number="7.5.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94360"

/codon_start=1

/transl_table=11

/product="Oligosaccharides import ATP-binding protein

MsmX"

/db_xref="COG:COG3839"

/translation="MAGVRLEHIFKKYPGSDKATVVDINLDIKDKEFLVLVGPSGCGK
STTLRMIAGLEEISEGKLYIGDRVNDVAPKDRDIAMVFQSYALYPHMSVYQNMAGFL
KLRKVKKDEIDKRVREAAKILDIEHLLERKPKALSGGQRQRVALGRAIVRDPQVFLMD
EPLSNLDAKLRGQMRAEITKLAKRLETTVIYVTHDQIEAMTMGDRIVVMKDGIIQQAA
SPEELYNLPANLFVAGFIGSPTMNFISGKLAEQGTSMHFIAPGVDVEIPQGKAQVLKS
RGYIGKEVILGVRPEDIHEEPVFLEASPNSVVFSTHVDVTENLGHEMLLYLSGVGNDTT
IARVDGRSNTRDGSTVKMAIDMNKVHIFDKETEVNVLLQDK"

CDS complement(5785282..5786499)

/locus_tag="EFAGFIKM_05070"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQSGDVHYMKLIPDLKQQIEVIIGTTLDEYEITIAEWMQSVVNL
VGRHENSETVDDKGEHQELSDQSASPISSDVISLNTGKRIFFKVRMNEHEETVVCWGC
PAKSITVETRQLIELLIRTNMALPDEVQPVVYENDREQYLTELGLWLKEQIEEPTKQE
SEAVPDRFVVPAGLNAEKILFLLQGDTDAHRLRSKELNKLLESYFGEEIVLIPLGEQ
EWMFMGDKEIVTEEAEDTTEAKKDSLNAFCLGLHELVASEWAGVFHLSASLPCIPAK
QLVSVTVLLRESVHLGRAFHVTQHIHLPWDLHLERLVASIPDDQRIRFIKETGKDTII
FNDSETLATLETFFSLDCNVSETAKRLFIHRNTLVYRLDKIKQEIGYDVRHFESAVLV
QFLLLMYKVTKKH"

tRNA complement(5786617..5786692)

/locus_tag="EFAGFIKM_05071"

/product="tRNA-Lys"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Lys(ttt)"

tRNA complement(5786699..5786784)

/locus_tag="EFAGFIKM_05072"

/product="tRNA-Tyr"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Tyr(gta)"

tRNA complement(5786795..5786869)

/locus_tag="EFAGFIKM_05073"
/product="tRNA-Phe"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Phe(gaa)"

tRNA complement(5786891..5786968)
/locus_tag="EFAGFIKM_05074"
/product="tRNA-Asp"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Asp(gtc)"

tRNA complement(5786978..5787053)
/locus_tag="EFAGFIKM_05075"
/product="tRNA-Thr"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Thr(tgt)"

tRNA complement(5787059..5787134)
/locus_tag="EFAGFIKM_05076"
/product="tRNA-Val"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Val(tac)"

tRNA complement(5787144..5787220)
/locus_tag="EFAGFIKM_05077"
/product="tRNA-Met"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Met(cat)"

tRNA complement(5787264..5787355)
/locus_tag="EFAGFIKM_05078"
/product="tRNA-Ser"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Ser(gct)"

rRNA complement(5787440..5790360)
/locus_tag="EFAGFIKM_05079"
/product="23S ribosomal RNA"

tRNA complement(5790572..5790647)
 /locus_tag="EFAGFIKM_05080"
 /product="tRNA-Ala"
 /inference="COORDINATES:profile:Aragorn:001002"
 /note="tRNA-Ala(tgc)"

tRNA complement(5790670..5790746)
 /locus_tag="EFAGFIKM_05081"
 /product="tRNA-Ile"
 /inference="COORDINATES:profile:Aragorn:001002"
 /note="tRNA-Ile(gat)"

rRNA complement(5790787..5790897)
 /locus_tag="EFAGFIKM_05082"
 /product="5S ribosomal RNA"

rRNA complement(5791000..5792550)
 /locus_tag="EFAGFIKM_05083"
 /product="16S ribosomal RNA"

CDS complement(5792902..5793171)
 /locus_tag="EFAGFIKM_05084"
 /inference="ab initio prediction:Prodigal:002006"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /translation="MKSILGSVLVISLLGLIVVLFKRIGLSFFTSFGIHLVLA AVG
 IYIVNYSGWITGTIPLNPATIGTVTVLGLPGVG LLLGLKISLFG"

CDS complement(5793206..5793481)
 /locus_tag="EFAGFIKM_05085"
 /inference="ab initio prediction:Prodigal:002006"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /translation="MFLWRNTRNSVEKHNRMLKEADQIYADIQMAKQEWERAMRQF
 EDAQGQDEIDYAIYVLEAAERKYQIHLRRAKRARANDDVTSQRGLSM"

CDS complement(5793666..5794265)

/gene="recR"

/locus_tag="EFAGFIKM_05086"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8RDI4"

/codon_start=1

/transl_table=11

/product="Recombination protein RecR"

/db_xref="COG:COG0353"

/translation="MYYPEPIAKLIDAFTRLPGVGPKTAARLAFHVLKMKEDDVIDFA
KALVSVKRNHLHYCSVCCNITDTPCRICQDKSRDVSVCVVQDSKDLVAMERTKEFDG
YYHVLQGAISPMEGIGPDDIRLKELLVRLSDERIKEIILATNPNI EG EATAMYISRLV
RPFEISVTRIAHGLPVGGDLEYADEVTLSKALEGRREMR"

CDS complement(5794302..5794613)

/locus_tag="EFAGFIKM_05087"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A3DHB8"

/codon_start=1

/transl_table=11

/product="Nucleoid-associated protein"

/db_xref="COG:COG0718"

/translation="MNNMNQMMKQVKKMQE QMLKAQEELADKTVQGTSGGGVVTA EVN
GHKKLLAITIKPEAVDPEDVEMLQDLVMTAVNDAMAKADEIANKDMGKFTGGMNIPGL
F"

CDS complement(5794655..5796400)

/gene="dnaX"

/locus_tag="EFAGFIKM_05088"

/EC_number="2.7.7.7"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WNT9"

/codon_start=1

/transl_table=11

/product="DNA polymerase III subunit gamma/tau"
/db_xref="COG:COG2812"
/translation="MEHIALYRAWRPQSFQDMVGQQHIIQTLQNAIREQRTSHAYLFS
GPRGTGKTSAAKILAKAVNCERGAPEPCNECEACRRITTGAVMDVQEIDAASNRGVE
EIRDLREKVKYAPTEVRQKVYIIDEVHMLTTEAFNALLKTLEPPPHVMFILATTEPH
RLPATIISRCQRFDFRRVSLEEQTARLTICEQEGMEADQDALQYIARLSDGGMRDAL
SVLDQISSFTDGRVTYQQVMDMTGGIASEQFAKLAASLLKGDVGHILQMIEGFMHEGK
SADKCMENLLYYFRDLLMIKMVPDADKLTDRVLNPESFRDMAESFTKEQLFHMIDTLN
RYQSEMKYAVQPQTLFEVALLKLCSIPAQGEASVQVGSSAHAAPADGGEINRLKQQLA
ELEKKLDRALKSGLSGGEGSSSTPSRPATRAPVSRGNSPAQLPAQLDQYVARKGAPEF
AEISKKWSQILQRVKEERVTVHAWFVDGEPVSLLDNVLVAFKNNIHRETTEKQANRE
VIERVLSEQLGRPARLVTMMLKDWTGAMEGASEAPKEDFKLEPEHEDGGSGNKQPWID
EAIQLFGEDLVVIKE"

CDS complement(5796989..5797186)

/gene="rpmE"
/locus_tag="EFAGFIKM_05089"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q03223"
/codon_start=1
/transl_table=11
/product="50S ribosomal protein L31"
/db_xref="COG:COG0254"
/translation="MKEAIHPNYTIGQVSCACGNTFETGSVKDGLRVEICSACHPFFT
GKQKFIDAGGRVDRFKKKYGI"

CDS complement(5797289..5798563)

/locus_tag="EFAGFIKM_05090"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MYLVYADEKGNVFDHPSLYGLARSGDMIVEIMEDELIPLPEGAT
LVGLPSTRPIGMDPDTGEMLPMPDTPQAVGALLPQGFTRLCLPGYVKTDKEYKLPLFG

YSAVVWKDGGFYVTASKSDSPEKWNPLNCDRDDVRSQVRLTEQYPENRLYTHLSNCA
LGYECLTSSNTFLNRWEGGVPVSYSCNAGCGCISEQPDDSGFVSPQTRMNFPRVDE
IVEVMLEHLKTPESIISFGQCEGEPSTQAKLIEAIREVRSVTDMGYININTNAGLN
DHIRGIVDAGLDLMRVSTISALDDHYNAYYKPRGYTLANVEKSMKYAAQQGVYTSINY
LIFPGVTDREEEIEAMIEFARRTDLRLIQMRNLNIDPESYLELIPSAQGDILGMKQMI
EIFEDELPGVVIGSYTHVPPAGMARPKRLITS"

CDS complement(5798660..5799985)

/gene="rho"

/locus_tag="EFAGFIKM_05091"

/EC_number="3.6.4.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AG30"

/codon_start=1

/transl_table=11

/product="Transcription termination factor Rho"

/db_xref="COG:COG1158"

/translation="MDLQISDLEEMKLTDLKYLAKKYQIPYYGTLKKKELIFAILRAQ
AEQSGLMFMQGVLEILPEGYGFLRPINYLPTSTEDIYISASQIRKFDLRTGDLVSGKCR
TPKENERYFGLLQVNAVNGENPSAAAERLHFPALTPLYPQKKLVLETSPNHLSTRIMD
VLAPVGLGQRGLIVAPPKAGKTLKKKEIANSISTNNPEIELFVLLIDERPEEVTDMR
SVKGEVVASTFDELPHENHIKVAELVLERALRLVEAKKDVILLDSITRLARAYNLVIP
PSGRTLSSGIDPAAFHRPKRFFGSARNVEEGSLTILATALIDTGSRMDDVIYEEFKG
TGNMELHLDRRLAERRIFPAIDIRRSCTRREEVLLSKEELDTIWAIRKNMNDSHDFVE
GFLKKLRNSKTNAEFLAAFDSAGNSPTSNSGTTTTRRSPRQTATSGTST"

CDS complement(5800451..5801704)

/gene="murAB"

/locus_tag="EFAGFIKM_05092"

/EC_number="2.5.1.7"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P19670"

/codon_start=1

/transl_table=11

/product="UDP-N-acetylglucosamine
1-carboxyvinyltransferase 2"
/db_xref="COG:COG0766"
/translation="MEKLMISGGRPLQGTVTISGAKNSAIALIPAALLAESEVVLDNL
PLLSDVAVYAEILEELGAHVTWEGSQMKIDPSDIKSIPMPNGPVKKLRASYMMGALL
GRFKEATIGLPGGCNFEPRPIDQHIKGFEALGATVTNEHGSIHHLHAKELRGAKIYLDV
SSVGATINIMLAATRAKGSTIENAAKEPEIIDVATLLNSMGASIKGAGTETIRIEGV
SELKGCRRHSIIPDRIQAGTYMIAAAATRGDVLIDNVIPKHLEALTAKLLEMVGIEEL
DESIRVIGKPSYNHVDVKALVYPGFPTDLQSPMTSVLTQATGVSVLSDFVYSNRFKHV
PELVRMGAKIRVEGRSAIIEGSALNAAKVKASDLRAGAALVIAGLTVSEGVTEVTGVE
YIDRGYDHLVTNLRLLGADVWRETD"

CDS complement(5801852..5802706)

/gene="fba_2"
/locus_tag="EFAGFIKM_05093"
/EC_number="4.1.2.13"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P99075"
/codon_start=1
/transl_table=11
/product="Fructose-bisphosphate aldolase"
/translation="MPLVSMTDMLNKALEGKYAVGQYNINNLEWTQAILGAAEEEEKSP
VILGVSEGAARHIGGFYTVVKMVEGLIHDMKITVPVAIHLDHGSSFDKCKEAIDAGFT
SVMIDGSHHSIDENIEMTKKVVEYAHAKGVSVEAEVGTGQEDDVIGGIMYADLNEC
IRIVKETGIDTLAPALGSVHGPYHGEPNLGFKEMEEVRDAVQVPLVLHGGTGIPKHDI
DKAISLGTSKINVNTENQIAFARVVREVLAAPDAYDPRTFIVPGREAIKETVKGKIR
EFGSNNKA"

CDS complement(5802967..5803353)

/gene="spo0F"
/locus_tag="EFAGFIKM_05094"
/EC_number="2.7.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P06628"

/codon_start=1
/transl_table=11
/product="Sporulation initiation phosphotransferase F"
/db_xref="COG:COG0784"
/translation="MEDKKVLIVDDQNGIRILLMEVFSSEGYNTFQAPNGKVALEIVN
NDKPDLVLLDMKIPGMDGLEILKHIKEIDPGIKVIMMTAYGELDMIKEATDLGALMHF
TKPFDIDEMRVAVNMQLRNGTANKCS"

CDS complement(5803583..5805187)

/gene="pyrG"
/locus_tag="EFAGFIKM_05095"
/EC_number="6.3.4.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P99072"

/codon_start=1
/transl_table=11
/product="CTP synthase"
/translation="MTKYIFVTGGVSSLGKGITAASLGRLLKNRGLKVTIQKFDPYI
NIDPGTMSPYQHGEVFTDDGAETDLDLGHYERFIDINLSKNSNVTTGKVYSSVISKE
RRGEYLG GTVQVIPHITNEIKERVFRAGREAGSDVVITEIGGTVGDIESLPFLEAIRQ
IKSDVGRDNVMIYHVTLPYIKAAGEVKTQHSVKELRSIGIQPNVIVCRTEYELS
KDMKAKIALFCDIDENAVVECRDADTLYQVPLNLREEGLDEIVVNHLKLTPAPDMSE
WEGLVDRINKLEHTVEIAIVGKYVALHDAYLSVESLSHAGFASNADV KIRWVPSEDI
TDENVGDLLHGIGGILVPGGFGDRGIEGKVS AIRYAREKQIPFFGICLGMQVSVIEYA
RSIVGLNGANSSEINPATEFPVIDLLPEQKD IENLGGTMRLGLYPCKLQEGSLAMACY
DDELVYERHRHRYEFNNEYRETIEKAGLVISGTSPDGRLVEIVELPGHPWFLAVQFHP
EFTSRPNRPQPLFREFVKASLENAQK"

CDS complement(5805639..5806208)

/gene="rpoE"
/locus_tag="EFAGFIKM_05096"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00357"
/codon_start=1

/transl_table=11
/product="DNA-directed RNA polymerase subunit delta"
/translation="MSTSLNLKIDKEKVKEIPLVDLAFMVLKAANTPYYYRDLNMNEVA
KQRGMTDEEINEFIAQLYTEINIDGRFACVGTSLWGLKRWYPVAGTEDSMTGAKRPRI
INDEDDLEDEDFGEEEDSYSSDEGFDSTKDDEEEDDEEEEDDIFDEEDSEEEVLVE
DDDLEDEDLEEDEEESENEDEFDDSDNR"

CDS complement(5806491..5806628)

/locus_tag="EFAGFIKM_05097"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNALIPPHGELALFLQKHILFVSKRAQGHMMMDGELEGSCGEPGE
E"

CDS 5806670..5807824

/locus_tag="EFAGFIKM_05098"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDYTGLLHQLIDGMRRPEPEQGGRYLIRFAKPQQYEACLVLSR
MRNEFTDLGAVRSSLARSIIAPVQRPEDLYRYGDEITIEADVPISLHATALHSKPSN
AQGIPWGVKQIRAPKVWSVSTGHRIGVIDTGADYHHPDLRYSLARGINLLNRSLLP
HDDNGHGTHIAGTIAAANSTAGMIGVAPRSLIYPVKAFDHNGSAYVSDIVLGIDWCVR
NKVDIINMSFGMKTRSKALLDVVNRAYHAGIVIVASSGNDGKRRSIDYPARYPQTISV
GATDKNRRIASFNRGAYVDVYAPGDKIVSSWVQGKHHEMSGTSMATSHVSGAIALLL
SKHPGLSPSEIKTLVKRATIPLRARKTTTAKSKVRGGEIDALKLMQEGGE"

CDS complement(5808113..5809792)

/gene="argS_2"
/locus_tag="EFAGFIKM_05099"
/EC_number="6.1.1.19"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q99W05"

/codon_start=1

/transl_table=11

/product="Arginine--tRNA ligase"

/translation="MTRNPLDTINERVSTAIGNAIVAAGIVTQEELPAITLEVPREKT

HGDLATNAAMQLTKIAKRNPQRQIAEEIIANLNLAEAGIEKAEIAGPGFINFKLDSYL

YPVLGLVQEQQNDYGRINIGEGRKVEMEFVSANPTGSLHLGHARGAAVGDALCNILDY

AGYDVTREYYINDAGNQVFNLARSIEARYLQELGQDAEMPEDGYHGEDIKGFQQLVA

EKGDELLSMHPGDRAAYFRDFGLEKELDKIKRDLNRFRVNFDFWFSETSLYDNGEVL

VLDELDRDNEIYEQDGATWLKTMQYGDDKERVLIKNDGTYTYLTPDIAYHRDKYARGY

DTMINIWGADHHGYIPRMKAAMQALGNDPEKLVVLIQMVSLFQNGEKVKMSKRTGKA

VTMEDLMDEVGIDAIRYFFTMRSMDSHLDFDMDLAISTSNENPVFYVQYAHARVCSVY

RQAAEQGIELLPLAQIDLSKLTTEHEYDLLRKMGELEEISAAATGYAPHRIIRYVYE

LASLFHSYYRAERVITEDAQQTQARLALIGAVRTVIATALRLVGVGTAPDKM"

CDS complement(5809789..5810214)

/locus_tag="EFAGFIKM_05100"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSNMRPVHIRLHSRYEGEDVLQEMQGEAVLKGSVLYVRYEEPQV

GPEGGTRRTLKLGQSIKIRHGEVESEQTFELNRKLPGFYRSPYMSFALSTHTQKL

ELSIQGLSARAAWSYDFYRFDEESGHFAISLHIQEEPIS"

CDS complement(5810481..5810750)

/locus_tag="EFAGFIKM_05101"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMKRQEPCKGCNDQYDVKISDAKMARLVEIASRSRETVQDEEYE

RRLSICFACPLQYGTTCRHCGCLVQVRAKLSESTCPFPYESQWA"

CDS complement(5810750..5811916)

/gene="abf2_1"
/locus_tag="EFAGFIKM_05102"
/EC_number="3.2.1.55"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94552"
/codon_start=1
/transl_table=11
/product="Intracellular exo-alpha-L-arabinofuranosidase 2"
/db_xref="COG:COG3534"
/translation="MAHEFLRLCELLGTEPYISGNLGS GTVQEMQEWWVEYITFDGESP
MANWRKSNGREEPWKLKYFGVGNENWGCGGNMRPEYYADEYRRYATYVRNYSGNEIYK
IACGPNEGNYEWMELMREAARFMDGISLHYTIPTGEWNDKGAATGFGEAEWFTTLK
KTLHMDELLVKHSEIMDKYDPEGRVGIIVDEWGTWYNVEPGTNPGFLYQQNTMRDAVL
AGVNLNIFNQHNKRVMANLAQIVNVLQSLVLTEGDKMLLTPTYHVFDMYQVHMDAQR
LDLNYESPGYTFGEETIPQLSLSASRNKDGVIHVTACNLSHTDELEVVCQLDAAQAAK
VTGQILHHTDFGAFNTFEQPNHVQPAAWEGLTLENNTLRFVLPASVGVIAVEG"

CDS complement(5811906..5812229)

/gene="abf2_2"
/locus_tag="EFAGFIKM_05103"
/EC_number="3.2.1.55"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94552"
/codon_start=1
/transl_table=11
/product="Intracellular exo-alpha-L-arabinofuranosidase 2"
/db_xref="COG:COG3534"
/translation="MVDVILKADSDEGLINRNIYGHFSEHLGRCIYEGLWVGEDSPIP
NTDGIRNDVLTALQKLNIPVLRWPGGCFAD EYHWKDGVGPKSERARMINTHWGGVEEN
NHFGT"

CDS complement(5812448..5813635)

/gene="hcf136_2"
/locus_tag="EFAGFIKM_05104"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01348"

/codon_start=1

/transl_table=11

/product="Ycf48-like protein"

/translation="MTTKSTMTWKRIGALALSLTLAWGMGPVHTLSGANAASSQACGK

GDHGLSATLKKGSGVEEQHLQFTDIDFLNDTTGRAGGEGFLIGTSNAGCTWQSIYIGQ

WQFTQLDFPNNVNGYALARVKDSPATYLIRTHDGGSHWTRLDTPGIQFKRIDFRNKDV

GYGYTYNGAYQTKDGGVTWSKMSTPANTRAAAFATEKQGYAVVVPGSGYHLKQTS DG

GKNWTTSLRVVSDTWSGADLYAHGQQVWALLYGDAGMSQQSYSLYASGNQGKNWTQVF

AQSTAGGGPAPGKNSTGKGNGPANPGGHPGNMALIGNQTAYLSAGSPAAGKVGIGRSY

DKGSTWKNIDLKDPGYSSRISFPSAKTGWLVTSDNSPAIQTTDGGTTWTQKMLLPS

EQD"

CDS complement(5813793..5814041)

/locus_tag="EFAGFIKM_05105"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRVIRTQLSMYPKWLTAVFIVFVINFLAVTIFLNFTLMVADLA

MLFAAYSIREYKYNKIYFSLCLLLSISFVILAVVTYPI"

CDS complement(5814704..5815573)

/gene="speB"

/locus_tag="EFAGFIKM_05106"

/EC_number="3.5.3.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P70999"

/codon_start=1

/transl_table=11

/product="Agmatinase"

/db_xref="COG:COG0010"

/translation="MKLDQAYSGNVFICSSDYENSKAVIYGMPMDYTVSFRPGSRFG

PSHIRQASVGLLEESPYLDKSIVDMTYFDAGDLLLPFGNAGRSLEVIHEYIGSLLADD
KFPVGLGGEHLVTPVVIQQMYKKYPDLILIHIDAHADLRENYEGEPLSHSTPVRKAAE
LMGGKNIYQFGIRSGSREEFQYGRENINFYPFEVAAPMKEALPKMGNRPVYVTIDIDV
LDPSAAPGTGTAEAGGITSKELLEAIHMIAGSDVNVVGC DLVEVAPIYDPTQQTQIVA
AKLIREMLLG FVK"

CDS complement(5815589..5816416)

/gene="speE_2"

/locus_tag="EFAGFIKM_05107"

/EC_number="2.5.1.16"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P70998"

/codon_start=1

/transl_table=11

/product="Polyamine aminopropyltransferase"

/db_xref="COG:COG0421"

/translation="MELWFTEKQTPVFGITAKIKQTYVTEKTD FQDLAMVETEEFGNM
LLLDGMVMTTVKDEFVYHEMAAHPALNTHPNPKKVLVVG GGDGGVIREVIKHA AVEKA
VLVEIDGK VIEYSKKYLPEIAGKLDEPNVEVLVNDGYMH IIEHKNEYDV IIVDSTEPV
GPAAPL FERG FYQGIYEAL KEDGIFVAQTDNPWF KADLIQKV NKDVKEIFPIVHVYGC
NIPTYP SGLWTFTMGSKKHDPLEVDETQIPEMDTKY YSPRLHKA AFVLPKFVEDLTK"

CDS 5816829..5818907

/gene="pbpG"

/locus_tag="EFAGFIKM_05108"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P70997"

/codon_start=1

/transl_table=11

/product="Penicillin-binding protein 2D"

/db_xref="COG:COG0744"

/translation="MTKPNQKTRKRGFPVRKLFKNLSLLAVLAMLATAAGLVYLYATS
LPLADSDRNSRLLDSQGEVIATLSAGGKDSVPVQLEDIAPDLVNATLAVEDRKFYNHY
GFDVQGMGRAVLVNLEHMQMSQGASTLTQQLARNLYLSHEKTWTRKAKEAMYTAQLEM"

NYSKDEILQMYLNEIYYGHGAYGIEAASRMVFGKSAKQLDLAESAMLAGIPKGPTYYS
PYNHMKNADRQKIVLNAMADIGKITQAEADKAYEKMLSFKPESERKTVESAPYFRDY
IRNLAIKELGISEAMLDHGGLNIYTTLDLRVQKAAEDAIKGMMDAKSELETALVSIDP
RTGYIKAMVGGKNYRTNQINHVLATTRQPGSAFKPIMYLALESKQLTSASIFNSEPT
LFHYDNRKTYKPGNFGDKYLGEIDLRQAIAASDNIYAVNTIMQIGPEQVVSMAKNLG
ITSNLSAVPSLALGTSPVSPLEMASAFSVIAAGGQRTPPVAILQVTDAAAGRVLYESPQ
TKAETVVEPAAAYVLRLMESVFENGGTGNRVSKAIKRPVAGKTGTTNTDAWLVGFTP
ELSTAVWVGVDQGSISTSDGRRAPIFAQFTEQALASVPPKIFTVPDHVVSVIDPE
SGKLAGNGCEEKRLVEFIDGTEPTEVCHGTTDDSDSGEDEKTRQVQNQQGIQEEKHSW
WGDFKRWWVE"

CDS complement(5819105..5819608)

/locus_tag="EFAGFIKM_05109"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDQNEQNGKKQIALNIVSAKSKHKGFGAGSIELNNLSPVIIDNG

EAKIDIGAMHAKSKVERNIKFSTNREDVPNGRQVWLWVAVDRTEEGQLYGGATACEM

WIDTEARRGWKLLAEHVNRM DYALKRRFMLDELGPEARAALKTLLISHNEDWWNASPD

VLKEALA"

CDS 5819710..5821701

/locus_tag="EFAGFIKM_05110"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIPRRAKSWLTASLALCVLAGGIWITLGYNRSTHSELPVLAPES

GKPKAIAPTPAPPESVQTPTAEVYSNRVVEYHMDVKLVEGNVLEGTQTITWTHPGKKT

VSELYFHMYPNAFSSADTTFMKESGGKIRGDVMPTNGYGSMNITEMKTEDGLSLLHRM

QYVQPDDGNIKDTTLIKVRLPKPVKGGESITLHTRFEVNLPKIFARMGTADNFVMAGQ

WFPKLSAYEPVGRRGRTEGWNLHQYHGNSEFYADFGIYSVRIRVPETYKVAATGFPT

QQAVVKNGEKVYQFYADDVHDFAWAASPDFVYAEFPFSAPNVPGVRIKLYLDPAHQDL

KERYFYAAKALANYSKWFGPYPYATLSIVPPKAGNGAGGMEYPTLVTAFGADDTTP
GYDLERTVVHEIGHQYFYGMVASNEFEEAWLDEGFTSYAEDKLMEQEYGLIPNLPVQS
GLITSPSSLTQESWKFDSSQNEYAANVYTRGKLVLLGIEHQVGAKKMERILSTYVKKYR
FKHPTSADFQNVVEQVTRTSWSDYFDQYVYGNGMADFAVEKIRVTPVQKDGQTLYES
VTIAKKGSDYSAPVRIAEDGHILTKQWNGKEDRITYKLHTHTSPVSWAMTDPLYSIV
LENRHMNNFLKSGLDERAKSRWSMSVTKLIEAIFGGLSW"

CDS 5821712..5822563

/locus_tag="EFAGFIKM_05111"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKAKIREGWFLVRQHMFIAALLFLYQLIWGYFFYRMVQSAVIPL
LLRYPNADAGELSTILFKMESQLNLSTHPEVHRYLWILGGMLLVRMLISPLIQAGLLY
SLQHFNSTEERIPFIRGIKNLWKPMLLLHTIRTLILLPAYWLIPKLYSILMDGFHSL
QLLLPGIPYVAAWIVYGWIIHHAILYMQFGVSAPEGEGGAHGTALKALWIALRHIAVI
GIALLLGGVHLLVFGAFTTASWLLTGLTGLILQQTYPLARCLLSLWKICSHFRLWQSK
ISKGESR"

CDS 5822950..5823420

/locus_tag="EFAGFIKM_05112"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFKKKLTAAVLSITFALSLGAGSAFADSKMDTVIDSAMGTTYKS
GGTTLNGFDCSGFTRYVFDKLGIDLARQSSSQFDMGDSVSRMEMRAGDLVFFNTTGKG
VSHVGIFVGDGKFAHSSSSKGVVISALSENWYANRYVGAKRIMSTDAYESLALD"

CDS 5823772..5824266

/locus_tag="EFAGFIKM_05113"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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EVEFGDAQLRQEQYAIVLDQNDRICGFAQYFPLQGVTRIGLGMHPELCGQGQGTAFTV
AIVQEAIRRNPTNEIDLEVLWNARAIQVYLKSGFVTQDTYERQTPSGLKPFHCMVYE
GPRG"

CDS 5824417..5824773

/gene="cccB"
/locus_tag="EFAGFIKM_05114"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34594"
/codon_start=1
/transl_table=11
/product="Cytochrome c-551"
/db_xref="COG:COG2010"
/translation="MHKWIMSGVFFAACALAVLMFTLPGKEEVAEEAKPTMPEVTLD
AGQAEALVKANCISCHGDQLQGGVGPALANIGSQDDLEKIYSTIVKGKGGMPSEFKGKL
QDEEIANIAMWLSEKK"

CDS complement(5824848..5825831)

/gene="rbsK_2"
/locus_tag="EFAGFIKM_05115"
/EC_number="2.7.1.15"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A9J6"
/codon_start=1
/transl_table=11
/product="Ribokinase"
/db_xref="COG:COG0524"
/translation="MSDYNQKQPLIAVVGSLNMDLVVKTDTIPEEGETVSGEELHYLA
GGKGANQAVAAARLGGQTTMIGAVGSDGFGERLLHSLTESGADASQVRILEDVTGT
SIWLSRGDNRIIVIPGANGQVPEMLEEADTVKSLTAAAVLLQLEIPLPAVTRAAQL
AAEGSALVVLNPAPAVPDLPQELLRCVDVVTNRSSELAVLTGRDHLPEDLDAVAEL
AASLGAADVTTLGPEGAVYAAASGGRVQAGRAGACRAPGYAVRAVDTTGAGDCFNAL

AVALARGDTLDAAVGFAMGAAALSVTKLGAQSGMPSAREVEAFLAEHAAEA"

CDS complement(5825876..5826172)

/locus_tag="EFAGFIKM_05116"

/EC_number="4.2.1.96"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A0R2K7"

/codon_start=1

/transl_table=11

/product="Putative pterin-4-alpha-carbinolamine
dehydratase"

/db_xref="COG:COG2154"

/translation="MVFSQEEVEAHLGRLEGWELEEGRWIVRKVFVFSNYMKGIAFVDE
VAAISEAFNHHHPFITIDYTTVTLRLTSWDAGGITSVDIKEAGQYNEAYDKMRSQ"

CDS complement(5826423..5826716)

/locus_tag="EFAGFIKM_05117"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGVKHGRDYEGLTDLTTAIGRIPDRYVFFEMDAEEWERLAASD
QLEVDEALAEFLFYALGEESIIPVGSVVIHDKEQHRIHILIGEEELTFVPLI"

CDS 5826950..5827750

/gene="pomA_1"

/locus_tag="EFAGFIKM_05118"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O06873"

/codon_start=1

/transl_table=11

/product="Chemotaxis protein PomA"

/db_xref="COG:COG1291"

/translation="MNISTIIGLILGLVSLVFGMFLKGAPLINLVNNPAAIIIFVGT
AGTIFIAFPMSEVKKIPKLFGIVFKNQVLIDRVSLIGTFMDWASTTRREGLLALESKV"

EEIDDQFLRGGMRMIIDGNDQEFVSDVLMEDIHATEERHRGSALIFAQAGMYAPTLGV
LGAVVGLIAALADLSDMEKLSHAIAAAFIATLLGIFSGYVLWHPMSNKLKRMSKQEME
IKLMMVEGLLSIQSGVSTIAINQKLSVFLTPSERKQLEEKEGSPGEKG"

CDS 5827737..5828555

/gene="motB"

/locus_tag="EFAGFIKM_05119"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P56427"

/codon_start=1

/transl_table=11

/product="Motility protein B"

/db_xref="COG:COG1360"

/translation="MKKAKKHEPHEEHIDESWLLPYSDLMTLLLALFIVLFGMSSIDA
AKFEQMASALNSALNGGSGILDHSSMNPDTPGADLGKNKQEPTEITKKTPAQITDAQM
AKKEQEDLEKLKERLDKYISKNGLSDQLNTKLNQSELKITISDNALFSSGRADV KPES
RSLAKAISSMLQEFPEYEVVVS GHTDNIPISNNQYKDNWDLSADRALNFLKILLNSQ
LDPSKFTPSGYGEYHPIASNDTNTGRAQNRRVEVSIIRKYQSNNTNVKAVGGGN"

CDS complement(5828769..5829470)

/gene="rluF_2"

/locus_tag="EFAGFIKM_05120"

/EC_number="5.4.99.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P32684"

/codon_start=1

/transl_table=11

/product="Dual-specificity RNA pseudouridine synthase

RluF"

/db_xref="COG:COG1187"

/translation="MRINKFISSETGYCSRREADKLVD SGQVTINGVKAELGSQAEEGD
DVRINGKPIKEKRKHVYIALNKPIGITSTTEQHIQGNIVDFVGHDERIFPIGRLDKDS
EGLILMTNDGDIVNRILRSEGRHEKEYIVTVDRSVTPSFLRGMSTGVKILGEMTL PCT
VTRMTDRVFRILTEGKNRQIRRMCSAFGYEVRKLKRIRIMNIHLGEMATG SWRELTP

AEKAELGGLLDYSLE"

CDS complement(5829489..5831876)

/gene="sasA_20"

/locus_tag="EFAGFIKM_05121"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"

/codon_start=1

/transl_table=11

/product="Adaptive-response sensory-kinase SasA"

/translation="MPYIARGYKPRGEQKNLSIKTKLSMIMSCSVLVILVLNIALSY

TTEENLRQDSETKMVLTAQIAIAVEQNQYSSDYVKRQIGNNLWLAAMAAEELDPDI

NNITNEELVRLSQKGVSHISLMEQTDDDIVSRSSDPREIGLSTKSMTYWYQAFKQL

FEKQQVTIPQGQKLEHFWSDGFEYSTSSPSDIDIWGYHHDGKRNYIINPFYNNTDEVDD

YVKISSPDEILNKIREVNPSILEITGINPLTFGSPNMGDDGRDSNFSKLNNRPIRFGT

YQYGSTDEDHRAVVRAIRTGQNVSVFVSETHEQKVLKSFIFTPNQSSYVISIVMDYK

QISSMVSEQLVSHASISLVLEIVFGSYLLAGYITRPIQSILGKVNDVADGHFDFRL

KVRRKDELGQLANRINAMIRNLGHYTSRLKQMYEENRAVKEHLESIINQTADAIHITD

LEGKVLRVNRAFEQLYGFRSREVEGRNLKIIPPEAEEMKRQHAQLVEGMSITSNETT

WMKKDGTRVEVSVSTAPVRDEAGEITALISVSRDITSRNRMEELLRRSEKLTTVGQLA

AGVAHEIRNPLTTLRGFLQLQQESNKLNRHLDLMLSELDRINLIVGEFLILAKPQAV

HFQNRDIRFILGDVISLLDSQAHLHGVEFVLRASSDSAMVHCEENQLKQVFINLLKNG

MEAMPNGGNIHIKHKHDEQSKRVRIERDEGIGIPEEMMPKLGEPPFTNKESGTGLGL

MVSQRIIQSHKGMMDIKSVMNKGTTVIIELPASEQQPEVIEVDQVTDLTDEEK"

CDS 5832161..5832667

/gene="tadA_4"

/locus_tag="EFAGFIKM_05122"

/EC_number="3.5.4.33"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P21335"

/codon_start=1

/transl_table=11

/product="tRNA-specific adenosine deaminase"

/db_xref="COG:COG0590"

/translation="MTDHLLQTDLAHLSEEAQHEHWMREAIAEAYKAEALGEVPIGAV
IVQNNQIIIGRGYNLRETTLDSTAHAEVMVAIRQASETIGAWRLDCLYVTLPCPMCA
GAIVQSRVPRVIYGTADPKAGCAGTLMNLLQEPRFNHRTEVIADILQPECSTMLTQFF
RSLRQKLK"

CDS 5832711..5833280

/gene="rimJ_2"

/locus_tag="EFAGFIKM_05123"

/EC_number="2.3.1.267"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A948"

/codon_start=1

/transl_table=11

/product="[Ribosomal protein S5]-alanine
N-acetyltransferase"

/db_xref="COG:COG1670"

/translation="MALTLYDTANGISLRLLPQDTQSYLDLIQVTRVPYQSLEPVRD
DEFYTLDAQTRRIEDRVKAAEDGTGYQFGIYTIQDSLLIGQVSINNVLGVANYADMG
YFIHPDYQGGGRMTAAVKLAVAYGFRALKLNRVQAAVLPSNKGSRVLEKNGFQFEGT
ARKYLKINGKYQDHQIYAVLAEDLDELAN"

CDS complement(5833540..5834634)

/locus_tag="EFAGFIKM_05124"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTKRMGALLLTLLTVSMALTACSSKQEPKEALKTAAANASKLT
SYEMSSNFTINELSYKPGDASQTDPTMTQFMSMLKDAQLNVTGVYQSEPMQTEMTLGI
ELKGDMGMTFNIPMVMTAEKLYVKVPNIPFFPIPENVVNKFLELDLKELAEQEGTEWN
PDAMDAAKTQKLSNEVMDAVLSEYDQAKFFKNLDTKDAKLPEGVDAKQVVQFSVNNDN
VKEAVTVLVTKAMPKVL DILSKEEYREMLQMDQADIDKAKEDLKITEADQAEMAKDLD

KLKDVLTINQFNIDFALDKNDFPVYQKMVADVLIKPEGTKDEVKLAFSGSNTYTKINE

KAAFKINIPTGDDVITMQEFEELMNASYGY"

CDS complement(5834870..5835022)

/locus_tag="EFAGFIKM_05125"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKPKTIPVPEAQASEQHRHSSKRSSMQEPLSGSKKVKQNQHVD

HLNPQG"

CDS complement(5835044..5835220)

/locus_tag="EFAGFIKM_05126"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTKAKAGVDKNLQNVVDDLEQPAVNSHHAQQIQQDINDRRHQDA

LNHDKTEDRDPSHS"

CDS complement(5835250..5835588)

/locus_tag="EFAGFIKM_05127"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNRELNIDQTELVGAWQERLPQVLNVGDQAQVMADEADQQAIRI

HIATAGHEMYSFDFKCAYVDSREVSQQLIDVERDGRITDERTEPIQELAHDYTRHIHE

CAQSLQSQTR"

CDS complement(5836051..5836836)

/locus_tag="EFAGFIKM_05128"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MRKISVTVEDKNETHVTLTNHEDHHINDGLSIDYFFTNNIHDSE
IEYVVNKIIKTKDWISNENGIYFINLKKLGTA YPSIFSQCQWMNGLINVSPTYEDGLG
DVRIFSLTISEDEIREKAPKKVFLSHKGANKPMVRKH YQLLKELGFDPWMDEEDMPAG
VQLMRSIRQGFKQSCAVVFFITPEFKDEQYLESEIDYALNEKLSRKQFTIITLQFEDG
QGIKGVIPLEMENYVWKSPKTELEAFKEI KALPIKVGQAIWK"

CDS complement(5836833..5837459)

/locus_tag="EFAGFIKM_05129"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MNELIVFQYKMKREN RKNIHFLNHLKKDYN SKVCVKQNGFE EK
FISVSYENIILLMFDSIFWIILKDESQNNHHIKRFEVGHSLPDCLMPIQLTNKKLIEY
FFEHEFSNNLLEMFIEGDDDEYFDKFLIYGEGLNYSSEYKQALKIPEINFEYIKLQP
KNSDSVLTRNNHLNVDGTASIDDTLNVAQSFNRFYQNYLKENG EILT"

CDS complement(5837490..5838773)

/locus_tag="EFAGFIKM_05130"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MMNPENSMLIVGNHEVKENSISNMKVSGSISPLVTIKPSVDEIT
TFRHSLKLLNQRELTSIINKYKIKIPSDAQKVSEVTYALEKSFGDGMLSKEIFHQFRQ
AAFNPELDTTDGGFFMSFN YKFTDISEVTLNSKILEWKKNLEQDRDSRNTFNADIELL
DFGSNSKGS LFKFTRRNERFVYNSQNMLSKNYFEVHQVIVEIYFDKQIVYFQTSNSVK
FNSVKTIVSNFLISLADDKHTKIKLTTPKMSKHLKFSFSEDGRSAKVYDNINPNTIKL
LDLFLEIENSTSFSSFQCVDIKFDHEDSLNKDLKDRIKSQAYGCDIGDLFNKSEVKTH
ILSKRVILQIEFKLVYTTLDANEIPRKHIILAGIVNDKSKINALRIYIENNEHTIKDI
VKDAYKDLKD VFIGSLMDSALKNEDKIKKMLGIGI"

tRNA complement(5840075..5840163)

/locus_tag="EFAGFIKM_05131"

/product="tRNA-Ser"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Ser(tga)"

CDS complement(5840361..5841644)

/gene="serS_2"
/locus_tag="EFAGFIKM_05132"
/EC_number="6.1.1.11"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P99178"
/codon_start=1
/transl_table=11
/product="Serine--tRNA ligase"
/translation="MLDVKILRNEYARVEEALTKRGKSLDLIAGFTEMDAKRRELLQE
SETLKSRRTVSAEVARLKKNRENADDLIVEMREVSDRIKAMDEEVRELEVKINDLTM
AIPNIPNESVPIGASEDDNVEIRRWECPKSFTFAPKAHWEIAQDLDFEAAKVTG
SRFTFYKGLGARLERALINFMDLHSDQHGYEEILPPYIVNRDSLFGTGQLPKFEEDL
FKLKDTEYYLIPTAEVPVTNYHREEILNVDQLPKHFVAYSSCFRSEAGSAGRDRGLI
RQHGFNKVELLKLSTPETSYYEELEQMTQNAERVLQLLGLPYRVLTCTADMGFTSAKT
YDIEVWLPESDITYREISSCSNCEDFQARRANIRFRREPKAKPEFVHTLNGSGLAVGRT
VAAILENYQQEDGTVVIPEALRPYMGGASVIARRS"

CDS complement(5841918..5842508)

/gene="pdxT"
/locus_tag="EFAGFIKM_05133"
/EC_number="4.3.3.6"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q8L1A7"
/codon_start=1
/transl_table=11
/product="Pyridoxal 5'-phosphate synthase subunit PdxT"
/translation="MKIGVLALQGAVTEHIRSIRAGAEGIAIKQVQQLEDLDGLILP
GGESTTIGKLMRKYGFMDAIRAFAAEGKPVFGTCAGLIVMAKHIAGQEEAHLELMDMT
VSRNAFGRQRESFETDLPVKGIEETVRAVFIRAPLIESVGDQVEVLSTYKDEIVTARQ

GHLLACSYHPELTDDYRLHTYFVDMARSYKHTVDSK"

CDS complement(5842725..5844113)

/gene="dacA_1"

/locus_tag="EFAGFIKM_05134"

/EC_number="3.4.16.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q05523"

/codon_start=1

/transl_table=11

/product="D-alanyl-D-alanine carboxypeptidase DacA"

/translation="MKAKHMNKKKRQMLKKSVASVMLINMLCMSTVMPVMAAADNSGQ

VLTAATTTKTEKAVQVPGVDSLGLEVRSVLMLEASTGQILLNVDADKAMPPASMTKM

MTEYIVAEQVKQGKFGWDDIVTVKKNAAQSIGSRIFLAEGDQHTVKDLYIAMAVGSAN

DATVALAEHVAGSEEAQVMMNDEAKRMGMKDTFFINSSGLDRADMPADFRPAEDKET

VMSALDAAILCRYIIMDHPDYTEFTTIQSYKFRPNDKAPIINYNWMLEANKNITNFKS

YAYEGLDGMKTGHTTNAGNNFTGTAERNGMRLISVVMGTDSEARFRETKKVLDYGFN

NFEVKQAVAGKTKVTGWEAVPLKKGKETTPVVTDNAVSVVPGKTQNLDTVFKANVT

EADKLVAPIKAGTKVGTVTYTYKADGIEPQEKTVNLITAEAEKGGWFRLFFRAVKDF

FVDLFDGIKNLF"

CDS complement(5844530..5845987)

/gene="guaB"

/locus_tag="EFAGFIKM_05135"

/EC_number="1.1.1.205"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P21879"

/codon_start=1

/transl_table=11

/product="Inosine-5'-monophosphate dehydrogenase"

/db_xref="COG:COG0516"

/translation="MWEDKFGKEGLTFDDVLLVPRKSETLPKEVDVSIRLSDTVKLNI

PLISAGMDTVTEATLAIAREGGIGIIHKNMSVEQQAEVDRVKRSESGVITNPFSL

TADHLVSDAEAVMAKYRISGVPIIEGDQKLVGILTNRDLRFIHDYGIKISEVMTHENL

VTAPVGTTLQEAEGILQKHKIEKLPLVDETNTLKGLITIKDIEKAIQFPHA AKDAQGR
LLVGAAIGISKDTFERADALVQAGVDLITVDSAHHHINIIEAVRQLRERFPSLTIVA
GNVATGDATRELIEAGASVVKVGIGPGSICTTRVIAGIGVPQVTAVYDCATVAREYGI
PIIADGGIKYSGEITKALAAGAHAVMLGSLFAGTAESPGETEIFQGRSYKVYRGMGSM
AAMKQGSKDRYFQDDDKLVPEGIEGRVAYKGPLSDTIHQLIGGLRSGMGYCGTSNLE
QLRNDTG FIRITGAGLRESHPHDVQITKEAPNYSL"

rRNA complement(5846358..5846469)

/locus_tag="EFAGFIKM_05136"

/product="5S ribosomal RNA"

rRNA complement(5846549..5849469)

/locus_tag="EFAGFIKM_05137"

/product="23S ribosomal RNA"

rRNA complement(5849777..5851327)

/locus_tag="EFAGFIKM_05138"

/product="16S ribosomal RNA"

CDS complement(5851768..5852319)

/locus_tag="EFAGFIKM_05139"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIGYFIIGCEIAFWVFVFAGLSVRYLLGMKRIGIGLLMATPVID

LLLLVATVMDLQRGATASMIHGIAAVYIGVSIAYGHQMIAWADRYFLYWFKGGENPRS

NKLYGREHASRERSGWFRHLLAWAIGSAFLLAMIWWIGDAERTAVFNNLIRVWGLILG

IDFLISFSYSLWPRKVPARNVKR"

CDS 5852406..5852996

/gene="betI_2"

/locus_tag="EFAGFIKM_05140"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00768"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator BetI"
/translation="MPKLVDHDKQRVLVAEAAWRIIRRDGMEQASVRNIAEEAGVSVG
SMRHYFSTQSELLRYAMNLVSERVSHRVQKMSFTGSPMDNMKCLLLEFLPNTTEEKLA
MEVWYAFTARSKTDPTLKEANTVYDELRQAVGSVINYLKHDLSRPDL DKELEIERL
YALVDGLGIHTVLRPDQMNAKLMDDVLT LHLASLCR"

CDS complement(5853080..5854417)

/gene="ktrB_2"
/locus_tag="EFAGFIKM_05141"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32081"
/codon_start=1
/transl_table=11
/product="Ktr system potassium uptake protein B"
/db_xref="COG:COG0168"
/translation="MKFRLHFAKFLSPPLILVGGFLLIIAGTVLLMLPISNQSGMHL
AFIDALFTSTSAACVTGLVVVDVGTTFNLFQGQFVIMVLMQLGGLGFMTMATLFALVLG
KRISLKDRLLLKEAINADSMEGIVRIIRKVLIFSFTIEGVAAVILALRWATEMPLGQA
VYYGIFHSVSLFNNGGFDLFGNSFQYYTGDWIFNVTASVLVSGGLGFVVLNDLFEYR
KRRRLSLQSKLVLSVSGALIGIGAIVLFVFEFTNGHTLASLTWSEKIYASFFQSVSTR
SSGTSTIDITEMRQATQFFILLMFIGASPGSTGGGIKTTTFLIMIGAVYAMIRGNKD
IVFFRQRPKELLMRALTIIMVSLIIFMIVMMLLTEDAPFLSLMFEAASAIGTVGL
SVGVTDELTNWGKIIITFTMFVGRIGPLTIAYALRPRKEKKLYRHPEGRIIIG"

CDS complement(5854621..5856132)

/gene="lysS"
/locus_tag="EFAGFIKM_05142"
/EC_number="6.1.1.6"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9RHV9"
/codon_start=1
/transl_table=11
/product="Lysine--tRNA ligase"
/translation="MTDEVLNQETELSELLQIRRDKLDELRLKLGIDPFGQKYVRTEEA"

GSILKKYEELTKEELEEKHIEVSIAGRIMAKRGMGKASFAHIQDLSGRIQIYVRQDSV
PEDKYAAFSLDLGDIVGVTVGVIKTKTGETSVKVKDLEVLSKSLYLPDKFHGLTDV
ELRYRQRYVDLIMSPDVQQTFIARSKIIQSMRRYLDSLGYLEVETPTLHTIAGGAAAR
PFITHHNALDMELYMRIAIELHLKRLIVGGLEKVEIGRVYRNEGMSTRHNPEFTMIE
LYEAYADYKDIMQLTENLVAHIAQEVLTGTQVIQYGDYVDLTPQWRRVTMVDVKEVV
GVDFSVHMTDEEAHNLAKEHKVPVEKHMTFGHILNAFFEEFVEETLIQPTFIMGHPL
ISPLAKKNDVDPRFTDRFELFIVGREHANAFTELNDPIDQRQRFEAQMLEKEHGNDEA
HEMDEDFIRALEYGMPPTGGLGIGVDRLIMLLTNSPSIRDVLLFPHMRPRTQD"

CDS complement(5856249..5856728)

/gene="greA_2"

/locus_tag="EFAGFIKM_05143"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80240"

/codon_start=1

/transl_table=11

/product="Transcription elongation factor GreA"

/db_xref="COG:COG0782"

/translation="MSDKEVILTPEGLKKLEEELETLKSVKRREVAERIKVAIGYDI

SENSEYEDAKNEQAFIEGRVITLEKLLRNARIINSDEIDTDAVSVGATVTVEDLEFGD

ITEYTIVGTAEADPLQNKISNESPVGKAILGKKKGTVVDVSVAPGVIQYKIMDIKKL"

CDS complement(5856980..5857999)

/gene="dusB"

/locus_tag="EFAGFIKM_05144"

/EC_number="1.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ABT5"

/codon_start=1

/transl_table=11

/product="tRNA-dihydrouridine synthase B"

/db_xref="COG:COG0042"

/translation="MLNIGGIEMKNQVVLAPMAGVCNQAFRLIAKEFGTGLVCAEMVS

GKAIVHGNQRTREMLFVDEREKPLSLQIFGGDRDSLVEAAKIVDKETNADIIDINMGC

PVPKVTKCDAGARWLLDPNKIYEMVSAVVDAVEKPVTVKMRIGWDNEHIFAVENALAV
ERAGGQAVSVHGRTREQLYTGADWSHIKDVKEAVSIPVIGNGDVHTPEDARRMLDET
GCDGVMIGRAALGNPWMLYRTIQYLSTGELLDPNGEEKIRVAILHMDRLIALKNETV
AVREMRKHLAWYLGKLGKSARIKDVIMEGTRDEMVMQILENFVSQLKSEGNLESEPMI
AGNAS"

CDS complement(5858096..5858299)
/locus_tag="EFAGFIKM_05145"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MENMQLANRIRAFRKLKGLTQHELAETGISLAILGTIERGNRK
VSQQELDRIAGVLAISIEELRGN"

CDS complement(5858251..5858799)
/locus_tag="EFAGFIKM_05146"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIAHSTSESSEAYIALGANLGDREQLFEALSLLDEHPHISVLR
CSALYETEPVGYVDQPAFLNMAVAVQAMLTPEQLLELLDIENRLGRVRDIRWGPRTV
DLDLLWMHGETRDTELLQLPHPRMGERAFVLVPLSDIVPEGEISGLYTFVHSSLSVLD
GKDGIQLWKTCNWPTESGHSGS"

CDS complement(5858809..5859171)
/gene="folB"
/locus_tag="EFAGFIKM_05147"
/EC_number="4.1.2.25"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P56740"
/codon_start=1
/transl_table=11
/product="Dihydroneopterin aldolase"

/db_xref="COG:COG1539"

/translation="MDRMVLHRMEYYGYHGVFAEERKLGQRYIDLEIDMDLGEAGRN

DDLTKTINYAEIHELVKQIVENKSFQLIEALGEHIASSLLDITYIINALTVKVTKPHP

PFDIHFEGVTVELRRTRK"

CDS complement(5859289..5860152)

/gene="folP"

/locus_tag="EFAGFIKM_05148"

/EC_number="2.5.1.15"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5XCA8"

/codon_start=1

/transl_table=11

/product="Dihydropteroate synthase"

/translation="MTLTPVIYERNYAWGPAELKLGKRTQIMGILNVTPDSFSDGGHY

TSVERAVAHAKQMMEDGADLIDIGGESTRPGSAVVGADDEELSRIIPVIEALHQQAPHI

PLSVDTYKADVARQAILAGAHIIINDVWGAKADSDMARTAAELGCPILMHNRQERNYT

DYLSDVVSDLQESIQIALTAGVKAEQIILDPGIGFVKDLGENLKLMSLGLLNEMGYP

VLLATSRKRFIQNTLDVGADDALEGTAATVAFGIAQGCQMVRVHVDVKPIRRTADMCD

MLYASPGIRRK"

CDS complement(5860149..5861033)

/gene="ilvE_2"

/locus_tag="EFAGFIKM_05149"

/EC_number="2.6.1.42"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AB80"

/codon_start=1

/transl_table=11

/product="Branched-chain-amino-acid aminotransferase"

/db_xref="COG:COG0115"

/translation="MQYAAISGELVNLAAAVVPVTDHGFLYGLGLFETFRTYQGVPYL

LERHLERMASGCKELGIPFTTTAAEVDWIQRLMDANGLRDAYVRYTVSAGEAPLGLP

SGDYSKPNHILLAKALPEPSPSLYESGKMLQRLSTPRNTPEGEIRFKSLHYMNSILAK

RELNGYGQHVQGA EGLQLTRDGHIAEGIVSNVFWVRENVLYTPALSTGILPGITRAVV
MEIASQQGIPCIETLASWEDLLQADEIFLTGSAELVPVTTLRDQDGAETIISNGHIG
PVTAVLLGMYRQKAGYTS"

CDS complement(5861035..5861610)

/gene="pabA"

/locus_tag="EFAGFIKM_05150"

/EC_number="2.6.1.85"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P28819"

/codon_start=1

/transl_table=11

/product="Aminodeoxychorismate/anthranilate synthase
component 2"

/db_xref="COG:COG0512"

/translation="MILVIDNYDSFTYNLVQYLGELGETVEVRRNDEIDLAGIEALAP
DHILISPGPCTPNEAGISLAVIDHFKGSIPIFGVCLGHQSIGQAFGGNVIRAERMMHG
KTSEMHHNGTSVFAGLPSPFTATRYHSLIVERSSLPDCLEITAETAEGEIMGLRHKEY
AIEGVQFHPESIITDHGHQMLRNFLSQQVKV"

CDS complement(5861666..5863411)

/gene="pabB"

/locus_tag="EFAGFIKM_05151"

/EC_number="2.6.1.85"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P28820"

/codon_start=1

/transl_table=11

/product="Aminodeoxychorismate synthase component 1"

/db_xref="COG:COG0147"

/translation="MTKPILLARMTGMEDFWRNAFKRSGALVYYQTIELATDGGRH
MTHLMTTYADWMEWAEQGWMTMPYITKSDEGPYHGGLPLSWEAAWQQASPYAIVLENG
KGGRYTFLGLDPVSVISGKGQEAVIHDVTQGTTLTDSGKPLDVLKRWTPYSAPKVNG
APDFGGGYAGYLSYDVARSLKLPALAEDNPALPDYWWMRFEIWAYDHEQQALFCMV"

HLAIEPNRNETDIRSLYSAAEARATAMQQRWLHIMGAAQAEQQALERRNKQVN RTP
QPEDAERESEGWETSFPQKDFEQAVRTVQEYIRQGDVFQVNLSLRQEKRLHSSAEYIY
EWLRLVNPSPYMGMLRSPDFQLVSGSPELLVKVENGKVSARPIAGTRRRGRDAAEDNA
MADELLSSEKERAEHIMLVDLERNDIGRIAAYGSVHVPELMSIEKYSHVMHLVSQVEG
RLAEGLSVFDVIAATFPGGTITGAPKVRTMEIIIELEPVRRGPYTG SIGWMDYSGNME
LNIVIRTLAIKDGIGYVQAGAGIVIDSDPYREYKECRNKARAMMRAVNYSEEAEASRA
IEQEQAERTEAVKLN"

CDS complement(5863420..5864358)

/gene="cysK_2"

/locus_tag="EFAGFIKM_05152"

/EC_number="2.5.1.47"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P63871"

/codon_start=1

/transl_table=11

/product="Cysteine synthase"

/translation="MAKVNNVTELIGGTPLVRLNRIVPEGSAEVFVKLEYQNP GSSV
KDRIAISIVEEAEKEGKLLGDTIIEATSGNTGIGLAMVAAAKGYKSVIVMPETMSLE
RRNLLRAYGAELVLTPGAEGMNGAVKKAELLKENPSYFMAEQFKNKANVKIHRETTG
PEIVEAIQSVGGTLDAFVAGIGTGGTITGTGEVLKEAFAGIKIVAVEPAASPILAGGK
PGPHKIQQIGANFIPEILDQEIYDEIIHIENDDAFETARQVAKEEGILSGISSGAAIR
AGLQVAKQLGEGKRVVIVPSNGERYLSTPLYNFEG"

CDS complement(5864704..5865654)

/gene="prsA_1"

/locus_tag="EFAGFIKM_05153"

/EC_number="5.2.1.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01145"

/codon_start=1

/transl_table=11

/product="Foldase protein PrsA"

/translation="MTRQEKGLWTAVIVLTGLMLVMGTVMMHGLRQGKDEADASHDA

NTEEGSTVATINGEVITDKEWTDALKRRYGSSELLQMLNRKAVYAEAIERKLIVTPRE
IARELAAAMDGYDSEKSYFDEMKSQGLGSKQELELEAGYRLLLEKIATISIQIKDADI
EHYWTEHREDYVSPEKYDLSIIVVKEEEEADSLDALEKGEDFEEAARKQSTDSFSRD
AGGRLGWIERNDPFQSEEILQLAAGLDVGDIAGPVRVEEGYVIIRLNDKEERQVQSAE
EVREEIRMQLALSQADPLPQVEQMLRNKYEAVILSEIPAS"

CDS complement(5865678..5866568)

/gene="hslO"

/locus_tag="EFAGFIKM_05154"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37565"

/codon_start=1

/transl_table=11

/product="33 kDa chaperonin"

/db_xref="COG:COG1281"

/translation="MENNNKHDLIRGTAMNGKVRAFAIQTTELVEELRRRHDTFPTA
TAAMGRTVTAAIMGAMLKGEELTVQVNGDGPQIVADANAKGEVRGYVSNPHVHL
PSNSVGKLDVAGAVGTEGFINITKDLGLKEPYRGSVPIISGELGEDFTYYFAQSEQTP
SAVGVGVLVDTDNSVIVSGGFIMQLLPGLTDPEITAIENAISTLPPVTTLLEQGLELE
ELLRRLLPDVQVMEGLDIHFSCDCSRERVEKTLISLGQTEMEQLIEEEGQAEVVCQFC
NEAYDFNKEQLETILEQAKN"

CDS complement(5866672..5867442)

/gene="coaX"

/locus_tag="EFAGFIKM_05155"

/EC_number="2.7.1.33"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81VX4"

/codon_start=1

/transl_table=11

/product="Type III pantothenate kinase"

/db_xref="COG:COG1521"

/translation="MILVVDVGNSNMVLGVYQGRELLHHFRLSTSRQSTVDEYGVLIY
NLFHMSGIRASDIEGVIISSVVPPLVNVIEAMCEKYVGKKALLVGPGIKTGLNLRYEN"

PREVGADRIVNAVAAVEKYGGPLVVVDFGTATTFDCIDEKGHYLGGAIVPGIQIATEA
LYERASKLPRIELEKPKKVIGRNTIHAMQAGIIFGYAGQVDGIVERIREEMGAKPRVI
ATGGLATLIAEETRSIEEVDPLLLEGLRIIYERNRER"

CDS complement(5867449..5868315)

/gene="nadC"

/locus_tag="EFAGFIKM_05156"

/EC_number="2.4.2.19"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39666"

/codon_start=1

/transl_table=11

/product="putative nicotinate-nucleotide pyrophosphorylase

[carboxylating]"

/db_xref="COG:COG0157"

/translation="MILNGYNEGLIESIKNWLREDVGAGDVTTSVTIPAGNQSKAIH

AKDNGVIAGMTVAELVFQVVDPLVDFSPKVTGDGDQVTHGTILAEVEGSTHSLTGERL

ALNLLQRMMSGIATRTRSYVDVLDGLETRLVDTRKTPGHRLLKEYAVRVGGGANHRFG

LYDAVMIKDNHIKGAGGITEAVQRARTVIPHTMTIEVETENLEQVREALQAGADIIML

DNMHPERMREAVELIREQAPHVKVEASGNVSLQTIRGIAESGVDVISVGRLTYSFESL

DISLDLNEKKEG"

CDS complement(5868312..5869943)

/gene="nadB"

/locus_tag="EFAGFIKM_05157"

/EC_number="1.4.3.16"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P10902"

/codon_start=1

/transl_table=11

/product="L-aspartate oxidase"

/db_xref="COG:COG0029"

/translation="MIPQYLVDFDLSALPMVETDVLVIGSGIAGLFTAIAKASEQQRVL

MITKKSLLSENTRYAQGGIAAVIAEDDSPAYHLQDTLVAGAGLCRSEAVEVLVNEGPD

GVKELIRLGTFLDLENGELALTQEGASHRRILHANGDATGYEIVRALAVEVNEHPGI
EVWDEHFVVDLIKDRDRGECIGALVQKDDGSQVFVKAQATVLCSSGAGQLYRYTTNPD
VATADGVAMAYRAGAIVRDMEFIQFHPTSLCYPGAPRFLVSEAVRGEGAYLRNVKGER
FMDRYHAQLELAPRDIVARAIVSEMESTNSTFVYLDITHEQPEMIKHRFPTIYETCMR
YGLDMTTDWIPVAPAAHYMMGGVKTDLSGESSISRLFACGEVSSTGVHGANRLASNSL
SEAIVFGRRIVDRIQSLSPGLSLQVRGTSTASVNMNSKIMEEQRPVSERRRLRLQKMMV
RQVGLRRNGEDLQKAMDKLQQELQFFDQTLTHKEELEYANLLTCAWLVTSGALHREES
RGAHYREDFPARDDIVWQKHSLQQREQAIVEELMS"

CDS complement(5869979..5870917)

/gene="nadA"

/locus_tag="EFAGFIKM_05158"

/EC_number="2.5.1.72"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WJK1"

/codon_start=1

/transl_table=11

/product="Quinolate synthase A"

/db_xref="COG:COG0379"

/translation="MEALALERKAEMNRELRLMELKKERNAILAHYYQRDEVQEV

ADFRGDSFLLAQKAAQTDADVIVFCGVHFMGESAKILAPNKTVIIPDERAGCPMADMV

NVDGLRKLKAQHPNAKVVTYINSSAEIKAETDICCTSANAVRVIQSVDSDEIIVWVPDK

NLGHYVQQHTDKKMIIWEGYCNTHDMLTVKDVVEMRAKHPNAEFVVHPECRPEVVEMG

DFVGSTTAILEYCKNSSAKEFIVGTEDGTGYQLRLDSPDKQFHFATKFLVCPNMKVNN

LKKLVKCLETMKPQIYVPPAVADKARESLERMMLLVK"

CDS complement(5871217..5873262)

/gene="ftsH_2"

/locus_tag="EFAGFIKM_05159"

/EC_number="3.4.24.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37476"

/codon_start=1

/transl_table=11

/product="ATP-dependent zinc metalloprotease FtsH"
/db_xref="COG:COG0465"
/translation="MNRFIRNSGFYLILFLVVGIVQFVSNGGEATDNPRYDQLRAAI
KANNVSELTVQFNGQTYLVTGQYKKAPDGAKSENFSTYIPPTDEAISELVAASETNNF
QYHQEPMKGDSIWLTLLTSFIPLIIMFLLFFFLFNQAQGGGGKVMNFGKSRARLYNEE
KKRVTFEDVAGADEEKQELVEVVDFLKDPRKFAAVGARIPKGVLLVGPPGTGKTLLAR
AVAGEAGVPFFTISGSDFVEMFVGVGASRVRLDFENAKKNAPCIIFIDEIDAVGRQRG
AGLGGGHDEREQTLNQLLVEMDGGFGVNEGIIIAATNRADILDPALLRPGRFDRQITV
DRPDVRGREAVLKVHSRNKPLTNDVKMDIIAKRTTGFSGADLENLLNEAALIAARRNR
KDISMKEVDEAIDRVIVGTEKKS RVISDREKRIVAYHEAGHTIVGYFLEHADMVHKVT
IIPRGRAGGYVIMLPKEDRMLVTKNELLDKVTGLLGGRVAEELFIGEIGTGAYSDFQQ
ATGIVRSMVMEYGMSEKLGPMQFGSSQGQVFLGRDIGHEQNYSDSIAYEIDQEMQRFI
NDCYEKCKDLLVKHSEMHIAQTLLEVETLEMDQIKQLIETGSLTPKAENDNDGEGT
PTEGGEPIDTIGDVRVRIQGKDETEPPAGDIPNEAPNLEKGNNNNPDDGGTKPTS"

CDS complement(5873363..5873902)

/gene="hpt"
/locus_tag="EFAGFIKM_05160"
/EC_number="2.4.2.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P99085"
/codon_start=1
/transl_table=11
/product="Hypoxanthine-guanine phosphoribosyltransferase"
/translation="MQNDIQEVLISEEEIQSKVKELGATLSAEYANRNPLVICVLKGA
FIFMADLVKNITVPVEMDFMAVSSYGASTKSSGVVKIIKDLDVSVEGREVLIVEDIID
SGLTLSYLIELLENRGAE SVRVVTLFDKPSGRKVELEAHYTGFDIPDAFIVGYGLDFA
EKYRNLPYIGILKPEVYSS"

CDS complement(5873955..5875394)

/gene="tilS"
/locus_tag="EFAGFIKM_05161"
/EC_number="6.3.4.19"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37563"

/codon_start=1

/transl_table=11

/product="tRNA(Ile)-lysidine synthase"

/db_xref="COG:COG0037"

/translation="MEALRWNNMLVKNVLDAAEEHQLWVPGDRIVVAVSGGPDSVAFLH
IMHEISKRHVPLELCAHVHHGFRSESDDEAEKMMELAQQLGITFEWTKADVPSYME
TGQGPQEAARNKRYAFLHEVASKYNAASIALAHHADDQAETVMLHLLRGTGLSGLSGM
KFKRREKNVELIRPCLRINKTDLVEACNTQGFMYFNDESNALRKYRRNAIRLDVLPFL
GQYNGQLTPSLNRLAEIVGDEDDFMEQSAYDTYRCLVQVNGGRQTFEVPSFLKLHVAL
QRRLIKILINYLPLDSDFVDFTRIETIRHKVMETHVTTWSLDIGQTLACTREYNLISF
GIRTDVQDQSYEYRLAQWSGTYELSLTPINRYIRLMTVSPEDYHVPESADQAAFDADQ
LLMPLVVRSLPGDTMKVMGLNGSKKVKNIFIDEKIPPYVRPRIPVCDGAGHIIWLP
GVRRSNVAPVREGTSAILYMTVGDSAIQG"

CDS complement(5875439..5876386)

/gene="yabT"

/locus_tag="EFAGFIKM_05162"

/EC_number="2.7.11.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37562"

/codon_start=1

/transl_table=11

/product="putative serine/threonine-protein kinase YabT"

/db_xref="COG:COG0515"

/translation="MTTLDASFPPGTVVTGKWNRSRYTIRKLLGKGANGIVFLVQRG
ENGKHYALKMGFDPVDLQSEVNVLSFQLQRNHEALRQSGIPSYLKDVDDYAVRGRDI
PFYVMRYVRGEALHHFIRRQGTDWTLVGLRLLQKLAQLHQAGWVFGDLKPQNVLVSD
YGQVELIDYGGVTSIGRSVKQFTEWYDRGFWNAGSRTADGTYDVFAFALLLIHVLEAD
ALKALAAEGLPQLRSVNQLVALVERSERLGPFRNWTTQALRGQFRDAGHAAQGWKEMM
ARPTPLRRRSKSTTPRWLKNFAVSVILLIGVLIYALLF"

CDS complement(5876370..5877122)

/locus_tag="EFAGFIKM_05163"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKQILLITDGCSNVGPSPVLAAAEALEEGITVNVVGVIDYGTIG
ELGSREIEDIARAGGGISQIVGTRQLAHTMQMMTRKTVVQTIQQAVNRELTQILGEKE
PKTVTDLEPAQRARVVEVMDDMAETTALQVILLIDVSASMKPKLAAVEEGIRDLMLSL
QARIGQSKLSVFHFPGRHIGEDAVMDIDWTTDPGRVRSLSFGRLQMKGATPTGPAIQKV
IDFYRYGTLEKQQEIEGNYRIEREGMLGDNVV"

CDS complement(5877208..5879712)

/gene="spolIE"

/locus_tag="EFAGFIKM_05164"

/EC_number="3.1.3.16"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37475"

/codon_start=1

/transl_table=11

/product="Stage II sporulation protein E"

/db_xref="COG:COG2208"

/translation="MEKWNVIQFPGMKAGKGGTEAREELSVRLKQWLGSRKAVQMIAS
RKWVLLLTFMGFLLGKAMILNELSPFAIAYFAVIAFMRRDYIIPVGAALLAGSLFAPF
PVPLIVASEIAIFYLLFRGLESYDRAELSYAPTMVFTTTFMVKLFAVVIGPSFSWYAM
LMLTMDSVLSFVLTLVFIQAIPIFTYRKKKFSCLKNEEILCLIILLASVMTGAVGWTIQ
SLSVEHMLSRYLILIFALVGGAPLGASVGVITGLILSLADMSAVYQMSLLAFAGMLAG
MLREGKRAAVALGMLLGSSILSIYLGPGDVMNSLWETCAAIVLFMLTPKSLMTAISK
YVPGTQDHTKSQHEYAKRIRDITAERVTRFSQVFRQLSRSFDQMSGAGEQVQKEGGMD
HFMNAVAESTCASC FKRTQCWD AKFIQTYKYMTDVMSTIEGNPEISGKQIPVDWNRVC
AKPEEVLEV MRAQYGLHQHNMQWKRQIIDSRLVAEQLSGVSQVMEDLAKEIQRESDE
MVQQEEQIRDALESLGLSIHSIEIINLEAGNVEIEIVHAYTRGFDECRKMIAPLISDV
LDEHIAVLHETMTDPRQGLATVTFGSAKTFEVTTGVA AAAKGGDVMMSGDSFSTVELGN
GTFVALSDGMGNGERARMESSAALNILEQLLQSGMDEKLAIKSVNSVLM LRSPEEMY
ATVDMALIDEYTAETTFMKIGSTPSFIKRGQEV IQVSASNLP IGIKDIEVDLVTVQL

QPGDILIMMTDGIYDAPGYAVNKELWMKRLIQEIDTDDPQDLADCLLESVIRYQQHEI

LDDMTVVVGKVEHFRPEWATLRVPGINRMERPRTVS"

CDS complement(5880188..5880721)

/gene="pnp_2"

/locus_tag="EFAGFIKM_05165"

/EC_number="2.7.7.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01595"

/codon_start=1

/transl_table=11

/product="Polyribonucleotide nucleotidyltransferase"

/translation="MAIEVGTKLEGKVTGITHFGAFVDLSGGVTGLVHISEIADNYVK

DVNDHLKLNLDLVTVKVINVDKDGKIGLSIKQAVDKPVEQQTQSRPPRAPRPERSGGDR

ERFSGGGPSGGQGRGGGGGGGFNRGDRGGRSFKPAAGKPSFEDKMSRFLKDSEERISS

LKKNTEGKRGGRGAKRV"

CDS complement(5880920..5881255)

/gene="ftsL_2"

/locus_tag="EFAGFIKM_05166"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00910"

/codon_start=1

/transl_table=11

/product="Cell division protein FtsL"

/translation="MGKTPVGRSKAPTQNGKSAGAKRRLMLWMTFMIVFVIWAGYTFL

VQTAQISDKSSHATQQASKEDTLKKLEQLKYEVSRLNDPEYIGQLARKKGYLPEET

PIQVEESGN"

CDS complement(5881267..5881836)

/locus_tag="EFAGFIKM_05167"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSPDTQWITLMWMLTSGVVMGMAYDSYRVLSGQLRFPRWSIHTL
DLLYWVASALFVFRMLYAGNHGQLRFYVFLGLIIGVCFYFWLLSVTTQRFVVMLIKLA
RTLIHWCGHILNILIVMPAKGIYKLIRVLFGFVIAILLFLGRLVLQCLVPFGKLFRRWM
FRPLLKHRVTPRFMIRVGTRIAAMWKRWF"

CDS complement(5881833..5882117)

/gene="yabP"

/locus_tag="EFAGFIKM_05168"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37558"

/codon_start=1

/transl_table=11

/product="Spore protein YabP"

/translation="MVEHGKAKQHHLSMQNRKLLDLTGVSNNVESFDSEEFLLQTELGH

LTIRGHNLHIKNLSLEEGLLSIEGTVSSLQYLDPGSQSKNGKGLFGKMFR"

CDS complement(5882291..5882569)

/locus_tag="EFAGFIKM_05169"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRLDKFLKVSRLIKRRTVAKDVSEQGRVLVNGREAKPSAAVKVG

DELTVQFGQKLTVRVERIAESTKKDEASSLYTLVKEEPIAKDNMGNW"

CDS complement(5882569..5882841)

/gene="hup"

/locus_tag="EFAGFIKM_05170"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A3H0"

/codon_start=1

/transl_table=11

/product="DNA-binding protein HU"

/translation="MNKTDLINNISTKSGLTKKDVESVLNGFLGEITDALASGDKVQL

IGFGTFETRKRSGRTGRNPQTGNEIVIPESTVPAFKAGNKLKEAVK"

CDS complement(5883149..5884642)
/locus_tag="EFAGFIKM_05171"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSAALTVVGLGSGDADQLTVGIIKKMKHAATLYVRTLDHPVLND
LKQEGLEMTSFDALYEAKSSFPEVYDEIANQLIEAARKGEAGTEIVYAVPGHPMVAEA
SVRLKERCQPQMGISLRVMGGESFLDEAFIRLGFDPIEGFQLLDASSLNTELVPQLH
TLIGQVYDVFTASDVKLCLMEVYPDDYPVFGHALGVQGGQEVHKKIPLHELDRIEGYG
NLSLIYVPKNTDDALRRRSFARLHEIVNILRSPGGCPWDQEQTHQSIRKNLIEETEV
IETIDEDDPDHMKHEELGDLILLHSQMEEEVGTFTNVYDVIEGLNDKLIFRHPHVFG
DNQAEDANEALQNWEQMKAEEKKRKGQDQKQSVLDGIPRDLPALMKGYKLQKKAHV
GFDWDDVEGVFAKIEEELAEKAEVQGGQSAEERKLELGDLLFAAANVARFIDTDPEE
ALAATNRKRVGRFQYIEERLREQGRTPADSNVEEMEQYWQDAKKAGL"

CDS complement(5884792..5886531)
/gene="murJ_2"
/locus_tag="EFAGFIKM_05172"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_02078"
/codon_start=1
/transl_table=11
/product="lipid II flippase MurJ"
/translation="MKQPSTGSRLQGAFFILGLAAIISKIIGAFQKIPLQNLGGDGVF
GIYNTVYPLYMLIITLAAAGLPLAVSKFVAEQNALGRPDESRIIRLSSLLGGIGII
MALLMYAGAPLIADMIGNRHVVPSIRAASWALLFVPVMTGLRGYFQGLQQMVPTAVSQ
VVEQTIRVTVMIVLLLWLMRRDASLETIAAGAMMGSVAGGMVGLLTMGLGYMVHHRKRG
REAVTEQLDSEWSSNGGEVGADRHEHSPVTSHKKTVSAINPALGERSRSNGEWIRTL
MYAIPVCLGSLAVPLMNLVDFTFTVPRLLRGEGLDELQTMVSFGIYNRGLPLVQLVTML
ATLSVLFIAPAMAEARLKGGEAVRQQAGLALRWFGLIGLAASAGLAVLAEPINRMV
GDAAGTEALRYMALTAAGSTVSIIAAALLQGLGAVRAPAFSMLAAAGVKALLNVMLVP
ALGISGAALAGAVAYMLAAGLNVALLARLVALRPAGAVLAKPALVIAAMSLAAVGTA

WAAEAVLGGMGVAADRRRLAAMGVSLLGIAAGSAVFLLAAARTGLLTAAELA AVPKLGP
RLAKLLRRLRVLR"

CDS complement(5886700..5887242)

/gene="spoVT"

/locus_tag="EFAGFIKM_05173"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37554"

/codon_start=1

/transl_table=11

/product="Stage V sporulation protein T"

/db_xref="COG:COG2002"

/translation="MKATGIVRRIDDLGRVVIPKEIRRTLRIREGDPLEIFVDRDGEV

ILKKYSPISELGDFAKEYAESLYESTGHVTMISDRDTIITVAGGSKKEYLDKQVGQLL

EGCMENRKILETNNGSYELSKDHDETLSSFVIAPISGGDPIGTIVILFNKDESVKMS

QMEVKMSETAAGFLGKQMEQ"

CDS complement(5887573..5888733)

/gene="prsA_2"

/locus_tag="EFAGFIKM_05174"

/EC_number="5.2.1.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01145"

/codon_start=1

/transl_table=11

/product="Foldase protein PrsA"

/translation="MLPKYKKVGKVLVSVMVAVLSLSLLAACGKKEEAKTPESTD TSA

VVATYDGGTITANEFDMQRVMKFLYPEY AQMMDMDDFKEYLVKQEVAYEYLSGKATE

DAKTAGTKAATEQFDKMKASVQADQWTEMLKAQNLTD DNIKDYMTTRIMTVIKDKETGV

TDDAIKAEFEKNKDQFTTASVRHVLINFTDPKTQKERKKEDALKIAKEVKT KLDGGAD

FAEIAKKYSEDPGSAEKGGLYENTPVGSWVEAFKEAAKTLPLNKISDPVET EYGYHVM

KVEARTEADFAKLTAEQKESLKSQLAAAEIDTFMQNELDKIVKEVKLPKTEK AEEGTT

EGTTEGTTGTGTEGEKTTEPKTDDSTGTDTKNDQGT TGTDKDATTDEGTSSK"

CDS complement(5888717..5892244)

/gene="mfd_1"
/locus_tag="EFAGFIKM_05175"
/EC_number="3.6.4.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7A7B2"
/codon_start=1
/transl_table=11
/product="Transcription-repair-coupling factor"
/translation="MLQALIQAFSKDPDFGSITAGIKSGMKEQLVSGLSGSARQIMLA
ALHQEMNRPLLVVTHNMFSAQKIAEDLQEALSPDQVLIYPANELVAAEAAVSSPETLG
QRIDVLVRCAQGFGRGVVPIFSGVRRYVPLPEVMANARILIKQGNTLQLDSFLLMVK
LGYERVERVESRGEMSVRGGIIDFYPTSSIA YRVELFDDEIDSIRTFDPADQRSIER
IEEITVLPCKELIADRERMEKAADAAALLLEQQLEKMTDRQAKLRLREEIHREIELLR
EHVYFSEMYKYISPLYPENKTIYDYPEDTLLVLDEPARLSETSKQLDRDESEWNLHL
MQNGKTLPLSADGDELLYERPFQTLFMSIFLRQVPHTQPQNILNFISRGMQDFHG
QMNVLKAEMERWQKAGVKVLM LANGEERLERMRRV LMDYDIPEPEMMIGNLQTFEMP
SIHLAVTEGEMFSQKQRKVRKPIRNVDNAERIKSYSELKVG DYVVHQN HIGIGKYLGI
GTLEVGGIHKDYMHIYAGGDKLSVPIEQIDLIQKYVGSEEKEPKIYKLG GNEWTRVK
NKVRTSVQDIADDLIKLYAERQTSKGFGFDKDSAEQQEFEDMFPYDETRDQVRAIEEI
KKDMEQNRPMDRLLCGDVGYGKTEVAIRAAFKAAIEGKQVAVLVPTTILAQQHFETFR
ERFSGYPFNIHVLSRFRSRKEQNETAKGIKAGTVDIVIGTHRLLSQDLVFKDLGLLIV
DEEQRFVTHKEKLKKLKTNDVLTATPIPRTLHMSMLGVRDL SVIETPPENRFPV
QTYVVEHSQALVREAIERELARGGQVYYLYNRVQGIQEMAAEISELVPEAKVGVGHGQ
MSETELEKTILDFLDGEYDVLVSTSIETGVDIPNVNTLIVHDADKMGLSQLYQLRGR
VGRSNRIAYAYFTYQRDKVLTEVAEKRLQSIKEFTELGS GFKIAMRDLSIRGAGNLLG
AEQHGFIA SVGFDLYSQMLAEEINKRKVTMLGEEPVP SDQWNTTLDLSIDAYLP SDYI
YDSIQKIEIYKKVAVIASFDDAMELEDELVDRFGDLPEAVINLLAVARMKVYVGKIYGI
ESISQRGEDITVKFYEGREHAFELSKIAHIGNQFERRVQFEQGPHMLIHAKGKGLGDK
QLMELVEKILESMKTAFKSKGELKDVTKV"

CDS complement(5892517..5892747)

/gene="fin"
/locus_tag="EFAGFIKM_05176"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37553"
/codon_start=1
/transl_table=11
/product="Anti-sigma-F factor Fin"
/translation="MSVNYVCRHCRTFIGRIDSARITEVELGFHFLTPDERRDIIAYN
SGGDITVRITCDYCKEALEHNPESLLASPLQ"

CDS complement(5892846..5893406)

/gene="pth"
/locus_tag="EFAGFIKM_05177"
/EC_number="3.1.1.29"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:B5XIP6"
/codon_start=1
/transl_table=11
/product="Peptidyl-tRNA hydrolase"
/translation="MKWIVGLGNPGSNYAKTRHNIGFMALDRLADRHNI SITQNKCKA
LIGEGNIGGVKTVLIKPMTYMNLSGESVRAYMDFYKVSLEDLIVVYDDMDTEIGKVRL
RYQGSAGGHNGIKSIIQHTGTQQFNVRMGISRPEPGHAIVDYVLSTFMKKEKEALDQ
TIEQTCDALEHSLTHTFEQTMKFNG"

CDS complement(5893852..5894805)

/gene="prs_2"
/locus_tag="EFAGFIKM_05178"
/EC_number="2.7.6.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P14193"
/codon_start=1
/transl_table=11
/product="Ribose-phosphate pyrophosphokinase"
/db_xref="COG:COG0462"
/translation="MTYFDSKLKIFTCSNPKL AHQIADYIGIPMGESHTTSFSDGEI
QVKLSESVRGCHVYIVQSTCLPVNDNLMEMLVMIDALKRASAKTINVVIPYYGYARQD"

RKARSRDPITAKLVANLIEKAGATRVIAMDLHAMQIQGFFDIPVDHLLGVPILAQYFR
SKQIENPVVVSPDHGGVVRARKLADFLNAPLAIIDKRRPEPNVSEVMNIIGNIEGKTA
ILIDDIIDTAGTIVLGANALMEGGVKEVYACCTHPVLSGPAMERLENAPLKEVIVTDT
IPITHANPTSKLKVLSVAPLLGEAIRVHEELSISKLFEIE"

CDS complement(5894907..5896307)

/gene="glmU"

/locus_tag="EFAGFIKM_05179"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A7B4"

/codon_start=1

/transl_table=11

/product="Bifunctional protein GlmU"

/translation="MKRMAIVLAAGQGKRMKSKLYKVLHPVCGKPMVGHVLDAAALSAG
VERSVVVVGHGAEAVQSFLGSRAEYALQAEQLGTGHAVKQVKSLGGETGSTIVVCGD
TPLVTSETLEGLMKLHESSGAAATVLTAAQLDNPBGYGRVIRGEDGSVQRIVEQKDCTE
QEDAVNEINTGTTCFDNAKLFAALEKVTNQNAQGEYYLTDVVGIFRNDGEVVEAYMSD
DIAESIGVNDRLALSQAEAFMRERLAVRHMLNGVTIIDPSSTYIGADVTIGSDTVLYP
GTILKGTTSIGEACHIGPQADVEDSVIQDGVTIKHSVVSNAEVGSDATVGPFANLRPG
TKLGRNVKIGDFVEVKNATIDEGSKVSHLSYIGDAKVGKNVNVGCGAIVNYDGYNKA
VTTIEDDAFVGSNVNLIAIPITVGKGAYVVGSTVTHSVPENDLAIARPRQENKPGYAE
KIRGRAKAKKQNAKPQ"

CDS complement(5896654..5896938)

/gene="spoVG"

/locus_tag="EFAGFIKM_05180"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P28016"

/codon_start=1

/transl_table=11

/product="Putative septation protein SpoVG"

/db_xref="COG:COG2088"

/translation="MQITDVRLRRVNSEGRMKAIASITIDNEFVVHDIRVIDGNNGMF
VAMPSKRTPDGEFRDIAHPISSGTREKIQA AVLTEYDRAATEEEVIEEGA"

CDS complement(5897127..5897918)

/gene="purR"

/locus_tag="EFAGFIKM_05181"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37551"

/codon_start=1

/transl_table=11

/product="Pur operon repressor"

/db_xref="COG:COG0503"

/translation="MTQYLLSRPHTVIPLTTFAERYGAAKSSISEDLAIIKEVFEEGG
SGELHTLAGAAGGVRWIPKVSRELALAFERLSTQLAQPDRLPGEYLYMSDLLGQPA
LMNEAGKIFATAFGNMNIDVVMETVKGIPLAYATGAQLNLPVVLVRRDHQATEGSAV
SINYVSGSHKSLHTMSLSRRAMREHSRVLIVDDFMKAGGTQGMIDLLAEFNATVAGV
GVLVESGSVDSEERLLTDYVSLAKLTAVDAKSRQISVKPGNYFDL"

CDS complement(5898052..5898906)

/gene="ispE"

/locus_tag="EFAGFIKM_05182"

/EC_number="2.7.1.148"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WKG7"

/codon_start=1

/transl_table=11

/product="4-diphosphocytidyl-2-C-methyl-D-erythritol
kinase"

/db_xref="COG:COG1947"

/translation="MKIYEKAPAKINLMLDVLHKRSDGFHEVEMIMTMVDLADRLEMS
ELPRDTIFISSQAGYIPLDEKNLAFQAARLIKERYNVRTGVHIIHLDKKIPVAAGLAGG
SSDAAAALRGLNRLWRLNIPDHELQELGAELGSDVPFCITGGTALATGRGEKLTPIPN
PPQCWWILAKPPINVSTADVGRFRSDKIVRHPSAAKMEQAIRNQSFTVEVCDQMGNVL
EDVTLKLYPEVQHDKDAMIRLGADGVLMMSGGPTVFGLVSKESKVARIYNGLRGFCKE
VYAVRMLT"

CDS complement(5899056..5899232)

/locus_tag="EFAGFIKM_05183"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSRRRRSVMSEDLKNELAKDLGFYDTVQQEGWGGIKAKDAGNMV
KRAIQLAEQAARKS"

CDS complement(5899484..5899759)

/gene="veg"
/locus_tag="EFAGFIKM_05184"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37466"
/codon_start=1
/transl_table=11
/product="Protein Veg"
/db_xref="COG:COG4466"
/translation="MAKNLLDIKRNLDAHIGQKIMLRANGGRRKTIERTGVLEETYP
SVFIVKLDEEQETFKRVSYSYADILTESVEVMVYDPGSQTHSSYMET"

CDS complement(5899913..5900809)

/gene="yabG"
/locus_tag="EFAGFIKM_05185"
/EC_number="3.4.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37548"
/codon_start=1
/transl_table=11
/product="Sporulation-specific protease YabG"
/translation="MNIGDLVVRKSYGGDVTRVEGLQLDAAVIKGTEFRLIADSPVD
DLIQVPYEPQSAKTRQAHIAHQTL SRLQQNRMEQAERNREGLVQDWSAQQEPAYFEM
PGKVLHLDGDPNYLKKSM DLYEQLRVPAEGQYVHESAMADTL YRLLPKVRPDIVVITG
HDGVLKTRQPYDLYSLGSYKNSQNFVSAIQVARQYERHLDALTIVAGACQSHFEALLR
AGANFASSPGRILIHALDPVYVAAKASFTSVRDTVNMSDVLHNTISGSQGVGGVETRQ"

SYRVGLPGLNDLSTLKVNPSTAV"

CDS complement(5900869..5901771)

/gene="rsmA"

/locus_tag="EFAGFIKM_05186"

/EC_number="2.1.1.182"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37468"

/codon_start=1

/transl_table=11

/product="Ribosomal RNA small subunit methyltransferase A"

/db_xref="COG:COG0030"

/translation="MKDMEETIEIATPKRTKEIIQRHGFSFKKSLGQNFLIDQNILNK

IVNAADLDESKGALEIGPGIGALTERLARVAGPVTAVEIDQRLIPILGEVMQPYSNVR

VHHGDVLKLDLAELFNTDFASVDKVTVANLPYYVTTPIMMKLLEEKLPVDSIVVMIQ

KEVAERMAAAPGSKDYGSLSIQVQYYSMPPELVCIPTVFIPQPNVESAVIKLVREQ

PPVEIPDEAHYFEVVQASFAQRRKTISNNLKARFFTKENREQADILLEQAGIQPSRRG

ETLSLQEYATLSTVMWEAGVRAAL"

CDS complement(5901776..5902321)

/gene="rnmV_2"

/locus_tag="EFAGFIKM_05187"

/EC_number="3.1.26.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37547"

/codon_start=1

/transl_table=11

/product="Ribonuclease M5"

/db_xref="COG:COG1658"

/translation="MIKEVIVVEGRDDTVAIRRAVEADTIETGGSAINQRILKRIALA

QERRGVIVLTPDHAGERIRKIIANKVPGCKHAFIPEADATRKGDIGVENASPEAIRH

ALARVHTSYEGAPSLIDWEDLIAAGLIVHPQAAARRMEMGNLLGIGYCNGKQFHKRLS

VFQITREEFSTALAQIEREGL"

CDS complement(5902477..5903661)

/locus_tag="EFAGFIKM_05188"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGTFQPEETHESRSSSKSFALRWKHENMRQMALIAIFSIALTIM
ILLVYVGQAGKQISLVIDGKAQVVETRTGMLQEMLEEQSITVSPHDKVSMNGAITD
GDRIVIERAVPVNITADGDTKLTLYTTDSSVEDAIQKSGIQVESNDKVYPALGTAIKAE
MKIRVVRVTKRTVEVEQPIAYKVIKTADPSLYKGDNRVVVNGKEGTIVQHIEKVFQDG
ELVSKKMVGKSVANNRVDKVIAGVTKAKPVVKEPEIQTVSAQTSTTKKATTNSKKTS
ASGSKVITVSGTSFKYSKVLKNVSMTAYSSEEPGIGTKTASGTRVTEGRTIAVDPKVI
PIGWWWVYIEGLGFRAEDTGGAIKGNKIDVYYDSVKHALNFGRKKGKTVYVIGPVKPE
AN"

CDS complement(5904430..5905200)

/gene="ycfH_2"
/locus_tag="EFAGFIKM_05189"
/EC_number="3.1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AFQ7"
/codon_start=1
/transl_table=11
/product="putative metal-dependent hydrolase YcfH"
/db_xref="COG:COG0084"
/translation="MMLFDTHTHLDAPQFDEDREDMIQRAVDAGVGRMINIGFNRETI
PTTMKLAETYDFIYAAVGWHPVDAITMQEGDLEWVASLCKHEKVVAIGEIGLDYHWDT
SPKEIQHRVLRQQIALAREVNMPIVIHNRDAHEDIIRILREEKAGEVGGVMHFSFGSW
ETAKSCLDMGFHLSFGGPITFKNAKQPKEVLEKVPMDRFFIETDAPYLTPHPYRGKRN
ETAHVRLVAEAAAEIKGISVEEIAAITTKNAMERFGIR"

CDS complement(5905525..5906802)

/locus_tag="EFAGFIKM_05190"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MEQRLTEEKVFKDPVHNYIHVQDPVIWQLINTPEFQRLRRIRQL
GTSYLTFFHGAEHSRFSHSLGVYEITRKIISQFERSHYSDWPKEEKIVALCAALLHDLG
HGPFSHSIEEAFDMNHEDWTCRIITGDTEVGAILRRYAPDFPEKVASVIQKTYEKPIV
VNLVTSPLDADRMDYLLRDAYFTGVNYGTIDLDRILRMLRPYHGRIVVKESGMHAVED
YLMSRYQMYWQIYFHPVTRSSEILRQIFKRAKTLQNGFQFRFMIDPLPQLFEGELS
VDEYLQLDEALIQTFTQWRKEDDTVLSELCERFMDRKLYKYVELEQVDLTMMEEIRE
AFVQAGLDPEYDLEIDFSPDNPDVFRPDESTDKQILLDRQDNLRELSEVSDIVRSI
SGLHRGKHHLIYPQNKVDIIHKLPSHIRPYFL"

CDS 5907120..5907374

/gene="abrB"
/locus_tag="EFAGFIKM_05191"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P08874"
/codon_start=1
/transl_table=11
/product="Transition state regulatory protein AbrB"
/db_xref="COG:COG2002"
/translation="MMKSTGIVRKVDELGRVVIPIELRRTLIGIGEKDALEIYVDGERI
MLKKYEPACIFCGNAENVTYFKGKIVCNECISEIPAPVTK"

CDS complement(5907657..5908541)

/gene="rsmI"
/locus_tag="EFAGFIKM_05192"
/EC_number="2.1.1.198"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P67087"
/codon_start=1
/transl_table=11
/product="Ribosomal RNA small subunit methyltransferase I"
/db_xref="COG:COG0313"
/translation="MTLHIQKSYAEQPEGSGKLYLVGTPIGNLEDMTFRAIKTLQSCD"

IIAAEDTRQTRKLLTHFEITPSMLFSYHEHNKGASGPELIRYIEGKNLALVSDAGLP
AISDPGSDLVQLALEAGITVIPGPNAALSALIVSGLPTERTFTGGFLPREKKDMRK
VLEAFDESNGTLLFYESPHRIRKTLVHLEEILGDRSIVLARELTKRHEEFARGTVREC
IDWLEEHPPPLGEYCLLVEGIKEEERKAEREAWWQLMSLADHVSHYEGEGHNRKDAMKK
TATDRGLAKRDVYNALIE"

CDS complement(5908542..5909321)

/gene="yfiC"

/locus_tag="EFAGFIKM_05193"

/EC_number="2.1.1.223"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01872"

/codon_start=1

/transl_table=11

/product="tRNA1(Val) (adenine(37)-N6)-methyltransferase"

/translation="MKANEVVLHESERIDLLSHDLRIIQSDEVFSFSMDAVLLARFA

SVPKRGRVLDLCTGNVVPILLTTRTQASLEGIEIQPRLADMARRSVQLNALDESIMI

REGDLRELVKETGHAVYDAITVNPYPMLNGSDLKMNTHQAMARHEIGCTLEEVQAC

SRLVRNGGKVSVMVHRPQRLAEIISLMREYKLEPKRIRMVHPRAHLEANMVLIEGMKDG

KPEVRMLPPLIVYNEEGNYCEEIMDIYYGQQAERTTKGGL"

CDS complement(5909417..5909701)

/gene="yabA"

/locus_tag="EFAGFIKM_05194"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37542"

/codon_start=1

/transl_table=11

/product="Initiation-control protein YabA"

/db_xref="COG:COG4467"

/translation="MIVKELLEDNQRLTIENEQLRKLLKREAPADLPISALAPVARP

AGPATGEDVVGEGYDNLARLYHEGFHICNVYYGHLRTEGDCLFCLSFLNK"

CDS complement(5909814..5910614)

/locus_tag="EFAGFIKM_05195"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYSVVGVRFKKAGKIYYFDPLDLPIEKENCVIVETARGVEYGKV

VVGKKEVGESDVVLPLKKVIRVAGDTDARVVDENKRAAKEAFGTCLNKKDHGLKMKL

VDVEFTFDRNKIIFYFTAEGRVDFRELVKDLASIFRTRIELRQIGVRDEAKMLGGIGP

CGRVLCCSSWLGDPEPVSIMAKDQSLSLNPTKISGLCGRLMCCLKFEHDNYESVREE

LPAVGKLVVTSLGEGKVVGINAGSRTVHVQLFDISKVKELPLDDVVIK"

CDS complement(5910732..5911703)

/locus_tag="EFAGFIKM_05196"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSFQQIMGQQAQKQMLQSSLRRAISHAYLFSGPAGSGQRKTAI

TFAKAIFCTELEDACGQCLECRKVDHGNHPDLTMLAPDGNNIKIDQIRDLQRIFSYR

SEAGHPKVYIIIEQA EKMTVQAANSLLKFLEEPQVPAVGILITDNGQAMLPTIRSRSQL

VPFSALNPEEMLQSLIEEGHPANLARS AVHLASGLEACREILQQNWFAEIRNVMLQLG

KESLGRGSTSLISAQQKLFKTGLSEHLDMLLSLFHLWFRDMLYVQYDRHEHIVFIDQL

DMLSQLAHTRSTEQWVS YMDMAAACRKKLRFNVNGQLCLEQFLIGLA"

CDS complement(5911713..5912156)

/locus_tag="EFAGFIKM_05197"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKINPGFRPIQSGISSTDSGSKPVQSKNFSDMMNHQGERASQAE

LNRRFSEIQLQGDR LARSMTIRELKAYKQLVKRFLEETVRRGVSMKETRGWDRRGRGK

RYKLIDEIDSALLSMADELLDTEEGKISLLQQVGEIRGMLINLSF"

CDS complement(5912501..5912830)

/gene="darA"

/locus_tag="EFAGFIKM_05198"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37538"
/codon_start=1
/transl_table=11
/product="Cyclic di-AMP receptor A"
/db_xref="COG:COG3870"
/translation="MKLIVAI IQDKDSNRLSSALVKANFRATKLASTGGFLKAGNTTF
MIGVDDGQVESVMNVIRSSCKVREQLVTPVTPMSGTTDSYLPLPVEVQVGGATVFVLP
VDRFEHF"

CDS complement(5912892..5913539)

/gene="tmk"
/locus_tag="EFAGFIKM_05199"
/EC_number="2.7.4.9"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q97R91"
/codon_start=1
/transl_table=11
/product="Thymidylate kinase"
/db_xref="COG:COG0125"
/translation="MQGRGKFITLEGGE GSGKTTMIGRIGSYFEERGIPYVVTREPGG
IEIAEKIRSIILDPLHTAMDARTEALLYAAARSQH LAEKVEPALRAGKAVICDRFVDS
SLVYQGYARGLGIENVWAINRFAIGD LMPDVTLYLDIEPEVGLARIDAHDGREVNRLD
LENLEFHRKVREGYFLLKEQFPDRIRVIDASMKQEDVLAAMILSLETGILKDFDE"

CDS complement(5913757..5914449)

/gene="cidB_1"
/locus_tag="EFAGFIKM_05200"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P60639"
/codon_start=1
/transl_table=11
/product="Holin-like protein CidB"

/db_xref="COG:COG1346"
/translation="MSAFILGIGMIALTIIVYIPATRLYKRLKWPILMPVLTTTAILI
LILVISGIKLDTYMLGGKWIQELLGPAVVSLAFPLSRHLHVLKQNIIPVGGTIGGSI
TGVSTGALIAILLGYPQEMVIALLPKSVTPVAIQLANQVGGNASFTSLFVMIAGFSG
ILLGPMLLKWAKVRSKHAYGIGLGSASHALGMARSFEYGENAVALSSVSMIVSAIAGS
IMLPLWVWIIYG"

CDS complement(5914419..5914847)

/locus_tag="EFAGFIKM_05201"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P60632"
/note="UPF0299 membrane protein YohJ"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGIPLKKYTGIVLQVLLMYGFYWIGNLIQAVLHLPLTGSIVGML
VLFVTIQLGWIKMSWGEESTWLQSHLQLLFIPPTVGIINHFDFFRANTLLLVI GLIV
STLITCLISAKLSEWLMWRSSHSGKKEAINCQHSSSELE"

CDS complement(5915378..5917222)

/gene="speA_2"
/locus_tag="EFAGFIKM_05202"
/EC_number="4.1.1.19"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P21885"
/codon_start=1
/transl_table=11
/product="Arginine decarboxylase"
/db_xref="COG:COG1982"
/translation="MDHKNKSSRAPLYEALLAYRDSKQRSFHVPGHKNQAYRHLVEQ
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HSEIGLVPDRSFLEMMEMDVTEITGTDDLHHPEGVIQEAQELAADCFGAEEFFLVGG
STAGNLSLLLTCDEPKSIVLVQRNVHKSVIHGLMLAGARAVFLESWVDPVSGLAVMP
SVETVQAAVQSYPEAKGVLVTLPNYYGMGADLTPIAEVCHAAGMPLLVEAHGAHYGQ"

HPPELVVSALSCGADGVVQSTHKMLTAFTMGAMLHIQGPRLNRSLLRQRLTMVQSSSPS
YPVMASLDLARRLLHVQGANTFTAGLTAVNAFKRGLAELPRFQLLQPAQPLQPAQPLQ
PEPPAGTAKPAGMSVSAQQTREGLTAAAMPSAAGYTAQDPFKAVIYDGTGVLSGYGL
QQQLEACGCVPEMSDERYVLLFSLGSTVQDAQYLLQALHHISSANGHEQVQSNAESS
HQLAKGSAHYISTWNNLQDKTHYSEPISTLQPIVEMDTINVPIEESAGCRSAEMVIP
YPPGIPLVYPGERISTSMVARIQLLRDEGAKFHGVSAASLQVLKVMKE"

CDS complement(5917479..5917664)

/gene="csfB"

/locus_tag="EFAGFIKM_05203"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37534"

/codon_start=1

/transl_table=11

/product="Anti-sigma-G factor Gin"

/translation="MEEHAEHTCIICEQRKREGIFIVSEFICDTCEAEMVHTDAQDAK

YNYFINQMKQIWVQKNA"

CDS 5918163..5918687

/locus_tag="EFAGFIKM_05204"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIAEPENKATFYQYRLLKKKAIARSVIYSYLCLPVIMLLFNLLA

FSWTGLFFFVLGPITIWVHYVIARTILLVVRTSYAKRWRWNMRMPWLGYIPDQHFSF

RMFVRVHLNMSWIGLCIITVCLIWSPSFTLSLIFWHLWLLGPRLYVVMVLSRERKDG

LIKLNQDVSYYLQ"

CDS complement(5919344..5919784)

/locus_tag="EFAGFIKM_05205"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLSWRRLGLQSFLLLCLTVVLAGCGEASGSVWTSYEGAVNEKSF
PVPKVANKSDQSENNSDMDYVRYTLSGISESTSLPEVYLDEIKSWGWTEKQAKGTSNE
SSTLRVFAKEGHTVHLAVHDGSFTLMVPRNDATQATVKSLAEDD"

rRNA complement(5920000..5920111)

/locus_tag="EFAGFIKM_05206"

/product="5S ribosomal RNA"

rRNA complement(5920260..5923180)

/locus_tag="EFAGFIKM_05207"

/product="23S ribosomal RNA"

rRNA complement(5923496..5925046)

/locus_tag="EFAGFIKM_05208"

/product="16S ribosomal RNA"

CDS complement(5925505..5926623)

/locus_tag="EFAGFIKM_05209"

/EC_number="3.1.4.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9HWS0"

/codon_start=1

/transl_table=11

/product="Cyclic di-GMP phosphodiesterase"

/db_xref="COG:COG2206"

/translation="MGLITLSEVKPGLKLGSDVQTLRGNVLLQKGKVLPKDMEVLRA
FMIQQVDIEQERMVSSSTVTKGASVSAGSSANDNNGERAGKTGNVTTAPVVTSLQDEY
EKMVALTKNAFLSSLAAELPVYELRTQLEAVFAHLKQYNVLTFSRVMQEHDYVYHHA
VLSAITSYQLAQWIDLPSKDWMQVAFAGLFHDIGNNKVDPQILHKPSTLTATEQEEIR
QHTKYGYQILKQAKAINEGARLAALQHHEKVDGSGYPLQLSGTQIHIYAKIVAIADIF
HAMTLEKIYRKAQSPYLVLEQIQSEAFGKLDPAIVRVFVQRSTQIHNGIRVKLSNNQI
GEIVFSDRDHPTRPMVSVEGTIINLMQQRQLHIEEVIG"

CDS complement(5926846..5929410)

/gene="gyrA"

/locus_tag="EFAGFIKM_05210"

/EC_number="5.6.2.2"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P05653"
/codon_start=1
/transl_table=11
/product="DNA gyrase subunit A"
/db_xref="COG:COG0188"
/translation="MAEEMNSQITDRDIGVEMRESFMDYAMSIIVSRALPDVRDGLKP
VHRRILYAMSELGMTPDKPHKKSARIVGEVIGKYHPHGDSAVYETMVRMAQDFSLRYM
HVDGHGNFGSVDGDMAAAMRYTEARLSKIAMEMLRDINKDTIDFQPNYDGEHEPIVL
PARFPNLLVNGVGGAIVGMATNIPPHNLGEVIDGVQAMIQNPDITSMELMDYIQGPDF
PTSGYILGRSGIRQAYQTGRGSVTMRAKTNIEENNNKARIIVTELPYQVNKARLVEKI
AELVRDKKIDGITDLRDESDRNGMRVVIELRRDVNPGVVLNNLYKHTSMQSTFGINML
AIVNKEPKILNLREVLHYLQHQIEVIRRRRTQFELKKAERAHILEGLRIALDHIDEI
ITLIRSSSNADAAREGLIERFSLSHDQAQAILDMRLQRLTGLERERIENEYNELMVKI
REYREILANEHLVLEIISTELQEIRDRFSDDRRTEITVGEESILDEDLIPREEVIIT
THTGYVKRLPVSTYRSQKRGGRGVVGMDTKDTEFVEHLFVTNSHNYLMFFTDKGKVYR
LKAYEIPELGRTARGETPIINLIQIEQGESVNAVIPVQEFESDRYLFFATRQGVVKKTP
LEDYTNIRKGGGLIGISLRDDDLIDVKLTDGLQEIIMGTAHGMSIRFSEGNVRSMGRS
ATGVKGITLDEQDAVIGMDVVDKELDLIVTAKGYGKRTPVNDYRMQTRGGKGIKTIN
VTEKNGSVVSLKMKVTEEDLMIITSSGTLIRMSMEGISTMGRYTQGVKLIHIRDEDSV
ATVSRIDKNEEEPDDDESLEGLEGEEPQATVVSLEEGTVSDAEVNEVEGDDDSGSEA"

CDS 5929838..5930785

/gene="yheD_8"
/locus_tag="EFAGFIKM_05211"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07545"
/codon_start=1
/transl_table=11
/product="Endospore coat-associated protein YheD"
/translation="MGIQRVSSKWAKTAVLQRSRIVNEYIPVTRKYSRQTLEQMTELF
ESNYIKPDRGTYGNVGMVRVTRTRYEPVNSEDDSTDAEVPEETNDRNLPDEPEASAV
ISRATYLTTTYHLQYGTEERSFHSLDELERALNDRIQEREYIIQQGISLMKHEDLPFD"

LRVLTQKNLQHNWETGVLGRVAAPGKIITNIHGGGRLATFEELVLPHLHQDGFKKLR
TELYRLGIHTAVQLQTSFPRLKEIGIDIALDEAGRPWILEVNTLPGIYAFGLLPDKEA
YRKIKRYAIAYGRLPSKKGKSSRPSPKAQASSAKKRVRR"

CDS complement(5930879..5932789)

/gene="gyrB"

/locus_tag="EFAGFIKM_05212"

/EC_number="5.6.2.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q839Z1"

/codon_start=1

/transl_table=11

/product="DNA gyrase subunit B"

/db_xref="COG:COG0187"

/translation="MSMNQPSYDANEIQVLEGLEAVRKRPGRMYIGSTSSKGLHHLVWE
VVDNSIDEALAGYCDHIEVSIHEDNSVTVDNGRGIPVGEHAKMKRPALEVMTVLHA
GGKFGGGGYKVSGLHGVGVSVVNALSEKVVTVKREGHIYQQEYRRGAPQYDLKVIG
TTEETGTTVRFPDPEIFTETRVFEYDILLARIRELAFLNKGIGLTLTDERTGATNSF
MYEGGIIEYVSYLNQKREVLHENPIYVEGSRDNIQVEVALQYNDNYTENIYSFANNIN
THEGGTHESGFKSALTRIINDYARKAGVIKDSTGNLSGDDVREGLTAIISVKIPEPQF
EGQTKTKLGNSEVRGIVESLFAEKLQEFLEENPSVSRRIEKGLQAARAREAAARKARE
LTRRKGALVSSLPGKLADCSSKDASISELYIVEGDSAGGSAKQGRDRHFQAILPLRG
KILNVEKARLDRILGNAEIRAITAMGTGIGDDFDIAKARYHKIILMTDADVDGAHIR
TLLLTFLYRYMRKIIIEAGYVYIAQPPLFKIERNKVIRYAGSERERDEIATLGENAKF
NVQRYKGLGEMNAGQLWETTMDPESRTMMQVSINDAILADTMFDTLMGDNVEPRRDFI
QENAKYVKNLDI"

CDS complement(5932935..5933183)

/locus_tag="EFAGFIKM_05213"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYIHLGGEKIIRSELVAIFDISIEKSSKISKQYVTHAEQEKTV"

EHIGEEAAKSIVVTKNIVYYSPISSATLKKRAHIFPDL"

CDS complement(5933198..5934310)

/gene="recF"

/locus_tag="EFAGFIKM_05214"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8RDL3"

/codon_start=1

/transl_table=11

/product="DNA replication and repair protein RecF"

/db_xref="COG:COG1195"

/translation="MFVNSIDLQNFRNYEHLRLDSFGPVNLLIGQNAQGKTNLAEAF

VLALTKSHRTSRDKELIRFGEERARLAAEVDKKYGSVKLELSLSQQGKKAKINGLEQR

KLSDFVGALNVVMFAPEDLEIVKGTGPGVRRRFLDMEIGQVAPGYLYHLQQYQKVLVQR

NNLLKQLWGKGASAQTMLEVVNEQLVEHGVKIVKKRKQFIKKLQKWAETIHQGITGGG

EVLRLAYLPSFSEAAEEDEAVLMDQFMIKLSQMKEQEIRRGTTLSGPHRDDLSFFIND

REVQTYGSQQGQRTTALSLKLAIEELIHEEIGEYPVLLDDVLSELDPFRTQLIETF

QSKVQTFITATGIESLNVDKLDASIYHVHAGQVER"

CDS complement(5934368..5934583)

/locus_tag="EFAGFIKM_05215"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNQVTIRTEYIKLDQFLKLADCIPTGGMAKALLQEGLVRVNKEP

EERRGRKLYPGDIVEVDGEGTFEVAEE"

CDS complement(5934600..5935742)

/gene="dnaN"

/locus_tag="EFAGFIKM_05216"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P05649"

/codon_start=1

/transl_table=11

/product="Beta sliding clamp"
/db_xref="COG:COG0592"
/translation="MKISIMKNYLNDSIQVSKAISRRTTIPILSGIKFDVNHQGVTL
TASDTDISIQSFIPLEDGDKSVVQVDQPGSVVLPKFFVEIKKLPSQEVHMEVKENF
NTFISAGATEIQLVGLDPEEFPVLPSIEENQTVSIPGDLLKNMIKQTVFSISTHETTP
ILTGVLWSLGDNELKFVATDRHRLATRSAMLDNAEGIRFNNVVISGKTLNELSKIVPD
QNTLVDIVVADNQVLFKIDRVLFYSRILDGTYPDTSRIIPTSYKTELVLDTKKLSESI
DRAYLLSREEKTNIVRMQTMDSGSVEISSSSSELGKVREEIEPAEFTGDPLKISFNSK
YMLDVLKVVESEQLMIAFTGVMSPHILKPLDDSHSLYVILPYRTTN"

CDS complement(5935962..5937308)

/gene="dnaA"
/locus_tag="EFAGFIKM_05217"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P05648"
/codon_start=1
/transl_table=11
/product="Chromosomal replication initiator protein DnaA"
/db_xref="COG:COG0593"
/translation="MDSHTSDLWQQILSIIQNKLSKPSFDTWFKATKATKLNDRSIVI
SAPTTFAVEWLESRYTKLVGSTVYELLGKQVDVKFVIEENKPAEPDPQLPAPTPKVQVQ
EEAVLSMLNPKYTFDTFVIGPGNRFAHAASLAVAEAPAKAYNPLFLYGGVGLGKTHLM
HAIGHYVLEHDPGSKVVYLSSEKFTNEFINIIRDNRGESFRNKYRSVDILLIDDIQFL
AGKESTQEEFFHTFNALHEERKQIISSDRPPKEIPTLEERLRSRFEWGLITDIQPPD
LETRIAILRKKARAENLDIPNEAMMYIANQIDTNIRELEGALIRVVAYSSLTNQDVTT
HLAAEALKDIIPSSRPKMITIHDIQQKVGEEYSLKLEDFKARKRTKAVAFPRQIAMYL
SRELTD FSLPKIGEAFGGRDHTTVIHAHEKISQAIKNDQDLYKVINNLTEKIKNPT"

CDS complement(5938179..5939726)

/gene="xylB_1"
/locus_tag="EFAGFIKM_05218"
/EC_number="2.7.1.17"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P35850"

/codon_start=1
/transl_table=11
/product="Xylulose kinase"
/db_xref="COG:COG1070"
/translation="MNNYMIGIDIGTTSTKSVLFTEQGSVVSTSTQEYPLYTPAPDVA
EQDPEEIVQAALRSVRGVMQSGVAAEQILFVSCSSAMHSVIAMGQDNKPLTRCITWA
DNRSAAWSAQLQENGLGHRIYLRTGTPIHPMSPLTKLMWLRHDEPELFERTAKFISIK
EYLFFRLFGQYVVDHSIASCTGLLNLEQLDWDAEAEVAGITPDHLSKLVPTTHILEG
MNHESA EKMALSSSTPFVIGASDGVLSNLGVNAIEPGVVAATIGTSGAIRTVVDRPVT
DPKGRTFCYSLTENLWVIGGPVNNGGMLFRWVRDEFAASEVETAKRLGINSYDVLTKI
AERVVRPGSEGLLFHPYLSGERAPLWNP DARGSF FGLTLHHQKEHMIRAVLEGVIFNLY
TVLLAMEEQIGQPTSIQATGGFARSPLWRQMMSDIFNQEVVPESFESSCLGAVVLGL
YATGRIQSLHAVSSMVGTT HRHTPVKENAVLYQELLPIFIRISRKLEEEYADIAEFQR
KMSLPRL"

CDS complement(5939793..5941154)

/gene="gntT"
/locus_tag="EFAGFIKM_05219"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39835"
/codon_start=1
/transl_table=11
/product="High-affinity gluconate transporter"
/db_xref="COG:COG2610"
/translation="MSTLFGLSHNATLLVWTLIAIVFLIVLISKYKWNPFITLLLSAL
MLGLLTGMPKPADVISSITGGLGGTLGTIAIVIALGTMLGKMMAESGGAERIATTLVDR
FGVKRVHWAMMIVGFIVGIPVFFEVGVILMIIIFTVARKTNMSLLQIGIPILAGLST
VHGLVPPHPAPMIAIEAFSADLGKTIYSLVIGIPTAIIAGPLFGKF IGKRIHTEPPA
ELAEQFATKTNSNMPGFGITLFTILLPVILMLIGSIASIIDPNATSGFTVFSEFIGHE
IIALLISVV FALFSLGFARGFTKHDISRFTSECLAPTATIILIIGGGGAFKQVLINS
VGNAIAEVATHANINVILFAWL VAGLIRVATGSATVAMTTAAGIVAPVLALTPGANIE
LVVLATGAGSLILSHVNDAGFWMIKEFFNMSVSQTLKTWTVMETLLSVVGLIFILLLS
TVV"

CDS complement(5941365..5942039)

/gene="gntR_2"

/locus_tag="EFAGFIKM_05220"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8GAL4"

/codon_start=1

/transl_table=11

/product="putative D-xylose utilization operon
transcriptional repressor"

/translation="MLFPSSWLQGASRGEAIACELRLRIISGTLRPGEILSENRIAAD
FDSSRSPVREALRTLSNEGLIRLERMGVWVIGLRIKDVEELYDVRFLIESFVQQRLAG
DVPESLIQLRNVIDKMQLAGRHQDAVEFAYQDLVFHETIIEAAQHSRISHLWKSIRY
VVM TVMLLTTRRVFVQGEQKVS AVIEKHLLLVEALES GDKVLIQAGVRTYFQDSGKTL
HESFDS"

CDS 5943107..5943457

/gene="rnpA"

/locus_tag="EFAGFIKM_05221"

/EC_number="3.1.26.5"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A0H5"

/codon_start=1

/transl_table=11

/product="Ribonuclease P protein component"

/db_xref="COG:COG0594"

/translation="MYKRLRLNRADFSRVYRYGKS FANHQFVVYGCRRKDTEQFRVG
VSCSKKIGNAVVRNRMRRMIKEIVRHHEHEIVTQMDLIFIVRKGALDMPYKEMEKSLL
HAMRKGSLLKSSKR"

CDS 5943533..5944411

/gene="yidC2_2"

/locus_tag="EFAGFIKM_05222"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9KDP2"

/codon_start=1
/transl_table=11
/product="Membrane protein insertase YidC 2"
/db_xref="COG:COG0706"
/translation="MSRLKTSKGKWILLIAVIAMVTVLAGCTPQGAGVTTEDLKNSDS
FWQANVIYWFSALDITFANWFNGEYGLAVLVMVLIVRTLILPLTMKQVRSSKAMQAIQ
PQLKEIQAKFKDTPKVVQETMKLFQENKVNPMAGCLPLIIQMPIYIALYNSIYGNSS
LRTHDFLWLQLGSPDHLFILPVLAITTFIQTWMMMRMNPAQQVGPMQFMLWVYPILI
FVMSYQFPSALPLYWFYSNIYTIVQNYFLYRNNDKIVAENVVKQNSSSSKNGAKRKNNGG
KATVSGKSGKAKKSK"

CDS 5944408..5945109

/locus_tag="EFAGFIKM_05223"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTKVITSGKTVEDAVNQGLTELGVSRDKVEIQVLEQPSKGFLGL
FGVRAAKVEVKLLPVPEVVPQPIKPAAYKSEVDALLEDVAAKNPYEEAAFLKEVAAG
MGLDVEVHIKKQRDGHIFNIAGEDLGMIIGRRGQTLDALQYLTNIVANRYSESFVRIV
LDAENFRQRRRKTLLEDAERLAGQAIRTGKEVVLEPMPPLERKVIHAKLQNHPQIKTL
SKGEEPNNRRVVITTK"

CDS 5945321..5946697

/gene="mnmE"
/locus_tag="EFAGFIKM_05224"
/EC_number="3.6.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q8YN91"
/codon_start=1
/transl_table=11
/product="tRNA modification GTPase MnmE"
/db_xref="COG:COG0486"
/translation="MISDTITAISTAVGEAGIAVIRVSGPEAVSETEKIFRSKTPLTQ

AASHTVHYGHIIDPANGEKIEEVLVTVMRAPRSFTTEDVVEISAHGGVVSVKRVMDLL
LQLDIRLAEPGEFTKRAFLNGRIDLSQAEGVMDLIRSKSDRAFSVALKQVEGKLSSKL
RDLRYTLVETLAHIEVNIDYPEHDVESLTSDFIKEKSSQVMTEIDKLLTTAEQGKILR
EGITTAIVGRPNVGKSSLMNTLAQDNRAIVTDIPGTTRDVIEEFITINNIPLKLLDTA
GIRETMDVVEKIGVERSRSAVSEADLILMVVSAEPLHPDEIELLEQIRGRQSIIMN
KMDLTPQVERDVLLRYIPEERLVPMSVKDDLGVDRLEDAISTLFFSGKLESADLTYVS
NVRHIALLLKKAKQSLVDAYEAAEQFIPIDMIQIDVRLAWEHLGEIVGDTAHDALIDQI
FSQFCLGK"

CDS 5946920..5948809

/gene="mnmg"

/locus_tag="EFAGFIKM_05225"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P64230"

/codon_start=1

/transl_table=11

/product="tRNA uridine 5-carboxymethylaminomethyl
modification enzyme MnmG"

/translation="MAFDGGSYDVIVVGAGHAGVESALAAARMGSKTLMITINLDMVA
FMPCNPSIGGPAKGHVREIDALGGEMGRNIDKTFIQMRMLNTGKGPVHALRAQADK
FSYQHMKETMENERNLTMRQGMVDRLIVEDGKCVGVVTQTGTEYRAKAVVLTGTYL
RGKVIMGELMYESGPNNQQPSLKLSNRELGFDLVRFKTGTPPRVHKDTIDFSKTEI
QPGDDKPKFFSYETESSDNEQLPCWLTYTSVETHQIINDNLHRAPMFSGLIEGTGPY
CPSIEDKIVRFSDKPKHQIFLEPEGKNTSEYYVQGLSTSMPEQVQLAMLR SIPGMEKV
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LKVQGKEPVILDRSQGYIGVLIDDLVTKGTNEPYRLLTSRAEYRLLLRHDNADMRLTE
IGHDIGLIPEERYAKFLDKKAKVEQEVARLKVAKARPVEVNAKLEEYGSTPIQDGSTL
LTLLRRPELG YELIEQLSPSEVELTADMKEQVEIQIKYAGYIEKQLIHVERLQKMEKK
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AARGQ"

CDS 5948809..5949531

/gene="rsmG"

/locus_tag="EFAGFIKM_05226"

/EC_number="2.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P25813"

/codon_start=1

/transl_table=11

/product="Ribosomal RNA small subunit methyltransferase G"

/db_xref="COG:COG0357"

/translation="MDDIQQQLQRRLLKKHGLELGELQLEQFELYQELVSWNEKMNLT
GITDREQVYTKHFYDSVSLAFYTDMTKVNKLADIGSGAGFPGLPLKICFPHIKLTIID
SLNKRIGFLQHVVLDLGLTDVELVHGRAEEIGRKEGYRDSYDLVTARAVAKLAVLNEF
CLPFVRKSGIFAAMKGGDPREEMKEAEFSFNQLKGRVKAVHPFQLPVEESERHIILIQ
KFDKTPYKYPRKPGTPMKTPLI"

CDS complement(5949436..5949651)

/locus_tag="EFAGFIKM_05227"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLIQSSISENKKKRMFHVKHPLYLCLKFYFVLTDFTITQLYQR
SLHWSAWFARILIWCFLNQNNDMTL"

CDS 5950047..5950865

/gene="noc"

/locus_tag="EFAGFIKM_05228"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37524"

/codon_start=1

/transl_table=11

/product="Nucleoid occlusion protein"

/db_xref="COG:COG1475"

/translation="MKEQFSKLFGLAERNNGDEIKQIPVNEIVSSPYQPRTIFDDDKI
DELLQTIKTHGVIQPIVVRNGSYEIIAGERRWRAVRKLGLDTIPAIVREFNDSQAA
SIALIENLQREGLTSIEEAVAYQKLIDLHQLTQESLAQRLGKSQSTIANKIRLLNLPD"

GIKMALMERKISERHARALLSLDTEELQMKLLGEIIEKELNVKQTEARVAFYKESSKI

KKSRRVSFTKDVRLALNTIRQSIDMVTGSGLDIKTKEADHEDHYEIVIHIPKRK"

CDS 5951055..5951816

/gene="soj"

/locus_tag="EFAGFIKM_05229"

/EC_number="3.6.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37522"

/codon_start=1

/transl_table=11

/product="Sporulation initiation inhibitor protein Soj"

/db_xref="COG:COG1192"

/translation="MSKIMAVANQKGGVGKTTTSVNLGAGLASLGKRVLLVDIDPQGN

TTSGVGINKADVANCIYDVIINEVPPQEIVETQIEGLHIIPATIQLAGAEIELVSTI

SREVRLKKSLAMVKKNYDYILIDCPPSLGMLTINSLTASDSVIPIQCEYYALEGLSQ

LLNTVRLVQKHLNTSLQIEGVLLTMFDARTNLGIQVIEEVKKYFQQKVYQTIIPRNVR

LSEAPSHGQSIITYDPRSRGAEVYLELAKEVISYE"

CDS 5951809..5952654

/gene="spo0J"

/locus_tag="EFAGFIKM_05230"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P26497"

/codon_start=1

/transl_table=11

/product="Stage 0 sporulation protein J"

/db_xref="COG:COG1475"

/translation="MSKRLGKGLDALIPSLSINDDDKVVEIPISQLRANPYQPRKVFD

EGAIHELAESIRQHGVIQPIIVRPVLRGYEIIAGERFRASQYCGNATVPAVVRNFS

DQQVMEIALIENLQRENLNAMEVAVAYQGLMDQFALTQEELSVKVGKSRSHIANFLRL

SLPEEVKDHVSRGTLSMGHARAIVGVKDEVVVKQLAKQTIDQQWSVRELEEAVQQQLDR

SKTGEAKAKSKLKKKDPFIDTLEESLRERFKTTVKIKHNKDKGKIELNYYSQQDLERL

LELLQ"

CDS 5952815..5953969

/gene="csd"

/locus_tag="EFAGFIKM_05231"

/EC_number="2.8.1.7"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q55793"

/codon_start=1

/transl_table=11

/product="putative cysteine desulfurase"

/translation="MEGVIIYLDHAATSWPKPPAVGDAMLSALEIAGANPGRGSHRMAV

QASRVLFEARKSISNIFGIKNANDIAFGSNTTEALNLAIQGSREGDHVIATMAEHNS

VRRPLEYMRRLRNVEIDYVPVNAAGAILDMQMERMFERSNTRLVVCTHSSNLLGSILPI

GEISLLCRKHGAILLVDAQASAGVMPVNVQQLGIDMLAFPGHKGLLGPQGTGGGLYIAP

ELDIEPLLHGGTGSQSEALEQPKVRPDRYEAGTPNTVGIAGLNAGVKHVLEMTPAVIY

QHEWELTQHIMDGLSSVKGIRMLGPEIGQPRTGLVSFTVDGYDSAQLAFRLDRNYGIA

VRSGFHCTPLAHESAGTTATGAVRASVGYNSTREHVEALVEAVLELTGAD"

CDS 5954110..5954610

/locus_tag="EFAGFIKM_05232"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAELNELILEQLLWIIIGGMALLTVILLIVSIVQGAKLRKFKRKY

EAMMAGSGVEDLESLLVNLKIQMDSIEDEHKLQTNQLQVVMQKLTRIQQKVGVKRYNA

YGERGSDLSFSMAMINDSQDGMILTGIYNRDGSYVYAKPLKGGESTYTLSPREEKAIT

LAQQAE"

CDS complement(5954585..5955190)

/locus_tag="EFAGFIKM_05233"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNPTSRSFSSQDMTSLKIPHTDPGIHSAITHRLMFHLYKAHSLQ
NVVIVCIGTDRSTGDCGLPLVGSALSKWDSPLFHLYGTLDPEVHAMNLQDTLHNIQKT
HHNPYVIGIDACLGQSSSVGCIQVVNGPLKPGAGVNKELPPVGDIHLTGIVNVGGFME
YFVLQNTRLSLVMRMSEIISSSLYSAIREWHTRSTLLAVPE"

CDS 5955308..5955571

/locus_tag="EFAGFIKM_05234"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDEWINDWMLIAFDSTQQALRAEMLLEFAEIEIDLFPTPKEITA
GCALCIQFPKEDLERVQKIIRNEFVEIRGLYFKTEDSYDNIPM"

CDS 5955586..5956524

/locus_tag="EFAGFIKM_05235"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLSFQFAQGEETSAAGAVNEALRWTDKVVWNIADPDIWLNIMFS
SIRIIIFIITRIVIKVVYRIIDRSMERKQEGKIRVNP RRFTV GELLKNATSITCNF
IMILLLLSEINIQVGPLLASAGVLGLAIGFGAQGLVKDVITGFFILEDQFAVG DVIQ
TGTYKGTVEVIGLRRTTKLVSWQGEVHIIPNGAIASVTNYSMSNSLAVVDIPMKADLSL
DESVHLVKKSLVGIEERDLNIVKVPDVLGIQSMSTSEYVVRIVAECMPNSRASVERQI
QGDVKKTLEYHEMSNQAVLEQAIALEKDEGDGTGGA"

CDS 5956514..5956723

/locus_tag="EFAGFIKM_05236"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MERKSFQLGDIVQMKKQHPCGSNEMEIIRMGM DIRIKCVGCKHS
VLIPRAKFEKNMKKVL RSAEDSTES"

tRNA 5956827..5956917

/locus_tag="EFAGFIKM_05237"

/product="tRNA-Ser"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Ser(cga)"

CDS complement(5957354..5957548)

/locus_tag="EFAGFIKM_05238"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGEKTEFEPGDKAPNDGEYTEVGEKSFVTEIQNPKRVTLQKGEA
FPETSNHNRKWKKLTKARVH"

CDS 5957751..5958044

/gene="rpsF"

/locus_tag="EFAGFIKM_05239"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P21468"

/codon_start=1

/transl_table=11

/product="30S ribosomal protein S6"

/db_xref="COG:COG0360"

/translation="MRKYEVMYIIRPDIEQEVVQATVDKFQGIISNGGGEVTAHDVMG
KRRLAYEIKKFRDGFYVLVHFTAEPVVTLERLMKISDEVIRYLITNDVKSA"

CDS 5958093..5958578

/gene="ssbA"

/locus_tag="EFAGFIKM_05240"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37455"

/codon_start=1

/transl_table=11

/product="Single-stranded DNA-binding protein A"

/db_xref="COG:COG0629"

/translation="MLNRVILIGRLTRDPELRYTPAGVAVTQFTLAVDRPFTSQGGEK

EADFIPVVTWRQLAETCANYLRKGRLAAVEGRIQVRNYENNEGKRYYVTEVIADNVRF

LESANRDNSGGGGGQPMREEPSYGGGGGRANNNNNNSRSNNQDPFSDDGKPIDISDDDL

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CDS 5958635..5958907

/locus_tag="EFAGFIKM_05241"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGFKQREGGDNDKRPARRGGRNKRRKVCFFTANKITHIDYKDTD

LLRKFISERGBKILPRRVGTSAKYQRMLTIAIKRSRQIALLPYTTE"

CDS 5959136..5959729

/gene="cwIK"

/locus_tag="EFAGFIKM_05242"

/EC_number="3.4.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34360"

/codon_start=1

/transl_table=11

/product="Peptidoglycan L-alanyl-D-glutamate endopeptidase

CwIK"

/translation="MNTSKRKGKQRKKRSLKTWIIATLLLSIIYVWLQQKGDIDNMWP

GTPIQDAVPITGLHPVVAENEELLVRKATRRGIEIVITHGYRSSEEQDALFNQGRSSA

GNIVTNARGGESYHNYGLAIDFALRTPEGDVVWDMERDDNGNGKADWMEVVDLAKELG

FTWGGDWANFPDYPHLQMDFDLSINELKRGRPPDSQ"

CDS 5960395..5961444

/gene="oppD_3"

/locus_tag="EFAGFIKM_05243"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P24136"

/codon_start=1
/transl_table=11
/product="Oligopeptide transport ATP-binding protein OppD"
/db_xref="COG:COG0444"
/translation="MDAFLHTNTIYGNYGVRVIDLNTELLEVRNLTSFRIEDDYAA
VDHVNLTVKKNEVLAIVGESGSGKSAFAFSLMGLHNKAKIEGQILYKGQDIANISPSK
LNKLRGKEMGMIFQDPLSALNPLMIIGEQIEEILTHQSKLSSREKREKVIHLLNQVG
IPRPEQIYKQYPHELSSGMRQRIVIAIAIANKPELLIADEPTTALDVTIQLQILELIR
DLKNEINAGIILITHDLGVVAEMADRVAVMYAGEIVEVADIFTLMNDAKHPYTRSLN
SIPTLSEERSKLHVIQGIVPSLKNLPRKGCRFKARIPWISESAHEENPQMHEIAPGHF
VRCTCYQHFFHPDQS"

CDS 5961459..5962391

/gene="oppF_2"
/locus_tag="EFAGFIKM_05244"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P24137"
/codon_start=1
/transl_table=11
/product="Oligopeptide transport ATP-binding protein OppF"
/db_xref="COG:COG4608"
/translation="MALLEVEGLKIHFPPIRGGLLKREIGSVKAVDDVSFSIEEGQTYG
LVGESGSGKTTTGRAIIGLNHVTDGKILFNGKNLATERRKNRQLQRDVQMIFQDPYSS
LNPKKRVIDIIAEPFRNYERLTATEEKQVRELLEKVGLSPESIIYKYPHEFSGGQRQR
IGIARAIALKPKLIIADEPVSALDVSVAQVLNFMQEIQKELNLTLYLFISHDLGIIRH
MCDQIGIMYKGRYVEQGTNDIFENPQHIYTKRLIAAIPDMDPTKREEMVAFRQQVKS
EYEHSYRNFFDEEGLAYSLKSISDTHRVALPQKG"

CDS 5962399..5963361

/gene="gsiC_5"
/locus_tag="EFAGFIKM_05245"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P75798"
/codon_start=1

/transl_table=11

/product="Glutathione transport system permease protein

GsiC"

/db_xref="COG:COG0601"

/translation="MWKTIVRRIIMIPQIFLLSLLVFLMAKAMPGDALTGLLDPSVD

PKALEAQRERLGLNNPWYVQYWDWIKNAIQGDFGQSFRFKMPVTDLIGQRVANTFWLA

LATLVLTYLIAIPLGIISGRYNDTWSDRLITGYTYLGFAAPLFIFALVMVWIFGFHFG

WFPTGGSVAPGLTPGTFSYVMSKFYHLLLPALSMALITTVSTVQYLRSEIIDIKHKEF

VITARAKGASESRIYNRHILRNSLLPIAAFFGYEITGLIGGTVFIESIFSYPGMGQLF

LSSISLRDFSVTALVLLYGVASILGALLSDIILGIVDPRIRIK"

CDS 5963391..5964296

/locus_tag="EFAGFIKM_05246"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WFZ9"

/codon_start=1

/transl_table=11

/product="Putative peptide transport permease protein"

/db_xref="COG:COG1173"

/translation="MSKANEVVVTSQKVDKSPSSLSILWRELVRDKVALISLIFLGLV

MLLVYGTSLILNQDDIVRVDLFALYEPPSAKYWLGTDYGGRDVFQQLVIGTRNSLTIG

IIVTLMTGFIGILIGLLSGYFGGMIDNLFMRVVDFFMILPMLMIVIAFVTAVPKYNII

SFSLIMTAFLWMGIARLIRSKALQERELDYVKASKTLGSSHLKIMLSQVLPNLSSIII

VTMTLNLAANIGLESGLSFLGFGFPESTPSLGLTVSYARNPQTLESRWWIWLPAVLI

LVLMLSINNVGQALKRATDARQRRG"

CDS 5964315..5966141

/locus_tag="EFAGFIKM_05247"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKGLFSRGLFFTMMMLVFVLVLAACSEKEAATPAPASNTEEGKT

EEKPANEEGVYSIEDFNNVKTNEGTAIEGGSITFGLVSDTAFEGTLNYNFYSGNPDVQ

VLQWFDEPLLTWDKDYVYTNDGAATYETSEDGKTFTLTIRDNVNWHDGKPVTAEDLQF
AYEVIGNKAYDGPRYDSNFTSIVGMEEFHAGKAKTISGIKVLSDKQISITYKESTPSL
LTGGVWWTYPLAKHIFGDMDVAKMSSSKEVREKPIGFGPFKVDVITPGESVTYVKNEDY
WRGAPKLDKVTLKVINPTTVVQELKSGGVDLVDAPFTDQYKDNANLSNVEFLGAIDRA
YTYIGFKLGTWDEENGKVVSNAEAKMGDKLRKAMWMAVDNDQVGKRFYNGLRWNATT
LIPPSHPEFHDSNNPGVTYDPEAAKALLDEAGYKLDGEFRTNPDGTPLEINFVSMTGG
DTAEPLARYYVQSWAAIGLKVNLEMVEFNSFYDRVNTGKDDPNIDVYQAAWGVGIDV
DPSGLYGRDALYNFSRFSSEENDKLLAQGISAEAFDVKRKEIYNQWQQYMVDEVPVF
PTLYRAVVAPVNKRVMNYAIGDGTGVYLSDLQVNADKAVVAE"

CDS 5966396..5967286

/gene="dacA_2"

/locus_tag="EFAGFIKM_05248"

/EC_number="3.4.16.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q05523"

/codon_start=1

/transl_table=11

/product="D-alanyl-D-alanine carboxypeptidase DacA"

/translation="MKKWWKRAGMLLALLLIYLGVPDMLVGKPGIKAESAVLMDMN

SEQILMDFNGSEEIAPAGVSKLMTTELLVMEAVINGDIGWNDLVNVSLYASSVGGSQLT

LKQGEQFTVQELFQVVAVYSANDAVALAEHISGTEQNFVQQMNQKATQIGLSEDTQF

TNSTGLSEKLLGPNRPMDIQGQTLMTAIDACKLARYLLNNHPEILRISSQMQVSMHQK

GMYSNTNWMLSSIGGPYAYDGNDGLKTGYDEDSGYHFVGTAERDGKRLISVVFGTDT

REGRFVETRKLFFNYGFSGSK"

CDS 5967623..5969212

/gene="bmr3_3"

/locus_tag="EFAGFIKM_05249"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P96712"

/codon_start=1

/transl_table=11

/product="Multidrug resistance protein 3"

/translation="MQKQMKWPLILFAIGVFMAALDNGIITSSLTTLNASFGVSPTWG
AWTITLYTLGLAVSVPIAGKLSDRYGRKKLFLIEVALFGIGSLLVALSTSFTFFLIAR
VIQALGGGGIFIIASSYVLSKFPAERQGTALGLLGGMNGVAAILGPNVGAFILDLTGN
WHWLFLINVPIAILLFIAGIRFIQEEQELSRAAVDWSGIAVLTGLVLSLMYSFSNLDG
VNMLQSLGSPMFYGGFFLAGVILLVLFYFMEKRLEGSEREPVVSTQLLGIASFRWTLLI
AFFSGAILASVIFIPGFVEQYLGVSNTASGYWFTPLALASGIGAGGGGYLVDRKGPIW
TLVAGLLSAIGFLLFPLWVEHIWQFVIASTLVGIGFGMMLGAPVNVVLTEQAGENNK
GIAVATSSLFRQMAMAIAPTIFAGFLARSFINLGSNIQAGFADKGIQVPPEMLEQYAS
GGASGSDVSSLTEGLSQIPDEGIRDVLLQAVHQTTGQGYNGLFWSAVVFSVLTVAAL
ITGRLRQKEKSQHVESVSTNG"

CDS 5969453..5970487

/gene="tagU_6"

/locus_tag="EFAGFIKM_05250"

/EC_number="2.7.8.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q02115"

/codon_start=1

/transl_table=11

/product="Polyisoprenyl-teichoic acid--peptidoglycan

teichoic acid transferase TagU"

/db_xref="COG:COG1316"

/translation="MKSRTKDKKKKRRKGLYITLVSLVLLIGGYLFRQQ LAVAAFDL

FLAGSVEDQLRSYVPQEGNNTPDPTVYRKEPFSVLLLGS DKRAYEKTRGRSDTVIYA

VVRPKESRVLLVSIPRD TYVQIVGRDANKDGEDDYDKLAHAYAFGGENMSINTVEKFL

DADVGYATINFDGIKKVVDALGGVKLPIDEDIVNKNPDHVQFTIEGGKPIYDGQEAL

YYVRYREDSDFNRTKRQQIFLNAMANEMLNLNQIAKIPELIQIMGDSFQTD MRASFII

DLAKQVLTQEKPQISSFTILGEGMKKDGIIYGQADEKD VQYAKELINNWM DQSTPAGE

VMIPDRQKIE"

CDS 5970672..5971097

/locus_tag="EFAGFIKM_05251"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MNIAFFLLPKQEVCVTSDSTLRQTLMERYHRFTAVPILNKEG
KYIGTVTEGDLLWYMKNAEGKISFENASKFLLKDVPLRLDIKPVSIDANMEDLINLAK
VQNFVPVDDMDRFIGIVRRSQIIEYCEGIVAKESIKAK"

CDS 5971363..5971665

/locus_tag="EFAGFIKM_05252"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MPKELDVAKRAKVIEWLKTVELDQVSRLFALWEGSTTRIGDSL
ASLIMSSYILGRRLGIPFKDLALLVEKLKKHKQEGHQLEDWYQDISALEDHMRKR"

CDS 5971668..5972582

/locus_tag="EFAGFIKM_05253"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLKFSFKSAVWSAVYLLLLLSLLTPLSVLAIFFMMIPGVILYAS
LSLKSFIVHLVPVAVILVVFHPIYLLLLLIFTLPAIVMGHAYKTRKSALFALMAGSGM
MLAEYLLLLLVGSVIFQFDLSSYIEDVVKLTIEPLTNTSNQMINGFAWTPEMTEDVAK
QTQLMIPFALVVTSMVMAFITHAIARPILNVMGVVSKLPPAREWRMPRALIWYYFLA
LLIEVISRQSDGTYWTMIAMNLSPLINLGFMIAIGFFFFLSHTKKWNPVIPYFLAAA
VFFIGPLRIIGIIDLAFPLREAIKSKR"

CDS 5972594..5974585

/gene="gdpP"
/locus_tag="EFAGFIKM_05254"
/EC_number="3.1.4.59"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A4ITV2"
/codon_start=1

/transl_table=11
/product="Cyclic-di-AMP phosphodiesterase GdpP"
/db_xref="COG:COG3887"
/translation="MPKFLKKRWHGYTVWAFILLLLLVMFVTIYNWTLGLISLILAS
ALGIVMIKAELAFRRELNDYINGLSIRIKRMEGEAVSMLPFGIVLYSEDRTVEWHNRF
VAEMFQEKTMVGNPLLNLFPKLPQPKEKKDGTKEHSSKEFHDEFQLDDRHYGVIHNPQ
ERYVYVYEITELAILRDKYENERLALGILVLDNLDEAAQGMDDQQRITALIARVTSEIT
SWAKRYEVYLRRLSSDRYLLMLNHKSLQELEQSRFVILDEVREMTADLKVPMTLSVGL
AFGSDSISEMGELAQSSLDMALGRGGDQAAVKSGQRLSFYGGKSNAVEKRTRVRARVI
AHALRDLMQESDRVLIMGHKIPDMAIGASIGVWKAASLYNVEARIVLDGINPSIERM
MEQVNKDEKLSKAFVSPEQATQMMTEHTLLVVVDTHKASMTMEPKLVQSATRVVVVDH
HRRGEEFINDAVLIYLEPYASSAAELVTELLQYIHDKVQFTPLEATALLAGITVDTKH
FALHTGSRTFEAAGFLRRSGADTIMIQRLMKEDLSEYIAKAEIHKHAKMVYGNIALAV
TDPGSKISQMMIAQVADTLLNMTDVVASFVISERPDGLIGISARSLGRMNVQVVMERL
GGGGHILTNAAVQLEGTLGEAEKRLTNVLAIEIEKEEGLFE"

CDS 5974582..5975025

/gene="rplI"
/locus_tag="EFAGFIKM_05255"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P02417"
/codon_start=1
/transl_table=11

/product="50S ribosomal protein L9"
/translation="MKVIFIKDMKGQGKKGQVKEVSEGYAQNFLPRGIARLATDGNM
KTLDNQKAAEERLKQEEKAEAEALAKKLEAEVTELKAKSGEGGRLFGAITSKQIAEAL
SKKGLKVDKRKIELDEPIRTLGVTVQTVKVHPEVKATLKVQVTEE"

CDS 5975027..5976388

/gene="dnaC"
/locus_tag="EFAGFIKM_05256"
/EC_number="3.6.4.12"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37469"

/codon_start=1
/transl_table=11
/product="Replicative DNA helicase"
/db_xref="COG:COG0305"
/translation="MGGEMLFDRIPPQNLEAEQAVLGAILLQGEALITAMERVQTEDF
YDKPHQLIFEAMIQLGEGNQPIDLVTLSLLKDKGELEDIGGVSYLAKLAHGVPTAAN
VDYYAQIIEEKSMLRRLIRTATQIVSEGYTGGEDVAAMLGEAERRILEISNRRSSSGF
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AFALNIAQNVAIRAQETVAIFSLEMSAAQLVQRMICAEANLDASVMRMGDFKGDWDWQ
KLTMGIAALSEANIFDDTPGITVADIRAKCRRLLKKEKGLGMILIDYLQLISGRGKAG
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FAM"

CDS 5976834..5978120

/gene="purA"
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/EC_number="6.3.4.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P65887"

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/db_xref="COG:COG0104"
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FEGAQGVMLDLQGTYPFVTSSNPSAGGVCIGSGVGPARIQQVIGVAKAYTTRVGDGP
FPTLHDAIGDQIRETGHEYGTGTGRPRRVGWFDSSVVRHARRVSGITGLSLNSLDVM
TGLETVKICTGYKFRGEVITHYPASLKMLAECEAVYEEMPGWSEDTGAKKLEDLPVN
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CDS 5978343..5979110

/locus_tag="EFAGFIKM_05258"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MKLLVWFVKILLTVLLVSSLTLLTGLIVQSYAKSLLASFNIQW
EGQPMGLTAMFQGALGGKTSEGNKSGNGTTDQPTGADEEHVPEDAVSVMGNGTESGQS
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GNGTGGTSGDASSGNDIVVSPDDITGTKDKLPAAEEKEKIFSLLMNKLPQKEMQQISG
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CDS 5979593..5981125

/locus_tag="EFAGFIKM_05259"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKGFRGIRQPGKDRVHEQSGEHRTAEDKNNMSMSTFSVNKKRVL
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DGEVIGIVKDQATADAILEQVQNKYISASAVRSSLKTKSVSANSSKKDEGPSTTLKSV
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EIRQHNPGIKETSQIGDELTLTPKPAVTVKSVEQVVEQIEIKPQVEVRKSADLKAG
TTKVVRPGQSGLKSMQYRITKENGEVQEEWLGQEVIKVAVTEVVLSTKVVGEGTGE
FAWPVSNATMSSSFGQRWGRQHKGVDLVGNRDVKASDEGVITFAGQKSGYGNVIIINH
RNGYETLYGHLNSIGVKVGQVVEKGESIGVMGNTGRSTGTHLHFEIKNGTVENPLTY
LN"

CDS 5981372..5982094

/gene="walR_6"
/locus_tag="EFAGFIKM_05260"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37478"
/codon_start=1

/transl_table=11

/product="Transcriptional regulatory protein WalR"

/db_xref="COG:COG0745"

/translation="MQGKILVVDDEQPIADILKFNLEKEGYEVICAFDGIRAVELALS
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PFSTRELLARVKAQMRRRQKLAITAGASEDEEKQVMRLFDLAFDMDMYTAYKGGEPLD
LTHREYELLYYMAKHSGKVMTREHLLQAVWGYEYFGDVRTVDVTIRRLREKIEENPSK
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CDS 5982094..5983944

/gene="walk"

/locus_tag="EFAGFIKM_05261"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q45614"

/codon_start=1

/transl_table=11

/product="Sensor histidine kinase Walk"

/translation="MGRFARFSFFRTIQAKLIIIVLLILIAMQLIGVYFVSAMKNSL
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SGKVLTTSLSSHSDYVGRKNTQTVVSRAHQGIRDNEEYIVDEDNVRKKVAKPVLSSG
KIIGAVYIAASMNELYSTMEGINKIFISGILIALVLTAVLGVILSHTITQPIKEVTRR
ATAVAEGNFDQQTPVFGTDEIGQLSRAFNMTSRLRDALSQNEEEKEKLTSILTNMSD
GVVATDEYGKVLVNRRASSILGMRPADIEGRHFALLGIDPEDAEALASGFTGSTLL
QIAPAGQEEPVIRMTFTPVHRRELGITGTIAVLQDVTEQEELEASRREFVANVSHEL
RTPLTTIKSYAEALDDGALEDPQLAGRFVGVQNETERMIRLVTDLLHLSRLDSKEAM
LRKQPTDILEMLEEVTDRFSFQMHQKDIQPVLSVENDIPAVPLDRDQIDQVLDNVVSN
ALKYTLEGGTITIAARRSDEHALAISVSDTGMGIPQRDLDRIFERFYRVDKARSRSMG
GTGLGLSIAREIVKAHDGSISLESEVDVGTTVTFTLPMREEGGEHREGTD"

CDS 5983928..5985208

/gene="ychH"

/locus_tag="EFAGFIKM_05262"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q794W0"

/codon_start=1

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/product="Two-component system WalR/WalK regulatory protein YycH"

/db_xref="COG:COG4863"

/translation="MKERIKSLVLATLVVASLVQSYFLIYRLPGGGDSIVTSETNYVK
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QSVNWDQIRKENPGFELSFKGIPVALLQRVMRLGTDLSLFQGETINRISIYTAKNETK
AHALFFSAKGDVVYEATQADLTVQDVQQHVDFTGNWTPYTLMEGGYYIPAEALETIEA
DVPTGQYTVEQMQRSLFFDPSMTRNIREKDGSEIYTDKRSLQVKQEQRWISYTDPA
PPAGQIDPAKDALSVDVFNQHGGWKGRSRMMLETADSKTQLEFQQYYGSYPIMDSMQ
FRFGTISMEMQQETVSSYERSLEYLNEGAETKKS VKLPGGEKLQALIKKVAGENRQVV
DVYPAYRPSTIEDGLKLIPVWVIRFGNGEETVS"

CDS 5985553..5986296

/locus_tag="EFAGFIKM_05263"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDWGRAKNVLIYAFLLNLVLGYQIWM DARETAGANLDFTSLAD
NTQQAMEEKG IQVLAPIPNETPKLPKLSYEFIEEDKAGVDMELEQPVDSKLIFSQSEL
EDALQREIPQIGTYRLDQLMAEDGAFVLHPLVDGKWPLFNVSELFYSDQKITGYRLT
PVRITTAESDQQVLPASKALGT LIENFLPND AIVKDIQLGYYGQLFNSDMQVAMPAW
RFVLESGEVLYVQGISGDVFS PKTDKPGE"

CDS 5986303..5987109

/gene="yycJ"

/locus_tag="EFAGFIKM_05264"

/EC_number="3.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SP91"

/codon_start=1

/transl_table=11

/product="Putative metallo-hydrolase YycJ"

/db_xref="COG:COG1235"

/translation="MGIYFTVLSSGSTGNATVIQHGGTSLMIDAGLSAKRLDALFQER
EISGAELDGILVTHEHSDHIKGLGAMSRKYNLPIYANLNTWAALEKSVGAIPEENRRV
FETGEQHDFGSLRVESFGISHDAAEPVGTYTFDDGTEKLSVATDLGYMSDKVRDAISDS
DVLVLEANHDEVLLRMGRYPWNTKRRILSDIGHLSNEAAGAALSELMNGRIKRTYLAH
LSRDHNMMDLAKMSVRDAMESRGCFYRDHEFKLCDTYDRPTPWDRVGEP"

CDS complement(5987078..5987290)

/locus_tag="EFAGFIKM_05265"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDRTRTLTAMDEVHMAAKLADLKDEHYRNTLALSTIIELLIDKG
ILTREEVERKAAELDSFMAHPPYPMA"

CDS 5988014..5989291

/locus_tag="EFAGFIKM_05266"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGLFGDDFYSTKVSRAEPEQKGKLQIIRPGGRARGRDRWSNPR
RSRTGISSTVKVAVISSVISSIVTMLFSFITQPASLPLANATGNNGGGGGAQTAQAAD
PYDRIIQAAAHVRPSVVSIVNHKTGSSLSMEDSALGSGVIFKKEDGKAYIMTNHHVVE
GASDLEIVTVDGETHKAKLVGKDRVSDIAVLSAEDKGLGAVAEIGDSSKLQRGQTVLA
IGNPLGLGGTLTSGIVSYTDRILPVSINQDGVYDWEQNVIQTDAINEGNSGGALVDL
NGKVVGINTMKISDTGVEGLGFAIPMNEVMKTVDLSLLNGKVSRLPYLGVYTVDLNPNY
APLDDEQRKDLKLPSHVDSGVVVLEASGPASDAGMKLNDVITEFDGQKITSTDLRKY
LYDQKKIGDTIEVTFYRDGKAEKVSVKLTDKPE"

CDS 5989591..5990112

/locus_tag="EFAGFIKM_05267"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKHLKKKMLGGTSLALSFLVLSACGSEVATTGASVDTSLQEKI

AGLEKKLVEQGAKSVEQEQKIAALETKNELSTNVIAGGAGGQTPVASGNNGSAGKGD

GVLITFAQYEKLEVGMSSVEDVIEILGGEGEALSEAENMVVYNYKGTAGNGANAVIAFQ

GGKLLTKAQSGLK"

CDS 5990486..5991451

/locus_tag="EFAGFIKM_05268"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFIKKSSMGVMLALCFMLILSACAGTASKTENAHSNAASAGNT

KSEETNTPAVELKVTTYNPGENSIFGVSSNLIEGPTEIVLVDAQFQKNDAEQLVKMIK

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LKENAPTAQIVPDVLDGAQLTVDGETVEIIGLDGSDPSHTFLWIPSIKTVLGGVPVYE

NSHVWIADNQTPESRDYWRQLLDQIIALNPERVIPGHYLGTSAGDISSVTFTRDYIAK

FEAEAETAKDSKELIAAMEKAYPDFTNTGDLETSQVIKGEISWP"

CDS 5991658..5991825

/locus_tag="EFAGFIKM_05269"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYVVCKEHVDIAIDMFVDEYEDAPDIVDLKETEFADWDPPAKCA

ECEQHAEFLVV"

CDS 5992205..5992489

/locus_tag="EFAGFIKM_05270"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISEfa8"

/codon_start=1
/transl_table=11
/product="IS3 family transposase ISEfa8"
/translation="MPKPQRRTFTTEFKKQMVQLFENGKSRAAIVEEYDLTASALDRW
IKQSQATGSFKEKDNRSPREENELMAMRKELQRLRMENDILKQAALIMGRK"

CDS 5992531..5993325

/locus_tag="EFAGFIKM_05271"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:ISfinder:IS655"
/codon_start=1

/transl_table=11
/product="IS3 family transposase IS655"
/translation="MCNVLEIAKSTFYHEAKEKPNDELTEAIVEIFHKNRKVYGRK
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EAKRFVWSDLTYVKVGHRWHYICVLMDFNREIIGHSAGPHKDAALVSRATVEGDL
SQIQWFHTDRGSEFKNHAMDQLLGTFGIGRSLSKGCPYDNAEATYKVMKTEFIYQ
MEFRNLRHLELELYDVNWFNRHRVHGSLGYLTPVQYRQEALKKVV"

CDS 5993728..5994207

/gene="rlmH"
/locus_tag="EFAGFIKM_05272"
/EC_number="2.1.1.177"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q45601"
/codon_start=1

/transl_table=11
/product="Ribosomal RNA large subunit methyltransferase H"
/db_xref="COG:COG1576"
/translation="MFIQIIGVGKLKEKYLTGIIQEYAKRLAPYIKFMIEVADEKAP
DTLSEAEVRVAKEREGERILAHVKSEAHVVALDGLWSSEELALEIDKLGTYGTSH
VVFVIGGSHGLSDEVLRRAKQRLSFGRMTLPHQLMRLVLVEQIYRAVKINRNEPYHK"

CDS 5994612..5995772

/locus_tag="EFAGFIKM_05273"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIQTLVNQLWDELQGNNPNKLLDKYHKYFDDYKDMFKEYDIPPN
TTYFRGRVGQKSLDVSIDDFDTTIQVSFNMSEISAVPPLFASGGRFNRAGYSYLYLSS
NIETCIAELRAEVGQVCSVGEFKNVELLRMLDLSSDSEDESYNFFKQLMLLPVNSQNK
NHYFLTQFISDIIREMGYNGILYNSSLSEGLNLVAFDSKQFQFVLYSDKMCKAKRIQY
DIEYVEEGYSKYKRYQDNLNGYNQKAEETKEQEIEYINKKADAMLFLSLREAVAQARE
SKVSKDEIYKEFECKCKSSMYFKTRINRMVARYLIHNDDLDGSIKFYINSLRDVKKG
VNCTTVFKMMLEDAPGLKSNRDFCIQLIESKCNENYLFELILDFDYLEKKII"

CDS 5995822..5996145

/locus_tag="EFAGFIKM_05274"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNSIHSCISEVIRELTYLYKRTYNNEWKSDYILNDVYDLVISLW
NAEIIEDSSVAMRLKFFYYDNKKYCFLEPADYTNYQSIESTASSQKDELIQELQKVKS
QKGIL"

CDS 5996289..5997044

/locus_tag="EFAGFIKM_05275"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGYQRYKLENNLTQTKKKLLSEYIVFYRGFIEEHGLDVLNVKI
PREVFASILDDIGALLNEHAIRLSSEEGERVKKFLEANPLPSNMEKLIPDEFRTFSLLL
NALKQWVSTESAATDKYLLGGKARQICQEAVDRCLVTGDELGENAELHHPLRDGRPPI
LLSKVGHDLIEQNYQKNDNEFINECDVWWNKVKQIRNQNNQSWIQLREGSNAIISKAS
TARPNAKSFANKVIREVGISAEEIEMLDVRGL"

CDS complement(5997118..5997867)

/locus_tag="EFAGFIKM_05276"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MANLKMHS LPINLGTPYLTNESAYFLGGIIAANETVSISNTECW
VSPVRYNYEYLTEAELRSHYTSVNAIANVLNNKTTYVDGSYININGFTLKVNKFTGRH
SGFVTLFPKKEKINVEELASLTEEVLKTSSEEVIRCFITGIFDGRGAIDFDYKKSIR
YIALDCANIQVATIFTSILNNFITNYNTSRDRLEGGIRRDNQFRIKDINYYYRSIGYI
SDVRFNKYLEGNPRVTTNYEDTILTGLKTIS"

CDS 5998121..5998309

/locus_tag="EFAGFIKM_05277"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGLEAEKWCSLEEIAEYLGVTKDTIRNWIKAHVPAHKIGRQWK
FKISEVDNWWKSGKSALD"

CDS 5998354..5999112

/gene="dpnA"
/locus_tag="EFAGFIKM_05278"
/EC_number="2.1.1.72"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P09358"
/codon_start=1
/transl_table=11
/product="Modification methylase DpnIIB"
/translation="MSETLSNLESNVLLL NEDCIDGMSNLDAGSVDLILTDPPYNLGL
FMKDRDTNLKKMRDNFFGAAGWDDLGFSDWEDSMNRFFAESTRLLKTGGAMIVFMSII
KVETLIKLAEQNGLYYKTTGIWHKHNPMPRNMNLHFVNSTEAWVYFTYKKKTGTFN
NN GKAVHDFFETSVTPGTERKFGKHPTQKPEQLLQQFIYLLSNEGETVLDPFMGS
GSTGV VAKRNRKFIGIELNKEYFQNAARIKETGVYET"

CDS 5999102..6000208

/gene="haeIIIIM"

/locus_tag="EFAGFIKM_05279"

/EC_number="2.1.1.37"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P20589"

/codon_start=1

/transl_table=11

/product="Modification methylase HaeIII"

/translation="MKPKVIDLFAGVGGMSLGFELAGCEVVLANEYDKSIASAYVENR
KESNMLVEDITDLPLTNTFGKYKGTIDIVIGGPPCQGFSQKGQRKTINDERNFLFKYF
FNVVSIVRPKYFVMENVPNLLTSENSFFKNEIIEIFGSIDYSLTSGVLNAADYGVPQS
RRRAVIIGKLNQVAPKLPEPVGYTVSIWDAISDLAYLKSGEGSEKQEYKCAPESNYQS
MLRSGSKILTNIHVATNHSSLALERLNLIPPNSGKEVLPQEHLTKSIYSGTWTRMRKED
VSVTITTRFDTPSSGKFTHPFLNRAITVREAARIQSFPDTFKFTGKGSQMKQVGNV
PPLAKSIAEVILNDRKKQEDYINDNSREFTRA"

CDS 6000177..6002033

/locus_tag="EFAGFIKM_05280"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTTPESLQEHRDIDLKLGKSSLSEVRETISLTFLWRSSGRVA
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VAFELIWRQAKVSFVEQSRFSFAERRGGIRYEKQLTFTKNMDLIDLLVAENQDTYMPIL
LKWATGFEIEIEDAAEEKLIKIFMLLSEEAIVKLTAAAGTDVIFNLNGVYKKLVEGNDT
VDINGELESKGLRILKSALSEGLNDFLSYRPGIVRLKDNRELDSEYQRRVSAYLS
LCNFKVIVRDNEFMVDTPVDEHTPLEATYNRILFGAPGTGKSYTLETEKAQFGDNYE
RVTFHPNYSYGQFVGTYKVPMDREITYKFVPGPFTRTLVKAINGTPQLLIIIEINR
ANVAAVFGDVFQLLDRRDGVSQYPIETSEDMRTFLASELESNFLSCTDETEKKRMLDK
YRKIVIPSNMYIWATMNSADQGVFPMDFKRRWEFEYIGIDGSDIEIYIVTLPNG
KQVSWNTLRKEINSILLKSKVNEKLLGPFFLGLSALANGEKFNEMFKSKLLMYLFE

DAAKQYRKVVFSGCDASTYSNVCIAYDNIGDEIFSLNLQDERQQESEDENA"

CDS 6002043..6003524

/gene="ydjA_5"

/locus_tag="EFAGFIKM_05281"

/EC_number="3.1.21.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34303"

/codon_start=1

/transl_table=11

/product="Type-2 restriction enzyme BsuMI component YdjA"

/translation="MRSAFFKELRRYSGEEIASLLQMTEEEAISLIRKLKSLGIVKEK

SKKALKDNEYVKDIDTEILYVELNSRNSHFVDFVGVINIGQYIICKYPKYISEVKTP

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NELNGEGEINWDKTIGEVYPILRESRAYYTELYTHGSFDDDFDYFKQLHECIITKCFL

KLKELGLSELFIDIEAILYDGELSDFGDEEYVLYRLSRELAVQFQNRKQIVLKTMYNY

IFKGKLREEENGLSLFGTNSFNFWWEKVCSDVFNNQLSTKLKYLSPQLAEQYSSEK

DYTLLELIEKPKWNLIEGGRLLKSHRVEETLIPDIISLFPKDDGVCFGIFDAKYYNIR

LDERRVDGQPGIGDITKQYLYQLSYNNFINAHNFTHIQNAFLMPTEKDTGEYVGTAEM

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CDS 6003883..6004968

/locus_tag="EFAGFIKM_05282"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIPFRNDHVGSLRPAILSQAREQYKSGNITYEELRVVEDQEII

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IAAYQKAIQAFYDAGCRYLQLDDTAWADLFSEAGHDKLRAKGLEPAEELKTMQRMINE

SLSHKPADLVVTMHICRGNYKSNYFSTGGYDYASEVIFGGLNVDGLFLEFDDERSGGF

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CDS 6004997..6006487

/gene="gabD"

/locus_tag="EFAGFIKM_05283"

/EC_number="1.2.1.79"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P25526"

/codon_start=1

/transl_table=11

/product="Succinate-semialdehyde dehydrogenase [NADP(+)]

GabD"

/db_xref="COG:COG1012"

/translation="MTIQADQETIIVEAFINGQNIKSLSQVAKENPTNPTEIVGYFPV

TTKEQAVEAIEAAAGAFKTWKQTPIDERIMMMRKAIEKIRAAENEIVHLLSREHGKPL

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LSTIKIAPALLAGNTIVLKPSPYAPLAAAKVAEIIASEFPAGVINVVHGDADVGVELT

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VISNFLTAGQICMIAKRVIYVHRSIYDEFVEKYIEAANRWIRIGDPFDSNTTVGPVNNL

KQKNYVLGLVEDAQKRGAKVIPLGQILDQKLFDQGYFLQPTLVLGCDVHDPiVVEEQF

GPTVPILPFDDEEQVIHLHNESIYGLTSSVWGKEEDAISVARQLEAGTTMINTAAVQG

LDVRFPPGGFKQSGIGREYGAEGIRTYTEKHVINVPKTLDPYIPE"

CDS complement(6006668..6007120)

/locus_tag="EFAGFIKM_05284"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTNNHEVGAVNELPENFEELKRAANRTSSWRDRLNAVNELGNWD

TAPTMKLLQHVLKNDQVFQVREAAYHKLKQLDEDVQMPAKNKGELFKGTNKILLRIKK

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CDS complement(6007223..6008182)

/locus_tag="EFAGFIKM_05285"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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/product="hypothetical protein"
/translation="MNSSLKQRMKSLLAPVFPGGIITILIFYLDYFQFELVEKFLLFA
AFVIVPLVILLDDHDAKNTYQRMMYAAMKWLFPAALLTLASVMSSKMWGLESTVIPIG
ILSLGWLLFTLLGLIYGLTTIVIAKGKAAEIAIGAGLVYFFIGGIWFTLYQYQLTLFQ
ANPATHALSSLHFHFSSAIVPIFIGALGRIMTKKSWYPWVVAIDIIGPILIAIGMIFS
KPIEYIGVALFACNIVVYTAYLLTYLRKNALDIKATIFLGLSCLAFYTVVVISIFYPL
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CDS 6008614..6009834

/locus_tag="EFAGFIKM_05286"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MHLRIKHLEKAIFIIIFMFVVFTYFNFISTEKMIYIGNVIEKKL
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IKEIESFKYRAKLKQVLENHPEIRKRRFSEDVLEVEQKLKDILVKYDMYIDKMMESID
TLKRYDYEELKLCVEEYKSIFNYSIVKKRILRFLSPEIKRIYPYDLNEKVSSEIIAK
RIYKIHKRLVEKIGSHMQNIEDINKSGDRSDALGLFLLFQNEIYGLGVKSISTVNSKN
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EMDGKTAYGDIYRK"

CDS complement(6010012..6010638)

/locus_tag="EFAGFIKM_05287"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
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/translation="MNRQLFPRSFRIIMACLLILAFV PATASAGYLGDKLTIGQSMA
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GSSLPANTTGDTLVMQSDGNLVLYNTTLTNSNYPNSWIPVWASNTGGR"

CDS complement(6010945..6011109)

/locus_tag="EFAGFIKM_05288"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSQAAPKLVFSSNLFKRTIGFFLAQETRSYNALDVSDRFRISYR

KIWLLYFLLL"

CDS 6011235..6013358

/locus_tag="EFAGFIKM_05289"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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AEFVSALVDMLKLNEVATAPAFKDVAANAAYADAIAEATHAGFIQGYGGNFYPDRDIT

REEAATILAKLVKDQATDKDATTIIASFEDGKSVSAYAIKPMAKLIDKGIFAGTDKKS

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CDS 6013710..6014255

/gene="ctc"

/locus_tag="EFAGFIKM_05290"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P14194"

/codon_start=1

/transl_table=11

/product="General stress protein CTC"

/db_xref="COG:COG1825"

/translation="MTTSFQAENRIPLNTSRLRDLRKSGRLPGIVFGKNTENEMIHIP

TIQFQKWLKQGTSGFIELQFEEKGSLTVLLEDLQRDPVTRDLLHVDFQQVQTNEILRT

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FAPDVTVISEGNESLLSVVKP"

CDS 6014670..6015287

/locus_tag="EFAGFIKM_05291"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDKLKNSGFYKLRFFITPEEFKSLQLLEHRQAQFYRTNAARTE

HDYNQVYEEYQTFYQYFVAGEKRDDIHPPFFVYSISIASDQESSGFFVRNEGVSPYYG

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PLRFSALDADAMKEQKPSVRISHDAMHDLSQSWIISKYGLVIHGK"

CDS 6015300..6015578

/locus_tag="EFAGFIKM_05292"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMFALKLICTWVLLVASCSAVWWSFRTEKLITFSWLAFLPAVF

QLVTAFRIGPGQAKSLIVFGCINLVFAALVGAGVWYLVQISNSYRRGK"

CDS 6015607..6016167

/locus_tag="EFAGFIKM_05293"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MKPMQEIETLAIEIAAAAKTSFCTLFENGERYYYCTLYTTGEGH
APSISAWSWEALALESARQAEESDTPVSTIADLIKWSYADSPYCCFGDDHFADVKQRY
NERPYIAELENDOWNRELDVRLNAMELAMKMLDDEGVFALNQPRESVCALVEVMPPDK
INTEIALRLNRAESPAMQVWLAEAAE"

CDS 6016443..6016781

/locus_tag="EFAGFIKM_05294"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGNRRPGAPSGYDPVQIYNSTSFNASGVVEYASIFCSNDRYSVQ
RDETWRSSDRGVCLVTRITATVRTPSGNIEAPYTSSGTSYSQFAIIQGVNQFRVTR
VTSAIRKCRK"

CDS complement(6016866..6017588)

/gene="yheD_9"
/locus_tag="EFAGFIKM_05295"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O07545"
/codon_start=1
/transl_table=11
/product="Endospore coat-associated protein YheD"
/translation="MLFERDKWLQYGILRDEPSLAERLPETQLLEKDTLTKMLLQYPS
VVLKPRNGSYGRGILFIKRSGANAYRIQENNTVIMRDNEQLLEWFEQTIKSDEYIVQ
KRLQLAQIKHRPFDIRIMVQRKKGSSTWNVTGSYAKVAAQGYQVTNVNNRPIPVLKA
LRLARIGDRLLVRAEQVSRLAAKRLGEYYPMLRQVGFDIAIDKKRRIWIIEGNYQPA
LRPFRLKDSSMHRRILWYKEH"

CDS 6018047..6019141

/locus_tag="EFAGFIKM_05296"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MIIGRQNGETIILIPSLEPDERLPAYVRQLREYGFTNIVIVDDG
SGEAYQSIFEELRENGCALLTHAENQGKGAALKTGFEYIGKQFDTSSFVVTADSDGQH
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TGLRAFGPGLLAFMQDVRGTRFEYELQMLISCIQSGIPIHTMPIQVIYENG NAGTHFK
AIQDSARVMGVLFNFLRFISSSVASSVVDLGIWFLIDALRPMLGEQHYLRILLATV
IARVISIVVNYVLNRHFVFRKEDSQGSLWRYLTLCGVVILLSSTGVYIFHTVLFVDEK
LAKFVCDALLFLLSFQLQRRWVFAARRKQL"

CDS 6019141..6021432

/gene="bcsA"
/locus_tag="EFAGFIKM_05297"
/EC_number="2.4.1.12"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37653"
/codon_start=1
/transl_table=11
/product="Cellulose synthase catalytic subunit
[UDP-forming]"
/db_xref="COG:COG1215"
/translation="MQNEKRQNIFFVITMILMSIYLVWRTFFTLPWGEGVLNVIFGML
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NACTFMDYDPKQKVHIYLCDDGARPEVEELARQFGVGYLGFPGNKDAKSGNLNNALSK
SSSPLIATFDADMIPQHTFLMKTVPYFMLSTFIKENEVWRPRREMDPKFKLGLVQT
PQSFYNPDFLQFNLYAEQGIPNEQDFFSREVNILRNASNAVAYTGSNTIISRQGMEDI
GGFPLNTITEDFETSIRLQQEGYITYATQEVQAAGQTTTTVKSMIKQRIRWARGILQS
LQNTRAPISGKLPFWTRVTYLSSFLYVWSFFNRLIFILAPILFALDFQIVNTTFWQI
LIFWLPSYFFYSVSMRYLSSNIRNQRRWSQVIDTIFMPYLIWPVLLETGIREKKFKVT
NKSRRASGRQWMSALLYALPHIFLLLLSIAAVIRYVNGKYGIALFFSSIIIFWLIHNMI
ALCYALFFMIGRRAYRETERIRAQEDVTIHDQANNLRYQAKTVDVSEQGIAFYVPYPI
YLAEQKIISLVVKTDREYANLDAVIVYVKQDGEGWRYSATVQPIDENDNRQYMQUIYD
RKHSLPEQMNLWDYDDMLRNVKKRIVQPRSDQRKMPRLSLQLPVHFTNEASCTLR
FNYRFFSATGFHGDIAAGAVVTFYTKSNIEVILQHTGKTTAREREVLLSVENIDDI

KGLIDQLLTDLIQPHSDRSTREG"

CDS 6021444..6023297

/locus_tag="EFAGFIKM_05298"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLIVLHFVMGVLLIFSFLGYMQFVRKALSLRWEFIPVFVFSSIA
CLVFLSGLAGQLFTGSLVILIAGLLLYGGMLFLRLRRGASLRMSFSIFQFSFLAGTFV
FLLVLFQNQLTHYDNFSHWAIVLKQMLSTDAFPTPDSNLIDFKNYPLGTSSFIYYVCR
FMGHSQSVMMLLAQGLLIFSCFYAMFGIVSEKKRFLLYAFLGLGLSTLSFFNLTIRITN
LLVDFLLPIYALTILAVIYQYRNEIKKACIVVLPLAGLLTIKSTGIIFAAIGLIFLV
YSWLKHKQKFSWKTALAVGTICGALIPYFGWSWRMATVFQGIDNKFDVATSGIQAGK
TPEQMQEILWTFLKASTDLTRPVIGIVIFQLIAAASVFAIVVLKKKWNLWKALIAL
DVVLLLYAGILALYLFMSPLDEAIVLAGFERYASSIVVLFAGGLVLCAIDLERSFH
YRIGEVDPDYQSFKTVETKGHYQKGIIGCMAVAATILLSEYNGIVSIAQSYDTTLPYKI
HAVTGDRWYSGGQEDNNRYLFYASDRDQQVTNYYMQYVGKYFLYAPHVDGIVLFYEDN
MDNLLSGYDYLVVVETDLNAKWLLKKHYGIDMQEGIYKITRSGDQIVLTLT"

CDS 6023485..6026364

/locus_tag="EFAGFIKM_05299"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRKWMVVIVILLAIGPWMGLWPLPVQAAHVFSGGGNGSPTDPY
IIRTAEDLDHVRDDLTASYKLQSDIDLTSGYNWLPIGTSANAFEGQLDGAGYTISGMT
IVSSADYIGLFGYVLEPATIHNVRLNVNITSSNTNSHYVGGLVGLANSSSVSNYYML
DRISVTGEIHGNGFSTGGIVGLSTYIALGNSDAHVSIYSNGYTYIGGLVGYNNSIIE
QSYATGDVSSSRNAGGLVGYSGGSSNVRNSYATGHVTGVSNAAGGLIGAGNSGTVGN
NYATGAVTRDSGIAGGLVGDNNIIIGSGMSITNSYWNLSDNLGLNTTGNQSGTDGAM
SQGAMKEWVTYIGWDSAIWGIHEDMSPPYLKSFSPVLRVDPLSSAAYSTELEDNHFMI
SGYVRDGSIGEPLVSYTIKDASNGTVTQDVYAINATSSNQTFNFPVMLEESSYTPGT"

YTINITASDSVPAHEQLQSLTFEVEDKSPPAAPIITIPSHGHMTNNTKPTISGTSEAR
ATVTVMMDGNIAGTTAAGSNGSWVWTAVSPLPEGMHVVKTRASDEVGNVSPDSAVHTF
TIDVKPPIITLIGSPSMQVKVGSAYTDPGATAQDAVDGDLTSQIKVTGAVNVSRAGSY
VLTYKVQDSSGNAAASVLRTVDVSSGGGGGAGAGGESGGSGSSSVEQSSNANLAQLT
LRVGGSTEELTPQFAPEITEYTMETSGEQLVLQWVAADSKAVVKLRSELVIDTTSIPL
VVGTVVKITVQAENGTRKVYTITVTRLDDNENASSSLECAFTDIQAHWAKTDICEAA
RLQIVEGVNTNIFAPDKTVTRAELAVMLMRTLQIPGVQQSAANPFSDKDSTPEWARLA
IHTGAVEGIFNGYPDGTFRPQQEIDRAEMAAMLAKKWETDPELDLTFSDRANIPAW
AQSYYVQAAYENGLLQGRGDNQFVSDGMTTRAEEAAVVMLRLWKSly"

CDS 6026498..6028252

/gene="sasA_21"

/locus_tag="EFAGFIKM_05300"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"

/codon_start=1

/transl_table=11

/product="Adaptive-response sensory-kinase SasA"

/translation="MNSTIEFVVMIASVMMTCIIFISVYGFRKERGVKYL LGVIVCRI

MYSIGVVLEKSSYELGDKLIFRNVHQTALNLMVPFFLLFTLELIGRDKFLRPRLKFVF

FILFALWSLLMWFNSELHMIYRSIKLHDGHLTTIKTGYSITFSMICYCIVAISFYLLF

QYIRNIRGDLRKPIMWVLFASFVFEIIRFVHPAWSPWLLSFTVYCSFIGMIMLVI

VRLRYKFFSIVPFARNMVLDTLQESILIANASGKIIDNNKQASDWFLKLGHASISGQNI

TDLLARWPNWYTLCESMQQGNVEIEVWLDGERKMYSINVYPLHTQRKQRQGVISLIFD

ITEKQQHLDQIAQLSQLKDQLVTIVSHDIRTPLAVQFQLVELLEEDRENFPDHRFII

EQLGNQTRTTLGMTNNLLEWFRSQSEDMVLRPQLLELTEVVEECLHILHIQSEVKQIR

VNYSIAPGTRVYVDREALGLIIRNLLSNAIKFTGVGGSIHVSAHLSGEKVTVSVRDNG

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FHFTMRGGTGDESSYRGR"

CDS 6028227..6028955

/gene="desR_2"

/locus_tag="EFAGFIKM_05301"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34723"

/codon_start=1

/transl_table=11

/product="Transcriptional regulatory protein DesR"

/db_xref="COG:COG2197"

/translation="MKVLIVDDEFAMLLAMKRMLSNMEGVGVGSFRDAAEALDFVRG
SNVDLAILDIMIAGDDGLELARSLRSICAELDIVFTTSHAEFALNAYDVYPLDYMVKP
ISRIRLAQTITRAMNKRSISSDDSTEKWTGNHADNEGESISNTSYVVEAPALVAPLTS
REREVLQGIAAGSTNEEIAEQLQISLSTVKVHVRHIFSKLEVHNRVSAVARAHD LAVI
GSGGNPITRSRGKFPHEKNDPGLS"

CDS 6029144..6030283

/gene="metE_2"

/locus_tag="EFAGFIKM_05302"

/EC_number="2.1.1.14"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00172"

/codon_start=1

/transl_table=11

/product="5-methyltetrahydropteroyltryglutamate--
homocysteine methyltransferase"

/translation="MSIQTEPKQRNVTPFRYDIVGSFLRPSALKDARLKYQNGEITTE
QLKEVENAEIVKLVQKQKEVGLQAVTDGEFRRSWWHLDFFWGLDGVERTIIDEGYRFN
GATSRPETARLTGKIGYSNHPFVAHYAFLKDTAGNDVVARQSIPAAAQFLFELDRADN
KESTQAIYPNRQELLSDIAGAYKASILAFYEAGCRSIQIDDCTWGALCDQQFITVMEQ
IGVNVEEYANELAKLNEEVVSGLPEDLVVTTTHVCRGNYVSTFAGVGGGYEPIAQTLTS
IDNYSGFYLEFDTERAGDFKPLRFLKDNQQVVLGLFSSKFGELNKEDILKRIEEAKQ
YVDLDRICLSPQCGFASTEENHLTEEQQWSKLAFIKEIAEELWK"

CDS 6030480..6031694

/gene="sasA_22"

/locus_tag="EFAGFIKM_05303"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01837"
/codon_start=1
/transl_table=11
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FLIFHLTFSRMKKQELYFEQLQQSERLKMIAHLTAABAHEIRNPVTVVVRGFLQLYQED
HSFEQPVRNKFALMIDELNTEQVTSQFLTLAKPNRELPEKVDVREVLEGVTGLLSS
YAMLSDRHMDVQVDEDCIILINTIEFKQLLINLIKNALEASDAGTTVQVTAKRVKQWV
EMRITDQGSGMTEEEVRS LGTPFYSLKTNGTGLGLMICYNIVEKEYEGTIEYHSAKGQG
TSVTIRLVAKTV"

CDS complement(6031758..6032558)

/gene="yusV_2"
/locus_tag="EFAGFIKM_05304"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O32188"
/codon_start=1
/transl_table=11
/product="putative siderophore transport system
ATP-binding protein YusV"
/db_xref="COG:COG1120"
/translation="MKPTHVFEAKQLVAGYENKTIHGVDIVIPSNQISVIIGSNGCG
KSTLLKTMARLIKPTSGSITLDGKAISKIPPKQLARVIGLLPQSPIVPEGISVADLVG
RGRFPHQSLFSGWTKKDYEAVAEAMTIMNITEFANYNIDELSGGQRQRVWIAMALAQQ
TDILFLDEPTTFLDITYQVEILDLLTELNRKHGTTIVMVLHDINLSARYADHIFALHT
GKLVAEGKPTEVITAPQVKDIFGLECTVIEDPFSGSPMVVPKGRYHAR"

CDS complement(6032558..6033589)

/gene="fepG"
/locus_tag="EFAGFIKM_05305"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P23877"

/codon_start=1

/transl_table=11

/product="Ferric enterobactin transport system permease
protein FepG"

/db_xref="COG:COG4779"

/translation="MRDQSIEFIMAGRRHRRRRWILVTSLAILACALCCAMLLLGNT
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LIGIGIQAMLDAVISYLLLVSSEKDIPAAIRWLTGSLNGSQMSALPPLVITVLCSPI
IMMLGKHLISILELGEQSAFSLGVDTDKTRIALIVSSVCMVAIATATTGPIAFVSFLAG
PIAKRLVGVGSSNILPAGLVGVNLVLASDLIGQFAFEYRFPVGVITGLLGAPYLIFLL
IRMNRKGEL"

CDS complement(6033586..6034626)

/gene="yfiZ_2"

/locus_tag="EFAGFIKM_05306"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31568"

/codon_start=1

/transl_table=11

/product="putative siderophore transport system permease
protein YfiZ"

/db_xref="COG:COG0609"

/translation="MNSTSLSDNRIRAHVPKNFILVLVICFILLGATMIASLVFGSR
PVRFHELIDGLFHPEVDSYGANIVRKIRSVFSLLCGVALGVSGALMQAVTRNPLAD
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KLVLAGAAISAALSSLVTAIMIPRSYVMDQFRFWQVGSVGSATWSGISTFIPFLVIGV
LIAFLTAPALNALGDDVATGLGVRTGTLRFIAALAGVLLCGAATALAGPIGFIGLL
STHVIRLILGPDLRFPMSAIAAGAIILTISDVGGRLISNPGELEVGVVTAFIGAPIL
IILAMRSKVRSL"

CDS complement(6034619..6035701)

/gene="fpuA_2"

/locus_tag="EFAGFIKM_05307"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q81L65"
/codon_start=1
/transl_table=11
/product="Petrobactin-binding protein FpuA"
/db_xref="COG:COG0614"
/translation="MNTKRKFPLTALLISLIFILALVGCNQNTADPAATPAASDSAAQ
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DYDLLSEIAPVVAYPTAPWATTWREQVTFNAKGMGMEAEQEQLIKDTEAMVNEKLAAY
PQIKDKKVVVWNFSAEDMSKLHIYTPVDSRVSFLGELGLVVPESITSQITDPNSYLS
LSAENAEALNDADILVGYGDAELLKAIQADPLLKIPAVKRGSVAFIEADTPLVAAGT
PNPLSISYTIDDYLLKISGAIDKINE"

CDS 6036062..6036826

/locus_tag="EFAGFIKM_05308"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MHNQIIKKLIVLCLVFVLLPATSVLAASSLIKDPVLAKVIRADL
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LKKLTFLAVEGNQIADISPLLGLTSLQNLVMDDNKIKSLAPLKNMRKLTSLLASGNQV
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YLANNPLNERAEQVVENLKKKGVVVSLVSEEADQTK"

CDS complement(6036981..6038090)

/gene="araR_3"
/locus_tag="EFAGFIKM_05309"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P96711"
/codon_start=1
/transl_table=11

/product="Arabinose metabolism transcriptional repressor"
/db_xref="COG:COG1609"
/translation="MKEVDYVKPKYQVIIDDIKSHILSGTYSIGEQUIPTTELALQESYT
VSRQTVRKAILLELSNEGFLRSEKSGTYVSNQYRSRSGGNTSKKTIGVITTYISDYIF
PSIIRGIESRLNEDNYSLLLASTNNDVAQEKKALEMMLS YGVDGLIVEPTKSNLYNPN
IAYYLSFKEQDVPFTMINAFYEELEVPPFFCLDDVQSSYLATRELISKGHTQIGIIAKM
DDLQGKYRMKGYIKALGEAKLRFHPEQVLSFDTASKPDLSSNVATYLDESRDALTAIV
CYNDEVGLEVVHACRQLGISIPDELSIIGQDNSYIAKNANIRLTTLTHPQEQMGRDAA
DWVIKNLQGKKDLPTNTYYQPVLVEGETVKEIVVE"

CDS 6038501..6040123

/gene="xylB_2"
/locus_tag="EFAGFIKM_05310"
/EC_number="2.7.1.17"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_02220"
/codon_start=1
/transl_table=11
/product="Xylulose kinase"
/translation="MIMSQDLKEAITKGATSLGIEFGSTRIKAVLIDERVETIASGS
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ALDSAGELLVPFRTWRNATTGAAARELTELQFNIPERWSIAHLYQAILNEEVHVPQI
DHLTTLAGYIHWLLTGNAIGIGDASGIFPIDESTHNYHPSMIQQFDEQIAGKGYPWK
VEDLLPKVYLAGENAGALTEAGAKLLDPSQDLQAGIPLCPPEGDAGTGMVATNSVRKR
TGNISVGTSVFAMIVLEKELSKVYPEIDMVTPDGSPVGMVHANNCSSDINAWVGLFR
EFSQAMGYEVDNAKLFSVLFNKALEADPDGGGLLSYGYYSGENITGLEKGRPLFVRSP
ESNFNLANFMRTHLFSAFGALKLGMDILTEENVAIDSILAHGGLFKTPVVGQRIVAA
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DVKGFEAFIERYSGLAIEQSAVDHLVENGRE"

CDS 6040125..6040820

/gene="araD"
/locus_tag="EFAGFIKM_05311"
/EC_number="5.1.3.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P08203"

/codon_start=1

/transl_table=11

/product="L-ribulose-5-phosphate 4-epimerase AraD"

/db_xref="COG:COG0235"

/translation="MLEQLKEEVFQANLELPKHGLVKFTWGNVSAIDRESGLFVIKPS
GVSYDTMKASDMVVVDLDGNVVEGEMRPSSDTATHAVLYKHYSEIGGIVHTHSTWATI
WAQAGLDVPMGTTHADTFYGAVPCARFLNQDEVDRGYEAETGRVIIETFEQRGIDVM
AVPAVLLHGHAPFTWKGDAKSAVVNSVLEEVCCKMNLARQLNNFAKELPQGILDKHY
LRKHGKDAYYGQK"

CDS 6041096..6042514

/gene="araA"

/locus_tag="EFAGFIKM_05312"

/EC_number="5.3.1.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9S467"

/codon_start=1

/transl_table=11

/product="L-arabinose isomerase"

/translation="MSAAKEFWFVVGSQLHYGEEALGEVKANAKITDALNASGVLPY
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TQFNESIPWATIDMDFMNLNQAAGHDREYGFINARLRKQNKIVVGYWERPEVQQQVAD
WMDVAVAYNESFNIKVARFGDNMRNVGVTEGDKVEAQIQFGWTVDYFGIGDLVQYVNA
VTEQEIDDLIAQYGDLYEFDYGTNSKEAWEASVRVQASYEIAIKRFLDEGGYSAFTTN
FEDLHGMKQLPGLAVQRLMAQGYGFAGEGDWKTAAALDRLLKIMAHNENTGFMEDYTYE
MAAGQEAILQSHMLEVDPTLASTKPRIIVSPLGIGDREDPARLVFDGKAGEGVVVSMA
DFGTHYKLLINEVSAFEPTVPAPNLPVARVLWSVKPNFQDGVKAWIENGGGHHTTVVSL
NLTTDQIVTYAKLVNLEYVVIK"

CDS 6042674..6043444

/gene="yokD"

/locus_tag="EFAGFIKM_05313"

/EC_number="2.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32003"

/codon_start=1

/transl_table=11

/product="SPbeta prophage-derived aminoglycoside

N(3')-acetyltransferase-like protein YokD"

/db_xref="COG:COG2746"

/translation="MYTKESLMQQLEQLGVDRQGTLLIHSSMKSLGEVEGGADTVLDA
FSDYMKEGLLVLPHTHTWSTINADNPMFHVENSVCV GILPELFRKRPGVVRSWHPHTS
VAALGRDAEFTKDDHLYDTPCARGSAWGKLLDRKATILLVGVDLKRNTFIHGVEEWV
DIPGRMTDEHEMLYTVLPDGSQISVPSRRHCGLPWSEHFWKVDEVLVREGAMRTGKLG
DAVVRVCDAAARTAEVITEMLKHNPD LFTDNLPLHAVTE"

CDS 6043781..6045478

/locus_tag="EFAGFIKM_05314"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNPLVWYDLFLFVLLFGVG VYVFATVRITNLHKVYFLFHGLMML
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VPAVIGAIGVVANPWNEFVIPLEGGYIERAYGPWFVWVMVILVSYFLMSLVLFRAVY
SSQTSAMIKKQVRITLWGILVLAVFATIDAILNVVLRAYLPFIIPGMTSLGIFLSDLF
FVYVIKRYNVFDLV SIAHEDVINTIPYGILVLDENEVIVEANKASRSFMDLHVGDSFD
MEAFLESVHVVGSCREFVNHYKKKENTLSHIEVIVERDNNIRHFILQSSPIVDSALVP
IGHILTFQDVSQERFYVKEMNRQNVTLQERNQALDLIRQELSEANR KLEELALTDSLT
NCYNRRYLTQHLNHEVITNIQYKTPFSLLLLDIDYFKAINDRYGHVIGDEV LVRTAEA
VKQSIRSTDILTRYGGEEFMIYLPHT EHDLANQIAERVRTAVESNHIMVDHEIMQVSI
TISIGILSFEDFEVVHVPDNPEG YLTQLFAAVDKALYQAKQNGRNRIEFAAFERGV"

CDS 6045676..6046977

/locus_tag="EFAGFIKM_05315"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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/translation="MLNKLKSQDVFGVSNLTVPSYIDRGKLDISVQRHLERPTHIAL
RGESKCGKSWFRQKNIPNSIVVQCRFGKSVVDIYTDALSQIGIKLILEETRGSSLKGR
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DFHYLSVEERKKFSFDLKTLDYGCYFVVGWSQSNLLTYLNADLSGRIVEMSIYWS
SDDLKSVIRKGNELNIELSNSLESVIDNCFGNVGILQKLILLLLDEAAIYEERETK
LDVSNKQYFNAAGASYADQLNAIYQQFARTVSAGIRKRKDSTGIYAHAMAVIVSASDD
KLINGLELDEIYQIAHSREARIKKGNLRTVLNKLLEELQVDEGGRLVIAYNDSTDQIS
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CDS complement(6047116..6047454)

/locus_tag="EFAGFIKM_05316"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTKLNSVGERIRAIRKAKGLTQQQLAELSGLDDAYVGSVERGE
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NILNEIKRAF"

CDS 6047672..6048487

/locus_tag="EFAGFIKM_05317"
/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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/translation="MRKSILKSLKPDIIVEMLDMAVAFENWNVKMERADMLYQCVQSI
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WMEDLNEVGMLVVQEFRHKALVNRVYALEIEAGQVQLLEEYVNFLEHPEEWLAGLKVI
TEAAVRHRWQIDRVLDVFEDQMQGEGTEINSSNNEGMYHYCYQRALYEQWMERPQEAV
EFILQAIRLAHKLGMDFYFIRCTVLLLESLREEATAEQIGRYRVMLEGIGQERI"

CDS complement(6048586..6049242)

/locus_tag="EFAGFIKM_05318"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLVKKIIDEWDPIDLFPYAPEDEYEEEVKQIEECTRNASLDKHN
LAKEIYTMFSEKFGSDIFTESLESCTNIANKILELPHFIGYTLSKLRTYEWVRYNMFA
REDLYHHTPGFYFRFFNPGKVYNELAICIDAFQGELQWKLYLGLETRNQNSLEPYEV
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CDS complement(6049401..6049832)

/locus_tag="EFAGFIKM_05319"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVDNNNAWSTEYPPVDIHTVKTVEKTWGIQFPSEYIHFIEKYHG
AEPAQRTLNISGKKVMFSSFLTIFAFDELIDLDIYNEQKNNLPPNHFPFAIDVEGNLF
CFNYSHNSQPNIIYIETINSYNPLGGHVAATDFTAFIQQFN"

CDS complement(6049873..6050976)

/locus_tag="EFAGFIKM_05320"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTKIQIPVDQMTHTIGVFKVGHGHLQQTLARLNSQLTPLLDGFE
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PGTPRTNDLVCGPNDPPPKRVSVEEHVDAFFNQAGENILAIGDSALQLGKDLIEHPLDT
AGNFLYDNTIGTVTDIGSGIAFSWNYAWDNGDTREQAEEKHIAAEFDKMKQEGGAEYAA
NITTSMLLGIFGRKVGKSIDGKQHHSPTDSGGGKGKEADTNLNSYSGAPFHYSQEP
TKRGGKSIADQIAERGWNDQRLGEAMHEPAGTVDWIDQRKGQNNAPVTVYYHEDGGYA
VRRNDTGEIIQVSQVDDPNWSTYWSDDDINWIK"

CDS complement(6051209..6051628)
/locus_tag="EFAGFIKM_05321"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRRYSLIVLMIATVMILILSSCRIEPNQVRVSKVPKELHTFYPG
DITQVDSIEMMSGSDGKRTTDDQVLIQEWIEKVRDLEIVLDPGQEDAAGVLFHVTMF
EQGKEVLYMTPTDMNHQRMQPQLELANRMSELYDALE"

CDS 6051999..6053549
/gene="nikA_1"
/locus_tag="EFAGFIKM_05322"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q2G2P5"
/codon_start=1
/transl_table=11
/product="Nickel-binding protein NikA"
/db_xref="COG:COG0747"
/translation="MNKKTPLLALVSLALSAGLLSACGSSESPAAQPSTDNKNVHFL
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SELVNPNTAIIDVSEPDIVNKPIGTGPFKLTSTPTGSKLELDREYWDGASPLDSIT
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ESMKDLNVRRALDALDRQGIVDTILLGYGEAAIGPFLPSLPFAPTYTDTATESGADV
AVKYLGEAGYTQQNGVMTKDGKPLQLTLLTYSARADLPLIAQVFQSDAKKIGIDVQIR
QIDTPEDYMASNRDWDIATYSNLTAPRGDAGYYLNATYHPKGALNFSGSEDPELTKII
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ITNKLDVM"

CDS 6053549..6054496
/gene="nikB_1"
/locus_tag="EFAGFIKM_05323"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P33591"
/codon_start=1
/transl_table=11
/product="Nickel transport system permease protein NikB"
/db_xref="COG:COG0601"
/translation="MFRILLRKFLFVIFILLFIMFVSFLFIRLAPGDPVLTILNVDEL
SVSQEQVEAVREEMGFNDSLPVQFGNWLLDFVRLDFGVSYSTGQPVMQTLMRALPATA
ELTIGALLVMLVIAIPLGSLSSALHRGSRMLSVGAAPPSFWLGLILIDMFGV
RFGNLPTMGRDGFSTLILPSLTLGLAISSVYVRLLRSSLLDSLSQEFVRSARARGLSE
GRIFMLHAFRHSLPPVITVFGVSLGSLIGGVVIEVLFAYPGIGKLVDAIRQRDYPL
IQGYILIMAIVVSLVNTAVDLSYRYLNPEMKLKEKEAHR"

CDS 6054493..6055347

/gene="nikC"
/locus_tag="EFAGFIKM_05324"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q2FYQ6"
/codon_start=1
/transl_table=11
/product="Nickel import system permease protein NikC"
/db_xref="COG:COG1173"
/translation="MKTIPPIPPTKSKKHSWQAIIGLLFALLVISASLYAFLYLKHD
HTLTDLRGRLQGASALHPFGTDHLGRDVLTRLLLGGGQTLGYSLLALGAALLIGIPFG
LIAGYKRGWVDKLFMRIADAFLAFPDTIVAIVLSGLLGAGIGNLVLAIVVKWVSAR
LVRSTVLSSESQKDYIRIARTNGLSDGRIMRKHLLPHIAGHVVLASLDLGKIILLISS
LSYIGLGAQPPTPEWGAMLNDSRPYFQSRPELMIYPGLAIVSVLLANMLGDYLRDRF
DVKKEVQP"

CDS 6055344..6056144

/gene="cntD_2"
/locus_tag="EFAGFIKM_05325"
/EC_number="7.2.2.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q2FVF0"

/codon_start=1
/transl_table=11
/product="Metal-staphylopin import system ATP-binding
protein CntD"
/db_xref="COG:COG0444"
/translation="MILSIEELSISSRDRTIVDQVSLAVREGEFMALVGQSGSGKSL
SQAIGRLLPPNLHASGRVMFEKSNLLERKPKEMRALRGSRSYIFQDYQGAFTPF
RSI
GGHFDEYQKVHGEKSSIRKKRAEEALESVGLGAELLRRYPFQLSGGQLQRASI
ATSL
MLSPRLLIADDEATTALDSVSGHRVLELLARKQAETGCAILFITHDWRHV
RRYANRLAV
MKEGQIVESGGKHRILDHPQHEYTRQLIDAAPVLSRSLKSGLKEAGTE"

CDS 6056141..6057112

/gene="btuD_17"
/locus_tag="EFAGFIKM_05326"
/EC_number="7.6.2.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01005"
/codon_start=1
/transl_table=11
/product="Vitamin B12 import ATP-binding protein BtuD"
/translation="MKTTTNDERRGLVQSEESGVRSHDFAKDVNHVDIDNAGINTTE
TDHAVTDADIDTAGSDNASLLSTLGNPVLHVEHLSRTYAGADRPVND
FSFTLNHGEC
LGLVGESGCGKSTLARCLLRIEDADTGSITLGGQDIARLSGRRLRPHRRKI
QIVFQNP
MAALNPCLKIADSLIDPYEQLGRNAELSHFTYTSKEAYVQKLLEAVELPSD
LAGRYPH
ELSGGQRQRVTIARAIGIEPDVVVLDEPTASLDVISQGAVLQLLTDLRTSL
GLSYVFI
SHDLAAVHRMSQRIIVMREGQIVDRFGADALFAERHPYTKELISIF"

CDS 6057491..6058996

/gene="mqo1"
/locus_tag="EFAGFIKM_05327"
/EC_number="1.1.5.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P65422"
/codon_start=1

/transl_table=11

/product="putative malate:quinone oxidoreductase 1"

/translation="MSQGQTSTDVILIGAGIMSATLGTLKELAPDWNIVFEKLATA

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WELSVKNLKSGAVERHKAKFVFIGAGGGSLLHLLQKTGIPEGKHIGGFVSGIFMVCKN

QKVVEQHHAQVYKASVGAPPMSPVPHLDTRFIDNKKSLFPGFAGFSPKFLKTGSNAD

LITSVKMHNLLTMLAAGVKEISLTQYLIQQLMLSKEQRMALRDFVPGAKSEDWDMVL

AGQRVQVIKDTVQGGKGTQFGTEVVTSADGTIAALLGASPGASTAVQVMLEILQRCF

PQHMEAWEPKIKEMIPSYGISLVENLDLLKEVHSSTAKALGLSDEKHVMHV"

CDS complement(6059242..6062373)

/gene="rcsC_17"

/locus_tag="EFAGFIKM_05328"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00979"

/codon_start=1

/transl_table=11

/product="Sensor histidine kinase RcsC"

/translation="MQEFEVNCRKLKSAMKPITYKKIPRYVVLISILFTILLGFRWIW

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FGQPATHAEAYRPERTAFTTSYVLDGSTELNLLVQTANFDDPYSGGITRSLYFGSPEA

IGNERGLSIDLQKITFAILHLSLYAFVMFLFIRKERALLTFSMLTLVAALTVASDHD

NLLLSWIPLNFTWIVKAKALSYPLFAFFLLQMARSFSHNLQWRKLFMYASVLGIYCL

FLLVAPVTLIYHVLEIGLSDFLYLFAIGWSVYLFFRMAAEKRSDASFLFAATSSLSS

VLWGIVNSHSEITNVYYPIDVIAAMFGFSAYWFRKYFRNSSEIEKLYEQLKEEDRQKD

QFLVNTAHELRTPLHGIINIAESIAVRERRKSGGQQAEDMKLLVTIGRRMSQLVDDLL

DVIRLKEKRITLQKKPLSLASVIPGVIGMFRFMAEGKPIHMQVDIPESLPLIQADERR

LVQVLYNLLHNALKFTDEGTITVSVRGHGEYVLIKVSDTGVMSEEIQQRIFEAYEQG

TPEARLSSGGIGLGLNISRQLTELHGGQLTVQSVPGQGSTFQISLPREDTASLSDQTEQ

QWDAHSFDEIAIAEPQQQTISQDKTAARILAVDDDPVNLRLISMLANEPYHIQPAAS
ALEALELLDKEPWDLLIADVMMMPHMSGYELTENVRKRYSVSELPILLLTARNEPADVY
AGFMAGATDYVTKPVDARELRRHIGSLIVLKQSIDERLRMEAAYLQAQIQPHFLFNTL
NSIMVLSEMDTERMQKLGDAFIEYLQTSFHFVNSEKMVEVTHELDLSRAYLYIEKERF
MDRLNVIWDIPDDLDSLPLTIQPLIENAVRHGILSKVEGGTVHIRIINQTASTLIE
IEDDGVGMQPEQIERALAWPKKGGPGGTGGIGLTNTHRRLTQMYGQGLTIVSSPGQGTK
VSFVIPLDRSMRA"

CDS 6062510..6063250

/gene="cheB_16"

/locus_tag="EFAGFIKM_05329"

/EC_number="3.5.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00099"

/codon_start=1

/transl_table=11

/product="Protein-glutamate

methylesterase/protein-glutamine glutaminase"

/translation="MRVILVDDEYLALSRLNKLLQEREDCEVIGSFLTAQEADQIEI

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VTRDRLEKTMKMYQRRTVSASLNVTEGPSMLIHCLGMLQIQVHPNEPPKHKMFRTTKI

RELFAYLLHHRNKPIKRDTLLELLWPELDERRGISNLHSGIHLRSMMN EFMGEDKMV

IRYQQFGYLLETGEFRIDAE EWESREPS"

CDS 6063369..6063653

/locus_tag="EFAGFIKM_05330"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHALWRNHAMQLAQYYIELGQNT EALTLYYRVQQFEPSLEEVGL

ALMKTYDRLGNKDPVVAQYNQLVIALEQEAGMRPGLEVELWYQQWKNSNS"

CDS 6063869..6069034

/locus_tag="EFAGFIKM_05331"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKVFKAMKISFLAFVLLSSISLAFVASAADGNIYVSSTGSD
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EIRNHIVKASVSQPATVISTSGGNSMVIQEGTIIHNNKVSGNVKENPPSVLSAGSGG
SLVIEDGLITDNEISDGNNGVIIGVGLYQSPNFRMTGGQITGNKLLGTELSEGETIGNV
AVFMRGDASQARFDFGGTAYVYDNFNADGDQRNVYLKNTTATGSAYLTLVGPMQSGSK
VG VYAKIMPDEDTPVVDIAIGRAPYQAVQEDQTFVSDINTTAAVAYDNQANKVVL
YRMPVNLELDTPLDFSTVGTKPTLKGSVTAGAVVTITMVNKSDPAKNIVGEATVNP
DG TWEFTPSSVLPPGEYTLRVATNNGISAEPVRRDIIIVDKSVGGTAGPGGVGTPALWL
RSDL SMGVASGEKVS IWEDQGS KINNATQDVEANQPTYWDDKNHNINFPVLEYNGTS
SFMNLDVSKLPQGKSPRSIITVSKTNKTGGLNYIISWGVQTPGAYTGMGMLQNNTRGG
LTFN SDRNQTLTYPEGFLGTTFPNEQFVTWTGGDTGINQARLYSKMKQVQQLNDWGK
DNVKLWDTGNSGGAVVGKLIPATGIEHWQGTEIIIVFDHALTDAERQKVSTYLAIK
YGYTMDQTTANSYVDSNMATIWD AQENAVYTHRITSIGRDDQSGLMQKQAKAQELGST
LTIALGNSVEDTNSANKNEFLKDSSFFTFGDNGASTEFTKPTKDGKLLGMERVFKV
QKANWTESQITLQVAETGGNPALPQYVVISNDAQFGNPNSLLLIENGQVTLNTSSFGP
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TGELDK EEYTPESWQTLQNALEVAQSVFDDENATPEQVEKAYQDLVDARKGLTKKPGT
GVDTSVLKNEHDRIKGENLTET EYTVESWEALKDAMNEAQRVLDDPAATQAQVDKALQ
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FDPLAKIEIAVG DGEWNEISSGTVSENLP LQVGGNKIVRVTD SLGHVTEYKINVTRA
SSDNGNNGGGNNGGGGNTGGNGGSTPAPTPTPAPVPTPTPAPVKDNLETT RDGNHQPF
ATSKPSNNKETLVQVDPAKLNVAMSQGTGQQFAIHSPNDGHMKVDGLTLET LKQLVDQ
GSKLNISNPLAIYPVPGGKMDVNGVSRQLGNAALNDIDVHVDIARSSDALIDSAETRA
ASQGYELLVTPVDLDTFTKDGQTVRSGQLNGYAPKYIALPEGIDPNRITTGVIINPD
GSIFHVPTVVTKINSRYALINDLRSSGSYSVIWNPQDFEDARSHWGKTDVN NIAARL
DLQNGDNTFSPNRQVTRSEFAEIVVLGLGLMRQDAPQNLFPDVND SAWFRSAVALAN

EFGIVRGYDNGNFYGNQEITREQGFAMVARAYRLIEPDATITPDQMNSELERYSDAAD

VSNWAKEDVAQLIAAGIIQGNGPEVLSPKTTMTRA EVTAL IARMLKVTNLIDQ"

CDS 6069377..6071485

/locus_tag="EFAGFIKM_05332"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNNTIYLRRANKLIIESNEGKQQLPKTYLATALKNIEALGYTFS

EELMQAMRQLSKEQFEAVYIQLVADLRVMVGAHVKYTPMYAGFPMQVMQADEAEYLN

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DKADIDTVLEHADPEDVDALLPTEIPFKENVGFVVASLLKHEKANIDRIGTYFKTASD

VLRLAVAWSGDGVDVSLAVASPFRKFKRRERRLLLGLLEQCGSITEDMLRYKDRWIRLGE

ILHPSEYKLRYPRCEEAFDILRNNKPYSTFNQSVELAFQYRNVWSLIDLLSQRPGFEFA

RRLDHLLRMTED EAYVLLAFGEVLEQVSTPVLLQVRQHFTQRNEPQDLRVFFPKGNVA

KAFVAVPNELPDIDEATCQEVVQLCERALVERFAVLPTLGKTYVDPLLHDYLVPFQSQR

ASKALRTIVRGSRVPM AEGDTIRFFNWWKEGDVNGQSTGRVDIDLSAVMYDKDWNYYVE

HISYTNLRSLNYKAVHSGDIVTAPYGASEFIDLHIPSIVAYGGRYVVATLLSFTSHPY

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CDS 6071654..6072526

/gene="rhaR_42"

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/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

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MYQSLTPELIDTIKGASNVQPLGLISASAHFSEGRMAEQGELDHYIGAATTKETPEGL
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CDS 6072878..6074503

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CDS 6074717..6075673

/locus_tag="EFAGFIKM_05335"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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YVLAPPTDEQVESVEEQLVFKLPTSINMMKLHNGGVPHYRHFPVSQAEAAKKVRIEV

AGILGIGREKAHSLGGEAGSRFIEQGGYPEIGVVICECPDSEVVMLDYRESGNAGE

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CDS 6076031..6076765

/gene="cpnA"
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/inference="similar to AA sequence:UniProtKB:Q8GAV9"
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CDS 6076832..6077251

/locus_tag="EFAGFIKM_05337"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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CDS 6077283..6077657

/gene="ytcD_3"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34533"
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YtcD"
/db_xref="COG:COG1733"

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CDS complement(6077718..6078788)

/locus_tag="EFAGFIKM_05339"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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VNTIEPIAPNLQHISLMQGYKVYGAHLGPFKTPAKETDAYHMPPEFNVDQQQFLEDQRQ
PGSSWTWSALRPSVVCGFALGNPMNLAMVIGVYASISKELNLPLRFPKGKPGAYHSLLE
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CDS complement(6079037..6079534)

/locus_tag="EFAGFIKM_05340"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS 6079710..6080867

/gene="cheB_17"

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/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00099"

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IQSGHLEAGYRLELGEAQLDSEQWEREIRQWKVVDASTVHVYEALHLYKGYTLGNYE
YMWAEPPERERLRYLWLYHMRQLSLYYQQHGLAEKVVESTQRIQHMLPDEEESYFMLMK
LYDEMHNLDLGVVEEQYRLLTTRMEQDLEIPISEDITEWYQDWKLGLTKVMKK"

CDS 6080819..6080971

/locus_tag="EFAGFIKM_05342"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVSGLEARFNQSHEKIINEITSNETYGPLQIFDHHANHFWSVNW
HALGMV"

CDS 6080952..6084008

/gene="rcsC_18"
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/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00979"
/codon_start=1
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YDSPYMGGISKPVRFGSQAAVDFSRWYSIGFQMLTFLVMLLHGMYACILYAFNRQERS"

LLVGAVLTLSVGITVTMGHDNMLWLPINYTWGIKIRLISLLLQNACILLLFQRLTV
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FRKQADRDIVFLLLTAGGITSNLIWSVAETAkdVTTVYYPIDIIFAITGFSAYWFKKY
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KPVLLHMEIPESFPQVMGDEERLVQILYNLLHNALKHTEEGTISVSAEIREGHALIHV
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DVMMPNMSGYELTQKVREQFSMSELPVLLLTARSQPPDIYTGFAFGANDYVTKPVDV
ELKYRIRALTMLNQSIQERLRMEAAYLQAQIQPHFLFNTLNSLMVLSDIDTEHMRKLG
DAFSSYLRI SFNYLNTGELVKLSYELELVEAYLFIEKTRFEDRLSVVLNVEPDLPLL
PPLSIQPLIENAVRHGLLSRNVGGTLCLSITRHEGYTRIEVKDNGKGIEPEKVAELLH
ATPGGKGGIGIVNTNRRLLQRYGQGLSIVSEPGEGTMVSFDIPDEI"

CDS 6084210..6085496

/gene="glnK"

/locus_tag="EFAGFIKM_05344"

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/inference="similar to AA sequence:UniProtKB:P40758"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0642"

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NSIAVRQMRL LHAEQEKRMEQMLSVNSGLYGEVFYLLKAMNTIEGITADSYDLYRDLR
EQDMNQYSQRTLGAQQIHEVKKDSQRILAGLLKLYDNEKTVNMSLSEVLNFASKANR
KYSEMLHKQVEINIEQQYDCESPYYIPLLTMNNLIANAIEHDGTIRIRIYEQEE
NVHFVVMDSGKGVPEAKRDVIFEPGYTTKFNEVGIAATGIGLSHVRDIVQSLEGRIKV
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CDS 6085468..6086361

/gene="cheB_18"

/locus_tag="EFAGFIKM_05345"

/EC_number="3.5.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00099"

/codon_start=1

/transl_table=11

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LMDLGIIGESGSKDIVALMEY AIDQKQVAEW PPLKESYEAVAQTYKSTPKDVEKESKA

MEQRIRRTVIAALTNMASIGLTDYSNHKFEHYAPLYFDFQDVRMKMRAMEEDQAGDKG

KVNIKKFLHVFYMETIEKMNH"

CDS 6086432..6086800

/locus_tag="EFAGFIKM_05346"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNITIDQQGNSKVAIIESNGIVINNAQDALDLMASVRYTDDADK

LIIDKSNITEEFFELKTKLAGEILQKYVNYHVKLAIVGDFEGHTSKSLRDFIYECNNG

KHVFFLKNKEEALQKLHNIS"

CDS 6086864..6087988

/gene="celE"

/locus_tag="EFAGFIKM_05347"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P10477"

/codon_start=1

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/db_xref="COG:COG2730"

/translation="MISNENLKVYALPEIGNLKVHGRRTGERLPLTLFWTGSVELNV

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RNGVLGAGDQHDFGSWQPDVVVVNLGSNDGGAFQSPWKDPDTGKVHKQRLNEDGTYH

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CDS complement(6088099..6088674)

/locus_tag="EFAGFIKM_05348"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:ISfinder:ISCac2"

/codon_start=1

/transl_table=11

/product="IS1595 family transposase ISCac2"

/translation="MNMSDNKTILYIAMS LDGYIARLDGSVDWLF DVEGDGGDNGYAA

FYETIGSVVMGRYTYEEVLT LSEFPYADRPTYVLSRSEQPLAPHAQFTTEGVETLIP

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CDS 6088744..6089652

/locus_tag="EFAGFIKM_05349"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MNHRLKLAIMRLMDSRQKFTARELAERFDVSVRTIQRDL DALQAL

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CDS 6089712..6090638

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/inference="ab initio prediction:Prodigal:002006"

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AKIIEKLYDANISNKLWSVSEELTGVYYRFDV"

CDS complement(6090620..6090859)

/locus_tag="EFAGFIKM_05351"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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VAPHSVNLIRAEELLPVYSIIRFTFLNSKIYTSNL"

CDS 6090910..6091179

/locus_tag="EFAGFIKM_05352"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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GRRVVQERNDEIRQLFAAGTTIDQLADQYCLSIDSIKKIVYCKKG"

CDS complement(6091269..6092135)

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/locus_tag="EFAGFIKM_05353"

/EC_number="2.3.1.189"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01698"

/codon_start=1

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/product="Mycothiol acetyltransferase"

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DMEFMVTCSSQAFGDSWDWTREYFMQTNESRVTYIAWQNQLPVGLVRVNSINATTAF

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CDS 6092404..6092598

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EDQKATAEEQQQALEMRQGL"

CDS 6092612..6092962

/locus_tag="EFAGFIKM_05355"

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CDS complement(6092957..6093310)

/locus_tag="EFAGFIKM_05356"

/inference="ab initio prediction:Prodigal:002006"

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CDS 6093464..6094072

/locus_tag="EFAGFIKM_05357"
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NLAPFSFFTASRNPPPTLLISIGPGVGDGQGTVKDTLLNIRETGEFVINMVPASLVEP
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CDS complement(6094210..6096078)

/locus_tag="EFAGFIKM_05358"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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DIA
TITGSNTTSYIMGDRWNPMNIGEHKHIWLPLTLNDSNGTASLECYTTWNIDAVTGTI
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LVNAVLWNNPGNWWYPTLHEVKMLGPATPEATGYSRFSSHNVDPDRYIRHANYTARVDA
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CDS complement(6096364..6097809)
/gene="dbpA"
/locus_tag="EFAGFIKM_05359"
/EC_number="3.6.4.13"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q814I2"
/codon_start=1
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/db_xref="COG:COG0513"
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MGFIETVQSIIQKLPQERVMTLFSATFPEDVAKLSRKYMNKPVEIEIKASGLTTATIE
HAVINVPEVNKTALLQDLFIVENPDSCIVFCRTQENVDKLFRVMADLDYPADRIHGGM
EQDERIEVMNAFRRGQFRYLIATDVAARGIDITNITHVINYDIPLEKEGYVHRTGRTG
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RKKDKREQLNQIMKLNFNNGGKKKKLRAVD FVG TIAKLEGVTADDIGIITILDNVTDV
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CDS complement(6098032..6098388)
/locus_tag="EFAGFIKM_05360"
/inference="ab initio prediction:Prodigal:002006"
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CDS 6098563..6098748
/locus_tag="EFAGFIKM_05361"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
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VLFFYQEKGDKICRESR"

CDS 6098730..6099419

/locus_tag="EFAGFIKM_05362"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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FMDKIKNLPQG"

CDS complement(6099564..6101858)

/locus_tag="EFAGFIKM_05363"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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RMEALIAKGGAMEGRKFKQLWSSKDASAFGEIQGTIRNLSIAYLKDAMKGVYEPKIQH
NWKITGVDLTAPERADVVELINDGIMSVPTTEDGKYTNIASINILDAVTQQEIDTLISA

KAGVSAAQFAGVKTGAFYQQLNKARKAAGNGEGATTPTPEKPTTPTVPKPTPTPGTS
KPGKPSAPSTGKPGTVTKGKQAKVTATYLNVRAGASSKAKVVAAPKGTLLLEVISTDK
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CDS 6102120..6103082

/gene="xynB_4"

/locus_tag="EFAGFIKM_05364"

/EC_number="3.2.1.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P23030"

/codon_start=1

/transl_table=11

/product="Endo-1,4-beta-xylanase B"

/db_xref="COG:COG3693"

/translation="MIKSKWFKTVGSLALVGILAASVAVGSVSAGLAKGSKFLGNIIA

NQVPSNFSFYWNQVTPENSTKWDAVEGTRNVMNWGQADMAYNYANNNGFPFKFHTLVW

GNQQPNWINSLSAADQKAEVTQWIKAAAGQRYSKSAFVDVVNEPLHAKPSYRNAIGGDG

ATGWDWVIWSFQARQAFPNKLLINEYGIIGDPAKADQYIQIINLLKNRGLVDGIGI

QAHYFNMDNVSVMNTVLNKLAAATGLPIYVSELDMTGDDNTQLQRYQQKFPVLWKHS

AVKGVTLWGYNQNTWQAGSHLVNSNGTERPAMQWLRNYLANNP"

CDS complement(6103220..6104380)

/gene="sotB_5"

/locus_tag="EFAGFIKM_05365"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00517"

/codon_start=1

/transl_table=11

/product="sugar efflux transporter"

/translation="MKSQQVNPLLILMLALGVFGIITEMGIVGVLPQVAHKFGISAA

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SLEIAFLFGAMVSVVALIGIWIWLPSMPVKEKMSYQKQLGILRKPGLWLNVAIVIF

AAMFSVYSYFAEYLGQVTHMSGSWISVMLTVFGVVMIIIGNLFGQFLRKSVVRTVLMF

PLLYVAAYALVYWAGPHFMWMVIVVILWASVHSGGLIVSQTWLTAEAQDAPEFGNSLF
VSFSNLGITLGAIGGWFIANLGIHQLIWSGMIFALIAFVLVWIKIKCFPAP"

CDS complement(6104692..6106032)

/locus_tag="EFAGFIKM_05366"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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GDVAMEHFHSIKRDFKYLPYIKEALTYPNQLQFFASPWSPPTWMKSPKAYNYGTLRWE

KDILEAYALYFVKFVQAYRDAGITIHQVHVQNEVIADQKFPSCMWTGEQLREFIGDYL

GPAFDQHGLDTEIWLGTINAPDPWEELIKKKTNDFDEYAGLVLSDPQAYSIIKGVGYQ

WAGKNAIQRTSASYPELRYMQTENECGDGNNSWNYAKYVYNLYQHYSNGVNAIYIWN

MVLEPKGRSTWGWEQNSMITIDPDTEVTRNPEYYVMKHFAHHIVPGARRVGLSGAWS

GKSVAFRNPDNSLVIVINNPFDQRRDLYLTLEEGQTLHMKLEADSFNSIVIQPK"

CDS complement(6106343..6107860)

/locus_tag="EFAGFIKM_05367"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRRMTLLLLVFILSLGASGQAMAYTTTDLGEGIIEDPALEDGLK

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DTLAINDAPLLMKNGKAFVPVRFISEQFNTSVGYIGSSKITILIFENKQLGESVQP"

CDS 6108236..6109132

/gene="dagK_2"
/locus_tag="EFAGFIKM_05368"
/EC_number="2.7.1.107"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31502"
/codon_start=1
/transl_table=11
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/db_xref="COG:COG1597"
/translation="MSMRQAMIISNPSSGKEEAQYVSQVREILESQQYEYVVNETAG
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FAYLKEGLKDLVNT PANHLTIEYDGQLWEGESPLFLAALTNSVGGFEKLSPDAEVDDG
LIHCFVVRNISVFNSLTLGTSLFLGSLKDHKDVDYFTAKEVHVRSDEAIRTNVDGEEG
PALPIHIRVLP RHIEVIVPEEV"

CDS 6109280..6110197

/gene="ydhF_2"
/locus_tag="EFAGFIKM_05369"
/EC_number="1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P76187"
/codon_start=1
/transl_table=11
/product="Oxidoreductase YdhF"
/db_xref="COG:COG4989"
/translation="MRTIKLGSSALEVPVAVGCMRINSLDGKEAEHFVRSAMEVGAN
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VKQPLVANQLQMSITNTT MIDSGINVMENDA AVNRDGSILDYCRLHDITI QPWSPFQ
YGFFEGVFLGSDKFPELNAKIDEIAAKYDVSNTTIAIAWLLRHPAQMQPVTGT MNIER
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CDS 6110470..6111852

/locus_tag="EFAGFIKM_05370"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MESTTTIRDHLESYLKREQMSISHFSETSGINSGTLSNILNKNR
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RLGLTNDQHRNLIASRFEYYVDRLDERYQLDALNELINAFGALHRWDKVQELSEKLK
VKASIHYEMNGRRKQEETKRPIVFYILYSDLAAGSACYHLKDYN GALKYVSLYSDNRW
VRNPDKDETVMNQFQEWAEANRYIYHLMGGHFEVLPDYLAYISTKENEIFPALCDIV
TAANRYDKDIDHVLKQYESYFTYQEQSNRIGKVSSQVTDDRYLRLLADLGAYYLKKDE
FHLGIEFVLDSLKFSIEISSGRGMLRGVGLFEQYREFASETAKQYKMIISEVQKLNE
EKVGFADSYL"

CDS 6111815..6111955

/locus_tag="EFAGFIKM_05371"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKRKLALLIATCSIVVFIVAPATESVPGKEIPNPEIMRPADHGF
GT"

CDS 6112094..6112264

/locus_tag="EFAGFIKM_05372"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDRLDLISRIEDARQLLYRMHMEYGSLLHPEVIQQSVVLDGLIN
QYNRVKVGKAMN"

CDS 6112364..6112744

/locus_tag="EFAGFIKM_05373"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKSTLDESQPIFHQIATMIMDDIVEGRLKVEEQVPSTNELSRFY

NINPATARKGLQELVDKGIIYKQRGVGMFVAKGAREALLVERKQDFYEEYIKPLLEEA

RRIHMNEDMIIDLIRGKKDKESSEL"

CDS 6112741..6113616

/gene="ytrB_2"

/locus_tag="EFAGFIKM_05374"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34641"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG1131"

/translation="MIHMEQVNYSYQKTPVLNQVTLHESEPIISAIWGRNGAGKTMM

SLLAGHNRPDSGTVQIMGQDPYNNLAAQGHLCYIQENHPLGKNWTVSDMVQMGQYFHP

QWNQELAERLIDVFELPEKKKIKFSKGMKTATQIILGLASNANITILDEPTNGLDAE

KRKFFYNALLESYEDNPRILISSHHIEEIQPLCESLIVLQAGEVLLNQPMEDMREKG

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DYLVNRTRNQEGVKP"

CDS 6113613..6114311

/locus_tag="EFAGFIKM_05375"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNAVKGTNRLIRDDMRLYLIGIFSSIALMLAVVYLAIGFIFDVS

ATQLFGPMYGGICTFAIGGIITLFPVAIGMGSTRIQFMKSFYMNSVWMVAGTMILHV

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MMKNAPLTMKSKKD"

CDS complement(6114475..6114993)

/locus_tag="EFAGFIKM_05376"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLNVEQKLEVLQSYPLQQRKDVSLGRVNFHYEDSAYDKKIVALH

IHPNGNGYIYAGLLPNYETDSKGFVNIRDYSETDLRLLDETIQAMSHNPNAVEFKEP

EQVKAAAPTATTSTGGGTWIDEDGHTLTLKYEDDMWYVYSGDNLDMAFESRSEAGEY

LKDEGFKPQAQA"

CDS complement(6115044..6115817)

/locus_tag="EFAGFIKM_05377"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WLN9"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/db_xref="COG:COG2513"

/translation="MSTLEEKAAALFQQYHVKGKPLVLINVWDAGSAQAIQSAGATAIA

TGWSVAAAHERDGEAMPFHLVLNLANLITASVDLPVTIDIEGGYGRSVSEVKRNIL

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APEHHNHSLLLEALIRSSHYADAGASGLFVPGQLQDHQLIQELCERSPLPINVMVTSPE

PSPKQLATLGVARVSYGPYPYLQVMEHLKELGRNLSGN"

CDS complement(6115895..6116947)

/gene="ada"

/locus_tag="EFAGFIKM_05378"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P06134"

/codon_start=1

/transl_table=11

/product="Bifunctional transcriptional activator/DNA

repair enzyme Ada"

/db_xref="COG:COG0350"

/translation="MISADLKEQYYEALVAKDSEYEGLFYVGVRTTGVFCRPTCPARK
PKFENCEFYETAQQALLASYRPCQRCRPLSHPNQVSDVVRILVEAVEKNPEKRWKEQD
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GFRDAFSRIMGAAPTQVDEGHILKASWIDTRLGPMMAIADEESLYLLEFVDRRGLERE
VERLRKRTKSAIVPGTTAPIQSIERELNEYFQGIRTAFTPLFCLGTPFQKQVWDELI
AIPAGETRSYQEIANALGKPTACRAVAQANGANQLAIVIPCHRVINASGELGGYGGGL
TRKNWLLTHEKQKQGS"

CDS 6117252..6117629

/gene="yneA_2"

/locus_tag="EFAGFIKM_05379"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_02014"

/codon_start=1

/transl_table=11

/product="Cell division suppressor protein YneA"

/translation="MRYSTYKSIYEFVYTKTSESRTMYVKGQFMQRVKPTWLMKIVT
ITLIIIGCSAVFTAFAAGDEQLLSGDQIVVSQGDTLWGISLVHQPQMDTRVYVEAIK
KVNKIEHNAIQIGQVLVLPGFDR"

CDS 6118000..6118575

/locus_tag="EFAGFIKM_05380"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKINIKKSVLCMSMLCISLFVSACGAKNNNESVQEHAYPQSKQP
VEEAGENSVPNADAKNNNSQGSASGDEGKPTAQSESTEPSEQIDIVIDQSEKPSEGNS
FDFGIKQVPKGYTLTEMRWTSNTVTIVNSLQEAIEHGGNGEFGFYFSGNGQFSGFIYS
DEMKGERGKATFVFTNDEGNEIMSEKEITLK"

CDS complement(6118683..6119600)

/locus_tag="EFAGFIKM_05381"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSSSLFTLTLIFTALLVIHIVYKIIAKLQPSKDYSIGIGQKIKTW

WGMFVIFCLATLFNPVSLISLMVLAFFSLKEYFSMIRSTRKADRRFLWAYLAIPVQ

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AYFPFATPEYGSKLVFLVLTQLNDVVHYLVSLYLGKRKVVPTANPFVTWEGFACAF

IVTTATSYFIHPYLTPFDWKFSLFIGVLISLAGFFGSLTVSVLKRDLLIGDDNKFDSL

KKSYLSRVDSLTYTSPVMFHVRYFFDFM"

CDS 6119697..6120251

/locus_tag="EFAGFIKM_05382"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTDERSIYILLTNTGTLFTKVIQSYTRAPYNHASISFDRELTEL

YSFGRKHPSNPLNGGFVKENIQGTYSKYPNTTCVIYKLQVTDREVEKMKRVLHIFIR

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QSERLQLVYEGKLSEYTLGNAEKE"

CDS complement(6120349..6120816)

/locus_tag="EFAGFIKM_05383"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

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/translation="MSVIGLAHVAIQARNYKDTLAFYTKVLGFKVGHSWSLPSFHTE

ACMLISPDQRTCIEVFDPKAVIPAEGEPATSPEAVRHGALLHFAFYVHDVEDIYERAL

AHGAKAYVEPDWISLGEPALRVRNALVHSPNGEVIEFLEEVDNFDRSSSSPPSI"

CDS 6120977..6121411

/gene="decR"

/locus_tag="EFAGFIKM_05384"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ACJ5"

/codon_start=1

/transl_table=11

/product="DNA-binding transcriptional activator DecR"

/db_xref="COG:COG1522"

/translation="MEHIIDEIDQQIMRLLQHARIPVAQISKEINMSQPSVKERILK
LEERGVITGYSTIYNLARLNRGTTTFILLKTEYCDELVQFCEQAIEVTDVYRISGEYN
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CDS 6121415..6122572

/gene="garK"

/locus_tag="EFAGFIKM_05385"

/EC_number="2.7.1.165"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P23524"

/codon_start=1

/transl_table=11

/product="Glycerate 2-kinase"

/db_xref="COG:COG1929"

/translation="MRETREKTFVLAPDSFKESMTAKEVCIAMEKGLRKIYPTAGYIH
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DAQGQPLARGGGALDQLAQIDVSGLDERLQEVEFIVACDVTNPLCGEHGASRVFGPQK
GATPEIVEQLDANLSHYADVVKQQLHKDIRDEQGAGAAGGLGAGLLIFTQAVLRKGIE
IVIEYTELREKLIAADVFTGEGGIDFQTKFGKTPYGVARAAKEAGKPVIALAGCVGE
GIDTLYAEGIDAIFGIVPGAADLDRLLREGPENVERTAENIARVLKLGILLS"

CDS 6123075..6126671

/locus_tag="EFAGFIKM_05386"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MNYRKIISLVLIMVLIAPWLAPAGKVSAGGSYPVPGKGGLITIK
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NQGDTSDFKQEVIDLFLNEQFIDKPDFKSLSEDDQIDITVHLLNLDPPTSDGYQNKGGQ
VQYLVQLALQALELPRKIGGSDSRIVLDEFYGKLAERKLHFDYPSVEEGYYERIDL
NLSSDIEKRMTAYIYERKIIGAPSIKKILGYRDTVSDTPFINKVVSSEDMMKVLDEM
EIQEGIESYNSKEENQEKPLGSFPLDISKWENLSSEEREKLADLMLSERLDEGYTSFE
EIQTAFNKFFPDNDSDPLTVLNTAKTNGNIAAMRLAMEDPDLGITLPNGYGALSQV
RDFIAGFLIEYVNKDYKNKEQVQYMMELAVLAQSVWEQRELSVLRNKDLLAQQLVNG
PNHFNDQQTYVLRSIGQQHLERSKVDKGVLAYNYLHLVAFERLEGVSKGDIVDPEIVL
NLLSMPIDSFEQATSIPRMDQWLDKAMKDQIKGEAFFSKYKFNLRGALDLSKRAELSP
EGQKELAEWVLNEQDSYEDVGNLQYVFNFFTPADVKGNDINNTLTGLESTMEISFDN
KLHWIDVAFIQKMDLSGNKTWVRYKAISDELPGRAVKFVFTQNGDSSTDNGNTPTPN
PGGNTGGGGSSTTTPVTSTPAPTTKQEQIWDVNGTNGTNLTPTITRTTETNGTIKD
LVKMTEAIAKESVEKAKQLNMNTARIVPDTKDSVSETRIELPKAAVKELNDGSLKLE
ISTENVVISVPTNSIAGFDQDLYFCVPLKKESERKEVEERAKKEQLIQQIAPNTNVR
VLARPVEIDTNMQSREVTLRPLRDSLPTDPAARQQALDNLAIEHSDGTELIQGGK
LVKLADNSEGIEFTVTKFSMFTLVVVDGLKASQSTHQPYIQGFGADFRPDAFVTRAQM
AAMLARNLPTEAAAGSVSSLSYKDVSAHWATSEIQKAHSAGIMNGMSNTQFAPEGSI
TRAQMATAIYRWTQQQASATTVNGPAVSFTDVSADLWAADAIAVYQSAGLMVGYNDGT
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CDS 6127058..6129739

/locus_tag="EFAGFIKM_05387"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKIRKTFSLLVSLMLMQGAAATYVSADSDPNSETSSSTSSS

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SANDAWQNLTYYYMMQVQTELYINGHPEAMIQDFPLQLDQLNEISEDMDQQQQLAEWM
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FTNTDRFEGKQIIVVRVRAKGNTPALKWTTLTFTSNTPTPNPGGNTGGGGSTAPVTTT
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IAGFDQDLYFRVWPLKKESERKEVEERAKKEQLIQQVAPNTNVRVLARPVEIDTNMQS
REVTLTPLRDSLPSDPAARQQALDYLAIIYEHSDGTKELIQGKLVKLADNSEGIEFT
VTKFSTFTLVVVDGLKASQGTHQPYIQGFGADFRPDAFVTRAQMAAMLARNLPTEAAA
SSANSVSYKDVSATHWATNEIQKASAGIMNGMSKTQFAPEGSITRAQMATAIYRWMQ
QQASATTKVTEVSFTDVSADLWAVDAIAYVQSAGLMVGYNDGTFKPSKLTAEAVKV
LNVLFNRTPLTGAVTPTFSDVPATHWAYADIEAAAQK"

CDS complement(6130029..6130601)

/locus_tag="EFAGFIKM_05388"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGKETAGNPNHSSLPDRHALRERVIEAIAANTMDLYGVNHTFGKL

YGIMYFEDRPMTLEEMKNSMNMSKSNMSYAVRSLTESQMIYKLEEKKERQDQYLAETD

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EQYYVWLQGFVDQLRDGKFYENASHTPDKE"

CDS 6130800..6131675

/gene="lacF_13"

/locus_tag="EFAGFIKM_05389"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29823"

/codon_start=1

/transl_table=11

/product="Lactose transport system permease protein LacF"

/translation="MRLKLWRESEAVLFTLPALIPLLIFWLGPLGYIVYLSFTDWDWM

SPDKLFVGLDNYSYLLTNSEFYRSLKVTLFGLGSVIPTIVGGLALAMLMNSKIKSSG

IFRTLLFSPWVTPTVAVSIAWSWIFEPEVGLANLMLGWVGVSPIGWLRDADWALVAVL

IVTLWKSIGWAMVFYLVLRNLPDDLLEAASIDGANGWDKFRSITLPLISPTTFFLSI
ILTIQSLQAYDQINVMTQGGPAGSTRLLYMYQSAFESFNVGEASSIAVVIILICVL
LSGVSFLLGRRRLVHY"

CDS 6131675..6132580

/gene="araQ_32"

/locus_tag="EFAGFIKM_05390"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MTMTLPNKKSKRMKRKELQNVSQPNFKISKLRILLAVIALGT

AFPFYWMVISGFKTNDEIWQFPPTFWPETFLWSNYVDAWNAAPFARYILNSTGVALAI

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CDS 6132618..6133991

/locus_tag="EFAGFIKM_05391"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNWSQASMTWKKRLRLNWKGGMSTVLATSFALLTACGTQAPAES

STTAAASGTEAQAKDPVEIEFWYGLGGNLDNMKKTIDAFNASQNEVVVKGIVQADYT

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QVDGKQYFLPMYGTQIMYYRMDTFKENGIDPATLTTWEKLAEEAAKMSKQENGKTF

YGWPEPMWGRDNMIDAVLGKGGQILSDDGKTVIDSPEWIETWDLFRKWINEDKIMGIH

YGGQGWEYWYKTIDVMMKNKAAGYTGSSGDQGDLDVVAAMQQPGWEGIGEGKPVAS

AISAGIPSAASPEQQQAAYKWLTYSNTASWSMNTGYIAVRQSAQQDPEFMKFSE

ENPQITVPLQQAHAHSAFQDPTGGKINDALKDAADQVQINNMPAEQALKEAKEKAQK

ELDRVTK"

CDS 6134088..6134858

/gene="gph_6"

/locus_tag="EFAGFIKM_05392"

/EC_number="3.1.3.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00495"

/codon_start=1

/transl_table=11

/product="Phosphoglycolate phosphatase"

/translation="MQDEMYVDGLPNPIEAVLFDKDGTLDDFTGMWGFWDTCVLNDFR

KQLATRGLRIDTDEFPQIWGTFHDDQGRMNGYDVRGPLAMGTMDEVYAVLTWHGYRAG

LNWAESKIMVRECLARAEEMEQRPAHPLPGVREFLEQCRSEGVVMGWVTADDTPSA

IKHLQWMGLDSFFDVVIGTDLVERGKPPDMLLLACERLGVSVQHTVVIGDTDGDMEM

ARTAGAGYRIGIGEPGKFRADRTIQSFHELLNGGLNR"

CDS 6134855..6135193

/gene="emrE"

/locus_tag="EFAGFIKM_05393"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P23895"

/codon_start=1

/transl_table=11

/product="Multidrug transporter EmrE"

/db_xref="COG:COG2076"

/translation="MTNSHAYLGWVLLALAIGLELSATILLKVSDGFSRLWPSVLMFV

CYGASFTFLNFAVKYMLAVAYAIWSGVGITLIGVVGHYYFGERLRLTSMVWIGFILI

GIIGLKWSDS"

CDS 6135193..6136287

/gene="cpdA_3"

/locus_tag="EFAGFIKM_05394"

/EC_number="3.1.4.53"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00905"

/codon_start=1

/transl_table=11

/product="3',5'-cyclic adenosine monophosphate

phosphodiesterase CpdA"

/translation="MRNEHTLEQPLATFQVITDTHVRDEADHIIHNRHLELALADIAKF

SQGSSGIMHVGDVTDRLPSEYRELQRIWKQHAESLPDIRYTVGNHDIGAVVWQDPPI

VLLEMKEDEVAELLEQEADIELVTKQTAESAALIEKLSGRTYTLSAVTSEQEGQDGG

PISSRVDPITVAGLWQRRLSDFEGTTGMRGSYHDHWIDGYHYIFLGTEQPHPKDCDMS

AEQLEWLDAKLSEHATLDHPIFLFLHQPLMDTVAGSLKEQGWWGVNQDAELKAVLAKY

PQAILFSGHTHWQLEAQHTMYDGAGHMPTMFNASSVGYLWTDQDEHLEGSEGLHVEIY

KDRVVVKGRDFVAGEWIEGVFTVRYPVER"

CDS 6136568..6138025

/gene="pnbA_2"

/locus_tag="EFAGFIKM_05395"

/EC_number="3.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37967"

/codon_start=1

/transl_table=11

/product="Para-nitrobenzyl esterase"

/db_xref="COG:COG2272"

/translation="MRELQVQTTYGTQVQGELLHDASVWKGIPYAKPPVGELRFKAPVQ

PESWDGIRQATQFGPENIQPRNHQPEGQTEIPNESEDSLYLNIWAPKEKRATPLPVMV

WIHGGSFVSGSGSQPMYDGTQLAVRGDVIVVTINYRLGPLGFLHMAPLGDSYVSNAGL

LDQVAALQWVKDNISAFGGNPDQVTVFGESAGSMSIAALMAMPAKGLFQRAIMESGA

SQFMPAEQASALREGMLKILGVDRDNLQKLNTIPVEQIIAAGETVKQQSGAGMALLFQ

PVLDGNTLPQMPLQAVSEGSAQDIPVLIGTTLHEGALFIQPHVPFSKEIDMVQGVDFM

TPDLDNRVAIADSYPKTADGQAQVMTDMFFWRSALQYAAAQQKYAPVWVMYRFDWVMPE

HPLLKRAIHSIEMFFVFNTLHVLKFMNAEPDEAAAALALKVQDAWIPFAKNGQPPEVAG

VNWPEYEQDRATLIFNHEIEVVHDPDAAKRELLGL"

CDS complement(6138188..6139339)

/locus_tag="EFAGFIKM_05396"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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SFSFIFYILAAYCLVILPFPPTTRDTCAQQAADTIYYNLVPFTFVKDIMKETPIVWSQP
SSYLSMIQGRAFLQVLFNVLMLPLGVYIRYFFQKRSFWKYALLGGFGLSLFFEITQI
TGFYGYYNCPYRLFDVDDLLLNTSGAVIGFFTAPILLALFPSRASIQAKSEQIVEQNR
VYTMPQLLALIIDGIIVVFLSNLISIFTASDVISDALSTSIAMVIVLFFIPWVRNGVT
PGSAILRFRYVDRQTGTPTSESLFKRFAALYVPWLLVTIIRLVNDYAFSGHQDVMLQP
YQMWISLGTFGIYMLVYAVLLVHVLIVLFSRGKRSFYFDEVSRTRASRK"

CDS 6139506..6139916

/locus_tag="EFAGFIKM_05397"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEYTVEIPYTCGNANRRMESLIHMSNLPNCPKCNSEYTYEDGNL
LVCPECAHEWSLEADNGNAEDAKVIRDANGNVLSGDGDTVVIKDLKVKGSSLVVKQGT
KVKNIRLIDGDHDIDCKIDSLGAMKLKSEFVKKI"

CDS 6140068..6140880

/gene="cmoM"

/locus_tag="EFAGFIKM_05398"

/EC_number="2.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_02057"

/codon_start=1

/transl_table=11

/product="tRNA 5-carboxymethoxyuridine methyltransferase"

/translation="MKRDHIIIEYSGFDEWGRLEREPIEFIINMHYIREHLPATGCIL"

DNGAGPGKYAIELAKLGKVTLSDLTPSSVD TARQKAQEF GFTQQFDGFHVLDATSLS
GMADETYDACLMLGPLYHLQADEERAAVRELYRVTKRGGVVFVAMQSRMRMSINSLQ
SPQHWKPNDNMAAIRSFVEKGIFNHQDQGRFTGAYYFNIQDVTPFMEQHGFETVDLIG
SSSLRAMLTDEQQQYWKERGEYDGLMQYMIEAAKDPSILGISSHLLYIGRKK"

CDS 6140991..6141248

/locus_tag="EFAGFIKM_05399"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQWKEVQERFPNEWVVF EATKAHSREGQRYIEEMAVIDSFDDST

KALKRYGELHQEDPRREYCFH T SRPEVVARERYVGMRGPR"

CDS 6141245..6141406

/locus_tag="EFAGFIKM_05400"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKISDGT TINDFQVEIGNMDYGLEIDGILGFNFMKQTGVVINAN

LVELSIDKL"

CDS 6141562..6142623

/gene="fgd_2"

/locus_tag="EFAGFIKM_05401"

/EC_number="1.1.98.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_02123"

/codon_start=1

/transl_table=11

/product="F420-dependent glucose-6-phosphate
dehydrogenase"

/translation="MEIGISTFVETNP DVKTGELISHAQRIRDVVEEIVLADQVGLDV

YGVGEHHRADYAASSPAVILAAA SQTKNIRLTSAVTVLSSHDPVRVYQDFATLDGIS

NGRAEIMAGRGSFIESFPLFGYDLNDYDELDFDEKLDLLLKLRDSEKVTWEGKHRPSFN
NLGIYPRPVQEKLPVWIGSGGNQESVVRAGLLGLPLVLAIIIGGRPQVFAPLVELYKKA
ATHAGHDASKLTVASHSHGFIADTTDEAVEKFFPPAQAVMNILGRERGWGHYSRATFD
AARSLEGALYVGDDVTVAQKIINLRKEVGITRFMLHTPLGTMPHNEVMRAIELLGKEV
APIVRKEIARWEAENEEAR"

CDS complement(6142759..6143418)

/locus_tag="EFAGFIKM_05402"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKDLNSGSTESAHTVTTFQEARLQHSDNLRQNIVHAAAALLQEH

GPEAVTVRRVAERMECSTKIIYNLFGKKEGLAKHLYLEGCSLMAQRFETIPRQASFEH

YFRDLAYVYWDFGISQSSFYQLMFGGSFSEFKPDGETLQGTATALKQVSALVEVAIEQ

GMLQVQDPLLAVRMIWAPLHGVIHLYLGGHIESEEAAKTYDHTLSMVIHSLVSTSAN

G"

CDS 6143667..6144482

/gene="fabG_11"

/locus_tag="EFAGFIKM_05403"

/EC_number="1.1.1.100"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O67610"

/codon_start=1

/transl_table=11

/product="3-oxoacyl-[acyl-carrier-protein] reductase FabG"

/translation="MIKEQHQQWVLITGASSGIGEIFALEMASKGKNIVLVARTESKLN

QLAERIERTYQVRAEVIVSDLSEVEAPQNVYEECQNRGIHIDMLINNAGFATHGCFEQ

LDGSRQQEEIMLNVLALTNMTHLFLPGMLQKKNGAVINVSSTAAPDPYMAVYGATK

AFVLSFTEALYEENRKRGVQFLALCPGSTETSFFDVVGADSVGKRDTPEHVAVAM

RALESGKPYAVPGAGNYWTAQFTRLVPRKLMLRIVGSMLRPRSKGGKAENIQV"

CDS complement(6144505..6145812)

/locus_tag="EFAGFIKM_05404"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTDSFIHLNTGQNISINESTQLQVTIQCTSSPSPLDVSCFMVNE
EGKVPSTDDYFVFYNQKADPHQSVLLQQAEEELKSSFVLDTNQLRQAPVEKCVFTATLDA
GGTFADVQACQAIVQAGSQQITYEITQVTAETALILIEIYKYRDGFKVRAIGRGFFGG
LQPLAESFGVEIESNDTSEAEQVLLTAQAEVAAASPEVLAPVAAPNTIHPPLNLT
LLKRKVTLSLQKKKIEPIQARVAVVFDASGSMYHLYRKGIVQEAFERILAIASAFDDN
GELDVWFFAKDFLRAPSVTARDFENYIERTYTLGSKGGTNNEPPVMQDVIRKYTIEEP
DVKMPTYIIFSDGGVSQKGKIMRLITESSTKNLFWQFVGLGQANYGILEKLDDMTGR
FIDNADFFALDDISKISDEELYDRLLTEFPGWIKERAKGILA"

CDS complement(6145918..6146382)

/locus_tag="EFAGFIKM_05405"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKKFDYSLNVEELDLRKHPELYTVGRGEQGVLMVEPYKGEILPH
WRFKTPEIATESSEKIYELFLKYKKKGDFVGMDMARKFLQMGYTRARRYTNHKGGRKY
SKEDGSILPYQNDKVKAEEAAIFKAQWEIAKTPDYMKMKEHREKYESDEA"

CDS 6146479..6146946

/locus_tag="EFAGFIKM_05406"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MGMSGRYLVVTKELVESIKSGEVSVDVAVDLIDKTWQMLQFT
LNGNLVEGEPPLGYVVPLAGEQYVGNYSMDLFLLSNEQVLEAYMALEQLTPEELKQR
YSLDQMIAEGVYPVMEDWDAEETFQEIVQTVDDIQALFQATVASGNGIIFYVF"

CDS 6147083..6147211

/locus_tag="EFAGFIKM_05407"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTQDQNEENKAIQEDEPDQFETPATAEDEETDEKLAEDQEQE"

CDS 6147419..6148927

/locus_tag="EFAGFIKM_05408"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAVPLVLLMVLTGCQAVGGVDVGKAMANGASIKSGESRQSMKI

NIEPAKEFATEKDLEMIELINSISLDIDQAKMKDAKTASIKGTLSMEGTKLPFHLSMN

ESQLVIDLDGAQKPLYISLDTLQDAQALPMVDTKALEKQLEEISPKLFSFVLKHLSNP

KNISVTPVQESVNGEALSLSKLHLEVSGEEILAMVKPFLTSISKDEQGLKELIGDLYD

VFYPVLEAVNEVEGGGDETLNSIVPESKDEAVASLYAIKVGLDMLVNYDQELNNLL

NETPEFKTVFGTETKLKLDLYLDSKLDIRKQNFELKVALPASEDLPVNSVTVSGDSEQ

WNIGGTAVVDEVDVSGGVMDLMKDDITPGQMLRNFDNSLAYQLLKDEAGITSKSVVL

FPDDEYAGAITVKNTTFVPLRYVSEELDAEVKWKTKGSNQIVIDDITGDEIVLTVGSK

KATVAGKEVTMVESAYVGKDGKTYVPLRFMAESLGATVDKEQETGWIYIDRP"

CDS 6149152..6149937

/gene="lvr_4"

/locus_tag="EFAGFIKM_05409"

/EC_number="1.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9LBG2"

/codon_start=1

/transl_table=11

/product="Levodione reductase"

/translation="MTERFAGKVVLITGGGSLGRSAAMEVAREGAKLALVDVNMKAL

EETKRVISEEVQHAEFKLIEGDVSDDEAVKKYVSDTVNEFGRIDAFFNNAGIEGKQNL

IENYETEMFNKVIDINLKGVFFGLKHVLPVMKKQGEGYIVNASSVGGIRAVPNLVAYG

ASKHAVAGMTKDAAIEYAEHGISVNAIAPGAILTDMVIGSFKQINPNDWESASKEFVK

DNPAKRLGEPKEVGRLVAFLLSGEAPFINGAIIPIDGAQSAKY"

CDS complement(6150070..6150528)

/locus_tag="EFAGFIKM_05410"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSLDVTIRHSSPTDLQDMVILMDQLGYPTTYAEMEERYTHISAD

ANFTTLVAEARGRVVGLIGLQTSYMYEKNGRHCRLALVVDQFRGSGIGRQLILEAE

QWAATHNVDSLNSGNRPEREAHEFYRQMGFTAGSTGFSKKPQILQHT"

CDS complement(6150525..6151445)

/gene="ddl_3"

/locus_tag="EFAGFIKM_05411"

/EC_number="6.3.2.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81Q29"

/codon_start=1

/transl_table=11

/product="D-alanine--D-alanine ligase"

/db_xref="COG:COG1181"

/translation="MKVGVIMGGTSSERDISLLTGQEMIANLNRDKYEVVPIELNTRK

DLIDKSVGIDVALLALHGKYGEDGTVQGTLES LGIPYTGCGVLASSVCMDKDMKQLM

QHAGVLTGEWLRVSHMEELSSIAVQQLTYPVVVKPNSGGSSIGTQVVKEASALPTAVE

AALAWDDTVMIEQYIEGEEITCAILDGKMLPVISIRSSAEFFDYSSKYDDHGADEQVV

QLPLDLHHRVEAAALACYQVLKCSVYARVDMIREGMPYVLEVNTLPGLTRNSLLPKC

AAAAGISFAELLDTHIELSLKERPKEDTTL"

CDS complement(6151458..6152909)

/gene="hisC_3"

/locus_tag="EFAGFIKM_05412"

/EC_number="2.6.1.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01023"
/codon_start=1
/transl_table=11
/product="Histidinol-phosphate aminotransferase"
/translation="MYSDLQLTEDRPVYIQVKDYMKRLMLKGGLQAKQKLPSTRELST
LMKVSIRSTVLLAYAELEDEGLIYAVKGKGNYSASIETPEAVANWELDWTTTEVSEYAI
KAEQYDLMKHGSGAERGEISFTSIAPDEKLFDLHNVKRAFLDRMSLEGEVLLNYGYAQ
GYRPLMNYLLRYMENKGVDLRGKDILITNGFTEGFDLLLGALRKKSGKALCENPTHHT
AIKNLKLHQFQLTGVMPEPDGLDLKQLEHELEASPYDLAYLVPSYHNPTGIVTSPAKR
VEIIRLMNKYQVPIIEDGFNEELRYSGSHVSPLIASMGKGNGLVYLGFSFSKVLFPGLR
VGWIIADAALIDYLESMKRARSHTSTLDQSLLYQYLSNGNFEKYLKRARTEYKRKYE
LVVRCLKQHLP MCRISGAGGLHLFVQFPSEYRTRELLAACKVKGVTFTPGDTFYLEPG
QGVNTMRLGFSRVSDENIRKGIRIIGETAAQMR"

CDS 6153583..6153939

/gene="uvrC_2"
/locus_tag="EFAGFIKM_05413"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00203"
/codon_start=1
/transl_table=11
/product="UvrABC system protein C"
/translation="MINITVPTPDVTITKQADPQLSHIYGFTDFHLITRELGGIFMFY
NAAGELLFVGKARKLRPRIKKHFEDTVSPIKNHREEVTKIEVCLVEDPVDREIYETI
INTMRAKYNVDKVLK"

CDS 6154081..6154893

/locus_tag="EFAGFIKM_05414"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNRSPKLSITDIPNTYEEVIVLIGRSGNPTLKDSTFENKGYGE
DRYQNYMTINGTVNKAFITLVILLGSAFATWMMFFNGQQVMPLAYGGGLIVGFILALVI

SFKPVAAPYLVPIYAVAEGFLGALSATYESLYNGITLQAALLTMAVFIALLVAYKTR
LIKATENFKLGVAATGGIMIMYLLSFVLGFFGISIPYLHDNSLIGIGISVVIVIVAA
LNLVLDFDFIEGGAERGAPKYM EWYGAFGLMVTLVWLYIEIIRLLGKLRSRD"

CDS complement(6155066..6155752)

/gene="sfp"

/locus_tag="EFAGFIKM_05415"

/EC_number="2.7.8.7"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39135"

/codon_start=1

/transl_table=11

/product="4'-phosphopantetheinyl transferase Sfp"

/db_xref="COG:COG2091"

/translation="MMITIRVLQVPEVLPGANWNQLLSQVSAERRAQSRFVRQADAY
RSVLGEILTRVALSKLTGLRAAELSFTRNSYGKPSLSHHSEVQFNVSHSGDWIALISG
STDELGVDVEKIAPIDMQIAERFFSPKESQFLAAEPDDRRLET FYRLWTLKESYIKAV
GMGLSIPLDSFAILPDEREDWHCKQAGTYLFLSQRLDDGHMLAACSAGGELPSQPEII
TLEDLYTELV"

CDS complement(6155913..6156785)

/locus_tag="EFAGFIKM_05416"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIELLNIAEIQAYLK RIGIDDIKEPTLEFLFELQRAHVQYLSWQ
TVDIFAGRPAEISLQESIQLILQGRSGYCFHLNGVFSVLLRSLGYTVDWHRGGVQPHG
EQPRVNSFHLGLSVLLPDADPTVERWLVDVGLGGMPFEPLPLRYGSYGSAPFRYQLMP
SSV VAGGWRLEYEPNGPSEGVDYAPEVVHDLEEFIPKHEFYSRAVES PWHNVFLLRQR
NENRSHEL RGCMLRTHDIEGIRKKEIRNYTEWRNVLTEIFYEPLVNYSELECQDMWER
VQSAHTEWKQAQEA"

CDS 6157075..6157551

/gene="greA_3"

/locus_tag="EFAGFIKM_05417"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P80240"
/codon_start=1
/transl_table=11
/product="Transcription elongation factor GreA"
/db_xref="COG:COG0782"
/translation="MANDEVILTQEGLEKLEDELKDLKTVKRKELAARLKLAISYGDL
KENSEYHSAKDDQAFMETRILILEKMLTKARVISSDNIDSNKVSIGSTVLLNDIEFAE
KIEYKVVGP AEADVADNKISYESPLGKEIMGKEVGSVIHV NAPMGVIKYELLQIKV"

CDS 6157835..6159190

/locus_tag="EFAGFIKM_05418"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNFSPKPNLDQDNAGKGERFSQAGFILAAIGSSVGLGNMWKFPYI
TGENGGAAFFLLFIVCLLLIGLPVLLAELAIGRSGRGSAAATAFIKAGGHKGWLAAGLL
QVLTPFIILSFYVIIAGWTLQYAITSFSGTLFNNPDYAGQFDSFIGGYMPIVWQLVAV
LITGWIVAKGVSNGIEKFNKVLIPAMLVLLIILMIRAVTLPGAGAGVSFFLNPDFSQL
TTESALVALGHAFSLSLGMGILVTYGSYVDKNQSLGAATVAVGAGDLIYAFIAGLII
FPTTFSFGIAPDQGPSLIFVALPAAFSAMPLGFLFGGLFFILLAIAALTSAVSLLEVP
VKYFMERLSWSRSRAVWVVISLAVFIVGLPSVLSLGLLPEWTIGSKSVFDWMDFVASNI
LLPVGGLLVITIFAGYFWKTAAEASGLRSGWFRVWLFMLRYVAPILVLLVLLHTSGIIH
F"

CDS 6159370..6160464

/gene="rlmN_2"
/locus_tag="EFAGFIKM_05419"
/EC_number="2.1.1.192"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q7A600"
/codon_start=1

/transl_table=11

/product="putative dual-specificity RNA methyltransferase

RlmN"

/translation="MNKSSIYGLTLEQLRSWLPEHGQKKSRAIRIWEWLYHERVHDFP

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TVCVTTQVGCNIGCSFCASGLIKKSRDLTAGEIVEQIMHVQRHLDAAGQDERVTNVVV

MGIGEPFDNFQHMMSDFIEVIKDRKGLALAAKRITVSTGLPDKIKEFADSSLQVNLAI

SLHAPNNELRTHIMKINRAFPQIEQLMDAVDYLLATTNKRIMFEYILLRDVNDQREHAA

ELAELLSSRRSMVSVNLIPYNPVDEHSQYQRSTEEISILGFYDTLKKNNINSTVRMEHG

TDIDAACGQLRSKQMKNNAVESEPGRLALG"

CDS complement(6160634..6161074)

/locus_tag="EFAGFIKM_05420"

/EC_number="2.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5HH30"

/codon_start=1

/transl_table=11

/product="Acetyltransferase"

/translation="MNTTIVEVTNQELLDACFAIRTAIFVEEQGVPAADEFDAYDTLD

AEARHILLYVDGVPAASSRLRIVEQVAKLERICVMLDYRKHGLGRVLIDKLEQMAVAD

GLEKAKLHAQVQASGFYERLGYAPASEVFMEDGIPHLLMTKKLK"

CDS 6161221..6161700

/locus_tag="EFAGFIKM_05421"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLTEKKEVLREIGMIARCLDSISNVEFQHLNLSRGQYLYLYRIC

ENPGIIPNQLAELIKVDRRTTAARAIKLESDGFIKQPAMGNKKNKVLYPTEAGLEAW

EFIRKEGVHSDQVTLTGLEEEIETAVMLLRMRHNIQVDWKFKKGRRSYMDISE"

CDS 6161802..6162911

/locus_tag="EFAGFIKM_05422"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRVNRKRLTWWIILSVSITAALTIFVKERFVMNESSPTVSFVQ
DHMINPNGTIATYLQDATSERADIVAGREALSESLGLWMQYAVAKNDQALFEESYELL
TTYFLMPQKYIAWKLDAKGDSQVTTNALGDDFRIVGALLKAADQWKQGREAKLETASE
ISRTLSQSVQNKGYVDFHDFASGHSTDTLSLVYVDLPSLQLMEKHQMVEPGTYAKYE
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CDS 6163040..6163915

/locus_tag="EFAGFIKM_05423"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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GFSIAMFKIEFLPLVMESLGSVRYAQFLEISGTIQKQIRYEDYKFFVDRGRFVIICP
MVNVEYLP LLTQRIKKAIMDIHIIDKKGNELQTVIRSGALVFQKEQFSKYEDIDAVIA
ALERNTETDLIGEYI"

CDS 6164070..6165365

/locus_tag="EFAGFIKM_05424"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/translation="MADFILILSIFSIWIAVFESIVIMAGAIRFINKQDKKGIQIPEN
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SQTSYMHNRNVKVMERKGTGGKSGALNDGMEIATGDWICIFDADAAPERNSLMFLTQKS

LENPEQYGVVFG RNKARNRGQNFLSKCINLEITSQRVYHTGLWELFQLGSIPGTNYI
IKTELIREIGGWDVTAITEDTALSFEILNRGQFVALAPQAEAYQQEPEQLSVYMKQRE
RWAKGNYQVVL DNIHNLFN RSSWRNKLLVIYYAVSYFWFMLAIIVSDIIFLVNLVYQV
IAIFKPEVSSPFQFAGDAYVFLVIGWALMYFIYVLQINLALAADIGQSNTRNFIYACV
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CDS 6165520..6166248

/gene="tam_3"
/locus_tag="EFAGFIKM_05425"
/EC_number="2.1.1.144"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00560"
/codon_start=1
/transl_table=11
/product="Trans-aconitate 2-methyltransferase"
/translation="MQDRGSDFYDDQANFEKYMERRKWQENANDTLEKPVMLELIGDV
TGKNILDLGCGDARFAAELMSREREGATYTGIEGSVNMIQAANESVKGLNARIEQAFM
EDWTYPAGAYDLVISRLAVHYIEDVESLFRNIYNTLKENGTFVFSVEHPVITSTLQPS
GTRTDWVVDQYFVEGYREQQWLGGSVKKMHR SIESYFMALQRAGFRVEHLRESAPQRA
YFVNEETYLRRQRIPLFLFLAARK"

CDS complement(6166440..6167222)

/gene="ylmA_2"
/locus_tag="EFAGFIKM_05426"
/EC_number="3.6.3.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31723"
/codon_start=1
/transl_table=11
/product="putative ABC transporter ATP-binding protein
YlmA"
/db_xref="COG:COG1119"
/translation="MIIDVQHVTWKRGPLTLLNDVSWQVNDGEHWALLGLNGSGK TTL
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KHATIGLYDKLSDDDLDDQAQELMQTLGCQHLWNREYRTCSQGEKQKLLIARALMANPR
VLILDEPCNGLDLFSRERLLDSIRELSQRPDSPSLIYVTHHTEILPVFTHSLLLRRG
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CDS complement(6167301..6168524)

/gene="fsr_2"

/locus_tag="EFAGFIKM_05427"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P52067"

/codon_start=1

/transl_table=11

/product="Fosmidomycin resistance protein"

/translation="MAQATLSKMQINSSANWALAGVSFAHLLNDAMQTVVPSAFPLFQ
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AFILLPHGQRSFLWLMGFALIGIFIQSLVSRWYRDKLAETHIRQQRPLKSSGAEPVAR
PVSRGFIAFTMGILILLFSKFVYIAGMTGYAFYYADAYDLPLSQAQICLFILQFAG
MVGTLGGPLADRYGRKPMIWFSIAGTAPFSLLLPYAGPVLSMVLCGMIGLILMSGFS
VIIVYAQELLPRHIGTVSGLFFGLSFGMAGLGSVVLGSLIDVTSIAFVIKLCNFLPL
GVCAVFLRKDQPRTA"

CDS 6168642..6169445

/gene="rhaS_42"

/locus_tag="EFAGFIKM_05428"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MELNMTLNGLELWKATGGFANEPHVHDDWYQLTLPVRGQCHLVQ
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TFMDPHLQRVLDYIHSAYTGPMIDSMAMVAHQSRYHFMRSFKALTGTPYQYLLNLR
VEEASRRRLRHTTDSVTTISYELGFSSVSQFYRAFQRVYVMTPEYRNHI"

CDS 6169803..6170720

/gene="yteP_36"

/locus_tag="EFAGFIKM_05429"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

/product="putative multiple-sugar transport system

permease YteP"

/db_xref="COG:COG4209"

/translation="MKKRMSTLFSLIIRDKYLLLMFSPIFLYLLIFMYLPMPGVLLAF
RNFLPGQGMLSGEWWGLRWFEQFVNSIYFWRLLRNTFLLAFLPLLFGFSIPILFAVCI
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DASWFRTIFTSSDIWQSFQFSSIIYIAAIMGIDPEMYDSGKIDGVNKFQELWHLTLPS
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VGLFNSVITFVLVFAANSMTRRLTKMSLW"

CDS 6170750..6171631

/gene="melC_7"

/locus_tag="EFAGFIKM_05430"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34518"

/codon_start=1

/transl_table=11

/product="Melibiose/raffinose/stachyose import permease

protein MelC"

/db_xref="COG:COG0395"

/translation="MQKSRSDRLFYGCYVLLTILAVVITLYPFLYVISISFSSVDAID
KQKVVLWPVGFTLSGYQMVLYQKELWVSFYNTLWYTVVGTLLNIVATCLAAFPLSRQQ
FFLRRKLNFFIAFTMYFSGGLIPVYMLITSLGLYNTRWVMVLPVLVITFNVMICRSAF
EGIPNEIFESASIDGANEMTMLYRLAVPIIKPTLAVLTLYYAVFHWNNFFTALLYLGK
QDMQPLQMFLRRVLIMASPEVMQKMGGTMTSGALAVSSLQVRYVSIVVSILPIVTIYP
FIQRYFVKGITLGAVKG"

CDS 6171700..6173295

/locus_tag="EFAGFIKM_05431"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRFKGAGRKSVIAAILAISLAGCSGGTGAGTDAGSTPSSSEPAF
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DAVNPRLAAGTGLPDIVLPDQDQLMKYINSGLFIPINELVEKYGVNLKKIYEKSPSV
KASLTTPDGKMYIYPQQLTRNYMPVFMVNVRWLDKGLSEPTTLDEFTAMLRKFSTD
DPNGNGKADEIPLSMEAKFVSMFAFGPAFGLDLSNQFYADDQGVHFSYYEPTYKEYLT
YLNGLYKEGLLGVDYASTTSDQVTSRISQDVTGATFNFSWYMSMVYSPLFKDYNPEEP
IIKGILPLKGPBGDQFYVGRTPVSGIFGITRDSKNPELAFRFLDYAVSEEATYYTWG
IKDDTYTEENGVKFTFDKGDNEYIQLGIGPVNLPNIQSTDSADSVVAPWHAKMDKE
LEPYVREPFPFVYALPDEASVESMAMPDITTYVEEMNFKFISGDASLDQFDSYIETLK
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CDS 6173329..6174312

/gene="exuR_4"

/locus_tag="EFAGFIKM_05432"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9JMQ1"

/codon_start=1

/transl_table=11

/product="putative HTH-type transcriptional repressor

ExuR"

/db_xref="COG:COG1609"

/translation="MILITIKDIAKLAGVSYSTVSKALNDDPRIKPATKQKVLAVAEK
HQYRKNNMLARQLSTGRSNIIGFVLDELSNPLFSNISGRLHTELKKRGYQMILVVADDG
VDVFSQLRVDGCILWDYALDNREMFWKKFATLNMPCFVLGTDEAPNSPYIKIDRKEGL
FKAVEHLKSLGHSRIGFIGNSQHIKLEGYREALQRTGLDFNEDHVLP AHSSWEDGYFA
IRNHAFGADSPTAFIGLNNLVTRGALRALLEAGYSVPRDISLIGYDDL PDMQYAEVAL
TTIGPPLDELAVQAAELIVSLIRDEQVDVPVVIQPKLNLRNSTAVNHTCIR"

CDS 6174339..6175451

/gene="yteR_3"

/locus_tag="EFAGFIKM_05433"

/EC_number="3.2.1.172"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34559"

/codon_start=1

/transl_table=11

/product="Unsaturated rhamnogalacturonyl hydrolase YteR"

/db_xref="COG:COG4225"

/translation="MQVQTQLSWSERIAATIIQQCDGDGYHAFPSGRWAYVEGMTLMA
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DQRYAEAAHLLAAQLAGQPRTSEGGFWHKKIYPFQMWLDGLYMSSPFLSEYAKTFHHP
ELWDEVAHQILLIERQTRDPRTGLLYHGWDESKEQVWADSSTGCSPHFWSRAMGWYAM
AIVDSVEHFPVNHKRGTIIGIFERMCHALVRVQEQESGLWFQVLDQGFRKGNYLEAS
GSSMFVYALAKGVRLRYLEPHFREAAEKGWQGLSSRLVEETADGVRLNGICHGAGLSL
DRDGTYNYYVSEAVVSDSFMGVAPLLLAALERLP"

CDS 6175448..6176503

/gene="pemA"

/locus_tag="EFAGFIKM_05434"

/EC_number="3.1.1.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0C1A9"

/codon_start=1

/transl_table=11

/product="Pectinesterase A"

/db_xref="COG:COG4677"

/translation="MTQQRLPNTALESSAPCLTVDS DGTGDYVTIQA AVDALPENGIG
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FIGADDFTAEGISFVNAAGPGKQVGQALAVYVDGDRAVFRR CRLIGHQDTIFTGPLPE
QPMDRSYFGGPRDGAERRKLRQYFEDCYIEGDIDFIFGSATV VFKGCEIFTKNRLTEA
EAADGQVNGWITAASTPEDVRYGYVFLDCDLTSNAPPQSVYLGRPWRHHAKVCFLNCW

IGAHVKREGWHNWNKTDAEQTVQYAEYNSAGPGAGCAADRVWAKILTEQEAAEYAVP
LILSGVDGWQPFERRGE"

CDS 6176887..6178458

/gene="chiD"

/locus_tag="EFAGFIKM_05435"

/EC_number="3.2.1.14"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P27050"

/codon_start=1

/transl_table=11

/product="Chitinase D"

/translation="MNQAVRFRPVITFALVFLLLITWFAPRADAAQWQAGTAYKKGD

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SITNTSVSLSWNASTDNVGVAGYEMYRNGVLVTSTSTTTAVVTGLTASTTYAFTVKAK

DAAGNISAASTSLSVTTSNGSSNPGPTGGKWLIGYWHNFDNGSTNIRLRNVSTAYDVI

NVSFAEPISHGSGTLAFTPYNATVAEFKSDIAYLQSQGKKVLLSMGGANGTIELTDAT

KRQQFEDSLKSIISTYGFNGLDIDLEGSSLSLNAGDSDFRSPTTPKIVNLIQGVKAVK

SHFGANFILTAAPETAYVQGGYLSYGGPWGAYLPVIHALRNDLTLLHVQHYNTGSMVG

LDGRSYAQGTADFHVAMAEMLLQGFHVGGSTGPFFSPLRPDQIAIGVPASQQAAGGGY

TTPADLQKALNYLIKGVSYGGSYLLQPAGYAGIKGIMTWSINWDAYTNNQFSSAHRP

FLNGLSTQTTKEVVY"

CDS 6178459..6180558

/gene="chiA1_2"

/locus_tag="EFAGFIKM_05436"

/EC_number="3.2.1.14"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P20533"

/codon_start=1

/transl_table=11

/product="Chitinase A1"

/translation="MIHLNKHTAFKKTARFLLGLSLLSVIIPSFVLQPATAAAADSY

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NEKSQTINVPNGTIVLGDWIDTGKTFAGDWDQPIAGNINQLNKLKQINPNLKIIS
VGGWTWSNRFSDDAATAATREVFANSVDFLRKYNFDGVDLDWEYPVSGGLDGNKR
EDKQNYTLLLSKIREKLDAAGAVDGGKYLTIASGASTTYAANTELANIAAIVDWINI
MTYDFNGAWQTVSAHNAPLNYPDAASAAGVPDANTFNVAAGAQGHLNAGVPAAKLVLG
VPFYGRGWDGCAQAGNGQYQTCAGGSSVGTWEAGSFDYDLETNYINKNGYTRYWNT
AKVPYLYNATNKRIFISYDDAESIGYKTAYIKSKGLGGAMFWELSGDRNKTQNLKAD
LPTGGTVPPADTTAPSVPGNARSTGVTANSVTLAWNASTDNVGVGTGYNVYHGSNLATS
VTGTTAMISGLTAGTSYFTTIKAKDAAGNLSAASNIVTVSTTTQPGGDTQAPTPTNL
ASTAQTSSITLSWAASTDNVGVGTGYDVYNGTALATSVTGTATISGLAADTSYFTV
KAKDAAGNVSAASNAVTVKTTAGTTNPGVSAWQANTAYTVGQLVTYSGKTYKCLQSHT
SLSGWEPSNVPALWQVQ"

CDS complement(6180712..6181569)

/gene="ytbE_2"

/locus_tag="EFAGFIKM_05437"

/EC_number="1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34678"

/codon_start=1

/transl_table=11

/product="putative oxidoreductase YtbE"

/db_xref="COG:COG0656"

/translation="MTTAQTAQHLQSTVTLHNGVSMFVGLGVFKVEEGSELIEAVKN

AIKHGYSIDTAIYGNEAGVGQAIAEALQENNLKREELFVTSKVWNADLGYEETLAA

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MQDAKVKPMVNQVEYHPRLTQVELKAFCEKHGIQLEAWSPLMQGQLLDNPVLTGIASD

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GPDPDNFDF"

CDS complement(6181766..6182980)

/gene="ydhP_2"

/locus_tag="EFAGFIKM_05438"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77389"

/codon_start=1
/transl_table=11
/product="Inner membrane transport protein YdhP"
/db_xref="COG:COG2814"
/translation="MLQDSKRSTWALLALAI SAFAIGTTEFISVGLLPLIADDLGISV
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WGWRAAFILIVVGVIGVAMIGNLILVPSTLKRGRTRTA FRDQLKLV TGGRLLLAFAITAV
GYGGTFVFTYLSPLLHDISGYSEKTVA FILLLYGIAIAVGNIIGGRAANRNPLKALF
YMFIIQTIILGV MYFTVPFKLAALLTIMGMGLLAFMNVPGLQMYVVT LAERYAPQAKD
VASAFNIAAFNAGIAIGAYLGGVINDSIGLIHTTWVGALMVLVAVILTAWAKTLESKD
QHASVEMEKASF"

CDS 6183145..6183540

/gene="ytcD_4"
/locus_tag="EFAGFIKM_05439"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34533"
/codon_start=1
/transl_table=11
/product="putative HTH-type transcriptional regulator
YtcD"
/db_xref="COG:COG1733"
/translation="MVRKKYNISVEATLEVIGGKWKCVILCHLTHGKRRTSDLKRIMP
AITQKMLTQQLRELENDGIVNRIVYNQVPPKVEYELSDYGRSLEPILNALCNWGDQHI
VKEYGDKSAVLEDNGLNDFNSDNRELVQP"

CDS 6183537..6184214

/locus_tag="EFAGFIKM_05440"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q5XDZ5"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

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VDNAHLVAWPHYVDYRIEKASQGWLSSVTSGEGLVCRFRGEGTILIQSRNPQGFGQWV
KQFIPAR"

CDS 6184349..6184810

/gene="slyA_5"

/locus_tag="EFAGFIKM_05441"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01819"

/codon_start=1

/transl_table=11

/product="Transcriptional regulator SlyA"

/translation="MTSSRYKNAQESPGYLLWQVTAMWQKEVRRVLEPLELTQPQFVL
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IITTEEGTRLAVEGIHLVEESDKAFFETLDERKGEYLEIMQEFLRQKTES"

CDS complement(6184955..6185929)

/gene="yajO_5"

/locus_tag="EFAGFIKM_05442"

/EC_number="1.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77735"

/codon_start=1

/transl_table=11

/product="1-deoxyxylulose-5-phosphate synthase YajO"

/db_xref="COG:COG0667"

/translation="MEYRRLGNSGLRVSAALGLGTNAFGKRADEAASTRIIHAAMDQGI
NFIDTANIYAGTESERIIGQALTGRRENAVLATKAGLPRHDGPHGRGSSRYHLQQUELE
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GISEQKGYVRYISTQTSYSLADRTPELELVPMCLDQGVGIIPYFPLAGGILTGKYNQ
TRVPSGSRADTDPSFNRFLLEHNIQLSEQVSAKAASYGCSPSVLSLAWLLTRPAVSTV
IVGATRTEQLEHNLASLDMSLPDELLADLDQISDSFRRREPFAZYRID"

CDS 6186045..6187085

/gene="tagU_7"

/locus_tag="EFAGFIKM_05443"

/EC_number="2.7.8.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q02115"

/codon_start=1

/transl_table=11

/product="Polyisoprenyl-teichoic acid--peptidoglycan

teichoic acid transferase TagU"

/db_xref="COG:COG1316"

/translation="MENSAAHLTRRKPKKPKKKWKKPLIITLSVLLVLGGLGFIYQKQ
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VDFYAAINFNGLKDIVDAVGGVELPIKKNIENKSKAHEKLFVEANKPIYNGEEALGYV
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CDS 6187274..6189862

/locus_tag="EFAGFIKM_05444"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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YSIVTFALYLGITLAYPFKHRMKLTWWDFALLAMNTSISCLMLYVLFVAGWQGL

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TVLITLYAWAVHSNSSSRERFKYSPLELGFLNGFKYVTLANLWLVLYESNELYVRA
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TMPALQPEVQQHTVAEIVGLLVLIIFNVGVFFAGRDLIAGIRGQFKSIEWYPVIAGV
YLLSVITVFLTQFQWGDVGLMFSLIYLLAILYIAYGFRRKYVMIRRLGLGLTLFAT
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PEEDQD"

CDS complement(6190282..6192240)

/locus_tag="EFAGFIKM_05445"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKGKMSKIILKAITVLLFFGLLAGDPSVVRFPDMASATAGPITV

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NIENYSKMVIRMKGANGGEQDHIQLSIGGLTRTLASFSGDTVTHFKDVEIDLAANGV

DLRSPGQLSMSFWHGGNSTIWIDEIRFE"

CDS complement(6192569..6192778)

/locus_tag="EFAGFIKM_05446"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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SNIEPEIQIISNTNTMVVVRCSQNI"

CDS complement(6193308..6194138)

/locus_tag="EFAGFIKM_05447"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNDSERRALGSLRNLRSSISPRDVGLPTGSRRRTRGLRREEV

AQLASIGPSWYTRLEQGRDSSPSVSVLESLASALKLTPNERRHLFLLSGESLPPQLNG

EEEIISPSVQMMLDELNPNPAYVIGRKLDLAWNRAAEAVFTISEPSPPHDYNLMWRQ

FTDPVWREGLNWEYVSQRIVAEFRTSRARYLQDVSKRLIDDLKRESTDFVRMWQHH

EASSTLDGYKKLCHPTLGAMEFEHITLQFPNDPDKKIMIYMPHTATKSRLENYLMESI

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CDS 6194265..6195038

/gene="barS1"

/locus_tag="EFAGFIKM_05448"

/EC_number="1.1.1.413"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9LBV3"

/codon_start=1

/transl_table=11

/product="A-factor type gamma-butyrolactone 1'-reductase

(1S-forming)"

/translation="MENISGQLLMDKVVMVTGAGRGIGAAAAKLFAEEGASVMLVSRT

ESELRTVRDEITATGGNADYFTADLSDASSVEEAVKATVRRYGRLNAAFNNAGIVTV

ASLVDEKEEDFDLIQSVNYKGVWLSMKAQIKAMLETSGSGAIVNSSSVGSLKGNPGLG

AYGAAKRGVNSLTQTAAIEYGPAGIRVNAIAPGTTMTDMIQQWVAINPKIIEQISAKT

PLRRPAEPIEVANAAWLLSDQASFITGVILPVDGGLSA"

CDS complement(6195493..6195834)

/locus_tag="EFAGFIKM_05449"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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/product="hypothetical protein"
/translation="MKESFQQVAKDNNKDTSSLVRDWISTYIAEHQRVDEEITDELYM
AGYQLQEALGGRENVSNFAKELQEFSLTNQKKFTQRILTTYMDLNLTPSCLSKTYK
GFAFSQCFCWA"

CDS complement(6196580..6196735)

/locus_tag="EFAGFIKM_05450"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNKKNIFIYVLLAFALSMTLTVLSRMNDDGGESLKGTSASETSW
LQMKIQP"

CDS 6196969..6197640

/locus_tag="EFAGFIKM_05451"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRETAKIVIRTPGQESDGSFAYVSQGRSITVGRYTGGSELDLSV
YNQMISKRHCRIHYDVQQQLWIEDLDSKNGTELNGQRLVPYEKYPFSEGDSLTLVNGL
IQLRTEGDLGETREYRVSDLFGEGVRLQDHLQTVQIGEVEIPLSKKEYQLFKLLYSQL
DHFVTRQIVAQVWPERSMLESEAVGIDEINSLIYRTNRKLGVBHFTIKSVYKKGVMK
SHVPE"

CDS 6197667..6198245

/locus_tag="EFAGFIKM_05452"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MFIIYLIPWLIWVTLICVISIVLVSWKNGISPMPTSSRVRQVV"

IQEVNRIPGYGDVLEAGSGWGTGLDVRHCPGKRLTGIENSIPLWSSQLIAYFSVR
LRRAKGNKHSLKGRLRFMRGDIYTSSYEHADCVICYLFPGAMTKLLDKFSRELPPGAK
VISVCFALPGKEPLSTITCRDALRTKVYVYSF"

CDS complement(6198475..6200781)

/locus_tag="EFAGFIKM_05453"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKNMITGSKLWSIAMITSLAACSSPATTSTTANAATSTTGTT

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ISEAGTYVLSGELTDGQIVNVADKGTVHLVLNGATIHNDNSAAIYIQKAGKAVITLE

KGTKNTVSDGKTYVYADATTEPDAAIFSKADLTFNGAGQLVTGNYNegITSKDDLK

IISGSISVKAADDGIKGDMMVAIQAGTITIEAEGDAIKSTNDTDTTKGYVAIAGGTFD

IQSGNDGIQAETALVTDGGTYNIVTGGGSANAPAKVEEGPFGGGGGGWGGGTPPTDMG

TPPDGEPPANMPEMPNNSGTNAGANTNGAATSSSANATTTTDDNNADADTATTATEST

SAKAIKAGTDLTVNGGTYTIDSMDDSLHSNNNVTVNDGTFNIESGDDGIHADQALTIN

GGTITIAKSYEGLEGAIITLNDGDVDVTASDDGVNAAGGETETATNTAASTDSATTAT

DAATTSNISVTETTGTSTTDQASQGTATTQQGRPGGMGAAASNNEFHINGGTLTV

NAGGDGLDSNGSINMTGGTVIVNGPTNSGNGALDYDGTFEISGGYLVAAGSSGMAQGT

SDASTQNTIVMTFPATQKAGTLVHVQDSEGNNILTFAPAKDYQTVVVSSPDLAKDGSY

VIHSGGTSTGKAVDGLYTDGTYSGGTQVVAFAQSTSNVTWVNESGVTTANTGMGGPGGG

GQGGFGGGRNRSQSGTTSdstgttDSAK"

CDS complement(6200808..6201488)

/locus_tag="EFAGFIKM_05454"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLDSLFSALTDTNLTfNNAVITIGLAILGLVISLTYMKTNQS

TYSQSFTLTMVVLPVIVAIILLIGSNIARAFSLAGAFSIIRFRSAPGDSKDIAYVLF

TMASGLACGVGAFGYAVLFTIILCVLMFVLSRFNFGGKKSQKTLKVTIPENLSYEEA

LNEVFHKNVFPDLKKIRTELGSLYELVYSVTIHESVSQKEFLDAIRTRNGNLDISL

TMSPTTEY"

CDS complement(6201481..6202299)

/locus_tag="EFAGFIKM_05455"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAIEVFNRYESKYLLTDEQYAHFYNDLLKYMELDAYNKKHEYYS

ISNLYFDTPQDSLIRASLSKPKYKEKLRLRAYGIPEENAKVYLEIKKKVFGLVNKRRT

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RDLRITFDTNIRSRRYDLKLEQGDYGEPLVKDGRWLMEVKAECTVPMWLSQLLSEHGL

YRTGFSKYGNEFRHLARTTNLNYQTERILVPGTDFNPSIEQDKTIIERERVLYA"

CDS 6202550..6203230

/gene="arIR_2"

/locus_tag="EFAGFIKM_05456"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9KJN4"

/codon_start=1

/transl_table=11

/product="Response regulator ArIR"

/db_xref="COG:COG0745"

/translation="MMRILIAEDEVHLAEAVSQILKKNNYSVDMVHDGRSGLDYAQSG

IYDLLLLDIMPEMDGITVLKKLRSEGNHTPVILLTAKGELSDKVTGLDYGADDYIAK

PFATEELLARIRAALRRKGEVVPEDGLKFGDIELNTTQLKLSVQGKEIKLNLKENELL

ELLIARKQAITSKEQIIKELWGFDSVEYNNVEVYISFLRKKLTFLNSAVRINTIRGV

GYVLEVTS"

CDS 6203230..6204573

/gene="sasA_23"

/locus_tag="EFAGFIKM_05457"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"
/codon_start=1
/transl_table=11
/product="Adaptive-response sensory-kinase SasA"
/translation="MFKKLNRNFLIVNLVSIIMMLVAFATIYTITYQNVQRETNMEL
YKVSDFYHSPYNSSKMMPRGEGQGSGTAGSTGSGSGSDSLPSEAMGGDNGGPGGDPNSP
PARSVSFMIKTDDQWKITNTHSRFDMEDTFYTEALQKVDQDKVGDSGRQTGGQFALDGT
DWAYVVDPSGDGHMIVFIDVTAQQGILTNIYTFVAVGLVMLIVYFLSRYFANRSIA
PVREAFEKQKQFIGDASHELKTPLAIINTNADVLLTNQEDTIANQAKWLHYIKSETER
MTGLTNDLLYLTQMDDSRSTMIHAKFNMSDAVESIILPMEAVIFEKNISLDYNIENPL
TVHGNSEIQKVILILLDNAVKYSGTKGAVNVTLQKQNNDDVVLAVSNTGEGIAAEHLD
RIFDRFYRTDSSRARKHGGHGLGLAIARSIVDQHKGEVYARSVIGEGATFYVRLS"

CDS 6204741..6205028

/locus_tag="EFAGFIKM_05458"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAEANAINEQEMMQYIADKTKASQANIALVLKHEQAYINKAHEN
AKGNDVDIDGDDLADYILSRKDVKLDELTVESILDAEMDYLMDKGHAGYVD"

CDS complement(6205488..6206255)

/gene="lvr_5"
/locus_tag="EFAGFIKM_05459"
/EC_number="1.1.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9LBG2"
/codon_start=1
/transl_table=11
/product="Levodione reductase"
/translation="MSTSYHTAVITGAAGGIGKELARRLAERKINLVLVDLNEEAIQ
QTIIDLNLDKHEHVIIVKANVSQEADVKNYVQKALDAFGRIDYFANNAGIEGPTGLIED
LSVEALDTVYNNIRGVFLGLQNVIPVMKKQKSGAILNTSSLAGLMGAPAVSPYIMSK"

HAVVGLTRTAANELAPYNIRVNAVLPGTINTRMMRQIEANSGNVEDYQSATVSSIPMG

RYGEPEEVAAMNLLSEEASYVTASLYTVDGGMVGQ"

CDS 6206451..6207089

/locus_tag="EFAGFIKM_05460"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLIEHPQDRRARRTQDAIIAAVSLILEKGADALTIRDITERA

DYNRGTFFYLHFPKGPELLQFILDDFMQGVGRAYAEPYAQLKEVDMTVLLPSTMPVFEY

IEAHQDIFRALITMHSDMSSRLCNMFRTYLTEDFVLVTEDSEWTINYDIMLSYLVSAT

VGVMHWAIEIGFKYSAHYMGEQLTALINIKPTRLLIEPGQKGRTIHERMLLD"

CDS complement(6207099..6207869)

/gene="sumT"

/locus_tag="EFAGFIKM_05461"

/EC_number="2.1.1.107"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34744"

/codon_start=1

/transl_table=11

/product="Uroporphyrinogen-III C-methyltransferase"

/db_xref="COG:COG0007"

/translation="MSRGLVSIVGAGPGDPLITVKALKRIQSADVIMYDRLVNDQLL

AEAREGALRIYCGKAPGLHSMSEQEMIGRMLAAHAAEGKQVVRLKGGDPFIFGRGGEEA

LVLAEAGIAFEIIPGITSAVGTSASSLIPLTHRGVASSFACVTGTGSDGSVSPVRWDL

LAHSVDTLVIYMGISQLPQIQHALLHHGKSGSTPAALIERGTTSEERIITGTLAELHS

LAKSHQVNNPALIMIGESVLIREQLLQMQAANASMTG"

CDS complement(6207866..6208747)

/gene="focA_1"

/locus_tag="EFAGFIKM_05462"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AC23"

/codon_start=1
/transl_table=11
/product="putative formate transporter 1"
/db_xref="COG:COG2116"
/translation="MDFVKPAEVLQSMVEAGESKARMNRVQMLIRGFLAGAILAFATT
LAYTAVSQTSVGLTGALIFPAGFVIIILLGLELVTGNFAMLPAMMKRRITWTDMLRN
YFWVITGHLIGCAFYALLYGLTITKIGTDMSNPLIQTLIQTSEAKTLGYQHLGGAGIV
LVTIKAILCNWMVTLGAVMAMTSTSTLGKIVAMWLPITIFFAQGFEHAVVNMFVIPAG
MMLGAQVSFADWWLWNQIPVLVGNLIGGAVFTGFGLYAAHHWGNPVKLSSKLATIQGG
RSGVASSDAASKLGTRS"

CDS complement(6208785..6209102)

/gene="nasE_2"
/locus_tag="EFAGFIKM_05463"
/EC_number="1.7.1.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42436"
/codon_start=1
/transl_table=11
/product="Assimilatory nitrite reductase [NAD(P)H] small
subunit"
/db_xref="COG:COG2146"
/translation="MNKFRIGHLADIDEKGARTFLIQDTEIAVFKLSDGSLHAIENRC
PHKGGKLSEGMVCGTAVHCPLHDWKIDLRNGKVHEPDEGCLNTYKTEVDGNSGEIFIT
IAG"

CDS complement(6209119..6211560)

/gene="nasD_2"
/locus_tag="EFAGFIKM_05464"
/EC_number="1.7.1.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42435"
/codon_start=1
/transl_table=11

/product="Nitrite reductase [NAD(P)H]"

/db_xref="COG:COG1251"

/translation="MSTTKKLVLVGNMAGIRTIEHILKLAPHAYEITVFGAEPHPNY

NRIMLSSVLAGGTSIEDIVINEWSWYEDNGIRVYPGDPVVQIDTKRKEVVSQNGVRAA

YDELIMATGSQAFILPLPGANKEGVIGFRDIKDCETMMAASQKYRKA AVIGGGLLGLE

AARGLLNLGMDVTVIHINGHLMDRNLDLPAGLMLQRELEDQGMKFLLNKHTEEITGKH

RVKAIRFTDQTVLEADLVVMAVGIRPQIELARNTGLDVNRGVIVDDYMHTSIPGISAV

GECAEHRGIAYGLVAPLYEQGMVLAKRLAGAATEGYEGSVTSTKLKVSQVDVFSAGQF

KDAADTRSIRIQDDVDGVYKKMVIKDGQLIGAVLFGDTTDGASLFSLIKSGENISGRE

KEILLGIPSGSGSGSPVAERMASMPDEEIVCGCNGVTKSSIGDAVLNKG CNTLGAIK

SCTKASASCGGCKPIIENLLTYAGDNVGEQTKEGICACTSYDRDEIVAQIKEMGLKS

VKEVMNVLGWNEPEGCSKCRPSLNYYLGMWPAEYTDERSKFTNERYHANI QKDGTY

SVIPRIYGGVTSPAELIKIATVAEKYDVPLVKFTGGQRLDLLGVQKENLPKIWEELDM

PSGFGYGKALRTVKTCVGN TFCRFGTQDSIEMGIRLEKKLDKMVAPAKVKLAVSGCPR

NCAEATIKDLGVVAIDGAWEIHVGGNAGVKVRAAELLCTVKTDAEVEEW TYSYLQYYR

ENAKWNERTAAWIERVGLDHVKEALADRDVRLALVERLEVTLGHTVDPWKEIIQDEKL

RKNFTPLSGAEPVTH"

CDS 6212151..6212744

/locus_tag="EFAGFIKM_05465"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRSLLVIRVQPTIAASSDAIPLTPERLLGANGYHVQVAGSEAEA

VKLARAAEASILHLSLADVEYWVNC LGKGKSDSPLLWWCAPDTASSSAESCEVETSFD

GILTPSMTGPEIHWTLHFAARRYMERKQWEQERKQLQSRLED RKWIDMAKAILSDLKQ

ISEAEAYDLLRKKAMDERKRMVDVATAIVKAHQLLQS"

CDS 6212763..6213839

/gene="trpD_2"

/locus_tag="EFAGFIKM_05466"

/EC_number="2.4.2.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8PD71"

/codon_start=1

/transl_table=11

/product="Anthranilate phosphoribosyltransferase"

/db_xref="COG:COG0547"

/translation="MDMSQILREVGRGKRGSRDLDNYTEALTVAEKILKQEVSPAQTAA
FLMAERMKMENVEELEAFVHACRNSAERFSIFQDGLDCAGPYDGRTKSFMATFPVAFV
LAAAGLPVTLHGSDPLPPKWGVTLVLLKEAGIDTRKMDREDARSAALRSGVMYVSSE
DWCAPLRKLRPLREELGFRTVFNTAEKLIDYNHSPYLVFGVFHNTFLDRIAKLLTRFN
YRRAYVVQGMESSEDLYIDRPTRVYAVEDGDMKLELVDPAAYELDMPVPELVWTAAKQ
LEVAESVLSGDGHIAFVNQVLLNGGFRLYAAGRVNSIEEGIYTCQGLLESGAAYRIYQ
QWCVSMGGELPDSRAVSIYPASSR"

CDS complement(6213881..6214429)

/locus_tag="EFAGFIKM_05467"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MREIPKPTMDQVEKKYVRETRCFKTARVFPTDVNNHNTLFGGK
LMSYIDDIASIAASKLCRVNTVTASTDSVDFLYPINPTDSVTLESFASWTGRSSMEIF
VKVIREDLKTGEKKIAATAFLTFVALDENNRKLIVPRIIPETEEEEKKLYETAPDRAAM
RKQRREESKKFADFLTVYPWE"

CDS complement(6214833..6215456)

/gene="satP"

/locus_tag="EFAGFIKM_05468"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AC98"

/codon_start=1

/transl_table=11

/product="Succinate-acetate/proton symporter SatP"

/db_xref="COG:COG1584"

/translation="MQTDSQTKVKIVNADPSAMGLFGLAIVTLVASSQKLGITDGLSY

AIPWAIFLGAFQALFACIQDSKRNTFGTTAFGAYAFFWFAMAANWMIKMGVFGSTLA
EQADGKQLGFAGYLVFTLFMTIGAIEANKVLLIIFILIDFLFLGLTFDAFGVAPHI
FHTIAAYAEMAIGIVSLYGTGASVLNAHFGYAFLPIGKPSGIFKPKA"

CDS 6215892..6216068

/locus_tag="EFAGFIKM_05469"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVMSLDLKNKIEKARHNLHMLVEHNKGGLGHPDVIRQSMALDEL
INEYNRISRNHSA"

CDS complement(6216242..6217171)

/gene="cheB_19"

/locus_tag="EFAGFIKM_05470"

/EC_number="3.5.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00099"

/codon_start=1

/transl_table=11

/product="Protein-glutamate
methylesterase/protein-glutamine glutaminase"

/translation="MRYFIVDDDPGVRSMLMDIIEDEGLGDIAGEAEDGAHIHAELLE
LHKVDVLLIDLLMPQRDGIQTVRALEGRFEGKIVMISQIESKNMIGEAYSLGIEYYIT
KPINRLEILSVRLVSELRMQQSIADIQRTLQGLSGLNSTERAAAPVPDKTITTAGH
FLLSEMGMIGEAGSRDLLDMLEYLEQVETDEHKLSPYTFPSLKDIFQNVAIRKLGEDA
SLAEVNKEIKASEQRRRAIFQTLSHVVSGLTDYTHPKFENYASKFFDFTEIRKKML
ELQNNVEPSLSQTRINTKKFVQVLYLEAKRLLH"

CDS 6217501..6218937

/gene="alsT"

/locus_tag="EFAGFIKM_05471"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q45068"

/codon_start=1
/transl_table=11
/product="Amino-acid carrier protein AlsT"
/db_xref="COG:COG1115"
/translation="MEQTIQDIVVIFNDFLWSKVLIIILLVCGIYFTAKTRFMQFRMI
GDMVKVLREPKSKEPGKISPFQAFCSMAARVGTGNITGIALAIALGGPGAIFWMWII
AIIGSASSFVESTLAQIYKVKDKGGFRGGPAYMERGLGKRWMGILFAILITLSFGLV
FNAVQSNITVAFENSFGTDRLTVGIIMAVIFAGIIMGGVKRIAKASEYIVVVLAVLY
IGVAAFVVLANITQLPAMIALIVKNAFGIEQVAGGTLGAALMNGVKRGLFSNEAGMGS
APNAAATADTTHPVKQGLIQAFGVLTDTLVICTSTAMIILLSGVYKGSDLGGIELTQA
ALSVHIGSWASGFLAVMVFLFAFSTLIGNYYYGETNIEFIKSNKVWLWVYRICVIAMV
VFGAVAKVQLVWDLADLFMGLMVVVNLIAILTSLKVTFEALKDYKKQKAEGRDPIFTR
DRIHIPGEVECWQSEEEVIGDKSIHVAN"

CDS complement(6219086..6219925)

/gene="yfmS_2"
/locus_tag="EFAGFIKM_05472"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O06477"
/codon_start=1
/transl_table=11
/product="Putative sensory transducer protein YfmS"
/db_xref="COG:COG0840"
/translation="MNVVDALLKVMPYISLILREPASLTVDHEKVLEVITTDKFDLG
FEKGMPLLESYQNFAILKNGREATLATLSKDVGIELDILNIPIFDDHQKVAVFCVS
YDQSNQNQLEDIIQENQTINGNLVDMVQHVAHAEEELQATSEQILQNTRLAVQNSSQI
NKVAGFIREISEQTNLLGLNAAIEAARVGEAGAGFGVVASEVRKLSVDAKQATSDIDT
SLRDVQQVIKQMEVEVSQIAASSSEQATLVASFTDVIEQLNETGERMKTLSQLISYS
VKK"

CDS 6220208..6220900

/gene="yeiL_2"
/locus_tag="EFAGFIKM_05473"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A9E9"

/codon_start=1

/transl_table=11

/product="Regulatory protein YeiL"

/db_xref="COG:COG0664"

/translation="MKEIMDFGLVRQLARENGLDQVLDEPALAELRLLEAAKGEMICA
KGERPERLYFLVQGKLKIYTTLPNGKSLLLRFSTPLALVGDELVNGKEAMNTVESVS
KSLLLGISYRALQNTYAENPKFLHFMLSQVTHKLYTFSNLSSLNMLYPVESRFASYLL
STMGQDESSEEIQTSKLTELADMLGTSYRHLNRVVQDLCNRDIIRKVQRKLVICDLE
QLRVIAGGNIYE"

CDS complement(6221037..6222275)

/gene="pepT_2"

/locus_tag="EFAGFIKM_05474"

/EC_number="3.4.11.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q81WU4"

/codon_start=1

/transl_table=11

/product="Peptidase T"

/db_xref="COG:COG2195"

/translation="MKDILIQRLSTYVQMDTQSDENSETCPSTPGQLALGKLLVEECT
SIGLQDVTMDENGYVMATLPSNTDKDVPVIGFLAHLDTATDFTGKNVKPQVIDNYDGA
DIVLNSELDVWLSNKDFPELHEYKGHTLITTDGTTLLGADNKAGIAEIMTAMAYLIEH
PEVKHKGIRVAFTPDEEIGRPHKFDVAAFgakYAYTDGGPLGELEYESFNAAAAKI
TVRGTNVHPGTAKDKMVNSLKIAMELNRRLPVEEAPEFTDGYDGFYHLLSLEGDVELT
KMSYIIRDFNREKFEERKTNLLHIANELKTKHGEKSIKVELNDQYYNMREKIEPVRQI
VDIAHEAMTRLDIEPVIRPIRGGTDGSQLSYMGMPTPNIFTGGENYHGKFEYVSVDNM
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CDS 6222503..6222694

/gene="ywhB"

/locus_tag="EFAGFIKM_05475"

/EC_number="5.3.2.6"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P70994"
/codon_start=1
/transl_table=11
/product="2-hydroxymuconate tautomerase"
/db_xref="COG:COG1942"
/translation="MPFITVKVLEGKTTEQKRQLIERMTQVACETLDVDPSKVFIIE
DLEKDNYGKNGKLFSDLDK"

CDS 6222743..6223777

/gene="namA_2"
/locus_tag="EFAGFIKM_05476"
/EC_number="1.6.99.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54550"
/codon_start=1
/transl_table=11
/product="NADPH dehydrogenase"
/db_xref="COG:COG1902"
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IAHAGRKAEDAPQPVAPSVVTFPGKEYKEPRALSTEEVEAMVQKFADGVRRAVQAGVD
TIELHGAHGYLIHQFHSPLMNHREDVYGQDLRSFGVEVIRAVKKEMPTDMPLILRISA
VEYADGGYDIDHTINIARAYQDAGVDMFHISGGEGPSGQRKPGNYPGYQVPFARRFR
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CDS complement(6223855..6224622)

/locus_tag="EFAGFIKM_05477"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
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/translation="MSFSYYGPLCTAVYDLTKPVGHSLGGDIEFYRHYLQRCKGRILE"

AMSGSGRVLIPILLEAGLKVDGIDYSMDMIDSCRSRCTERALPMPPELFVSDLEKLDLPY
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SLPDGDTITVEVKTIEVNLLQQYKVSLIRYEQWHQGSLVATELQQLTLRWYGIEELRL
ILENIGFSHIKVYADFNPDQPPTQSNQKFVYEATRR"

CDS 6224850..6225278

/gene="yndB"

/locus_tag="EFAGFIKM_05478"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31806"

/codon_start=1

/transl_table=11

/product="putative protein YndB"

/db_xref="COG:COG3832"

/translation="MDSSSSSSSALPDIRQELVLHAPVEKVVEMVSTEQGLKTFWMPG

NLEPVEGHEFVLEAGPFGQSPCQVTEVLPLHKLSFRWGKDWTLTFLNEQPEGTDFTL

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CDS 6225519..6228614

/gene="rcsC_19"

/locus_tag="EFAGFIKM_05479"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00979"

/codon_start=1

/transl_table=11

/product="Sensor histidine kinase RcsC"

/translation="MRKHWIMLTISFICIVIVPLGWIAQTLISERINPQATDGKIDLT

QWDFDRKGAASLKGWDFYPGQLLSPADIEASVSGRKPLPASSGTQVPARWNKSLGQA

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MLLISLVVMFYTLRAMFYWLKGRPNDSHFALVSMMSILMVVVLYTLGAFTTLDTAFFA

LIELLLFVFAQMIVTAIRFAQSFRDVEALSERLLAIDSLKDEFMANTSHELRTPLHGI
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DLESVARTVVEVSGFTFEDKPVILIQQWPQSLPLVEADEDRLRQVLYNLLGNAYKYTE
QGEIRLYASVEGDWVKVSVADTGVGIALDKQEDIFQAYEQSNGTIERLNHGTGLGLSI
TRKLVELGGGEIWVESKPGQGSTFHFTLPVMKMPLLQTHSKPAAARYVAAQSGSAKEL
VTRESDEQDDLTEAEHTILIVDDDPVNRQVLLNLLSTERYRVIAADSGSTALKLREEF
PSIDLVITDWMMPKMSGLELCRKLRHSSSELPIMLTARGLPEDIKHGFQAGANDF
LSKPVDAGELRARVRTLIEMRSSVQEAIRTEMAFLQAQIKPHFLYNALNVIIATCAVN
PDKATDLLIELSHYLRGSFDFQNRQLVPLTKELELVESYVHLEQARFEERLVVEYEV
ESDVHLYLPPLSIQPLVENAIRHGVMERAAGGTVHLRIFQSEHVVVQVQDDGVGIPP
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CDS 6228744..6229907

/gene="cheB_20"

/locus_tag="EFAGFIKM_05480"

/EC_number="3.5.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00099"

/codon_start=1

/transl_table=11

/product="Protein-glutamate
methylesterase/protein-glutamine glutaminase"

/translation="MRAIVIDDEKPAQLHLERLLRTDGRITPVQCFSTARDGLHFLAK
ERVDVVFLDIGMPENMGLEAAEYIQLDQSIRIIFVTAYADHAVEAFELHALDYVLKP
VSSARLAKTIDRIAGIMSHKSQVAATAEVQASESVVELDIEVPGLLTFKHLDIYRSL
DQGAEKHKWRTTKAQELFAFLFHHREEVWSKEILLDKLWGDVSQEKGLTHLHTSVYQI
RKLFKEWNMTGKLEYNMNRRLSGNLVSDVDQFEKSMVYHVITSDNVDDL RHMIPLY
RGDYLEEHDYRWAQAKARELRRKYTGLVMDIARWDMEHGRGKEVIEQLTILQEREPYS
EEICRLMMEVYASMDQDQGIFRLYHSFKLTLNEDLGHQPEPDTSRLYQNLTDQ"

CDS 6229944..6231290

/gene="phrA"

/locus_tag="EFAGFIKM_05481"

/EC_number="4.1.99.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9KNA8"
/codon_start=1
/transl_table=11
/product="Deoxyribodipyrimidine photo-lyase"
/db_xref="COG:COG0415"
/translation="MKLFIHRKDLRTDDLAAFDYLREHQEESVHVLIYDPFLLRQGRE
KEHSGVNFQRHAAELGRQYFEAKRKLHVAYGKPAEVVEFILNEFKGEINEIVVHRDMT
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MNEHPNPPSATTVAELKVSDRQIEWPDAMQVPLELLEGSGSNDDDPHLLLDQFLSDRI
AEYGDHRDEYEAYETSHLSSYVAVGAVSIRKMYDAASRTAEAGEWIRQLCFRDFYLYR
AVYESHYFTYEKVYDLSALHDDHFEQWCKAETGIPIIDAAMTELNETGHMPNRLRILT
AMFLTKNLQCPFTLGEAYFRRKLRDYDNIQNRGNWLWCASLGENAAPYFRVNNPVTQS
EKYDPQGDIYRKWLPELKDLSKDIHQPRKDAIVDLKASRQAAIDVYKQILASRGK"

CDS 6231572..6232744

/locus_tag="EFAGFIKM_05482"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSETLKRERIPELNLVRALAIIGVLSVHSTSYATVDMTGSGYYW
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MYFVLLHFTHYQGRPFGESAVSFITKLFTGKAYTHLYFVFINMQFYLLFPLVLWLLKK
YPSVVKWSVPIGLLIQWAFIVSNKYGFQVPNKGSWAFSYFSYFMLGAFIGVYFPKIKQ
WFVISRANATKGRVASWILLWAVWIIAGLGHVYIYYLLRLKIATYNTLWYEFFWNVHT
FACALVLIQIAYLLYRKGPSLIVKPLNRLGALSFGIYLIHPFLLVYRNYPPTGVSW
LVHLWYAGGFGVALIASWIVVGLTARFVPYAWVIFGNLPKPKPRLVPQQNSGQLDV"

CDS 6232963..6233082

/locus_tag="EFAGFIKM_05483"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MQDILEYVEHILHECSEQTQEYNSKDYQAYSHEGVHEQM"

CDS 6233127..6234758

/locus_tag="EFAGFIKM_05484"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="METGPAPFRQGKTEQEARLSKTCMYCGQQRPMSEFRRRTGKRAG
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GRTSHGMEQGSATVSESERSQPSVESSSSNDDEHADLVTSSPSSSGIRKKRRRRRKSK
RSESITGNELRETSLEHDGLAGEVGDEPQPGEHWRGEEGHSQGHAAANEKGSARAGA
RAAAAVQAAEQAAAAQQALLPAEPQGPAAPMAADQPTAAKRKRKRKRRAALAPGA
GQARSVAEAHAPALSDRGDATTVAAPTAAEAQAAAAGREPGQAPGAAAEAGPPAPVR
QPGSPGSKPRQARERAPKASGEDAARGASGQRPAHASRSHGAGTDGRPRRQTPSAPVA
IDPEDPASLRNTRQGMVRMRGKTDKGRRWHQEVDMEAVTLVKEKAAVVVNRYTIRRL
FSNKDFKRYILTRDHYTCYFCGSYGDITDHLPRAKGGHTTPLNCVCACNLCNQSKAA
MDAEEFMRSIGPEWNAAHQAELIELAMQEAQLEEG"

CDS 6235027..6235686

/locus_tag="EFAGFIKM_05485"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MTPAALDIMSYTEENIRFWLEKFRSLGPLPGILLTFMKSFVPP
LPTLLIVGVNGAVYGLWAGFIYSWIGMVLGCTVTFLIVREIGKSAFVERWARKPRVQR
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IGSNVEQFLEHPIRWVGVLFFIAVSLWASRKLERHFTRSSSDGEDLHDLNQPTGKSIS
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CDS 6235754..6236833

/locus_tag="EFAGFIKM_05486"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIEDIFGFSRMLNRMNEHELRTLLRVLYMKSELVVKRQEKQSEK
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QEKRYFFSMDDNYAVGPLGDLTRRVDLQRRHLWLTERLCLNDRQAYALHELDLSELN
TRLQSIDDRTSIIWYANNSHENTGLLYAMHLLRSESPIYLIETSGLYQQLFNRPDI
QYDVLHTGEILPEKLLAMWHVCSEQEPLSKQERRQLEQDWLELSVQPGLLRMMENGVI
RSLTEDALDEYIMQKVRELTPNWEPGKYIRAARIVGEVIGTSSQHISDAFVEYRLRQL
VLQGQLEMDGKPLAMRYYSIRLAER"

CDS complement(6237111..6237629)

/locus_tag="EFAGFIKM_05487"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNERKKDIETLFLQDDGVIPNHPTLPVLLYKNVWAEELHAESL
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AGTGHKRLESSTDFRIAGAYPGGMSYNTRTGEEDDRAKALQEIREVPIPDTPVYGQH
GPLLEIWNGKKS"

CDS complement(6237954..6238130)

/gene="csbD"

/locus_tag="EFAGFIKM_05488"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P70964"

/codon_start=1

/transl_table=11

/product="Stress response protein CsbD"

/db_xref="COG:COG3237"

/translation="MSNSTGDKIKAGV NKAKGEVKDQIGNATNNRSLQAEGKKDKAKG
AVQDKIADIKDHH"

CDS 6238816..6239262

/gene="yjlC"

/locus_tag="EFAGFIKM_05489"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34633"

/codon_start=1

/transl_table=11

/product="putative protein YjlC"

/db_xref="COG:COG2427"

/translation="MSQSPTQQEVPVTEGANVSERQSLDVLDQLMKPEVQESLTVLVE
 NLPKLAEMVTAMTKAYDFAQSVATDKVLISDTMSAMGEFAKPVVDKAKGVASAAIEAN
 DRAQTEQTSVGLFAMLKMLKDPNVQQSLRFAQSFLSILNERQQPKR"

CDS 6239287..6240468

/gene="yjlD_2"

/locus_tag="EFAGFIKM_05490"

/EC_number="1.6.99.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80861"

/codon_start=1

/transl_table=11

/product="NADH dehydrogenase-like protein YjlD"

/db_xref="COG:COG1252"

/translation="MSKQILILGGGYGGLLTALTARQYLSPEEATITVVRYPHQII
 TELHRLAAGSIAEQAVALPLEKLLRGKNVNLKIDTVDTIKPDEKKVLMTSGSTYSYDA
 LVVALGSETAFFGIPGLQEYSFTLKSVDANRIRAHVEARLDAYKQSGNKADATFVIG
 GGGLTGIELVGEFADLLPAVCQEKGIDFKEVSLYTVAGPSILAGFPPELVERAKSSL
 EKRGVNFIVGVAITEMKENEVLLKDGSSIPTNTLVWTGGVQGNNAVANSIEVDRGRA
 KVTEVLQSTSHKDV FVAGDSAVVFPSEGARPYPPTAQLAWQMGETIGHNLGVMFKGGA
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CDS 6240785..6241429

/gene="yhfK"

/locus_tag="EFAGFIKM_05491"

/EC_number="4.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07609"

/codon_start=1

/transl_table=11

/product="putative sugar epimerase YhfK"

/db_xref="COG:COG0702"

/translation="MNVLVIGANGQIGKFVVEQLAQEGKHKVTAMIRKPEQADALKEL
GADVVIDLEGSVEDLAEAMKDHNAIVFTAGSGGSTGQDKTLLIDLDGAVKTMEAAEQ
QGISRYILVSAYGADQREKWSESIKPYVAKHYADRVLFASDLNYTIIRPGGLKNEPG
TGKIAVGTDLEPGSIPREDVARVIVASLQEEKTYRMAFDLIAGEHPVEDALGKL"

CDS 6241485..6242237

/gene="arlR_3"

/locus_tag="EFAGFIKM_05492"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9KJN4"

/codon_start=1

/transl_table=11

/product="Response regulator ArlR"

/db_xref="COG:COG0745"

/translation="MNEAVLVIEDEPKIARLLELELQYEGYQVGKAGSGTEGLEKYAD
GQWDLILLDVMLPGLSGIEVLRRVRKDATVPIIMLTAKDSVEDKVSGLDLGANDYIT
KPFQIEELLARVRAALRLSAVASVSSASSTPADTGTDS SGHQA EAEAGWLTAAGLKL
NEG TREVSRDGV AIELTPREFDLLVYLLQNQRQVLSRDQIVQAWWGYDYYGDTNVVDV
YIRYVRKKVDNVFTPPLIHTVRGVGYVLKEQL"

CDS 6242234..6243610

/gene="sasA_24"

/locus_tag="EFAGFIKM_05493"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"

/codon_start=1
/transl_table=11
/product="Adaptive-response sensory-kinase SasA"
/translation="MSLRSKIYGYSSVLFVLLIAVNLSVYIVFERMSIDNEVNRVEA
EAESIVKGVQRQSAGSIPPDDLRLAYAPVNGMLRIVNEDGTSSPVTTTAASEQLSKLPY
KYESEKKSEYTQVEQIGYVWVSPVVIWPDGEVVNVQVTESIAETENRLSVLRTVLVAV
TIIALIPAISSRILANRMTRPIQQMTRTMTDIQSSGQFKRLPLEEGSKDELKTMGQT
FNRMMDLLESNFERQERFVSDASHELKTPLTIIESYASLLQRRGKERPEVFDEAVEAI
LSESVRMREMTEQLLLLAKQPEQWNVQLERVDITRLATDSTRAFREAYHREVRCEDPG
SIWAISDESKLKQLLFILLDNARKYSEDAIEVRLEAKGQECRIRIVDTGIGMREDELE
KVFDRLFYRVDPARTRSLGASGSLGLSLAKELAGAVGARIELTSTEGEGTEASIILPL
SVQNGPLS"

CDS 6243689..6244489

/locus_tag="EFAGFIKM_05494"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTEHERRPPEMKRHEQGNIGWAKSRRSLWWGAGLLVVLIVAAV
WWKPWQSTGAVLTADAAAQSVLDQYPGEIVNSTLKDGTYIMQLRSETGLYDVQVDAVT
AAVNSIKRLESNPQAEKTLWSREQIKTALLKQQTDNQLVSLELVEQQGSPVYTAVK
AKDNSREELTIDPYTGETIASKTIAAPTTEPTKDDPKPQFLSEKQAKQKALAEVPGEV
DDIELRGTNNGNPYYLVEIDLEDGREIVQVNAISGAIRSVTWDEDDDD"

CDS 6244728..6245360

/gene="ykoJ"
/locus_tag="EFAGFIKM_05495"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O35012"
/codon_start=1
/transl_table=11
/product="putative protein YkoJ"
/db_xref="COG:COG3212"

/translation="MMMKNKHLWIGSLSAVLLGGSAVAASGNVNGQSVQTTPTSTTQ
SATQNNQNSTGKMLNASQAKALALKAADGKVDDVDLERRNGQTFYEVEIDRKGTNDVVV
RLDAYTGKILAVVNDEDYDDDDDDYKGTVSGNTSNNSASKQVKLTASQASNIALKQVTG
GKVTKVELDHDDGRYVYEIELRTAQGEADVDDIDANTGKVLSDQDFDDQD"

CDS 6245722..6247230

/locus_tag="EFAGFIKM_05496"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAMNDGWLKKNTHSRRFTRRLSYLLALVLALQSIGMLLAPGPNA
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LKNWEYRNDVLTSSSAAELNISNIERP KVIYNSATGKYVLWMHKENGLDYGEARVAVA
TSNTVDGNYTYVGSYRPLGYDSRDMTVYNDNGTAYLISATRVNADLNIYKLTPDFLGV
ESLVTTLWPGQYREAPALFKDDVYFLITSGATGWNPNQAKYATASSITGSWSGLSNF
GDSTTYGSQSTYVVPVEGSQTTSYLYMGDRWAGAWSGPVQDSKYVWLPLSFPSATSLA
MNWASSITIDTATGTVTGVTDPDVPNASYQLISRKSNKLLNVIGGSSANGADLEQR
ADGEMTSQQWQITDAGGGYVKIINRSSGKLIGVENGSTNDGAVIEQWNDGGWASQQWQ
LVHVGGGYKLNKRSTGKVLDISSQSLADGAAAIQWTDNGGTNQHFQIVKVQ"

CDS 6247465..6248250

/gene="lnrL_5"

/locus_tag="EFAGFIKM_05497"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94440"

/codon_start=1

/transl_table=11

/product="Linearmycin resistance ATP-binding protein LnrL"

/db_xref="COG:COG1131"

/translation="MSEQQVLSIESLRMRYNGRYVLNGIDLEVNRGEMIGYIGPNGAG
KSTTVKILLGLVEGYVGTVRIFGKDIADGDVEYKRRIGYVPEVAELYQLTPAEYLT
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LDEPLSGLDANSVMVKEILSQLSAKGTTIFYSSHIMDVVEKISSRIVLIAEGRVAD

GTFKQLQQSMEGSLEEVFNQLTGFNEHKAIAERFVSIVQEVY"

CDS 6248252..6249919

/locus_tag="EFAGFIKM_05498"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEESSDFRTLKILDRFRPIIARTGADYDVLRLILRVKFQMDQRR

VPTILSNNSGKKERKEGNQFLRSLWLYGLMGLMMVPIVWDTGHFMLQMGLVFGILMF

MIMTSMISDFSSVLLDIRDRNIIMTKPVNGRTVGMARAIHAGVYLLLLTGSLTGIPLI

AALVTHGIGFFLIFLVELILINMLILVTTSLIYLFMMKFLDGEKLDKMINMVQILLSV

GIAIGYQLVIRSFSIIDFGMVFTPAWWQLLLPLWYAAAYEWLFAGGGNVWIYTFTTL

AVLVPPVSMIVYVKLMPSFELYLEKMAHSGQSSGRRRGRWDRISKVVSRSREEQACF

RLSASMMRNEREFKLKVYPSLGLSFVLPYVFWFTELQSSSWAEFRQSSFVYTFYIVLM

LVVTVVMLKFSGQYKAFWTFRAAPMANDSALYKGALKAFLCNMFLPIFLANAVLFTW

TFGLRILPDIAIIMMTATALVPLAGKLLLRKPPFSQSFSMAQQSDGWYVFAALPVLAM

LWGVHVFFRSVAGGVWIYGALLIVANVLLWTLLFREKKTAKKGSVAV"

CDS complement(6250296..6251510)

/gene="ldh_3"

/locus_tag="EFAGFIKM_05499"

/EC_number="1.4.1.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q53560"

/codon_start=1

/transl_table=11

/product="Leucine dehydrogenase"

/db_xref="COG:COG0334"

/translation="MQLWQEMEREGMEELIFCHDADSGLRAVIAIHNTVLGPALGGCR

YWTYASEEEEAVRDAMKLAKGMTYKNAISGLPYGGGKVVIWNVPFVKNKPDENGCGSQ

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GRYVTGLDLGTTATDMDQIRLETAHVTDTTGSLGAQDDFTAEMTAYGVHIGIVTSLRQ

QGIASLQGIPVAVQGLGKVGYALCRYLHAAGARLIVADVPERVQRALVQFSGAISAD
PAHIHAADCKVFAPCALGGVLT PATVEELRCSIVAGAANNQLSERQLVAGRMQARGIL
YAPDYVLNAGGIISTAYELEGAGPDLIRQKVAGIAGTLSKVYAEAAQSAISTADAADR
LAESILRSGHKK"

CDS 6251856..6252371

/locus_tag="EFAGFIKM_05500"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P61544"

/note="UPF0316 protein SA1727"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFKILVFIFLIQIVYVSAYTLRMILT LKGQKYIAALISMGEIVI

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HGGFWTRSIKK"

CDS 6252393..6252545

/locus_tag="EFAGFIKM_05501"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQSCFFGFILSDAFMLPRYIPETLLPKLTLYDSRLTVQFLVVP

AIPVYM"

CDS 6252662..6254089

/gene="pelB_2"

/locus_tag="EFAGFIKM_05502"

/EC_number="4.2.2.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:D3JTC2"

/codon_start=1

/transl_table=11

/product="Pectate lyase B"
/translation="MKTKFRSLCSTALALTGLTLLSGQASVQAAGNADYNLTGFSQG
NAGGGIIESNTATYKKVYNATDLALALKKNSGVKVVEIMNDLNLGWNEIPSAAQTS
FAKHNDALHPVLKQTGVSKLTIDGFNGLTIFSANGSIKHAAISVKRSSNVIIRNLE
FDELWEWDESTKGDYDKNDWDYITLEENSNVWIDHCTFNKAYDGLVDSKKGTSGVTIS
WSLFGDDGSSNSWVTQQINELEANKASYPMYNYLRSSAVGLSKADIIAISGPQKKGH
LVGSTSLESANANLSMTLHHNLYKDIQDRMPRLRGGNAHAYNIVMDSTGARA
AKAKIT
TAMATAIASKGYKFDIIGNGAISTESGAVLVEKSVIKDVLPVRNNQTD
PADPTYTGK
IRVTD
TMYSLDGSSFRGSSDTSGSPLAIPAVVKSFSWNGFSTLPYSYTTDDPSTLNA
RLTASNGAGSGKLTWSKDNWLKTSY"

CDS 6254416..6255093

/locus_tag="EFAGFIKM_05503"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
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STDHRRR"

CDS complement(6255169..6256245)

/gene="exuR_5"
/locus_tag="EFAGFIKM_05504"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9JMQ1"
/codon_start=1
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ExuR"
/db_xref="COG:COG1609"
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GVSGELKEKIKVLAVEMGYRYNAAARSMKEGLTHNIGVIIPERFTGPTQSFYVRVFQR
ITKHL EEQGYYGILHILNVEDEEELTPKLYSDNKVDGFIVLGQISKEYIELVRSMEV
PKMFLDFYDEHSDIDSVVTDNFYAAAYELTNYLVQQGHRNIAYVGNLYSTSSIQDRFLG
YYKSLL EHLPMNPDLVLNDRDERGT FIEIDLPEQLPTAFVCNCDQVAHLLVQKLTSM
DIQVPGQCSVVGFDNDIYAMLSDPKLTTVEVDVEQMARTAVHSM LKKVDNPNRSFGRV
HVKGNIIYRDSVSAVSASSDTMDI"

CDS complement(6256385..6257569)

/locus_tag="EFAGFIKM_05505"

/EC_number="2.4.1.281"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:E6UIS7"

/codon_start=1

/transl_table=11

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VPLHWRFDLNETTNPHFMERLGINATLNP GAIYFNGKYVMVIRTEGLDRKSIFALAES
DNGIDGFRFTGKPLVWEDIDAE TNQYDMRLVQHEDGWIYGIYCSEKDP EAPAFDTS
SAVAQAGLVRTRDLTSWERLPNITTNSPQQRNVVLHPEFVDGKYAFYTRPQDGFISTG
SGGGIAFGLCEDILNPVIHEETIIDERQYHTVYEVKNGQGPA PLKTD RGWIHIAHGVR
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LT"

CDS complement(6257566..6258756)

/gene="ce-ne1"

/locus_tag="EFAGFIKM_05506"

/EC_number="5.1.3.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0DKY4"

/codon_start=1

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/db_xref="COG:COG2942"

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DYTGEALDTSKHVYTQSGFVYSLSEYYRATGDASALELAKTLFALIEDKGLDAELPAY

KEQFDRTWKEQPNEMLSENGVIADYTMNTHIHVLEAYTTLYRVWPDQQVKAALERLLG

ILYEQVYDQDTKFLGVFFNKQWESIIDLRSFGHDIEASWLIDEALKVLGIEQHPQYAA

MVTDIAYNISNVAVNADGSLLNEQEGEHIDDKRIWWVQAEAMVGFYNAYQRTGDPLFL

ERVERLWYTKENIIDQRAGGEWYWSVDGNGTPDQSEIAGPWKCPYHNSRFCIELIER

MGSE"

CDS 6258981..6260294

/locus_tag="EFAGFIKM_05507"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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ALGSWAITQIQGMTDTPDDIGFLPFPTNASEVVVPLSADYNIGMNVNSENKPAKAWI

DWFLAKSNYAVEQGGGMDADKNAELPPILDQYKDVQFSTLTPAKEGQEGLVDKIDNEG

EIGLWQPDFKKRIIEAGIGNRKESYDDIMKDLNDKWVKARAECLK"

CDS 6260492..6261379

/gene="ngcF_5"

/locus_tag="EFAGFIKM_05508"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O50500"

/codon_start=1

/transl_table=11

/product="Diacetylchitobiose uptake system permease

protein NgcF"

/db_xref="COG:COG1175"

/translation="MKYLKVSNWGYSAQRIFIICAFSIIPLALLFTFAYLPVINMFKY

SFTDWNNGYSKRFDYVGFENYTRIFSDPEYFKVFIVSLYYFVATFLQMGLALYFATILS

FKVRGKNFFKGILFFPYLLNGVAIGFIFLFFFKPDGTLMLMHAVGLGQYTLWLGNP

NIINVSLAGASVWRYMGFNFIIFLGAISSIPKNVYEASDIDGANRWQQFRHIILPSIT

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LLIVILVTLVQRVTMKGEE"

CDS 6261382..6262215

/gene="araQ_33"

/locus_tag="EFAGFIKM_05509"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MTQLKYTLASVVKYASLVLAAFIALLPIVVILFASLKTNAEYAT

SSPLAPPANWLNLFANYTKAFVDGNMLVGFKNTIIILIISIIGATLTGSMIAYVLDRFK

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QFLGSISSALDESAMLDGASYFTIYWKIILPLLKPAIVTVIIVKGVNIYNDFYTPFLY

MPKTDLQVISTALFKFKGPFQSGQWEVISAGIMIAIPTMIIFLLLQKYIYNGFAQGSV

K"

CDS 6262484..6263521

/locus_tag="EFAGFIKM_05510"

/EC_number="2.4.1.319"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:E6UBR9"

/codon_start=1

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/product="Beta-1,4-mannooligosaccharide phosphorylase"

/db_xref="COG:COG2152"

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PVKGIARIFNSAVVPYEGKFIGVFRAETVNGRPHLHMGASEDGLEWTIEEERIAFVDE
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NGVLFPRKIKDNYVMLSRPSDSGHTPFGDIFLSESPDLVYWGKHRHVMSKGGQGWQWS
VKIGGGPAPIETSEGWLMFYHGVGTGTCNGFVYSMGAVILDLDEPSKVKYRSSNFVLTP
EKWYEEQGFVDNVIFPCATLHDADTGRIAIYYGAADTYVGVAYTTIEEIVNYVIETDE
VIAGDHEEGKL"

CDS 6263521..6264468

/locus_tag="EFAGFIKM_05511"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHMEYIKGFTFGWMSGRGDFRKPEAKESLRLMAERTGSSHVIFA
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FFDIDVPCEPKWKDWFRSYTAFQKHAAAIEQEKCEMFIVGCEMVQSERRDEEWREVI
ASVREVYTGLVSYNTDKYQEGHVKWWDAVDVISSSGYYPIGDWEAQLDRIEQVIAPYG
KPPFFAEAGCPSRSGSAQVPNDWGLEGEVNTTEEQERFYEAMFRHVSQRDWVRGFGFLWD
WSAHLHAEKEALTDDGYGVYGKPAEQVIRRFYEGIAVEV"

CDS 6264763..6266397

/gene="nikA_2"

/locus_tag="EFAGFIKM_05512"

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/inference="similar to AA sequence:UniProtKB:P33590"

/codon_start=1

/transl_table=11

/product="Nickel-binding periplasmic protein"

/db_xref="COG:COG0747"

/translation="MSVQHRKSSALTATMLLLLFVIVGCSNTGSGDESSAASDQTS
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KVYTFKLRQGKVFSDGTPFNAEIVKKNFDAVMKNKDTHSWLGIVGVLDKTEVVDDQTF
RLTLTEPYYPVLQDLSVVRPFRFLGEAGFPDDGDTSQGIKEPVGTPWMLAEYKQDEY

AVFKRNPNYWGTAPKVDQITVKIIPDGETRVLA FEKGDLDLIYGEGVISLDAFQQLRD
NDEYVTQLSDPVGTRSLLLNSSNPKLSDVRVRMALQQGFNKQAMVEGVTSGLEEPADT
VLSKNYPYTNVDLEPITYDVEKSKALLDEAGWKLPVGGTVREKDGQQQLDFEMIFDKTD
PIQKAMAETIQAEWSELGVKVNLTGLELTVQIKRLKANFDLYFWYNYGAPYDPHSFI
NVVASPGFGISETLSALPMKKELDDQVHAALSSTDETKRQELYGSILKTLQEQAIVP
ISYIKKTAVYQKKISNFIFPANRDENPFVGIELGNQ"

CDS 6266473..6267417

/gene="nikB_2"

/locus_tag="EFAGFIKM_05513"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P33591"

/codon_start=1

/transl_table=11

/product="Nickel transport system permease protein NikB"

/db_xref="COG:COG0601"

/translation="MISYIGKRMIAIPIVFIATLVTFALIHISPVDPAEAYLTAAHI

YTPPELLAQKRHEFGLDQPLLTQYAHTIQKIAKLDFGTSYLTNKPVWDEVKLRLPATA

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KLDWLVPVEGRGSWENLVLPTITLSLILIAVYTRLLRSSVLEQLQETYVKYARTRGIRE

RVIMLKHV LKIAISPLITGMGMSMGKLLGTIIVEQVFSWPGFGRYFVDAIFNRDIPV

IQCYVFLAACLFIVCNLLVDLVQLVMDPRISAKGRAEH"

CDS 6267414..6268244

/gene="gsiD_5"

/locus_tag="EFAGFIKM_05514"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P75799"

/codon_start=1

/transl_table=11

/product="Glutathione transport system permease protein

GsiD"

/db_xref="COG:COG1173"

/translation="MINKWRAVFKGQRAIQICSVIILLFFVIALLPWIAPHDPVKVN

LLQKLASPSLEHWLGTDLGRDNLRLMYGARVSLGFATLIFLSSLLIGVIVGSISGY
LGGWVDSLLMRLCEGIMAFPNLVLVLGIVGIFGPGLMQVLLALMMVQWVYYARICRNM
VVSLKERNFIAAARISGSSSWTIIRRHIPNVQRPIVVMGTLEMGWAIMDISALSFLG
LGIQPPNAEWGAMIHEGTGYIRSHPELMIYPGALILLVVITFNILGEALSERYGIAKR
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CDS 6268284..6269090

/gene="cntD_3"

/locus_tag="EFAGFIKM_05515"

/EC_number="7.2.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2FVF0"

/codon_start=1

/transl_table=11

/product="Metal-staphylopin import system ATP-binding
protein CntD"

/db_xref="COG:COG0444"

/translation="MDDAAKVLEVRGLQVNLRTAEGSVPLLEPIDFELKKGRVFGVLG
ESGSGKTVTCNALLHLLDPCRMEVSGSIHLNGRELGSLSGEEMRRIRGKEIGFIMQNP
MNAFTPVYTIGSQFIETLRHTGTMSKVAARERAIAALADMNLPEPAKLMKRYPFQLSG
GMLQRMIAISMCLRPALVIADEPTTALDVVNQFKVLQELDRLRTEYGTSILLISHDL
GVISQMADEVAVMQGRIVEQADVYQLFDHPQHEYTRMLLNARPSMSLGR"

CDS 6269257..6270057

/gene="nikE_2"

/locus_tag="EFAGFIKM_05516"

/EC_number="7.2.2.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8FVN0"

/codon_start=1

/transl_table=11

/product="Nickel import ATP-binding protein Nike"

/translation="MLQVRGVSHSYGKRNLDRSGARPSVLADISLTIEKGVCLGLLG
TSGAGKSTLGRILLGLEKPSQGQVLFQGGQDIYRSSKPVLKGLRRELQVVFQDCYSAVN"

PLMTAAQIIIGEPLDNYERLSGKEQLRVIGQLLEQVGLTPEDGSKLPHQFSGGQLQRVN
IARAIALKPKLIVLDESISSLDMVHQTQILSLLAELRASYGLSYLFITHDIRAAMTIC
DRIAVMDQGRIVYSGDAGDSVMKSDHPAVQQLVTAILPEHPSGRISFR"

CDS complement(6270657..6271235)

/locus_tag="EFAGFIKM_05517"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

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FNMNLEGGYRNKLPLEPDLLQAQEAIKWAEHLVWVFPIWWGGPPALLKGFVDRIFMPG

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VRITPVDQVGKKSDEQRKNWLDKIEQLGRKMG"

CDS complement(6271548..6272180)

/locus_tag="EFAGFIKM_05518"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLIAFWLVITYYTIMKNKSHVDSKKKDILQAAMRLFATKGVDGI

SVKEIGDAAGVTDAAIYKHFKNKDAVALEAFTQYCVDTALIDGYVRQEGPVLERFKQ

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DSRLTAVLVIGAITRMAVSSMQGELPELLVPYTGETVHRLASMLGQVPQE"

CDS 6272299..6273282

/locus_tag="EFAGFIKM_05519"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVGSVNEELDAYSWVTPEGMLNDQYITSREQLYKGMNGRYVERF

TVPSGESYIFKPLTNPVQHGRERWMYERVMSGLPPIYPQLIAASDLTIAPAQSWMIYE

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DELLSRLNMQLSASDWDKISRILTAEEELPTVLCHGDLHPGNMAEVDGSLVILDWEH
AHLNTPLWDIYHLVDLSHPLFPRTVTPVLRERVMDVYLDKLGSLGVQIERVSFAEWYD
AYAIVFSLWMFRLIDGDLRSEECVWPKEQLRNQWHETAVTLEQCMKHLGEE"

CDS 6273301..6274299

/locus_tag="EFAGFIKM_05520"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRKVGLVMRKIQFTEAQGPRVFADRLKQIGLELGVDIVFISPER

HVSGYDWLPGYEHEKGDLVNYDIVLDQIHSQNIEHVIYTVSGFTFLKMFLPKSVLFPH

SFPDPALTGYEMMKPFYTMVDKAIQTEFLKTELGRNFGVHDVNVPIGFSEELANRH

YDPSQVVHNRVLWIGRDEANRRPDLVLEYARQNPDKVYMFVGGVRYKETMKKYDIPS

NVKLKFALTQDEIFTLMNSSKVYWSCSAFDTFAMPLTEAMAMGKMVVKPEHACYGHIR

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CDS 6274353..6274637

/locus_tag="EFAGFIKM_05521"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEVLILWTLGMWAVQLLIEWFIYRLQGRRMTWVQYILPCVALLG

GAVVIMISIDIGGWNGIGYALLGASLGTSGMLTLITVAIRDVVLRRRGRK"

CDS 6274751..6274912

/locus_tag="EFAGFIKM_05522"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNHEMLNNRISQLPIAMAGIVHTFLTNGRSLSNFEYTEVNICEK

MPALTSFGR"

CDS 6275011..6277092

/gene="btuD_18"
/locus_tag="EFAGFIKM_05523"
/EC_number="7.6.2.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01005"
/codon_start=1
/transl_table=11
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LMRLMARLNKPDEGQLMIKKDTRMGYVAQVPEGLDDHTVLDVLSLGFKELMICRTQMK
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GWRFGSLSGGEQTRVVLASQLIVRPDLLLDEPTNHLDLERVEWLEGFLREYPGTIVL
ISHDRYFLDRVVRTLELEDGEAETSAGGYTEYMKVKEQRLLQQFEFKEQQKVIKKM
KETIRQLEEWGRVGGNEKFFRRAASMRKAIERMEQVKRPVLERRNAEFDVRPTDRTGK
RVAVLEQVEKSYGEREILRGISGLLEYGDKIALIGRNGSGKTTLFKLLLGDEQPNAGK
LEWGARVDVGYLAQQEPTNPCLNVLEYFRLEAGVEEGEARGILARYLFYGADVFRSV
GQLSGGEWTRLRLALLVQRKPNVLLLDEPTNHLDIASREALEESLVDFEGTVLAISHD
RYFVNRLASRVWELEDGQMTAYLG DY EAYREKKLDMQARAAATTQAAAGGGVSSRGNA
KSEMKSGLTSAPGGTARSGKKSGVTSTLNGSTVVAADGSQDHAASTVSGKALTPSAVA
ASNHRSGSGNQQSAEKLQTLARLEAQIQVLDQQLETVQNNPLELEQIWNDREQLSAE
YNDVLAQWAEI"

CDS 6277530..6277952

/locus_tag="EFAGFIKM_05524"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLEQISVTRDELFMRLVLDATLVKNKLWAHLSNECQDGREHAVY
VTAYEQQMPDVYGAAIADAALAMCKMSSMYSPEYMLWNGSSFQEELTASSTYTMELA
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CDS 6277952..6278236

/locus_tag="EFAGFIKM_05525"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSDQERGQASKPGSKAKLVAFSLMLAVPAVLSGCGSNNDCECDPE

YDTGCEYDSSSGHYHYGGSSYRSNKDSNSSYSKSKSKSSGFGSFFRSSGG"

CDS 6278241..6279443

/locus_tag="EFAGFIKM_05526"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRQVVQLPFSHEEVFQGEAEQQIPYHRMYGKQYCVALTIVYSPS

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WLEFYANQGLKGPVTFSTFGEHVEDRTNTEYLMKRCQEAGYEVFYAPLEELEIVPGEA

LYHQGREINLLYRLYPLEYLIDDRDETTGVDIGAALLELVREGRLGLMNPVQHVLMQS

KGFMAAIWSLYERNEQTPEYCGFTLFDEAEMDVISRYLLPTYFSAEPFELNAIPYVAK

SYWGREGRGTTTTLDGGTDNAFGKQDMEHPLNEALESNLASGATDEDEEITAYYENQPK

IYQQLVPM"

CDS 6279623..6280027

/locus_tag="EFAGFIKM_05527"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MENLGLNLVNVAVGVGILLVVLVCGYFAFSKLTRYNDSEIIAKD

NEAAGMYMGSKLLGLCIIVGMVSFSTHSWLDMLLWSAFGIIVLCLVYIIFDFLIPKMR

VCDEIARGNMAVAQLLRSLIIGVPIVIGTFLM"

CDS 6280085..6281032

/gene="rihB_1"

/locus_tag="EFAGFIKM_05528"

/EC_number="3.2.2.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P33022"

/codon_start=1

/transl_table=11

/product="Pyrimidine-specific ribonucleoside hydrolase
RihB"

/db_xref="COG:COG1957"

/translation="MRRVIIDTDAGDDTIAITALHHFQVEGITITGGNVQFDQEVE
NALYTVQVAGHGGKVPVYKGCERPLMAYGKAQHRTVEDVHGDDGMGGAHFPKADQRPE
SGHAVDFIIEKVHAHPGEIELLAIAPLTNIAMAIQKDPTIIEIAHLYIMGGTNNALG
NITPAAEYNFYVDPEAAKIVLHAGIPITMVGWEMCTQYSVMDDDDHAEIAALGTSGAD
FFTAINKVVMQFNKSVHKLNGTTHPDLLMAVAADESIMTKSGQYYVDVEAAGELTRG
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CDS complement(6281117..6281638)

/locus_tag="EFAGFIKM_05529"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSNVDINHIRKGDVCNLTMTTEKLKEMQQEEKDLVFGTFNSEM
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SSWHTALRLRNENQTLEQDFNLPTSEYVLAGGAFPLILKNEGQVGTITVSGLPDEEDH
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CDS 6281819..6282310

/gene="lspA_2"

/locus_tag="EFAGFIKM_05530"

/EC_number="3.4.23.36"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00161"

/codon_start=1

/transl_table=11

/product="Lipoprotein signal peptidase"
/translation="MLFYFVALLVTLVDQGTKIAVRMYMEVGDMRLGNSGMQLQHYE
NSGMAGSMFQGNARLFGVIAVLFIAGMLYYRSKGEIRGFWMQAGAGFMVGGALGNAID
RFIYARVTDFLVFPSSGRGILNLADVAINIGVVMIIIGMLIRAYQSYRAKRLRNALPKV
ERS"

CDS 6282573..6283811

/gene="msmE_6"
/locus_tag="EFAGFIKM_05531"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q00749"
/codon_start=1
/transl_table=11
/product="Multiple sugar-binding protein"
/db_xref="COG:COG1653"

/translation="MRTTLTKALGTMLLCGMMAVLLSSCTSGDSANGKVQIEFFQKNP
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AQSDIFTDLKGSSLLQTIDPNYIQMLKDLTGMDVETGIPYATNANGIMYNKTLFKEMG
LDVPKTWDELIATAQKIKDAGETPFYFTYKDDWQTSLPFNALASNLVGIDFYQERRDN
KVTFKEKYREVAEKQLELMKYGHGDNFNGKAYS DGNRAFANGEAFMYIQGTWAISEIRK
ANPNVDIGFFPFPTGNDASEIKLVNGIDSLFTIAADTPNREQAETFIAFLLEPENIGR
YIDEQTLFSAVEGVKQDDPAVQELMPYIEQGKVIDFPDHYIPAAVQLNSIVQSFLQNQ
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CDS 6283836..6284702

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/inference="similar to AA sequence:UniProtKB:O34706"
/codon_start=1
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protein MelD"
/db_xref="COG:COG1175"

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GIYFLPNILSVLIVGYIFNYLFSNVFPIWQGQNLGINALSTNILGSESLAWIGIVIVAV
WQSVALNTILYLAGLQTIPTTLYEASNLDGAGKWREFWSITFPLIAPFFTINMVLAMK
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QIRFLQRREMDL"

CDS 6284702..6285529

/gene="melC_8"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34518"
/codon_start=1
/transl_table=11
/product="Melibiose/raffinose/stachyose import permease
protein MelC"
/db_xref="COG:COG0395"

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FFKGLYYYYFVSAMFIPFPIIMLPIVKLTASLEMTNLVGLILLHTVYGLAFNVFVYVGY
IRSIPVALEEAAFDGATTWGTFWKIIFPLMAPISATVGILTCLSTYNDLPLLIIS
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CDS 6285890..6287653

/locus_tag="EFAGFIKM_05534"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
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NAEKHIHQTAQASGRDLALIAQVNSLTAQVADESYVQRLLSDEKQGNPATFNQRQAL
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ADPEDPGVLLAIRRINLLDHSFEHGGYVVVRMQRSFFQLNDSNGTDGSQDSIMLMDGA
GEVVTSDLEINLDPKAILDSGSVVQNGEESYIVVRQKSELTGWTAVLTPLRETTEGV"

SILRTALLVSGIIGVVLFLIMSFFLSTMITRPLIRLMRAMRSAQPGAMRPNLMVSSTM
EINELNNVYNQMVYRQNELTRVVHEKEVMQSRAELKALQSQINPHFLFNTLEAFYWSL
EEKGDEEMARMVVAMSRLFRYIISSSHQDEWVTIADELEHAERYLQIMQMRLGERMQW
EIQLSDTVRKVAIPKLLIQPLVENAILHGVESKLGPGKISVHVDASTEKNLVRIEVD
DGPGMDELRLQSVIHALHGGPAVSNKGTGVGLINVHRRMLLYFGSQLGERCRLFITSK
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CDS 6287643..6288437

/locus_tag="EFAGFIKM_05535"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5HJF7"

/codon_start=1

/transl_table=11

/product="putative response regulatory protein"

/db_xref="COG:COG4753"

/translation="MIHDKTILIVDDEPRTRREGIRKTLEGWSAGRNIHQTAENGVEAV
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VEYMLKPIDKEQLLQTVEKALKFSEQRRRIQTMQEMVDPKLLDVKERGEQRLNSQISE
ALTYVDAHLGEHVTMREIADLLHLNSSYFSVLFEQIGINFSEYLTRKRIQRAKELLV
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CDS 6288552..6289871

/locus_tag="EFAGFIKM_05536"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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PDVGVTWAAGFLEPYVKG NLFAPVDDLLSDSLGEKFIAGTTEAYAIDGKTYALPIELN
ISPIYYNKAIFAKYNLQPPATYDEFLSVLKTLTENGEVPIALGNKDRWTGSLWYMYLA
NRLGGDALEKAINGSGKFDDPALTQAAAQVQKLVD MNAFNKGFNGLSNDEGKSEFMNE
KAAMYL MGTWELPNFTTNP DIPQEFDKIGFFKFPTMEDGKSDINSWVGPGVGLFVA
QNSKVKEEAQKFVQYFVEKWGESSVTEAGVIPATKVDTA AVQLPQLYIDLLNELNQAS

SLTLFADVQMKPAAAQAHLDMIQALFGKAVTPEDFVKNHQAAIDKGN"

CDS 6289910..6290791

/gene="ngcF_6"

/locus_tag="EFAGFIKM_05537"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O50500"

/codon_start=1

/transl_table=11

/product="Diacetylchitobiose uptake system permease
protein NgcF"

/db_xref="COG:COG1175"

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AVVGS�KYFDLIYVMTDGGPNGSSEVMASYMYRQAFRSFDFGYGSAVGFFLLICLLV
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CDS 6290822..6291709

/gene="ngcG_9"

/locus_tag="EFAGFIKM_05538"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O50501"

/codon_start=1

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/product="Diacetylchitobiose uptake system permease
protein NgcG"

/db_xref="COG:COG0395"

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TVLFASLVTFАITRMRWKGRSLVLGLFMVGLMIPVHSTLIPLFSFLKLHLDHPLSV
ILSYIAFNMPITIMILLGFYYALPREVEEAАVMDGCSVHRIFRIVLPMTSSVISTTA
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FLILSNRIVEGIAAGSVKG"

CDS 6291946..6293355

/gene="yeeO"

/locus_tag="EFAGFIKM_05539"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P76352"

/codon_start=1

/transl_table=11

/product="putative FMN/FAD exporter YeeO"

/db_xref="COG:COG0534"

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RTHGYTKETMYVAVFMNVIHVVGNYALIFGHFGLPKLGVEGAAISTVGSRFICLLIFF

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AMATKQYAGNISSYIYLFMSAIGMGTSIIVGRLVGARRKDDAYKRVFDSVKWALLATV

IIDVIIIILFRVPLMSIFTDNPEIIKLGAQVILLSLLLETGRTCNIIGSLRAAGDAK

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HELVEHDDEEVGAQPVPVAV"

CDS 6293591..6294487

/gene="rhaR_43"

/locus_tag="EFAGFIKM_05540"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

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/translation="MSRYRAMIQQLFYIETHLHEQIGLEEVASEALLSPYHYHRIFR

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PLTHMETEYEMSDEPLNLSFEE"

CDS 6294573..6295424

/locus_tag="EFAGFIKM_05541"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTELLDPRVDFVFKRIFGSEQNKDVLLAFLNSTFIETGESPLTE
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QIKKGENYSLLKKCVTINILNYSCLDNERYHNVFHLREDHTGIGLTDDIEIHVMELTK
LDEYSVPMKEGGLVNWLLFLKGIDTSNWEVLAMNEPMLKKAMDTLEFLSQDASTRMAY
DARMKALSDEKSMIEGARAEGAAGKLEGKREMARELLTLGVDLSAIVKASGLSEDEI
KKLLPKQ"

CDS 6295820..6296530

/gene="phoP_7"

/locus_tag="EFAGFIKM_05542"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P13792"

/codon_start=1

/transl_table=11

/product="Alkaline phosphatase synthesis transcriptional
regulatory protein PhoP"

/db_xref="COG:COG0745"

/translation="MNKKVLVVDDESSIVSAIAYALRREGYEVDTASDGEEALVKVAS
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KEFDLLTILMSNPERVYTRDDLDRVWGM EYAGGTRTVDIHIQRLRKKIGDTDQQKLQ
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CDS 6296527..6298032

/gene="sasA_25"

/locus_tag="EFAGFIKM_05543"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01837"
/codon_start=1
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/translation="MRVSIKLFKFSVFLAALLILTVVVLSSLVLRGIERNQQSQIEGIL
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SSISSGESAIQDTLNYALQNKIAYHEQGDITLLYAAPLDGPDGQMGAVWMQYQVQSYH
EFYTRILQLFIWAGITVVALSFILGYLFYNRFAVAITRLKKSADSIREGNYITESPLK
RKDELGELGQGIYYMSTSIQQNITAMHAEQQLQLAIEKLQALEQQQKQYIGNISHEF
KTPLTSIKAYVELLDMYKDDPQLDDATSNIGKETERLYEMVEKVLHLSALEKYDFEN
QAEDVEVSALLEDACGRMRGKAEKFALNMELDLEPAVIRSDRESLMHIFINMLDNAIK
YNVPDGVIRVKNELRMQDHQAVIRIYNSGTPIPAEAREKIFEPFYTVNKDRARKTGGT
GLGLSLVKQFVEKQGGTITLLSGDPEDGEGVTFQLMFPLADSSLQVRNKSE"

CDS 6298093..6299199

/gene="tolB"
/locus_tag="EFAGFIKM_05544"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00671"
/codon_start=1
/transl_table=11
/product="Tol-Pal system protein TolB"
/translation="MNWKQAAMGTFGAIALTTAACGGITEPGGNAQGGKTGTDITVK
DNTNTSVYQSFKLEKIDKLPNMRGIAWLSDDWIVSDKENKSLKPVTIEGQERYPHNLY
MYDLTKGTDTPKKESEVSLGAPLVSDGKYLKYREPEENTGKGYFLNLHNGETTPAGK
EDGFIQEGAWLDNEHVVFPMKGDILASVDGTTKVLVETGNFNVRSIKVSGSMLYYI
TGEDGQLNAYDVKTGEVKQVLKSVEWVPSNDGTRLAIVKRTADTKRALVLTDLLEGNE
KATLARGTQIFGTSWSGDDSKIAYTINSENDNEKGLFVSNTESAEQFQISADMDNASD
PLAWSPEGNKILLSQAVLENESYHFVTSVITISE"

CDS 6299438..6300325

/locus_tag="EFAGFIKM_05545"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P67330"

/note="UPF0176 protein SP_0095"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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EGINGTVSGTPEQTEQYMKDMLANPLFSDMVFKIDDVEEHAFKKIFVRHKAELVTFRV

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PEWIRENLGDMKDKTIIITYCTGGIRCEKLTGFMINEGFQDVAQLDGGIVTYGKDPEVQ

GHLFDGKCYVFDERISVPINRTEEDIVIASCYHCGTTHDRYINCPTCNLQHVSCEDCE

ETHNRFCSDACREAAPVHA"

CDS 6300338..6300985

/locus_tag="EFAGFIKM_05546"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLIVKREEERTTREQILFMLKQQGTLTAREMTADLGLTGMAIRR

HLTALEQDGWIEVREARATAGRPSSVYQLTVRGDSFFPKSYSSLTLELLEELSDSAGS

GVVDALFESRRDKLLRSGLPQMEGQDLAGRVEELARIQNANGYMADASRDADGTYVIT

EMNCPIVQVASVYKQACRCELELFRSLLQAEVERTECYADGGKRCKYEIREASGN"

CDS 6301148..6301465

/locus_tag="EFAGFIKM_05547"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MHEPEPALKKAMNLLKELSEDEEFRQQYEARQKFLRDQVSMMEG

AREEGLKKGMEEGIQKGIEGEAESKRKIAMNMLNLGLDQETIVKATGLTSAEVKAIQ

QEK"

CDS 6301786..6302835

/locus_tag="EFAGFIKM_05548"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKKFWMSLMMVASMIVAAGCGNNSGTGSESESGTTGGGSEE
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ISGDSKNDLVLG IATPSALALAQQVKDKPLLFAAVTDPLGAKLVTDMDKPSGNVTGAS
DTNPEAIVQLADFIAKNLPDVKT VGLVINEGEPNAVVMADNAEKALATHNIKLVKAPV
TNTSEVKQATDSL VGKVD AFYITLDNSVVS AVDTIIQTANSNKIPFFSSDRDTVEKGA
FATVGFKYYDHGYQVGEMAADILKNGTKPGDMKVTVPDKLDLILNLKAAEAQGITVTD
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CDS 6302969..6303889

/locus_tag="EFAGFIKM_05549"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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INMRILGAPNKSIMGMDNPFSGEHVMVLIIVVLVFKIMLDLFMKTDVGLALRATGDN
KRMIRSF GANTDVT TIVGV SLSNGLVALSGAFIAQQSGFADITMGIGMIVIGLASVII
GEAILGARTVFWATLAAIVGSIYRIVVALALQVEWFDTSDLKLITAVIVIIALVFPT
MQRSMKQRSLARKRTEELMRSGGHQAKGGM"

CDS 6303892..6304686

/gene="nrtD_2"

/locus_tag="EFAGFIKM_05550"

/EC_number="7.3.2.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P38046"

/codon_start=1

/transl_table=11

/product="Nitrate import ATP-binding protein NrtD"

/db_xref="COG:COG1116"

/translation="MLEITQVTKLFNPGTTDEKTALVGVNLTMPGDFVTVIGSNGAG

KSTLMNIISGVMKPDMDGLINDRSIKNLPEHKRSSWIGRVFQDPMAGTAPHMSIEEN

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MATFTQPQILLLDEHTAALDPSRAELITELTETLVREMLTTLMVTHNMEQAIRLGNR

LIMMDKGRILVDSEERKRTLTPPELLGEFERISGKKMADDRVVLG"

CDS 6304879..6306057

/locus_tag="EFAGFIKM_05551"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSLQLDEGTYTVTRRTESIRLLAKEFALLHFLYENKEKAFTRSQ

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LITKEIPFEERLYWLLIFVHPLIEPADSIQLYEKALNSAALSADQLRELRLNIVEV

YVEVGQYQRAKEQLEETYRVIDTDELKNFRLPVALAALYVELWGGSGEAVEAQMAYLR

SGLKDAPYLREIGRFQVMEGLWLLRQGRIREAELRMDDGLDVLKMSLNAPLYLNAAYQ

ILLFLGHHRIEGRIRSKYRQVYVEIGKSYGVPAYGQQIVDEIRNFLSPTSPSSDLPLI

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CDS 6306127..6307473

/locus_tag="EFAGFIKM_05552"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTVISNEPTSNESTESPASSAESSKSLTNLRFVRMFIAYSLAT

FGDWFDALAIQVMVAYRWGADPLIILIPVCMVPGILLGSFAGALADRLHKVKIMIL

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DGSAASEQDGSESLFSQWKQGWRFIKSSRTVLSTILFGCFGLMAILMIDYQFTTLFRE

IKPGNESLLGWLGSAGAGAVTILLNRLPRIGYGWGLGGGYLFVGAGIAALGWIGP

QTPEIWVWIWGLCIGLGNGLFMVTLNLYLLQKETPPAYVGRVFGIQNSLSSVVLVAPL
AGGALIRVAGPSPTFQYIGLATLVIGLAGILLQRILWERKQPLITEAKENIPQESA"

CDS complement(6307594..6308175)

/locus_tag="EFAGFIKM_05553"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPNNNVFNPLSQPVYTSNTNTYTSPGIVAPPENNAGSTGNLYNA

GSTNSTTLGLLGGTVIATVQLANPAGSGKTLVSRLSGGITVSLNLLSSFSGSMSLTA

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VVPPGQAINLSVSGSLSVGGLMASTAYFAWWEV"

CDS complement(6308209..6308751)

/locus_tag="EFAGFIKM_05554"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDEITNYNIFNQSNGLFTQLTNTFSAPGIEASPDSGAAAAGSF

FALTTNNTAIPASQNLLLQILNGAGSGRTLRISSLTGGTTAAATLVIYSGGTVTAGST

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CDS 6308942..6309439

/locus_tag="EFAGFIKM_05555"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSRTAKRSKKRTKQPTKYDSRRRSRHSCRAKLLKPPCSRITRPR

FKQGASSRTKLPGAIHCFTEHTYVGAETSSSIHSLPAQDTSSLSMYTYGVVNRGKHPA

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AQRMP"

CDS 6309485..6310867

/locus_tag="EFAGFIKM_05556"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPNFTTFNTNPDNLRTLIFGQDSTGTAQPVRTDTSGNVVGIILD

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TAGTLTNLLNGTITSVLGATITAGTITSVLGATVTAGTLTNLLNGTITSVLGATITAG

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GATITAGTLSSVTSISQKSFQESQLISTPTANTFTALPAVTTSVFGTYSFFVYNRGP

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CDS 6310947..6313229

/locus_tag="EFAGFIKM_05557"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQNRLLGIHMIVQNEEHHLPRCLDSLKHISTECFITDTGSSDRT

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LLYRHGYTMVAANILIQCMTSEELDAEGLFWLGETLVAKGYHDQALSLFEQALERE
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CDS 6313186..6315156

/locus_tag="EFAGFIKM_05558"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRAERISLCMIVKDEEELLPHCLASVQGAVDEIIVVDTGSSDRS
PEIAQQYGAVVVRFEWCEDFAAARNAGLERASGDWILFLDADEALDRAAREQIRSWTS
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AFHVTDMVIHHYGYQTAIVERKDKVNRNVRLQQAVEEEDQPFHHYNLGVYLRVGE
AERALETFGVARMGIDPAVTSYAHLLFKYEVRCQLHLNRWQEALDRIDAALELFP
EYT
DLMHHRGVCADALGDADRAEYSLREAVRMGPPPIYHTEEGIGTYQTYTLGRLL
EGR
ADLEGAVDAYVEAVRAKSSLLPPLYRIFRIMRVSGQEHQIPALVRERFALSSEE
ATHK
VLGILEQSRCYEALQLLSVISSQPSAEMRERLSVAEAMLIKQQGRWNKARLKLE
PVQ
RKKGLLAISSARWLERLEWIEGKEVNGDDPLALWLKRSSQLGAVTNEESAVQ
TGRTVG
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QQLAGE
GLSVGESVRVKEKEKEMEGKKENGKVSDIESFPGASDTLTGTSWLVKGLVSA
ADHHL
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CDS 6315239..6317293

/locus_tag="EFAGFIKM_05559"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNMGIGISLCMIVKDEAGSLQRCLNAVRNVVDEIIVVDTGS
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KTELMR
LLAASRDDVWGYWIQVTSLLGVSGEEHVTDVAVCRLFRNDPRIAFQGRIHEE
IASSIMA
LAPQGVVHSGLEVIHYGYLEQVITAKNKGARNMQLIRFALNQEGDQPELLY
ALAAEW
F
QQAKYDEALRLLQPLLAQLTPEGYHSDLVLKTAYAWREIGSPERALAVVEAW
APVYE

DFPDLLELGAVLELDQGREVALNWLKQAKSAASTASRYTSVSGAGTYRSLTLEGMAH
ERAGRWAEAEAAAYTAALGMQPGSLPAWQRLLLAAATGRQHAIASVTARVSLPPAAWQ
ALIPAALAAHRPDWLLRHAAALVGPLRAQPLAAGLALAQLGEDAAARAALQPWAAHAP
HGREAAALALWALGHKQPGRRNARAAARHAAALPAAAHAAEALLQRGALEGSSTLACSS
GLAGNPPRGATPSGPAAPAPGGVLAAAQALAGVGAWAAWLRLLQALPPSGALALLAAL
PPAARCGLLRAPASVREGLLALCGTPDGAQQPHADEVPAERTAHAVLAGTLALLAGR
QNLAREWAESAQVTARQSAATGRPATTIPPGLQTLLRLTAPGAASADEYTNQCNMLLV
HL"

CDS complement(6317544..6318215)

/locus_tag="EFAGFIKM_05560"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMDTPKATEFMESRYIRQSDPKDTLVFPLHPAWWSRPYEYEW

RRFARPDDVVLDAACGISHPFKFWLAEHCREVHACDWDERILSEEAIRLDIVSDFSEQ

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KPNGQLIATFDVPEMRPDLLLETIMAVTGLTIEDKLNVEEPDDAIWSDMYGTPIRCFA

VICKG"

CDS complement(6318212..6319753)

/gene="mshA_4"

/locus_tag="EFAGFIKM_05561"

/EC_number="2.4.1.250"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01695"

/codon_start=1

/transl_table=11

/product="D-inositol-3-phosphate glycosyltransferase"

/translation="MGVVSILTHSFTDGYNREFGRVFGGGLERYILDLCVIRGLGHI

PEVHQLSYFEAFQTRTEQIDVFGYSYDMDNVPEAFDRMAAAAARGPVIYASCLWQPITY

KPGSLGICHGINWDRPGLPLETKQQVAEHIQLALDGLVRIVSVDSHFQTCRAACTYT

DPRQVVLIPNAVDTSYFTPAPPTRTFEQEQEDELVAWKNDLASHEENVGAVISGVQA

VEGKDGTSAGAGANSKANRDGGGDTSDQEPEGKETVDFHLQLSKLEEVEADGETYRF
AHNHRNSTDWATEILVEADAQVNGPIQGGQVEKKTVDARITSPRPIRIIYPRRISME
RGIIPMMLAADKLLGAFPDLEIEFAGELVEGSTVGRVFRYWHRTHPHAERINQRTYDF
RDIREAYHQADIAVIPTVFSEGTSYACLEAMSCGLPVIASNVGGLNDLIQDGFNGLLV
PPGEQELTAALVRLVQDRAERERLGIYARETALSVDLARWRSRWSTVLESFLAETGLK
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CDS complement(6319755..6320747)

/locus_tag="EFAGFIKM_05562"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLDPKKRRQQLNGPMVHRDIRTETTYTPTETVDRTHTDALGNGD

RTPDHAQPTQDIRSQVHHWGDSQGQAEQNAAITQEETSVFKEPLSIRRVKSKGNKLT

AMLQVRNERGRYLEEVLHDLSEFVDEIVVDDASTDGTDPICKAYPKVVRLEVLEKPL

FAEEWRLRNTLWQAAAGTCPDWLLSVDADLYSSEAKKAIRTLINQEYADWFAFRFYD

MWGGRTHYREDDLWSLHKRHTASLVRYMPGYFYFYPQQNHHVPRPLSCTVLPGVSTE

LKVQHHLGWAGSLEDVRKYLRYSKRIDPGGEWGNLAHYESILDPEPRLIPWKEGP"

CDS complement(6320747..6322039)

/locus_tag="EFAGFIKM_05563"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEKPAPLPGEDTEASLDKASTRQPPVRYVLFPRKGGWSSFYPYD

IAALLSIEGEVYYYVSSLTQTEDVPSVITVISLPEAEQLLLEPRTVAVVAHPYWLMAAA

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LGGEDPAPAGTMQKDDLEVALRDYELLFLHALRQILSGTPDSVTLLQCSVRADFYRQL

RAKAGAHETISFLAAYEYLLEDPRVHSLQEAFTHAVMNGRSDCVTSHYRFLSAIHA

RAGQLEDALRVYGISAADQERHHYELCRWLEAGEDQLVRAELLRMNDDYGNALRIL

DELGGETARHWKFRIYQETGRVEEALALVHAVDIQDDASRRDYQQLSGSALALRGERH

GAVRHFLETALEDEDALARIVELELLDHAVQQLLGEVP"

CDS 6322512..6322772

/locus_tag="EFAGFIKM_05564"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTERELMRTILDSLQGKMMIWVTDHLIGAEQMDELIFMENGKIA
MQGSHEQLLAGEERYCRLIELDRPGWTGRQQEQPLPPVASR"

CDS complement(6322880..6323869)

/gene="tagO_1"

/locus_tag="EFAGFIKM_05565"

/EC_number="2.7.8.33"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34753"

/codon_start=1

/transl_table=11

/product="putative undecaprenyl-phosphate

N-acetylglucosaminyl 1-phosphate transferase"

/db_xref="COG:COG0472"

/translation="MVDGSETSEFMVYILAFIVSFAVVLLIPPLGRLAHRDFVDKP
REDVERKLHRQPIPLTASYAIFTGFFLTYYALTKEITWETAALVAGGMMLLTIGTVDD
WYKTKGKDFPALPKMLVQVSAAVLVFASGIAFTGFVNPFNAEYVMLPIWLQFILTILW
IFGVTTVINFSMDGLAGGLSAISAITLFIVALAKGQTDSALMSIILVGVGTIGYLYK
NKAPAKVFMGDAGATFLGFILAVIALDGAFKQATMLSIFIPILALGVPIFDNIFVVIK
RFIQGKAIYQADASQAHYRLLRAGLNHKQVVAVLYLVSTCLCLSSIILMLVEM"

CDS complement(6323958..6324773)

/locus_tag="EFAGFIKM_05566"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDKKAACKILLSTFWGGGGWKTTSLPFSGEEFEYAKSKGVMFDPL

TITHDEIVQRLYDMHQDDSFKERVISAFLHSLSTKKVYLR
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ERPSLHPNTSACGDCNFLRLQSDKEYSNVDLNV
LNFERIKWGGVRHGWLIYCLMDLEL
LLQDKDANYEVTPEQAILVNLLEAAQTEDPKDSARS
LEKKWKDLFPSSKQERDALLE
IWAAAGILAPGDKPRKRKGGSSDFVFAATWQGD
DGYHAEAVKH YFGSYLPQIQ"

CDS complement(6325002..6325319)

/locus_tag="EFAGFIKM_05567"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MASELKLTTVCNALGDIPIRMKIAHCLAS
SGEKNCSAFEVDHISK

STLSHHIKILREAGVIQPRIEGKQHFYSLRKEELDVR
FPGLVNMILNTTAEYVTQAPD

KLN"

CDS 6325504..6325893

/locus_tag="EFAGFIKM_05568"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTVNTTLLNNYFRLFDASRADERAMQD
LLSLFTPDAEIVLNG

TSRSGFDGFMKAFYEYNKDVKHMWDWVQQPDGSYQTN
WAVCGQAADGTVYAKAGIDI

ARVNDAGQIVYLENVQADQNAFSKYNQ"

CDS 6325944..6326075

/locus_tag="EFAGFIKM_05569"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTEEMLNSVEFLTEFSPENQELEKRFF
FYFRTVAVAAPGYFNRT"

CDS complement(6326471..6328021)

/gene="xylB_3"

/locus_tag="EFAGFIKM_05570"

/EC_number="2.7.1.17"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P35850"
/codon_start=1
/transl_table=11
/product="Xylulose kinase"
/db_xref="COG:COG1070"
/translation="MASSPYMIGVDIGTTSTKAVLFEQNGTIVAQGSADYPLHTPTPA
IAEQDAEDIFKAVIESVKQATSKAGVKPEDILFVSFSSAMHSILPVDQHGTPLMRAMT
WADNRSAEWTEVLKSEMNGHEIYLRTGTPIHPMSPLTKIMWLTRDQPELFRQTHKFIS
MKEYVFYKLFSEYVIDHSMASATGLMNLEKLDWDAEALHVAGITPEHLSRLVPTTHVL
KHGLHPEYAKEMGIAVTPFVIGASDGVLSNLGVNAIDPGVVAVTIGTSGAIRTVVDK
PVTDPKGRFFCYALTEDAWVIGGPVNNGGVIFRWIRDEFAASEVETAKRLGIDPYEVL
TRVAENVPPGSEGLLFHPYMTGERAPLWNPARGSFGLTLHHKKEHMIRAALEGVLF
NLYTVMLAIEEKIGRPKKIQATGGFARSELWRQMMADIFDQDVIIPESIESSCLGAAV
LGLYALGRIDSLSAVSGMIGSTHRHQPDPSVRVYRELLPIFIRISRKFEEDYADIAA
FQNKTMQG"

CDS complement(6328287..6329114)

/gene="araQ_34"
/locus_tag="EFAGFIKM_05571"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94530"
/codon_start=1
/transl_table=11
/product="L-arabinose transport system permease protein
AraQ"
/db_xref="COG:COG0395"
/translation="MATKHLKSLVLYTGLIGGMLISMFPFYWLIVMSTRTTSDIYKFP
PQLWFGGELWNNITRVLQQIDFWGAFLNTLFVSGLVTLVLFDSLAFAGFAKFEFPG
KKWLFILLATMMVPSQLSLVPSFVLMATFGWVGSFKALIIPGMVNAFGIFWIRQYAT
ESIPNDLLDAGRIDGCNFFRLYWNVALPILRPAFAFLGAFTFIGVWWDYLVPLIVLTD
ERKYTLQIALSQLNGLYNTDYAMVIAGTLLAVIPLIIMFLFISRQFISDIAAGAVKD"

CDS complement(6329135..6330085)

/gene="lacF_14"

/locus_tag="EFAGFIKM_05572"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29823"

/codon_start=1

/transl_table=11

/product="Lactose transport system permease protein LacF"

/translation="MAVTEPRLTPDPGNARPDLDQRKSLWARMWEHRALYVAISPFYI
LFAVFGLFPIGFSLYLAFHKWDGIGVMTYNGFNFKYMLTDAEFWQAVGNTFMIWIYS
TIPMLFFALIIAFLHAPFVKFRTLFRVGYFLPNVTSIVAVAIIFGALFANNYGFLNY
LLQSVGLPVVEWLNAPWGKVAISSMVVWRWTGYNAVIYLAGLQSIPQTLYEAAKIDG
ASAIQSFFRITIPMLRPVILFTVITSTIGGMQLFTEPQVLVGNDGGAGAAGMTIVLYL
YRESFINNYFGYGAAVGWGMFLIILFSIVNWKLQVQKSS"

CDS complement(6330130..6331404)

/gene="lacE_2"

/locus_tag="EFAGFIKM_05573"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P29822"

/codon_start=1

/transl_table=11

/product="Lactose-binding protein"

/translation="MIRRKRTCWTAILMVCVLLISGCSIWPGQDDSAANNKKVALTLWY
WNRSIDDKLIARAKEKFPNIELTAQKIGGDFKAKLKTTLAARSGEPDIALNDWIMEL
FPSEDRFYNLVDLGAGDIEDQYLPWKWKQGVTPSGQMIGFPMDTGPTALFYREDLFKE
AGLPSDPEDVTRQINSWDAYAAAGEKLKEKFGGKVFLTDNIATVYNQVISQSAERYFR
PDGSFIGMDSPIVGKSWDTAVAFKEKGLLANADGWTPSWNAAMNNGEIASFVGAVWMK
QVLQEAAPDTSGKWRVARAPEGDGNNNGSFLSILKSSEHPQEAFELVRWLQSPENQLE
QYQTLNLFPSAPGVFDDPAMKEEPPFFGGQATGPVFAESAQEVDAFFGERYPSVHNI
ITRRLNDVAKQNADPQQVWTDTVHRVERELQR"

CDS 6331728..6332495

/gene="ribBA_2"

/locus_tag="EFAGFIKM_05574"
/EC_number="3.5.4.25"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01283"
/codon_start=1
/transl_table=11
/product="Riboflavin biosynthesis protein RibBA"
/translation="MINSHIIQLLAPKIQTFPSGKEFIYLVGPIKLPVNLDGETKTFQ
WYSWMKSDKAMESGKLIESLAEELAERQQSSVLVYGDFAEAEALIRMHSICHTGDI
FGSKRDCGFGLEQSMKMIAAHGAGALFYLANHEGRGIGLFSKAMAYILQEEGLDITVD
ANLQLGFTDDARNYDDAIAVLRALRSAPVTITNNPRKLAALQEAGLNVGGRVPLWGD
RSAFNEKYLQTKVNRSGHLAESDGWAGAETLLPHAQA"

CDS 6332689..6333258

/gene="glpP"
/locus_tag="EFAGFIKM_05575"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P30300"
/codon_start=1
/transl_table=11
/product="Glycerol uptake operon antiterminator regulatory
protein"
/db_xref="COG:COG1954"
/translation="MPFEGQRILPAAKSMKQFEAMIEGPYTYGVMLETHIAQLQSVMD
EARRYDKKILLHADLVQGLKNDEYAAEYLCQHIRPAGLISTRASVIQKAKQKGITAIQ
RIFLLDTHALEKSYLLLAKTQPDYIEVLPGVIPHIIAEVSVRTGIPIIAGGLIRSPPE
VELALGVGATAVTTSNVDLIRHFEKSLTP"

CDS 6333287..6334774

/gene="glpK"
/locus_tag="EFAGFIKM_05576"
/EC_number="2.7.1.30"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P18157"

/codon_start=1
/transl_table=11
/product="Glycerol kinase"
/db_xref="COG:COG0554"
/translation="MEKYILALDQGTSSRAILFNRGGEIVHIAQQEFPQYFPKPGWV
EQNANEIWSSILAVMASCLAESGIKPVQIAGIGITNQRETVVVWVKETGRPIYNAVWV
QSRQTADICEELKTQGLGDLFRRKTGLLIDPYFSGTKVKWILDHVPGARERAKEGELL
FGTIDSWLIWKLSGGTHVTDISNASRTLIYNIYDLQWDELDDILDIPKTMLEVRGS
SEVYAHTTDYHFFGHRIPiAGAAGDQQAAMFGQGCGCYTKGSMKNTYGTGCFMLMNTGEN
PVQSNHGLITTIWGMNGKVEYALEGSIFVAGSAVQWLRDGLRMLRSSKDSSEYASRV
PSTDGVYMPVAFVGLGSPYWDSEVKGAVFGLTRGTTKEHFIRATLEALAYQTKDVLGA
MESDSGIPVHALRVDGGAAANDFLMQFQSDILGIPVERPTVNETTALGAAYLAGLAVG
YWTSADELTDHENTERVFQPVMAEQQRTELYTGWKRAVNAAMAFK"

CDS 6335176..6336834

/gene="glpD"
/locus_tag="EFAGFIKM_05577"
/EC_number="1.1.5.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P18158"
/codon_start=1
/transl_table=11
/product="Aerobic glycerol-3-phosphate dehydrogenase"
/db_xref="COG:COG0578"
/translation="MTETFSSAHRTEYLQSMANAHFDVLIIGGGITGAGIALDAASRG
LKTALVEMQDFAAGTSSRSTKL VHGLRYLKQYEVKMVAEVGRERAVVYENGPHVTP
EPMLLPiYTAGTFGRFSTSIGLMVYDRLAGVKRSERRQMLNAGAVSDREPLLRKQGLL
GGGLYVEYRTDDARLTIEVMKEAVKGAQAVNYVKAKGFLKENGKITGIEAVDQIDGQ
AYMLKASKVINASGPWVDGLRELDGSRQGKTLQMTKGIHLVFDGERFPLRQAVYFDTF
DGRMVFAVPRDGKTYVGTTDTVYQDDPAHPQISDSRDYVIDAVNGMFPDVHIGTGDV
ESGWAGVRPLIHEEGKNPSEISRKDEVWVSESNLITIAGGKLTGYRKMAEMVVDLVAR
QMEQESGHSIGPCVTMMPISGGDVGGSAGFISYAEHKIKDGVALGLARPAALRVRT
YGSNVEALYERMPDPRTKSELHGMPQELLMLRYAIDEEMAVTPSDFLVRRTGDLFFR

IDEVRRYKAAVISY MAGCLNWSEEEVVKHTQELDQLLLEASGKI"

CDS 6336903..6337907

/gene="ligC"

/locus_tag="EFAGFIKM_05578"

/EC_number="1.1.1.312"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9KWL3"

/codon_start=1

/transl_table=11

/product="4-carboxy-2-hydroxymuconate-6-semialdehyde
dehydrogenase"

/translation="MTLQIGIIGTGWFSKVHADILARMEGVRVASVCGTSLEKAEAMA
SVYDAVGYGEEHMLEGEKLDVYICVPPMSHGSIESELIRRGIPFLVEKPLSTGMDV
PRQVLDQLQKSGLLTSVGYHFRYQEAQVLQQSMKEQTVGMALGRWMGGMPGVAWWRR
QDGGSGGQFVEQTTHIVDLLRYCAGEVTEVYAVAAQRSMHEKHEHVTVADVANTLKE
SGAIASIANTCLLPDGEAGLQFYTDAGVWDWTPERLLLPSAAKHAMAGLEIPAGHN
PYERENEAFIHALRTGDRSRLSDYADACRTQEITTAALASADSGLPVQLQPSKHLSH
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CDS complement(6338012..6338347)

/gene="yybR_4"

/locus_tag="EFAGFIKM_05579"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37486"

/codon_start=1

/transl_table=11

/product="putative HTH-type transcriptional regulator

YybR"

/db_xref="COG:COG1733"

/translation="MKLKKVKSPSPCMITQAIDIIGKKWVLLIMYQLLSGPKRFTELE
AEMAISGRLLSERLKEMETEGIVTRHMFPEIPRVEYELTPKGRAIEPVIDQIYSWSS
DWLKQKQKSE"

CDS 6338736..6339116

/locus_tag="EFAGFIKM_05580"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKILGYVFLVVLAVGVFVMTGFNKGADMMIQTFFESFSYPTWT

MYLLGAAELLSAVGLLIPRTRILASGILTFILIGAVGSHLIYAQYAAVPPPAVLLVAN

IIVLVVGMRRLEAEEEGQMDAIQA"

CDS complement(6339242..6340081)

/locus_tag="EFAGFIKM_05581"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNAKPDLFIPEDIFLRKGARKATEIPEHIRNWLQAGHIESVNLT

EWLAVDHSVSLFQKVTHEWGLDAETRAITEQLTQMDEQRIMKIIPAIALQWLNLLNRLT

MNEQTNLFRSIAEHRSDSVRCWAAYIIGLD SGLNLTEKLEHIRPFAADHHFGVREIAW

MAVRESISAE LSSALQH LIPWSVDPDPLIRRF AIESIRPRGVWAKHIQELKENPAMAL

PLLDVAKSDAHKYVQDSVSNWLNDASKTNPEWVRQVCATWTQQSDTQHTQRIVTRATR

SLT"

CDS complement(6340159..6340854)

/locus_tag="EFAGFIKM_05582"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDKILYLSQFDLMSSLSEADLIEMDGMT CITTIPKNRQIQTPDT

FTEGFYFVKRGKVRLYTLNPEGKQFTLDILTEGNVFGEMNGISLGTRAVCIETMEECD

ICLMNKQRFEQFLIEHPEFMMRLMNVLSERIKRMSELTQTLALGNLHEKVIHNLFRLA

EQMGWIEEDEYCRIQLGLTHQEIAWMAGATRESVTIVMQELARAGRIRTGFKSVSLHR

DEIANLRKITAHL"

CDS complement(6340982..6341500)

/locus_tag="EFAGFIKM_05583"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKRTGMKRSLDRLGRIVLPKEMRDTMEIHIGDPLEFFIEGKELI
LRKYKSTLCIFCGDVDTEMYFKEQFICRTCAIQLKHPDDSPNWFVPQNKQAPAPVERP
ASKSAPVSSPAREEGTTADNQEYPDLRPKTARMLQQMKEIVEQNPGLAQQQIAEKLGI
SQGRVSQLKKLL"

CDS complement(6341607..6342287)

/gene="cidB_2"
/locus_tag="EFAGFIKM_05584"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P60639"
/codon_start=1
/transl_table=11
/product="Holin-like protein CidB"
/db_xref="COG:COG1346"
/translation="MIGFLCLLLTVGIYAVAKRMYRNLPKVYLSPLLITPLLVGILL
ATGTDYATYSSGGKWLSLLLQPATVAFAVPLYTFFHVLKKHISEIVFSVMTGSVVAVL
SSALLAKWLRLDGLIHSLIPRSITTPIAMNVSATIGGIPAVTAVFVIMTGLLGVIMG
PSIVKMLRIDGEIARGTLFGTGAHGTGTSKAFELSSLTGTISSISMVLAALFTLAVAP
VLSKLIFP"

CDS complement(6342284..6342655)

/gene="cidA"
/locus_tag="EFAGFIKM_05585"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P60647"
/codon_start=1
/transl_table=11
/product="Holin-like protein CidA"
/db_xref="COG:COG1380"

/translation="MKKWGLGIAQVALLMVFSLLMDLLARTLHLPVPGSILGMVVLFI
LLQTRVVKLRWIEVGAAWLLGELLFFIPSAVGIMNYMPMLEHDGLQILFIVLLSTFL
VMSC TGLVATRIAKRKERHTG"

CDS 6342819..6343703

/gene="cynR_1"

/locus_tag="EFAGFIKM_05586"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P27111"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator CynR"

/translation="MDIRHLQYFLEVARQQSFTKAAEVLYITQPTISKTVKSLEEELG
ITLLDRYGKKVELTDAGHVFFRQALEIEKSFRSLSSELDDLMNLKKGHLRIGLPPMVG
SSFFPMIIGEFHKAYPQVTIQLFEDGAKKVEADVISGALDIGVAVLPTVDELDDHFVF
VKEKLNLLVHPSHPLAGKESVALHELENDAFVLFREDFALHDRIIVACQHAGFQPRVV
YESSQWDLLSAMVAANLGVALLPETICREVDHMRVRIIPVVEPVIPWQLGMIWRKDRY
LSFATREWIGFTQSMLGE"

CDS 6343815..6344672

/gene="nit1"

/locus_tag="EFAGFIKM_05587"

/EC_number="3.5.1.128"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0DP66"

/codon_start=1

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/product="Deaminated glutathione amidase"

/translation="MKLRVSAVQYQLHTISSFEQFAAQAEHYIRTASEYGTEFVLFP
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NTAHMFYPDGRIGRIARQDKIHITPTEVQEWNMAPGEGLEVFDTDKGRIAMLTCDIEFPE
IVRMAKAKGADVIFCPSTDDRHHGFYRVRYTSHARAVENQVYVVLGTGTVGNLPTVDFM
RANYGQAIIPTNDIPFPPRGILAEGEINNDMIVTADLDLDLLEVRSGSVTTWRDR
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CDS 6344746..6345420

/locus_tag="EFAGFIKM_05588"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYTKEMLITDPERNGKRVKAVVRNYVTADFEELIRIQAESFPPP

YPEELLWSHEQLTSHVQHYPEGAICIEVDGELAGSMTSLRMQWDPAHPASHTWAEVTD

DGYIRNHQPDGNTLYIVDL CVRPKYRKWGLAQLMMQAMYHLVIAQGMDRLLGAGRMPG

YHLVADQLSAQEYLDQVAAGERRDPVISFLLRCGRMPVGVGTADYLDDEESCNYAALME

WQNPFK"

CDS 6345467..6346138

/locus_tag="EFAGFIKM_05589"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEFTRITSIKDPLFAQMHKLMQEIPREEVLDFPLWEEPLEDPG

IRVFVAVHEGQVVGATEYRYEDWNVAMTDFTIIGREGLGIGSFLANHRKRD LQKLAA

ANGKELFGMFAEIYNPYLSQDHEFGGIKPMDPYVRREVL SHLGYQRLDFPYVHPSWQG

DGEAVGGLDLCFMPGDESLGELPASLVADFLNRYAVLPNKPQEWLAMVEQLTARKSV

ALLPL"

CDS complement(6346705..6348687)

/gene="mdoB"

/locus_tag="EFAGFIKM_05590"

/EC_number="2.7.8.20"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01070"

/codon_start=1

/transl_table=11

/product="Phosphoglycerol transferase I"

/translation="MSRSSLTRFLSGPFIFFTIIMMIKSSLAWIVIFDDIPVWKPLLT

ELPLIWIGFCLIEWFAAKRRMWIYLAMNLLLSGIFFAAIMYYKYYGVIVNYHALAQVN
QVTSVKSSMFSLLDPYYLFIFADVLIIGGILIRRRRIKLGSTERPNRVPLERRARRRVA
SVILTLSMILCMLNIYPNRASMSSELTQAEQMGILGYEAYTILDRPDKVPPIAHIDQTD
IDQLKQTTELPAIVEQGAASGRNVIMLQLESFQNFLIGLEVDGQEITPNLNQLARQSL
YFPNFYQQVGQGNTSDAEFVVNTSFYTPPNGAATTYADKALPSLPKLMSANGYQTAT
FHTNDVRFWNRDQLYMALGFDQYYDIDYFGTQDSIAFSASDEVLYSKTLDKLESMQSS
GNPFYAHIIISMSAHHPYTLPKNKVKLTLPERYKDTLPGDYLISQHYADEAVGQLIAGL
KERGLWENSLFVLYGDHLGLPIYSLDRDDKVLMKELYGREYTSADMINIPLIISAPGV
TPGVQLEQIGGQVDILPTIAGLTGVSLEDQLHFGQDLLHEGGNLLPERYYLPSGSVLN
DASLFIPAKGYGDGTHYSLADAGRQDAEQQQMNVPSEDTTKISGDEESPAIATPNNSG
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CDS complement(6348859..6349356)

/gene="isdG"

/locus_tag="EFAGFIKM_05591"

/EC_number="1.14.14.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01272"

/codon_start=1

/transl_table=11

/product="Heme oxygenase (staphylobilin-producing)"

/translation="MYIYLVPSPIPDALAAYPHLTLRSEEHVRLAIESAERLMNIESD

DKVAAYEAFDAAGSWTGGGYAVLNNIPVTEDGRNDFEERFKNRARKVEDEPGFVGIRV

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TYTIE"

CDS complement(6349448..6349762)

/locus_tag="EFAGFIKM_05592"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSSELLNRMIGIGGIVAGLLFAILIIFTRLIARKHNGLDERYL

YCITRAKAFSWNATTISLALAWILVVMLDGISLSFFIITAVFVIHCLSSIAANLYYSA

RN"

CDS complement(6349752..6349964)

/locus_tag="EFAGFIKM_05593"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQNLIRDKRIHMHITQEELSQQLKVSQRQTIIISLESGKYKPSLVL

AHKLAQLFGCQIEELFIFEGDENIEF"

CDS 6350179..6352446

/gene="dinG_3"

/locus_tag="EFAGFIKM_05594"

/EC_number="3.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_02206"

/codon_start=1

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/translation="MYRSGSIRPGFRTNASMQEGTRIHQRVQKEYTEEDLKEIVLEAE

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VQHDEPRMQVQLTYVHSVTHEERRFRRMAERQEEQFAAEVIAGYAPYAEMIAAYEEK

RDISVKELPFPFRKYREGQRKLAGAVYKTIREGQGLMAKAPTGIGKTMSVLFPTVKAI

GEGEASRLFYLTARTTTRVAAEEAFARMQSEGLKMHVISLTAKDKICFKEEEACDTGQ

CGMCEGYDRINGAVLDMLEHETLMTRPVIEQYARKHRVCPFEFSLDAAYAADAVID

YNYIFDPRISLKRMLEEQKRKTVLLVDEAHNLVDRGRMMFSAELEKAVFLDVKREFQS

LDSSVPAAKAIVDYTGAIKYLITLRKNGGEEGKIIQQEAPEELIERLEPFVMVAEQC

LVEGGSGNAETDQLLLDAYFTAQNFLRIAKLYDERFITYAECVRSEVRVKLFCLDPSV

LLRQTAKGFRSLIHFSATLSPLRYRDMLGAEEDYTLQIPSPFQREQLDVRLPLSV

RYKDREQSRRPIAEMLRQLVSEWPRSRLMVFFPSYPYMREIYETAEPLSEADTVIQK

QGMNELEREQFLDGFQPNPERTRLVFAVMGGVFSEGVLDLPGDRLNGVVVGAGLPQIG

LENNVLRDYYDRTGRNGFNAYIFPGMNKVLQAGGRLIRTEEDRGVLVLVDDRFIQEP

YRSLLPEEWRDYKRI"

CDS 6352650..6354131

/locus_tag="EFAGFIKM_05595"

/EC_number="3.2.1.98"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P19571"

/codon_start=1

/transl_table=11

/product="Glucan 1,4-alpha-maltohexaosidase"

/translation="MKRNHTMMQFFEWHLAADGDHWKRLAEMAPELKAKGIDSVWVPP
VTKAVSAEDTGYGVYDLYDLGEFDQKGTVRTKYGTKQELVEAIAECQKNGITVYVDMV
MNHKAGADETEVFKVIEVDPNDRTKEISEPFEIEGWTKFTFPGRGDQYSSFKWNSEHF
NGTDFDAKGERTGVFRIAGENKKWNENVDDDEFGNYDYLMFANIDYNHPDVRREMIWVG
KWLIDTLQCGGFRLDAIKHINHEFIKEFAAEMIRKRGQDFYIVGEFWNSNLDACREFL
DTVYQIDLFDVSLHYKLHEASLAGRDFDLSKIFDDTLVQTHPTHAVTFVDNHDSQPH
EALSWIGDWFKPSAYALTLLRRDGYVLFYGDYYGIGGPEPVDGKKEILDILLSARC
NKAYGEQEDYFDHANTIGWVRRGVVEIEGSGCAVVISNGDDGEKRMFIGEHRAGEVWV
DLTKSCEDQITIEEDGWATFHVCGGGVSVWALPEQNEDCADA"

CDS 6354716..6355345

/locus_tag="EFAGFIKM_05596"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSPKRELNRRFFPLVMYLFVIAVCLGACSLGPNQGPAGEPKRTDE
YTLNSERRDLNERVTKRPESFQKDTLDEYTLTAMVDVSYESGVDRITYEILVNEARVP
MVNVIQSFTLDPNMINRIDAGELFHSNVSNTHEISLGPDKPEPLGLSLRSYVLKPKAE
IDSNILQRYADMYIKISYGPNDQRTEDYFHVQAEPRLRTIEYMKSWERD"

CDS complement(6355431..6355709)

/locus_tag="EFAGFIKM_05597"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MEYRIEQGYFLIYSPARSTSSG DIMVVKLLERP FFKDRVEFLINS
KNYECTTHHEYLNF EPTSHHKPEKPGAFS MERSEFNRMWDTMNQYFEK"

CDS complement(6355774..6356517)

/gene="rbn_2"
/locus_tag="EFAGFIKM_05598"
/EC_number="3.1.26.11"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01818"
/codon_start=1
/transl_table=11
/product="Ribonuclease BN"
/translation="MKLTFLGTGDMFSVEQH HNSMLAEFGGTHLVIDFPESNAKALKE
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MRYTTDGERTMSDYYDVVPLPDGGTFELGGVTFETFRTQHVPGMVSNGLLAKPYFYYS
ADSTLDQARVEQVAADVQLIFHECHMHD LVIKSH TSLKDLEQLPAEVRQKT VLMHYHD
EYADADRRDQFNREHDLRMIGTLESFELE"

CDS 6356721..6358163

/gene="uxaC"
/locus_tag="EFAGFIKM_05599"
/EC_number="5.3.1.12"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34808"
/codon_start=1
/transl_table=11
/product="Uronate isomerase"
/db_xref="COG:COG1904"
/translation="MKSFLDEQFLLHNETAIKLYEDYAKDMP IIDYHCHLSPQE IYEN
KTFGNLTEAWLYGDHYKWRLMRANGIEEQYVTGGEGVTDYDRFLAYAKTVPM MIGNPL
YAWSHLELQRYFGVYEV LNETSAPAIWDKVN AKLNSDGF GARDLITKSNVT VVCTTDD
PTDSLEYHLKIQEIEGFD TAVLPSFRPDKGLELNRDTFVEWVGKLSQASGTAISDYES
FLAALES RVEFFHSVGGRVSDHALDYVPYGVATREEAAA IFAKALAGQKV TREEEDKY"

KVTTLTFLGKLYAERGWMQFHINAARNNNTRMFAKLGPDTGYDAVNDTPLSAAMIGL
LDALEQQQALPKTILYSLNPRDNEVLAAIIGSFQGGGIPGKIQLGAAWWFNDTKDGML
AQMKALANVGLLSRFVGMLTDSRSFLSYTRHEYFRRLVCNLIGEWAEQGEAPQDLELL
GQIVQGIAYNNAKEYFPFASVPKTVSASQS"

CDS 6358564..6359106

/locus_tag="EFAGFIKM_05600"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTGIDPVAQKLLYSIMQFNKGKWRQHKPHGRNHNEIMVLGCLLH
GMHPGEQLNWQDNPPDFNDTIESNHHPGMKVSEISALLRVKSPTITPVIRGLEDEGLVK
RTMDPEDRRRAVRITITEAGREIIRAAHQERMEIFNKLVEHLGEQDSTQLAELLTKVYT
FFDTLTSLQKDDSTRGDDKP"

CDS 6359103..6360830

/locus_tag="EFAGFIKM_05601"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WQJ1"

/codon_start=1

/transl_table=11

/product="putative ABC transporter ATP-binding protein"

/db_xref="COG:COG1132"

/translation="MMKLFRMLKPYQIPIIFILVLVLFQSLAELYLPTLMADIVNDGI
IKGDIPYIWQIGGWMLVIAIGGTACSVIASYLSSRTAGGFAKQLRSRVFRHVENFSLQ
EFDKMGTASLITRTTNDITQVQNVLTMMMLRMMIMAPLMCIGGIFMAVSQDAKLSTIFL
VVLPLVGGAIALIGAKGLPLFKTIQKKLDRNLNLVREQLTGIRVVRSFNRGEHEKVRF
NGANTEL RDSSIKVNVLMATIMPVMMMLVMNFSMIAILYFGGMRIDSGNMNIGALIAFI
QYAMQIMFSLIMVSMIFVMIPRASASAERINEVLDMQPDLSNPEQPRGMKSMQGMIEF
DNVTFRYPGAENPALSNISFTARSGETTAIIGGTGSGKSTLLSLIPRFYDVTEGSRV
NGTDVREIWQEDLRAKIGFVPQKAVLFTGTITENIRHGKDDATMDEVVHAARTAQAEN
FITEMKEGYDSLIAQGGNNVSGGQKQRLSIARALVRRPEVYIFDDSFSAIDFKTDAKL
RAALKSETTEAAVLIVAQRVSTVMDADRILVMDEGRIVGSGTHKELLEHNEVYREIVS

SQLTEEEIA"

CDS 6360827..6362704

/locus_tag="EFAGFIKM_05602"

/EC_number="7.6.2.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WQJ3"

/codon_start=1

/transl_table=11

/product="Fatty acid ABC transporter ATP-binding/permease protein"

/db_xref="COG:COG1132"

/translation="MSERTERKSHRPPGGPGPGMGMRPPAEKAKDFKGLRRLIRY
LQPHSSRLLGVLVAAILSTLFSIISPKVMAEGTDILSKGAAILQGVQGAGIDFPALM
KVLYLLGGLYLSAAFMYVQQYLMAGVAQRVVYDMREQISAKVGRPLPKYFDSRTTGE
TLSRATNDVDNISNTLQQSLAQFITSIVTIVGVIIMMLTISPWMTLITLPLSVVV
VMLVASRSQKHFAQQKSLGELNGHVEEMYTGHKVVKAFGREEQSVQQFEKVNEELYE
SGWKAQFISGIIMPLMSFVGNLGYVLICVVGIFVTRGSISIGDILAFQYSRQFTQP
INQIANISNIIQSTIASAERVFELLDEEEVPESKQPVQLQQPKGAVAFQGVNFGYKE
NELLIHNMNIDVKPGQTVAIVGPTGAGKTTLINLLMRFYEIQDGRITIDGADIKDMER
GKLRSFLGMVLQDTWLFNGTIRDNIAYGREGSTEEDVIKAAVAHADHFIRTLPEGYD
TVLNEEASNISQGQKQLLTARAILANPAILILDEATSSVDTRTEVFIQKAMNDLMKD
RTSFVIAHRLSTIRGADLILVMDHGNVIEQGNHDELMASQGFYADLYNSQFAEQQPQA
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CDS complement(6363363..6363956)

/locus_tag="EFAGFIKM_05603"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIPATLEQLEQVRKECRTMVRKRATASAGTTLVPLPGTDVLADV
GMLMQLLPAINNKFGLSQKQLDGMDPETKSMIYGFMVSIGSKVIGRMITKELVVQVLK
RVGVRVATKSVAKFVPFAGQGLAAALSFTAMRYVGNKHVDDCYEVVKRMIEQRELIPG

EPAPSALEEANSDDVKVEVKSSISNNSADDPAKESKDQ"

CDS 6364272..6365168

/gene="bmrU"

/locus_tag="EFAGFIKM_05604"

/EC_number="2.7.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39074"

/codon_start=1

/transl_table=11

/product="Putative lipid kinase BmrU"

/db_xref="COG:COG1597"

/translation="MEFNKALLIHHSKANKRENTVGLVAGVLAPAVHELIVVRTDE

PGEGEKLCRERGEQFDVVFILGGDGTVHECVNGLADLQHPPLIGTLPGGTCNDFARSL

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SYFISTLQTISHTPEFRYQLEADGKEMEAGEAVMIYAANGRFLGTNALPFAPDALQDGE

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CDS complement(6365209..6365799)

/locus_tag="EFAGFIKM_05605"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSPPKPSPRIPRLLETSRIYLRPFITDVDAYFPGLFDAEMRRL

TGTQNSFTRAQVERYVENAAQDDSRMLLIALQENDQIIGDVVLMMDHAKNRSahirv

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KRDVLFYNHQYHDAVQMSMLEDEFQRQHMKDRAGNV"

CDS complement(6365890..6366516)

/locus_tag="EFAGFIKM_05606"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MSKKTNI PRSPGRPKTGVDQASVQSNILMTASRLFMEYGYEPVS
LQQIASLCNVTKASIYYHFSSKADLFTVAITRMMAMGMQQTSLRLDEPGTLQERLVKV
AEAKMQHSHIETETMMREAEKHLDPEQLAQIREAEVRIFEVLATHFQKEMDNGYLRVG
NPMLLAHAFTSLLMLANREDVRNMNGGSIEELAQELVALFLDGAVKRN"

CDS 6366694..6368925

/gene="apeX"
/locus_tag="EFAGFIKM_05607"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q81QL7"
/codon_start=1
/transl_table=11
/product="Apo-petrobactin exporter"
/db_xref="COG:COG2409"

/translation="MQEGSGYGRWVAGKRSKWITLLWIIIAVVLGMVWPAVGDTRETN
NAQDLSESKPSVQAAALAEKEFPGGEGLPALIVWRQAGGLTDEQIENIQALTERLDQD
PVEQQQSVVPLYQLPPQALKGQLSEGDSTLVMPLFFNEGADSEQLKEAIEALEQKTQD
IFGANPFDVAIDDTNTLIARVTGPVGISIDASGLFSSADVSLLIATVVLVLVLLLLLIY
RSPVLAIIPIIIVGFAYMVTSPILGFMADQGWITVDAQSISIMTVLLFGAGTDYCLFM
ISRYRQILYHEPDKKKAIFQAITGSSGAIAMSGFTVVAALLVLLLAEYGAYHRFAVPF
SLSIFIMFIASLTLPALLAIFGRGSFYFPVPRTHEMEVERAKKKGKPAPAPRKIKES
WIGRIVTKPWTVLAILTVLLGGLAAFASTQVKFTYDLLSSFPEDVPSREGFTVIGEQF
SQGELAPVKVIVDAEGKETDLKQRLES LDYISKVGDAQQAENANITAFDVEFNLPY
SMEAMQHIPDLRATAEQALQDAGVTNADSNVWLDGQTAEQYDIEVTGERDAKIIIPV
IGMITLLLLLYLRSVVATAYLIATVVLVSYFSALGLGWIIIIHYGLGADAIQGAIPLYSF
VFLVALGEDYNIFMISSIWQKRKTMPLRQAIREGVGETSSVITSAGLILAGTFAVLAT
LPIQVLVQFGIITAVGVMLDTFLVRPFMVPAITALLGKWAFWPGKYVPIAEKNEEKQN
QSM"

CDS 6369196..6370149

/gene="rihC"
/locus_tag="EFAGFIKM_05608"
/EC_number="3.2.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01432"

/codon_start=1

/transl_table=11

/product="Non-specific ribonucleoside hydrolase RihC"

/translation="MTNQNLNVYFNHDGGVDDLVSFLMLQMDNVHVTGVSVIPADGYL
EPATDASRKIIDRFGTYSVEVSKSNSRGKNPFPAAWRLHSFYVDALPVLNESGKMEAP
LSAVPAHQHLIEKVRNTEGKTLTLLFTGPLTDLARALDEAPDIEEKIDKLWVMGGTFER
GNVEEPEHDGTAEWNVFWDPAAAYRVWQSGIQIDLVALESTNKVPLTPAVRNRWAAER
RFEGVDFLGNCYAGCPPLVYSETNSTYYLWDVLTTASVGREDIVKKKTVNCIVIPDGP
SQGRTEQADGRPVQLVYDTPDPEAFFTYMTDLGKKAAPQRY"

CDS complement(6370301..6372019)

/locus_tag="EFAGFIKM_05609"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNSLFMRIFLFFSCLMLAAGAVLGITMYRSSAQLVEQSMGMQAAQ
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NTYFYVVDGAAADVAEDDFSPYGSAEETHYEGMLQAFEQNEPIRGELTQDEYGATITA
YVPIHGADGKVLGLVGADLDSTAVYELMSRNRMTMIWTALAIVLLSVLLVYGFAHYLT
RPLVKLKKLITQVGKDLTVNVLSRKDEVGQLASEFKHLVTGTRDVMTGIRQSSDSL
LQAAEGVSKHSQATAEASQRIAEHTNHTASGAAEQVARAGEVTVAMEEITRSMQHIAN
SSSMVADVVSQETTNAVQGGANINTAMDSMDKIHQANVQMVASTSQLEQYSGKIESVA
HLMKGIASQTNLLALNASIEAARAGEYGSFVAVASEVRKLAGESEQSSQHVTETIAE
MTRQTALLSEHMSASTSAVQSGLAVVQEAGRSFTSIHTGIETMNKRLHEVSAASEQLS
ASAEVVSASVEDMEHISRESSSSSIQKVSHATGSQLQSMDEMSASAESLRVLSSSELNGL
ISRFKI"

CDS complement(6372294..6373040)

/locus_tag="EFAGFIKM_05610"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11
/product="hypothetical protein"
/translation="MDMTHMNHMQMEHEAGTSYLWIIVGAIVLLFSIAAYIWASRTQG
KILDHMKKKERADIQKQSRSLRLAAHVMIASIIITFGLFFMQGAGKTYNVADLESNAT
IDVTDDKYYGADHTEDPIQYEMTIPTSGPHNPHDIKFGFYTDFPGYNYLVHNLEHGDI
IIYYRENASEDLKEHLKYLAKFREAGAGILAVPNKDIPEGSEVVVTAWTKTMKLDQFD
DAKVGTFINKYINQGPEKIPASVRQGGGTGTM"

CDS complement(6373404..6374318)

/locus_tag="EFAGFIKM_05611"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKCPVCNHENGDAHFCERCGSNLTQTTSSPTPVTNSESAASEPE
YTRWSSTQATSSQASVPPNTPSISIHKEQARESTGTNDHASAGDNSSNQWNNIVQNEK
VQQAKEVSKQYLSYFLSVLARPYQTMKTVGDQHSLNGWLTMALIAVLSSTYFLITFSR
IGMDGLFIGGFLRPLFFTIIILIASIALMYAILKIEKITFRPKTLVAQFGTLLVPAVV
SLVLANLFIIISYSIAISLLAVSYIIIFVALNSVLFQYPLNRTKAAIDSMYSVLIANV
VVFFILYRLLGEIIIIGLIGMMLSPFGRL"

CDS 6374693..6375037

/locus_tag="EFAGFIKM_05612"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MELLDSNESKKKMCQYYNEISKELFGFGTLLRVTIDQNIVTFY
AKHRRSPRSDALEGEAPGLKLEVDFRMSVLYKKKFREKLEQHMGLPIEAILRDYDAST
QWAITNVILEQA"

CDS 6375285..6376358

/locus_tag="EFAGFIKM_05613"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMKKWISGLAAVAMTSVLLAGCGSSTDDATGGSGSGGTAANKLV
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QQGIDEGLFKIDRSKIPNVNDIYDIKAPLGEDYGPAYTVGQLGIAYNPDLVSKEVT
SWSDLWDPAFEGNLTIPNITATAGPMVVDAASRVAGNDTFNEDAAFAELKKLSGNVVK
FYSQTSEFVNMFSQEEIAGGPIMEMYFKDLKAAVPAKFTVTPSEGAYAVMNTINVVK
SKNKELAEFINWQLSQDVQAKSAKAKVDSPVNTKVELTAEAAEGVTYGADVVEKLNK
LDMEFVNQQVKGWTDRWNREIAQ"

CDS 6376457..6377395

/gene="rihB_2"

/locus_tag="EFAGFIKM_05614"

/EC_number="3.2.2.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P33022"

/codon_start=1

/transl_table=11

/product="Pyrimidine-specific ribonucleoside hydrolase

RihB"

/db_xref="COG:COG1957"

/translation="MSEAQNRILDVDTGIDDALAILLAVKSRKLDILGITTVCNV
LQQATENTCKILELAGAPEIPVIAGAAGPLTRKSHYHRVHGQDGLGGALPDPALSKK
AEEGFAPDFIVEQAKLYPGELTIMTAPLTNLALALMKCELPSSLKEVIFMGGVVRG
HGNITPTAEYNTYADPEAARIVLHAGIEKLTQVGLDVTRQTLLNEATIERLTHPALRA
YVAQSTEIYINRYEQMNGVRACALHDPLAVGVALAPELVGRKSYVVDVETASRLCDGQ
MVCDFQNRLGEQPNTLVCETVDAEAFLELFINALNA"

CDS 6377675..6378496

/gene="potB_1"

/locus_tag="EFAGFIKM_05615"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AFK4"

/codon_start=1

/transl_table=11
/product="Spermidine/putrescine transport system permease
protein PotB"
/db_xref="COG:COG1176"
/translation="MKKSVIYWLLLPGFVFLAAFMIIPIVLTIGSTFFQENSFTFEGY
MHFFRDPYFLKILLTTLQVSVTTIVCVVLGFPTAYYISQKAPRRKGILLALAIPL
TSPVVRFSWMIILGRKGLINNTLVGLGIVDKPLDILYTPAAMMIGLTHLFLPLMIIS
LVGVLENIDGDLKAAQSLGASRVTAFRRVVFPLAVPGLVIGAVLVFVGSALTAYTPA
LLGGKQRVIAFLYQNAMTLNDWYLASVVAIMIVITFVVVGVMNKMMAKTLNPKG"

CDS 6378501..6379292

/gene="ydcV_2"
/locus_tag="EFAGFIKM_05616"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AFR9"
/codon_start=1
/transl_table=11
/product="Inner membrane ABC transporter permease protein
YdcV"
/translation="MREKHIGLGLFSLLVFIFLLGPLLIISVTSFEPGTVLKFPPEGF
SFRWYENIFNTGGFLRTFQTSIIISLLGNLLALVLGVPAAYALSRYDFKGKSVLNALF
LSPVLIPGIVLGFTLMKYLVIVYHLPYLGLLIGHTIIMLPFIIRVIASSLSSFDFAV
EEAALSLGAGRVRTFFTIVLPNIRSGIIAAVLIAFLESFNNVDISVFMTGPGVSTLPI
QMLTYVENYFDPTIAAISVLLMVLTGLLMFVIERIMGGFSYFTKR"

CDS 6379311..6380369

/gene="potA_2"
/locus_tag="EFAGFIKM_05617"
/EC_number="7.6.2.11"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P69874"
/codon_start=1
/transl_table=11
/product="Spermidine/putrescine import ATP-binding protein

PotA"

/db_xref="COG:COG3842"

/translation="MALLTLDHVSVAYDKQIILKDFQLELEKGKLLSLLGPSGCGKTT
TLRLIAGFLEASQGKFMFGGKDYTKVPANKRNFQFVFQSYALFPHLSVYDNVAFGLRM
RKVKDKDISSRVMRILEVVNLNGFEKRFPQELSGGQRQRVAIARALVIEPDLFFFDEP
LSNLDANLRLNMRVEIRRIQQELGITTLYVSHDQEECFSSISDQVAIMNKGVVEQLDRP
ETIFKYPATEFVARFIGFHNFIIEFAERRDAGELITLSAGGRTFTATAHPGTARPGARK
GAIRPDDLIVSGDTSADVNNALPGIIKVSTYLGRSYQYVIETELGDFTANQEMETPYL
SGQRVSLIFPQDKLVLE"

CDS 6380546..6382285

/gene="ade_3"

/locus_tag="EFAGFIKM_05618"

/EC_number="3.5.4.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q72EX7"

/codon_start=1

/transl_table=11

/product="Adenine deaminase"

/db_xref="COG:COG1001"

/translation="MRADQLIVNVHVYNSYYKRFEMNNVAVLGGRFLYVGPGGPELIQ
ADEVIDARGRYMIPGLIDIHLHIESTMVTPETFSHGLIGCGVTSIVAEPHEMANVFGL
EGVQEMMAVSRETTVDMFYAIPSSVPATPMETTGGSEIEDMDVLLATGEIICLGEIM
NYVDVIRDPECKTNQILQHIRKNYPDLVIEGHTPKLLGLDLHRLIYAGVDSHHTHQSI
EGLQARIAAGMFIEIQEKSMTPPEVMKYLIQHDAQHFCFVTDDVMPDSLVERGHLDHI
VRKAIQMGMRPEDAIYAATSTPASRMKMTDRGSVAPGKVADYVLLSNLEELSIDQVYK
NGRKAYDDYEPYKQERITGQFPPHFYKSVQLEKLGVTDFAIQLSDPKVSGLGVALAGE
GEYQCRVMMVKDGSTFVEEHIAPVQSSDGELLWEESGYAQIATFERYGVNGNRAHGLI
GGDTIKRGAIATTYSHDNHNLVVGRRNREDMILAANTVISSQGGFCVVEDGKVLSHLE
LPVGGILTEEPLAVVSHQVKELRAAMLSLGYVHYNPIMSISTHSLAVSPALKITDHGL
IDVNAGKVVSLLVI"

CDS complement(6382466..6382897)

/locus_tag="EFAGFIKM_05619"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MWKEYFKGISEEYTFSSPASGDEIAKVESLFHVTLPHHELKEILL
ETNGVRAIYDLGLIWSVDRINNENKHYRDDHFQDYMPFDNLVFFGESGIGDLFAFPV
TGDGICRADVFVWNHENDSRKWVAPSVSKYVEWSLQGKIKI"

CDS complement(6383058..6383321)

/locus_tag="EFAGFIKM_05620"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MFTHEEIQSWENETAfvqkhnkkfIDPRKAKLKDHRKGIKSTHY
NKECKPARKQHYRLYRTKMKRLMYHEKYDLLHNYKRTSGWLTW"

CDS 6383606..6384172

/locus_tag="EFAGFIKM_05621"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MNEINNAKTIFFDVDDTLyDHLQPLRGALQDVLGLPDDFPYAEA
YHRFRYYSDWLSAQEDLSAVPEADAVERMRRRRFELTMEEFGLPLQLGQAEELQAQYL
SRQFEIVPFKGAYELIRRLQAEGHTVGLITNGEGEHQRRKLEALDVLSLVDEHLVFIS
GTTGYAKPDRRLFNYVSKQTGTdarSSy"

CDS complement(6384514..6384765)

/locus_tag="EFAGFIKM_05622"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRIFQFKQESGKEITKFDSNFVMSRITQTNKAAHIGCMHLAEGG"

VIGYHQA VVPQ LLLIVSGEGWVRGETNEYIEVRCGEAVL"

CDS 6385127..6385606

/gene="dps2_2"

/locus_tag="EFAGFIKM_05623"

/EC_number="1.16.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8RPQ2"

/codon_start=1

/transl_table=11

/product="DNA protection during starvation protein 2"

/db_xref="COG:COG0783"

/translation="MSTIQTRNNTFANNATALQDVLNRQIAGWSVLYTKLHNFWYVQ

GPHFFTLHAKFEELYNLATANMDEVAERLLAIGGRP VATMAQQLRLSPIEEAQQQLSA

ERMVESVVADLRTMVEVIRQGIHEAGEAEDNATEDMLIGFTAALDKEVWMLNAFLGK"

CDS 6385734..6386948

/gene="nos"

/locus_tag="EFAGFIKM_05624"

/EC_number="1.14.14.47"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34453"

/codon_start=1

/transl_table=11

/product="Nitric oxide synthase oxygenase"

/db_xref="COG:COG4362"

/translation="MRSDLEQLQEEAEWFIYTCYEELGHSREDVQARLVAVIGEIEVT

GTIVHTTEELEQGCKMAWRNSNRCIGRLFWDKLRIVDARHADTAGTAAEAVLNHIHVA

SNGGKVIPMITILPPDGPNGTPVRLWNHQLIRYAGYETEQQIIGDPASVELTKAAMSL

GWQGAGSPYDVLPLIIQAQGQAP EWYVIPEEEIVEVMIEHPERAEIAELGMRWYG VPM

IADMRLEIGGISYPAAPFNGWYMGTEIGARNLADTFRYNKLPAAAAFGLNTSSETTL

WKDRALVELNVAVLHSFKKAGVSIVDHHTAAAQFAMFEQREEKAGRELTGDWVWLIPP

VSPATTHIFHSSYRNEIVKPNFFRQDQAYTLKDGVASAAEPRSSEQQNAQVENNPQPQ

AGDTPMKCPFAH"

CDS 6387103..6387570

/gene="nudC"

/locus_tag="EFAGFIKM_05625"

/EC_number="3.6.1.22"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00297"

/codon_start=1

/transl_table=11

/product="NADH pyrophosphatase"

/translation="MGYIETLRGMVGNAPVILLRPSILILNKTGEILLVRHLDDTWGV
 PGGFMELGESVEESAMREVREEIGIEIKKLHLYGVFSGKELYTKLRNGHEYNNVIGY
 ICTEYEGELKPDGVEVLEAKFYKPTELPERTDPYLKSKIQENAVHIATLLGEI"

CDS 6387590..6387751

/locus_tag="EFAGFIKM_05626"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVYLASCKANELSASYRTNYCGMINLTFRGVIPASTCLKPMQE
 QQNKEIAPL"

CDS complement(6387880..6389232)

/gene="mdtG_2"

/locus_tag="EFAGFIKM_05627"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01528"

/codon_start=1

/transl_table=11

/product="Multidrug resistance protein MdtG"

/translation="MDIRRNLPLLMTICFLSQMGGMILPLFPLFIEEFGLSGWMMGV
 IFALFYVGKVIGGVPAAIYKKLGGKKALILMLILLAVCMGGFALSSAAVLFGLLRLL
 QGLASTGLTVVRSIIGDGGNVNDRGLYNGYISSSEGGGMVLGPVISGWLALHWPLSV
 PFLLVTCCLMAVVAAMGMKTTAQARANHESGNTLSDHLLLEDHSAVVKQKPLDNSAHS"

VLHMDDTPPLPSTTSDALHTQAADTALFNQAPNSTMSGPTTTLTQRQQLIGYGTVHFL
EMSAYAVFLTYFALYAAHIMHWDPFATSLAFTVSGISTLAAAPFVGYLSDRMGDRLLL
CMLGMFLIGIEVVFLSTSSHLWVYAGMLIGGVGGACYMDSFFAHIGDHIPDESRSV
IGKIVSAAEIGSIVSPLVAALLMEVGSLYSVFVFNLLIAAAIVVQAVMRSRYKTRRV
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CDS 6389488..6390597

/gene="potA_3"

/locus_tag="EFAGFIKM_05628"

/EC_number="7.6.2.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A679"

/codon_start=1

/transl_table=11

/product="Spermidine/putrescine import ATP-binding protein

PotA"

/translation="MSEQQPIIRFEAVTQQYDQDEAVLKAVSFEIERGKFYTLLGPSG
CGKTTILRLIAGFAEPTQGSIFYNGALINRVPAHQRVNTVFQDYALFPHLNVFENVA
FGLRIKKMKTAEIRSKVLEALKFVNLSGYENREIGEMSGGQRQRVAIARAIVNEPEIL
LLDEPLSALDLKLRTQMRYELRELQQRIGITFIFVTHDQEEALAMSDEIFVLNGGVIQ
QSGTPNDIYDEPINRFVADFIGESNIVSGKMKQDFVVEFAGAQHECVDQGLQRDEPVE
IVIRPEDLEITTEDQGKLVNVDSQLFRGVHYEISTYDDAGNEWLVHSTKKAVVGARI
GLYFDPEAVHVMRFNETEEEFDKRLEAYQEAAHAD"

CDS 6390587..6391420

/gene="potB_2"

/locus_tag="EFAGFIKM_05629"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AFK4"

/codon_start=1

/transl_table=11

/product="Spermidine/putrescine transport system permease
protein PotB"

/db_xref="COG:COG1176"

/translation="MQTKASTRNAYLIPYVLWMVLFVVAPVLLVIYYSFFDVEGNFTF
GNYARFFTPVYLQMTLSSFWYAFLITAFSLLISYPTAYMLTRTKHKQLWLLLIILPSW
INLLLKAYAFIGLFGTYGLTNSLLEVVGIGTQQILFTDFSIFVSVYIFIPMILPIF
NALEEMNP SLIYAARDLGASSWLTFRRVIFPLTISGVKSGCQAVFIPALS LFMITRLI
AGNRVITLGT AIEQHFLVTQDWGMGSTIAVFLIAMA IIMFLTGSGKKEVRNGKKRKA
V"

CDS 6391395..6392204

/gene="ydcV_3"
/locus_tag="EFAGFIKM_05630"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AFR9"
/codon_start=1
/transl_table=11
/product="Inner membrane ABC transporter permease protein
YdcV"

/translation="MGRNGKLSNVYLAVVFAILYAPIAYLIFYSFNSGGHMRSFEGFT
LEWYKEVFADTRLLIIVLNTFIIALLSSAISTILGVAGALAIYHVR RKRTKNTLLSLN
NVLIVSPDVIIGASFLILFTMIGIKLGFTSVLLSHIAFSVP IIVIMVLPKLQEMSPTL
MDAARDLGAGSWQILTRVVLPYVKPGIFAGFFMALTYS LDDFAVTF FVTGNGYSTLSV
EIYSRARQGVSL SINALSTLLFLLTVLLVVGYYFINRRATRIPP GGKGLRP"

CDS 6392201..6393274

/gene="potD"
/locus_tag="EFAGFIKM_05631"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0AFK9"
/codon_start=1
/transl_table=11
/product="Spermidine/putrescine-binding periplasmic
protein"
/db_xref="COG:COG0687"

/translation="MKQLVRTFAIVFVA AFALMILASYLNKSQGYSGGNTLTIYNWGD
YIDPDLLKEFEDETGIKVIYQTFDSNEAMLT KIEQGGTTFDVAIPSEYAISKMKEEDL

LVPIDHSKLTNLSNIDPRFLDLSFDEGNKYSIPYFWGTVGVVFNPELVDGLTFDSWND
LWDPRLKNQILLLDGAREVIGMGLNSLGYSLNDTNEDHLQEALKKLSTLTPNVRAIVG
DEIKMLLANEEAAVGLVWSGDASEIMDENDKLDYMPVEEGSNLWFDNMVIPKTASNIE
GAHQFINFMLDPDHAARNAEYVGYSTPNAEALKLLPEDISEDERFYPDEKLTGKLEVY
DNLGKKMLSHYNDLFLEFKMHSK"

CDS complement(6393606..6394106)

/locus_tag="EFAGFIKM_05632"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAKRTILAPVLILLGVYLILNQGGSLGPGTIFATFWPTLFVIPL

GLFFHWLYFSMIGRGGVLLVPGGLLLTVGIVCQIAMLFNNWSTMWPGFILAVAVGLFE

LYWFGGRNKWLLIPINILTVISLLFFAVMSIGTMLSSLSFIQPFVAIVLIMGGAWIMV

GRKKRM"

CDS complement(6394357..6395253)

/locus_tag="EFAGFIKM_05633"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPDEVQLREMKAPTYEEQLEKFKNRKMTIENDVEAITLKRIH

YYRFTAYALTFKQDTSNDYIEGTTFNKVYKHYLFDAALRNHFMKIVEYIEIALRSQIS

YKLAHKYGS LGYANAANFSKIQFHQRFMEDLQKCIQKQHKEVLIAHHRENYQDRYPIW

AAFEVSTISMSSLYKNLKTSDKKSIDREYPSRNISYRELENWFHVLTVFRNRCAHY

SKLFNYRIPVTIRYTRNDELLGLDKAFLFGAIYNAKYLIKDRTIWDSWVTELSSLIEA

YTIVDISLLGFPTNWEHLLRKQ"

CDS complement(6395426..6396427)

/gene="zitB"

/locus_tag="EFAGFIKM_05634"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00552"

/codon_start=1
/transl_table=11
/product="Zinc transporter ZitB"
/translation="MAEQPKSESFMSLVKKGNTSSAVAMAGNAVLAVCKGGAFLFSGS
GAMFASAMHSLADAINQGFVFGSVLSEKKPTRRFPTGFGRVINIFCMIAVIVVTIMA
YETIHEGIHLLQHPVGHTGGLWINIGVLVLNILIDGAILIKAMKEILKEARAPKAAGF
ALVPAAIKNVGRAAPPTRLVIFYEDVVAVLGALLALISVVVIALTNFALLDGIVTTIIG
CLMIAVAFRVGYDNMIGLIGVAAPQDIEDKVSQTILADTHVADIQMMRIIQEGRYYHV
EGLIELTKGLSLADADDIKFRIQEKLMTNPDIAAISIIEDDGVNSWGKKHSDVVK"

CDS complement(6396571..6397167)

/locus_tag="EFAGFIKM_05635"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MPEQRIYELMEELDMLLEEKVQDEENQELLEAYREFEGVTDEQL
DAFEREQGIRLPADFRAFYKRKNGSGYGFHVLPSLEERRESEPFYLLSLEKIQKEQS
TLVENRMDDYFTEEEIRELDPRIKPYLFQKKWITFGMLGGGSLYLMFDFDPTEQGTVG
QIIMYVHDPDFVYYVAGTFTELLEQSNRNLRELEASEAIEY"

CDS complement(6397490..6398260)

/gene="ygiD_2"
/locus_tag="EFAGFIKM_05636"
/EC_number="1.13.11.29"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P24197"
/codon_start=1
/transl_table=11
/product="4,5-DOPA dioxygenase extradiol"
/db_xref="COG:COG3384"
/translation="MMPSLFIAHGAPSLALEENVYTEFLQKLGQELPKPKTIVLFSAH
WESTTQLVSSVPNYETIYDFGGFQPELYQIKYPAQGQAETTAEVERLFAEAGIPVQTD
DVRGLDHGAWVVLRLLYPDADIPVIALSVNRYLTGEQQYQVGQALASLREQDILVIGS"

GGTVHNLRLRNWESDGVDPWASEFDNWLHDKLVSWDTESLFSYDKLAPSAQAAVPTPE

HFVPLLLAMGAGDQNKQASLLFKAYQYGNLSLSCWKFE"

CDS complement(6398260..6398934)

/gene="estB_2"

/locus_tag="EFAGFIKM_05637"

/EC_number="3.1.1.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q53547"

/codon_start=1

/transl_table=11

/product="Carboxylesterase 2"

/db_xref="COG:COG0400"

/translation="MNSPYIHEVRLPSHYNPQRYPVIFALHGMGSDEQDMLRLMEPM

QSDFIIVAIRGPVQGGSGYAYFQIKSIGNPIRELYDASVLGLQQLVVDLSAKY AIDPT

RRYIAGFSQGAIMAMTSLIMGDAIKGIVAMSGYIPQFVKDEYKLQPNSEL SVFISHG

DQDHLFPLQLGEDNANFFRQHTNHVTVYPYNGGHQMTPDLYQQFQHWLR TDANLTED

PKGLNS"

CDS 6399018..6399527

/locus_tag="EFAGFIKM_05638"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKIYHGFIVGSIFFLYDEYKLFIKNLEWFYNKCRCAWFISYSR

GRDQDVKKYRAYFEIFDENKAREFYLGylGFQLDWEHRFEQDMPLYMQISLDSIVIHL

SEHHGDCTPGAALRVETDNLDTFHGALRQKEYKNARPGIEETPWQSREMTVTD PPFGNR

IIFVEASAE"

CDS 6399595..6400134

/locus_tag="EFAGFIKM_05639"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
/translation="MDIGLAIRTIRKQKQITIMQMCEGTGLSKGFISNVENNKTSPI
ATLESIADYLEVPLPYLLLTPEQRMNVVRKNERKETTAGSGQIKVQQLTAKGAMRMSI
VELPPGASTGISKHAGEESHVLVQGKIRAEQCEDVEVLEVGDSTWNAIVPHEVTNIG
EPAVVLIAVSKELGLDHL"

CDS complement(6400427..6401146)

/locus_tag="EFAGFIKM_05640"
/EC_number="1.1.1.325"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q8KES3"
/codon_start=1
/transl_table=11

/product="Sepiapterin reductase"
/translation="MELKNKTAITGAGKGIGRAIAEALAKEGVHLGLIARTASDLQA
LQQSLSQEYGVKVTSAVADISDRTQAEAAVAAIEMELGAVDILINNAGIGKFGTFMEM
EPEEWERILHVNVMGTTYVTRAVLPSMIKESSGSIINIASTAGERGFATGSAYCASKF
ALLGMTESLMQEVKSNIRVTALTPSTVNTLATNAGLKIGDEDRMMQAEDVAELALA
TLKLSDRVFVKAAGIWTTNPQ"

CDS complement(6401225..6402124)

/locus_tag="EFAGFIKM_05641"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MSTKKWLALAVICIGIGLLGTSIYGVQFGDERENYSKRWDFKED
ELQNIIMNANFSADIEFVVSPDSNGYIEVDGKWDP AIVKSFEQATLSNGTFQLSQTER
ERLQLFTLYWNRDSTITVALPEGHQLNEVKLDSSSSDWDLTGLSAKQLELNNTSGSI
RLENIKVPNIELALTSGDITASMIDGDMTVKQTSGSLTADQVVGHVNSEIESGDIEIT
ELNGAADVQFTSGSIHIEQSHSAPINASGTSGDIFIQAAPDFDGIYDAKATSGSVDVP
ESPMVSRELKARTSSGSIEITK"

CDS complement(6402121..6402714)

/locus_tag="EFAGFIKM_05642"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNRQQFMQAMEIHLRPMEPQERAELLADYDQHFELGLREGKLEE
EIARELGQPEEIAKEALGDRYDIHTPGSDAFYAPTYREMRSRPNSTRATRNFFTAIGL
LFLNLMLGIPIGLTLWSVWLTLASLSLLVLAPVAAVDFVFLGQLDKPEIFVAIGA
VGICFAISKYVFRAFKNITLQYIQWNKNMMKGDVSA"

CDS complement(6402707..6403036)

/locus_tag="EFAGFIKM_05643"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNVNIQFKKGVLELCVLVLINRQDRYGYELAQAVSKHIEVAEGA
LYPLLRRRLVNDGYCTTYLQESSEGPPRKYYRLSDTGRDYMTALTTEWNDFVRNVANLI
EEGTHNE"

CDS complement(6403332..6404876)

/gene="petC_2"

/locus_tag="EFAGFIKM_05644"

/EC_number="7.1.1.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01335"

/codon_start=1

/transl_table=11

/product="Cytochrome b6-f complex iron-sulfur subunit"

/translation="MSDNQQPKTGLPPVPESLWRATHEFDAYPKLTEDITADVAIIGA
GIAGITTAYLLAQTGMRVVVLEAGKVLDTGHTTAKVSAQHGVIFDEIMHHFGQEQA
RMYEENADAAKWMRNLVKEKQIDCQWAEEDAYVYIQSEENIKKLEIETAYGKLNIP
GEWVDPLPIVPARAGIRMPGQARFDPLAYLHYLLDSAVKQGVRIEHTTVTDVEEDA
SLHVRTYGDGPSVTAEHIVVASHFPVYDPGFYFTRLHAERSYAVLVEPEKAYAGGMYI
SDDKPYRSLRTVLHDGKELILFGGENHKTGQGICTFGHYERLEQFAAETFGIRNIPFR

WSAQDLISIDKVPYIGPITGRHERVYVATGFAKWGMTTGTMAGHLLADRITGRDNPHA
AIFDPAFKADPGMKHFIVENNVNAKELISGKVGIVHKKVSDIGEDEGAVVRHNGKRA
GAYKDTSGKLFLVDTTCTHLGCEVEWNEGERSWDCPCHGSRFDYAGHVIEGPAVEDLK
FLDAQE"

CDS 6405246..6408068

/gene="xyl3A_2"

/locus_tag="EFAGFIKM_05645"

/EC_number="3.2.1.37"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:D5EY15"

/codon_start=1

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/db_xref="COG:COG1472"

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VATLKHFLANNNEVDRGSGSSSIDPRNMREYYLKAFEKPFKEGGAQSMMTAYNSINGT

PALLHPFVNEIIGEWAMDGFIVSDAGDVMGIKNDHKYYDSHTPGTVESVKAGIDSIT

DDAELSKQALREGLEEGTLTMDDIDKALFNTFRVRFRLGEFDPEEGNPYAAIGEESSM

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VSPLEAIRGKVGSDKVAFKDGNDRITLTSVANGKKIGLAEGEKSPVIASGEAETFMVS

DWGFSGSYTLQAESNGKYLTDEETVTASADEVYGWVFVKEVFHLLPQQDGSVGLTTWNG

KTVTAPNGGNDFAVSEELKTFGATETFKQDVVNGLEEAVAAAKAAETAIVFVGNNP

LVNGKEEIDRPSLDLAESQQRLVEAVYAANPNTVVVIVGSYPFTSNWVQENIPAVLYT

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SSDVQLVADLTVEGETIPARNLGVATRAENYDAYLGVDLDESKEGGSASVRVIGEQQWI

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CDS complement(6408164..6409003)

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/locus_tag="EFAGFIKM_05646"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O06477"
/codon_start=1
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/db_xref="COG:COG0840"
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VTQVASFIREISEQTNLLGLNAAIEAARVGEAGAGFGVVAKEIRKLSVDTKEATARIE
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DGK"

CDS complement(6409220..6409729)

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/locus_tag="EFAGFIKM_05647"
/EC_number="1.97.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A9N8"
/codon_start=1
/transl_table=11
/product="Anaerobic ribonucleoside-triphosphate
reductase-activating protein"
/db_xref="COG:COG0602"
/translation="MNLYGYIPESVNEGTLRAVLFI SGCRHACPGCFSPDSWSFRAG
EPFTEERQQQILHEVTTHPLLDGVTLCGGDPFFSAAECTSWVRQLRAARPDLTVWAYT
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IVTMQLSML"

CDS complement(6409726..6411687)

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/db_xref="COG:COG1328"
/translation="MNMLEYANPPASDLLSDLGRRRIIGAEDADTLRENANLNGDSFSG
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RKGQRLFGEHTLLEDEQLHLDSIEAKNQCPRAYAFAYEETELETGQAAESLIHNLNTM
SSRAGGQIPFTSLNYGLCTSAEGRVSRSLLEATIRGLGNGETPVFPQHIFQCKQGIN
QAQGEPNYDLFRLAVTCSSRRMYPNFVNVDASFNLFPYHPEDPDTIIATMGCRTRTLA
DRFGRNRQSGKGNLSFNTINLVKLGIRFGICQGARAADRAGFYTALESVMHNAASGL
LHRYRIQTAQPAKASDFMMREGVWEGGEQLGPNEPVADLLKHGTLGLFIGLAECMTA
LYGRHHGQDPHVHREALNIIRTMREFCDRMSEQHNLNITLFATPAEGLSGKFTKIDRE
RYGLIAGVNDREYYTNSFHIPVYHTLPAYRKIELEAPFHTLCNAGAIYSVELDGNVRA
NTAAFLRIVQYALAQDIGYFSINHPIDRCPACGYEGVIGDVCPNCEAHENHVHFQRLR
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CDS 6412170..6413807

/gene="rcsC_20"
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/EC_number="2.7.13.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00979"
/codon_start=1
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/translation="MGTAEGITRGFYEDIKEAAAHIVDVLSGILKVNTIFVATNDGVT
NVILEAFNRTEELVVKGSALPFTDSYCSLVLRDNGSVLTIEDTCEHPMTRSMGVTSGL
GNRFFVGVPIMRRSGETFGTICLMDDPGYVISETDMKTLKAMAVFLGYVVDLESTLHV
QERKLSDEQMQEQLQAEKERAESEAMTKTQMLKLMSHEIRNPLNGILGLTDLIRTPD"

MPREEQSEYVNMIETSGNILLSLLNNMMNFMNINEAGKTVIHDDPFDLVGTIENTVYLYA
GIATGKNIELGLNLELNVSQVFVGDEVKIGQLLAHVVIQYALDSTREGSVLITAVVNGE
ELEETGTLQLKVKYTGQMLSDKKTPTFNSQDENLNIQKLIGSNLGLAVSQNLAILMHG
RIQVSSVKENETEFNISLPLRRYWELPQLASVQQRLKGKKVLLAKDPDILQGVSSLMR
RWEMDVHMTSGLTLAHDWIKEGFMPDVAVDMGLLEGGAVDFVHELKQRLEDLPVIVL
VPYGMHIELHEAEAFDAVLTKPVRQADLLNALSITLP"

CDS 6413971..6414909

/gene="gpr_4"

/locus_tag="EFAGFIKM_05650"

/EC_number="1.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q46851"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0667"

/translation="MDYRRLGGSGLKVSEISLGSWLTYGGYVERENAVKSIETAFDEG
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CEASLKRLGVEYVDIYYCHRYHTETPIEETLRALDDLVRQGKVLVGVVSQWTAAQMEA
ALGTADRLLLLDRIVVNQPVYNMFDRIENIIPLGERKGIGQVVYSPLAQGLLTGKYT
SVSDIPENSRAAKLGWDEGKINADRIGKVRQLIEVADKLDLKVGLALAWILRQNNVS
SALVGASRPEQVKENAAASGVKLDAATIVEEIESILA"

CDS complement(6415050..6416162)

/locus_tag="EFAGFIKM_05651"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFSTFFINICVMITFMVSGIIAKFYISIRLPFPSLRVQLIGLL
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IYPLQMTISFAGGLFIYFIAEFINKSNEMLFLEKRASTDHLTNLSNRRQFEKSLQLE

LQRARDYQQKLSLLAIDIDRFKKVNDTYGHSAGDAVLKQLGQLLVEHARSADIVSRNG
GEEFAILLLLDCGHRQAVATAESIRQAVEKYHFALPDGHTTRLTISIGVAVYPDHCDDH
DDDDFFEQADRALYEAKNTGRNRVCALTFRSLPLTL"

CDS 6416436..6416831

/gene="perR_1"

/locus_tag="EFAGFIKM_05652"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q97FU2"

/codon_start=1

/transl_table=11

/product="Transcriptional regulator PerR"

/db_xref="COG:COG0735"

/translation="MRTLNLTIQRQAVYDVVRHSEDHPTAADVMNRLVEQGYNLAYGT

VYNSLRYLTDKELIRELKLGETASRYDARMDDHQHIMCEVCGKVDEVMTEVPPQWMKQ

VAETGYAIDHAHVVFGGVCGECRNKRIK"

CDS 6416807..6417613

/gene="czcR"

/locus_tag="EFAGFIKM_05653"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q44006"

/codon_start=1

/transl_table=11

/product="Transcriptional activator protein CzcR"

/translation="MQKQTDQVKIKLPGRRLPLRVKPALSDAAPLVDNCPVTRRVILI

SPMPGQVHELKALTDSCFDVLVFHRWEPDLHERLVFDLLIYDLSVAGTIDAFAGISS

RLNREAHTTPCLYLVGEKMIGSASGPMLQEELLVWPARPQEALYRVQRMIGNSPALP

NRGFLPEEGHRIGFKDLWLDREMSVQRDNNRIHLTKTEYDLLLKLIDAKGAVISREE

MLSDIWETDFTGGSNVVDVHIKSLRKKLGDNASSPQYIVTVRGVGYRLAD"

CDS 6417901..6419367

/gene="katA_2"

/locus_tag="EFAGFIKM_05654"

/EC_number="1.11.1.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q59337"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0753"

/translation="MMTERMTTNQGAPVGDNQNSRTAGRRGPTLLEDYHLIEKIAHFD

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DPTKTWPEDVLPFHTVGTMTLNRNPQNFFAEVEQAAFSPSALVPGIEPSEDKLLQGRL

FSYPDTQRHRLGPNYLQIPVNCPYAPVRNHQRDGLMNVNQDPSPVNYEPNSSGNSPQE

DPAYRDSQVPLQGHVTREKIEKTDDYTQSGELFRSFTPVEQQHLLDNLINDLKGVSD

IQMRALCHFFRADGQLGGRLAHGLGVDISAHMPSQDGK"

CDS 6419576..6419992

/locus_tag="EFAGFIKM_05655"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRIHNFKVGERGLNRFFGPLEAKIMDILWAHPGSSIREVQTALE

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FGALALNHMLDALDEADAGLIERLEQKIKQWKKDSD"

CDS 6419994..6420854

/gene="htpX"

/locus_tag="EFAGFIKM_05656"

/EC_number="3.4.24.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00188"

/codon_start=1

/transl_table=11

/product="Protease HtpX"
/translation="MWKTRSKLLFTVGFGIPLLVMQMFMYAMYKIFGWDIPFNLLWL
CNHWMSRLGWLSVGHFLLALVLLTFAGTGWLLTVRMIKTRAAVRKLRSM EVRTL SREL
ESRYHHLGQPGFIVVDKHSPVAFTIGLWRPCIVLSTGLLTMLDAEEETAVVYHEVHHL
WHRDPLKTTLLSVFAIMMPYIPVLKHTSKHYNIVREILADNEAIERTGNVAGIGSALL
KLLRACPEPWGAHELT VQSSFADTSVNVVRISRLLDPEQDVT LRLPRYAVLMSATVFL
LSILFWWSIG"

CDS 6420899..6421318

/gene="catD_1"
/locus_tag="EFAGFIKM_05657"
/EC_number="1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54720"
/codon_start=1
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/product="Putative oxidoreductase CatD"
/db_xref="COG:COG2259"
/translation="MNMNNSKVEIGLLFSRIMIGLIFVLHGWSKFEGGISGTVGFFES
IGIPGFLASVVAIIELVGGAAMILGLGTRVFAALFAIVMVGVLFTAKVGEPFLSGTEL
DYLLLAGSLTLLFTGSRL LAVDYLFSRQGNARQNVSA"

CDS 6421613..6422314

/gene="yhhW"
/locus_tag="EFAGFIKM_05658"
/EC_number="1.13.11.24"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P46852"
/codon_start=1
/transl_table=11
/product="Quercetin 2,3-dioxygenase"
/db_xref="COG:COG1741"
/translation="MINVIPSDARSSFDRGWLRGSHGFSFG EYQDPENTAFGPMRVAN
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EHNASDTEEVRLQLWFMPQTKGLEPSYETTSFDPAALAGALVPIVSPDGGPRVAAIH
QDMTIYLGRLAKDETLTFNQDTGRRMYIFSIEGKLGLDGEYLLNEGDTARVEQQDSIE
LQGNEDTFYMIIDL"

CDS 6422359..6422694

/locus_tag="EFAGFIKM_05659"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MAQQEWFMVKHAVTGRGLANSKTDLSYRFQQEGTGFTVTGL
DEQIVEQIMELRQELNVFRFVQRKDQPLLKHWWYVDGERVVYDRESHTLSIYAKSEIR
YVPEDYFAD"

CDS 6422870..6424465

/gene="gerAA_2"

/locus_tag="EFAGFIKM_05660"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P07868"

/codon_start=1

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/product="Spore germination protein A1"

/translation="MADKTSGKDKSRQPGRASEEKKHIPLGLPSPFLRQPISAVHET
QIQAVKEIFSDCSDVFRNVMITPEVKGLLVYIEGIVNSADIQEHMLRPIIRGLVQQR
TDEPDVPLDDTTVELTQVKRVNTWAAAAEGLASSALLVIDGSAEAWMFNVKGGVRRG
VEEPQTESVIRGPREGFTETLRVNTALLRFKLKTPALKMVSMTLGTTKTDIVLTYLE
GIADPKVVQDVKDRLEKIKIDGILETGYIEELIEDHPYSPFPQMHYSERPDTVAGNLL
EGRFAILVDGTPFALIAPVTMWQMLQASEDYERFFITNLLRWIRFLFVAIALFLPAL
YIAITTFHQDMLPTTLILSIAGAREAIFFPALVEALIMELSFEALREAGVRLPKTVGQ
AVSILGALVIGQAAVQAGIVSAPMVIIVSMTGIASFTIPRFNFAITVRLLRFPIMLLA
GMFGLYGIVIGLVLVISVHLTQMTSFSVPYLSGLSPYSKTDKIDILMRVPWWKMINRPS
TVQRDQKRMAEKINGSPEAEEGW"

CDS 6424470..6425669

/gene="gerBC_2"

/locus_tag="EFAGFIKM_05661"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39571"

/codon_start=1

/transl_table=11

/product="Spore germination protein B3"

/translation="MFFIRKYRTVVMLLICTSFISGCWDRKEINDIAFVIGIAIDKEK

DNYRSSLQIALPGQSGATGSEGGGGGTSGDKSWFILSNTAKTFHGTSLLEGQKALSRRI

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GLAIFKKDKLVGMIDKAPADALILAMGEANAPEVMVEAPRGEGDIFIKNENNSSLHP

SVKNDKVKVNIQLYAKGVVDNESNYGDRREEEILKLNDAIHKKIKSDIEEGIRLVQQ

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EEEVIHD"

CDS 6425662..6425883

/locus_tag="EFAGFIKM_05662"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIKPLLFTYLGMAIVVILMDFRHMKQAAAINRWISYGLIALGTG

IWFYVTHLSKTLVYTIWISHVIQRLLPLP"

CDS 6425940..6427082

/locus_tag="EFAGFIKM_05663"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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IQQVNMDNLMPYFHVDVAGVGKGSWYIFSFYGEMIALPFVIKGSDFRFSVLGGMIIIS

ALLMMLILVETITAIGVPIASRLVPSYELARQLQISDFLDRFDLALAAATMPTMITK
IAFDLYFVCWGLKRMIPKVSGKVM TGPVALVGFVSAFWFFRNAIQLNRFTREWTWIAI
VFEVLFPLVLFVFLRPRKKDKQKSKDARKDGEKRRQDSHG GELQPS"

CDS 6427213..6428043

/locus_tag="EFAGFIKM_05664"

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/codon_start=1

/transl_table=11

/product="hypothetical protein"

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TVSALKKRKLTPVRDDD GSTDGLIREFAPHDLAGKKV MLQLHGETAPKLVAWLEE QG
AIVRQVLPYRHVPPEEAELEQLLNEILKFEVDAVFTSGPQVRFLTQYAASQDKLEPM
LAAFRQGVIPASVGKVTANSMREEGIEALVIPEEEKMGALIVELGRYFAAGRAAKIKD
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CDS 6428485..6429204

/locus_tag="EFAGFIKM_05665"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRTVCVTGAARGLGLALTAQMLKRGYLVYAAGLDVEDSEGIRML
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AEMA EVFNVT LGTLRVTHSLLPLLLQGQVKLIVDISSEAGSIEQCSR DGWYAYCMSK
AALNMQARLVHNGLKDEGGQV MLVHPGWVQSYM RGELDVAADLTPEQSAQHIAVLDR
HEQFKGDQPAYVDYKGEKLPW"

CDS 6429248..6429886

/locus_tag="EFAGFIKM_05666"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDHRKKALLLGDYTHPDWHPLQGVD AEISRIFHDTMTVQCSENR
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KQMIGAKFLHHPAYAPLEFTVTAESHPVTEGISNFTMEEEPYQFEFGSFAETKILLEY
QSEEGPKPAVWAHRYGVGRIVYLMPGHHVPSFAHETYRKLLLQAGKWAARYV"

CDS 6429959..6430339

/locus_tag="EFAGFIKM_05667"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MSDLFKKAISLGLGLTVVSKEKIEKTVDDL VKRGELAPGESKAL
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PQLQPDESPAPLEVPPPLKGNEIE"

CDS 6430340..6432010

/gene="ubiB"

/locus_tag="EFAGFIKM_05668"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07443"

/codon_start=1

/transl_table=11

/product="putative protein kinase UbiB"

/db_xref="COG:COG0661"

/translation="MAVRIKHVGRYREIAMALVRHGF GYMVEELGLFQLLALPRRWMS
REAHTTKTLSERIRLVLQELGPAFVKLGQLASTRADLLPESVIRELVKLQDQVPPFSS
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VQRDL DILRELTAMAEKRWDWVKYQIPQMVEEYAQALMAELDYTV EGRNTEKIAQQY
QQDKKVKIPTIYWDQTSSRVLTMEYIEGIKLN DREELVRRGHDLN NIAERLVDSLLNQ
IFIQGFHADPHPGNLMVLKDGR LAFIDFGMVGSLSD EMKQQLASLIIGLMRKDTDSM
IRAIEKLGMMPPDDMDLRGLHVDLDKLR TKYYDIPFSKISVGQALNDLFGVAQRHRVVM
PADILL LGKSLTMEGVIEHLDPSLSIVDMAEPFGRK LIKERFSAGRIKNR LFRSAAD
MAESVIGLPGQLRQLSSIISKGKLRLEISVPELDALMRRMDQISNRLSFSIVLLAFCI

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CDS 6432528..6433979

/gene="bicA"

/locus_tag="EFAGFIKM_05669"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q14SY0"

/codon_start=1

/transl_table=11

/product="Bicarbonate transporter BicA"

/db_xref="COG:COG0659"

/translation="MNTLKQQWFGNIRGDVLAGITVALALIEAIAFSIIAGVDPMVG
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RFFKGIPAPLIAIVVMILTIVFHLDVRTVGNMGNITSTLPMFHPNIAWTWDTLMIL
LPYSFTMALVGLLESLLTATIVDEMTETKSSKNREVRGQGIANFVNGLFGGMGGCAMI
GQSVINVKSGGRGRLSTFTAGAFLLAIIIIIFSGVVKQVPMGALVGVMFMVCIGTFDWS
SIKNITRVPRAEAFVMIVTVAIVVYTHDLSIGVMVGVLVSLHFGWKQTKIRVQASQE
QGQKVYRVHGPFFFGSSSRFVDEFDAEADPKEITIDFGGSHIWDNTAVVAIGKLKFKY
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CDS 6435372..6436898

/gene="cshA_2"

/locus_tag="EFAGFIKM_05670"

/EC_number="3.6.4.13"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01493"

/codon_start=1

/transl_table=11

/product="DEAD-box ATP-dependent RNA helicase CshA"

/translation="MANFEQLGIRPEWCEILKHQGIAPTPVQERSIPVLLGGRDIIA
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GFLDDVETILSELPHKRQTMLFSATMPKGIRNLAKTYMKDPEDVKVSSQSVIPIKQIR

QQVLECTDRGKLEALRGMIDTYRPYLAIFCRTLRRASKLNQDLREAGYASDELHGDL
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CDS complement(6437390..6438322)

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/inference="ab initio prediction:Prodigal:002006"

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CDS complement(6438325..6438468)

/locus_tag="EFAGFIKM_05672"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS 6438731..6440524

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CDS 6440802..6444191

/locus_tag="EFAGFIKM_05674"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS 6444193..6446640

/locus_tag="EFAGFIKM_05675"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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RERSSGGS LRRQAEQSRAEHPEVGYFQWVAWSDSEPGSVREALLGLIRDKSMQLESAR
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CDS 6446726..6448009

/locus_tag="EFAGFIKM_05676"

/inference="ab initio prediction:Prodigal:002006"

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RHLALSFGIGGAVSGLLAGLLLEWGLDGSNVGDTFVRLGAMLILSGVLTLSWIVPIK
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CDS 6448029..6448676

/locus_tag="EFAGFIKM_05677"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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IRQRDEDNMVIASTGKADIRFSIRYKSGFFQKRKSVLITVTAEPVPKEALCYVRKQG
GVPLNKEDGTVYPFVSDFAPGRNEMPPVEVAKDDYVRLFFTDGPKYGAAYRLISD"

CDS 6448767..6450026

/locus_tag="EFAGFIKM_05678"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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FDVAGEGMVEQDYLGLHGQHIKNSAGILFMVDPLQIRSIRDKIRINLGNPEGEWTPRY
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VHRDWFDLTFENIDGEIRRFIEKVDRPFKGTMDVYFKDTAYFAVSALGSPVDMKLQ
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CDS 6450026..6453235

/locus_tag="EFAGFIKM_05679"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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GVGSPTQVLSALKMNEVLFKRLLYAVMQSVATRRKVYISLDLPAEEVTAGAKGLLRLL

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CDS 6453731..6454615

/gene="yusV_3"

/locus_tag="EFAGFIKM_05680"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32188"

/codon_start=1

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/product="putative siderophore transport system

ATP-binding protein YusV"

/db_xref="COG:COG1120"

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LFLDEPTTFLDMAHQLEVLQLLEQLNATANRTIVMVVHDLNHASRYAHHMIGIKKGNA

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CDS 6454855..6455334

/gene="gpx1_4"

/locus_tag="EFAGFIKM_05681"

/EC_number="1.11.1.22"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P74250"

/codon_start=1

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/translation="MSVYSYQAVTTANQEVSLDLYQGKVLVIANTASKCGLTPQYGEL

QKLYDRYRDQGLVVLGFPCNQFGGQEPGTSEEAESEFCQINYGVNFPVFTKVDVNGEDT

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CDS 6455819..6457180

/gene="nox"

/locus_tag="EFAGFIKM_05682"

/EC_number="1.6.99.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37061"

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ELVEAFQMNGKEVTLIDSVDRLNKYLDPEFTDAIEDTLTGRGIKLALGQTVQNFTGE
NGKVTKVITSKGEFETDLVILCIGFRPNTELLKGQVDMLPNGAIIVDKYMQTSQKDVF
AAGDSCAIHYNPTGKASYIPLATNAVRMGTLVARNLVRPTTPYMGQTGTSGIKIYEQN
IAGTGMTEMSAADEGLIVESVPLEDSYRPEFMPTAEKLLLKVVEQATRRIVGAQVMS
QVDLTQSINTISVCIQNNMTVDELAFIGFFQPHYNKPWNFLNTAGLQALPPIEVKSP
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CDS 6457555..6458406

/gene="focA_2"

/locus_tag="EFAGFIKM_05683"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AC23"

/codon_start=1

/transl_table=11

/product="putative formate transporter 1"

/db_xref="COG:COG2116"

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LDIRVIASAPAEWGSLVNLIGAAVFPVGLILVLIGGGELLTGNMMAVPLATIARKLSV

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SGIGCNWLVALAVWLSYASDTMSGKVLGIWFPTMAFVAIGFQHVVANMFLIPAAIFEG

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CDS 6459037..6459231

/locus_tag="EFAGFIKM_05684"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS complement(6459280..6459939)

/locus_tag="EFAGFIKM_05685"
/inference="ab initio prediction:Prodigal:002006"
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CDS 6460505..6462568

/gene="ynfE"
/locus_tag="EFAGFIKM_05686"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P77374"
/codon_start=1
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YnfE"
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HRFVKLDMPHAAYLDQLPTPSGKIELYSETMEQRGLPPLPTYSALVEGYDGEHPAGP
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CDS 6462757..6463983

/locus_tag="EFAGFIKM_05687"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

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FSYHLSFVLNGVTSAGFAIFFWYYLSRVEPDQGEVHLTKRITVPDGPVWALLGNTRL
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AVLNRRNREVKEYGMDT"

CDS 6464271..6465818

/gene="cheB_21"

/locus_tag="EFAGFIKM_05688"

/EC_number="3.5.1.44"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00099"

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/translation="MYKVLLVDDEFMISDGISSVWNWSRLGTELIGIAQDGLEALASI
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CDS 6466046..6467011

/gene="yteP_37"

/locus_tag="EFAGFIKM_05689"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

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/product="putative multiple-sugar transport system
permease YteP"

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DGAGRWRQLLHITLPGIMPTIVIMLILRMGAVMNADFQKILLMQTAPTYETSDVISTF
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CDS 6467027..6467896

/gene="araQ_35"

/locus_tag="EFAGFIKM_05690"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

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/product="L-arabinose transport system permease protein
AraQ"

/db_xref="COG:COG0395"

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CDS 6467924..6469573

/gene="lipO_16"

/locus_tag="EFAGFIKM_05691"

/inference="ab initio prediction:Prodigal:002006"

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GYRDFLETMAKWYKEGLIDPEIMTNDGKAFDYKVTSNLAGAYQGGVFSGMGKYFNLMR
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CDS 6469666..6471441

/locus_tag="EFAGFIKM_05692"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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FERIIWLKNVLILVYLIALVLALGMVFARSLTRPIRQLISQMKEVQYGDLENIDAN
LSIPTHQHMDDELGLLQRTYRLMITHINTLIKENYASQLVIKETEFKALQAQINPHFLY
NALDSIHWLAKKNRQEQISSMVLSLGYLLRSSISFKQNIITIAEELEIVNHYITIQT
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ALIVEDHGPMEPEYVEQVLRGEVKTRGTGIGLLNIRERVRLAFGEEYDVLLESKPGL
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CDS 6471420..6472709

/gene="yesO_5"

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/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31518"

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/product="Putative ABC transporter substrate-binding
protein YesO"

/db_xref="COG:COG1653"

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LSQYSSLQLLEDMPYMQSGLIDTTDIEKEQLEIGSLNGKTYGLSLGVNAMLSIYDPE
VLMAHDIELPTDTWTWADFDRMGELLGKGIYLGTYFTPEQFFAYYLRQYGSKLYAED
GKRLGYEDDGLFIEYFGRMQQLAEEKLIFAPDIWTSIDIGQPDNDPFYLGALFSWGYS
NQFISTAQRYGKPLTISPMPGPNSQDGLFLKPGMFFSMAGNSRHKEEAAKFISFFVND
LDANLLLKGERGVPVSSSVKERMKLVEPELAQVFDYIDWVADNSTQMDPPDPIGAPE
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CDS complement(6473056..6474768)

/locus_tag="EFAGFIKM_05694"

/EC_number="3.6.3.-"

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/inference="similar to AA sequence:UniProtKB:Q99T13"

/codon_start=1

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protein"
/db_xref="COG:COG1132"
/translation="MLRRFMSYYRPYKRLFILDFSCAIAAALELAFPLAVNRVVDQL
LPAGNWSMILAACVGLLGIYLLSSFFHYAVTYWGHKLGINIESDMRRELFQRVQKQSF
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FIIVPLMIYLSLYFSRKMSKAFKRMFADIADYNARVENNVSGIRVVQAFANEKHEVGR
FVENNERFRLTKLITYRIMAWNSSLFILMKFVSLFVLVCGTWVFVIQGSMTYGEFIAF
VMLSNVFLGPIEKINSVIETYPKGIAGFRRYLELLEAVPDVEDTPQAKPIPDVKGDIA
FHNVTFSYGEHKPTLSQVNLDIQAGQTVALVGPSGGGKTTLCSLIPRFYDVDAGHISI
DGIPVKDMTLESLSRHIGIVQQDIFLFDGTIRENIAYGKLNASDEEIWQAIRRAQLEE
LVQSQPDGLDTMIGERGVKLSGGQKQRLSIARMILKNPPILILDEATSALDTETAAI
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AQFG"

CDS complement(6475009..6476037)

/gene="yxeB_2"
/locus_tag="EFAGFIKM_05695"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P54941"
/codon_start=1
/transl_table=11
/product="Iron(3+)-hydroxamate-binding protein YxeB"
/db_xref="COG:COG0614"
/translation="MFAAKKRFSGLLLMLAIIMILAACSSGTGSTATEQTSAAGTETT
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VVIPYGTFTNVYDEIRGFGELMNKSEEAELWLTQYDERIEAARAKVKTVIKPEETFSI
LEVSDKSYGYGDNFGRGGQAVYSALQLAPLEITKKELMGDTQWKEISREVVG DYAGD
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ERAEQNRK"

CDS complement(6476148..6477794)

/gene="rhaS_43"
/locus_tag="EFAGFIKM_05696"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1
/transl_table=11
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/translation="MNISKPIYHKKSLSRPISLQKIQSVPVALFKLCHLVQLHDREAF
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LLDILRDHVAHSAHEDHSWLDVLRHIHQMYTHPLTREQLARDANVSPEHFSREFKKH
TGLTFVEYVTRLRIRMAQEHLFANPTLQDIAQLTGYRDTFYLSRKFKQMVGSAPTHY
RKMPKKIVSLTYNYTASLLALGHTPHMGAVASWMEEKLGEHGHGHEQFEQHSEYELV
KHTDLIANAQPDVIIGYAPHPASDELRLIAPTILMPFEEIDWQEQLLLLGRITGLESN
AQALLDQYHQLEQEANHTLDQQMEGTRGSAVCMFMIGEDGAYIYGHGWGRASHVLYQS
LGFTPPSRMEQDGQLLTGYVHVPLSEIHLAADHMFVAFPEEPAEREMLDNLLNQESW
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CDS 6478324..6479313

/gene="rbsR_4"
/locus_tag="EFAGFIKM_05697"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0ACQ0"
/codon_start=1
/transl_table=11
/product="Ribose operon repressor"
/db_xref="COG:COG1609"
/translation="MATIKDVAKLAGVALSTASYALSGDSKVSATKAKVLEAARELN
YRKNGFAMD LKRSRTNTIALILTDLSGPYYSELIRSVQDVALANGYDLIACSSMGGRD
STAVRFLREKRVDGAILAHNIHDDILVESAGHRFPPIIVMDRQLSSDHLVNVLDGEQ
GGYLATRHLIQAGHQKIAYISGPSNSYDNALRYQGYLRAMREAGLEEKSKWRLNGNFV
REGGYSATKMMIMQGDLPFAVFYGNDEMAIGGLKALEERGVSVPDDISVIGFDDIQLS
EYVHPPLTTIRQPKHEAGSLAGHLLFQMLNGEEVDPSYTLTISMIERSSVRSV"

CDS 6479475..6482867

/locus_tag="EFAGFIKM_05698"

/EC_number="2.4.1.333"

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/inference="similar to AA sequence:UniProtKB:Q92AT0"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG3459"

/translation="MTTMINEPIRLSAGELSFTFLNSGDLYQATSGTTMLNQLLSNQI

DGSLNNLYLRVHEGENISSFPLLGVHSNSKVITSKAQSSNQLIWEGTVQLEGSEKGIG

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PTLANETYQYEFAYTALQSELLNLNGEAQVVFYGLAKPNHAEGISALEFGDEVTAAWN

EVQALTVENGDTLEQVKLSSFLGEPLVTLDTLQDEIHDLPDRQQEEHSGEELLSFFT

GSYEHIVLKAKELLVERPHGHILMSGGNVQLGAQVITTTSYMYGIFNSQLVIGNTNFN

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HNMLVHYSVPHGLEQYGGAAWGTRDVCQGPVEYFMATQKYEQVRDIKMMVYTHQYEDD

GNWPQWFMFDKYFAIQEESHGDIIVWPLKVLADYLTATRDYAILDEKVPYTVKHSFG

FTEETATVLDHAKKEIEYIRSHFLHDTFLSSYGDGDWDDTLQPANAQLKQYMVSSWTV

ALTYQSVNVLSQALKFKDADFAQELDVLAQGIREDFNRYMLGTDVIPGFVYMEEADQA

KLMLHPTDTETGIQYRLLPMTRSMIGELLNAEQAESHYALIREQFLCPDGVRLMNRPA

QYAGGVSTHFKRAEQASNFGREIGLYVHAHIRYVEAMAKLGKTDQVWNGLAMINPVG

IGEVVPNAEIRQANSYFSSSDGKFNTRYEAQEHFDQLRKGTQVKGGWRIYSSGPGIY

MNQLISNALGIRQEGGDLVIDPVLPAELNGMQFEFEYAGEPVTFIYHLNEGAVSRVAV

NGKDIRTERTANRYRQGGVSISLDEFQRARSATERTVVDIYM"

CDS complement(6482947..6484143)

/gene="COQ5_6"

/locus_tag="EFAGFIKM_05699"

/EC_number="2.1.1.163"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01813"

/codon_start=1

/transl_table=11

/product="2-methoxy-6-polyprenyl-1,4-benzoquinol

methylase, mitochondrial"

/translation="MNIKEAASRLGISARAI RFYEEKGLILPAKQSSNGYRTYTENDI

WRLQTIAALREIGMSLQDITQALGEIDQGNQQRLEEYLELQQAVIYAQWIELKRMMDT

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VSTEHPNSEDRHHSATPSPISDENEVSHPNHNVGHSTPGDSNDTVQSSFYLYHNYDEA

LEQTAHWISPALGEKGLDIGTGTGNLAGKLLQHGADMTAIDQSREMLRRCRTKYPEMH

VKLGNFLALPFTDHSFDFVSSFAFHHLSPDQQLLALQEMQRVLT SRGRIGLTDLMFV

DATHRDSYIRQAETTGHEEQLRALRERHFPLLSELCSWLEQQGYVTKNVRHNELLHTL

LAVPLR"

CDS 6484418..6484918

/locus_tag="EFAGFIKM_05700"

/inference="ab initio prediction:Prodigal:002006"

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/translation="MLTSHTFTIRPSEIKDAAQLMELDALVWDKYTSPAPMHWRSRQQ

YLQHCPPGSQLIAVEGERVCGYVGFQPATGMPVNRHVYEIHIAPHDRRCGIATALM

DAIKQHAAQQGVRKRLRLVLSSNPGAITFYTQCGFVTEGRLVSEFYIGGKYVDDILMG

YFIQIK"

CDS 6484945..6485733

/gene="fabG_12"

/locus_tag="EFAGFIKM_05701"

/EC_number="1.1.1.100"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O67610"

/codon_start=1

/transl_table=11
/product="3-oxoacyl-[acyl-carrier-protein] reductase FabG"
/translation="MDMGLQGKKALVLASSRGLGKAVAAQLAAEGADVMLASRSEEKL
AAVKQELLALGGGGRVEYCATDVTRKEDIEALIHKTAEMFGQIDILVNNSGGPPSGSF
ESLTDEDWERAFELNVLSYVRLIRGALPYMKESGGHIVNIASTSVKQPIGLVLSNTL
RTGVFGLAKTLSQELAPYGILINTVAPGRIATDRIELDAARAEQNGISEDEVSEQFR
KEIPLGRYGQPEEFAKAVVFLLSGANTYITGTSLIVDGGMVRL"

CDS complement(6485847..6486395)

/gene="ydaF_3"
/locus_tag="EFAGFIKM_05702"
/EC_number="2.3.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P96579"
/codon_start=1
/transl_table=11
/product="Putative ribosomal N-acetyltransferase YdaF"
/db_xref="COG:COG1670"
/translation="MFTYSLDEYTELRPLAMEHTKPLFELTDRSRDQLRHWLPWVDHV
TEVEHTSNFITNALKQGAENGGFTAGVWSKGDLAGVIGFHEINWTNRSVSIQYWLKKG
FEGQGLMTSACRVLVDYALVTLDLNRVEIRSATNNKRSRAIPERLGFVLEGVIRQAEK
LPKGYVNHAVYGMLQHEWELLR"

CDS 6486952..6488685

/gene="glnS"
/locus_tag="EFAGFIKM_05703"
/EC_number="6.1.1.18"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9I2U8"
/codon_start=1
/transl_table=11
/product="Glutamine--tRNA ligase"
/db_xref="COG:COG0008"
/translation="MKGLIPVDNRTTPPNFIKNIITEDLRSGKVQEVITRFPPEPNGY"

LHIGHAKAIWINFTLGGEFGGKTNLRFDDTNPVKEDVEYVQSIQEDVKWLGYEWNKR
FASDYFDEMYNRAVLLIKKGKAYIDQSADEIREMRGTLTEPGKNSPYRDRSVEENLD
LFTRMRAGEFKNGEKVLRKIDMSAPNINLRDPVIYRISHAHHHNTGDKWCIYPMYAF
AHPLEDAIEGVTHSLCSLEFEDQRPFYDWVIAECEMENQPRQYEFGRNLNSQMVTSKR
KLKLLVDEGHVDGWDDPRMPTISGLRRRGYTPEAIRDFVYETGISKNYGVIDLQLEH
FVREDLKLKAPRTMAVLHPLKVVITNYPEGQVEWLEAENNVENPEMGNRQIPFSREIY
IEQDDFMENPPNKYFRLFPGNEVRLKHAYFIKCNDVIKDAEGNVTEIHCTYDVETKSG
SGFTGRKVKGTHHWVEATQAVPAEFRLYEPLILDEAPEAEVEVAVAGAETEVVEEQPE
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CDS complement(6489355..6490548)

/locus_tag="EFAGFIKM_05704"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVSLKLYNFFIYGAISIFAGFLQLYLQEIGMTKLEIGSLMAIGP

FVSLFANPFWGFWSDKSRNIRIILMIMMGGTFLVAQGVFYAPTYTWIYVAMIFFYFFQ

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MIATAFVLSVFLPRQPIASDTPVVTFRRFQKVMFNPFYMAFIGLGVLSVPNAMNSTF

MSLYIVEMGGDKQMGVWAIFTSSILEVGVFLLLDRLKMKMSMLLASLILISVLFALR

WQLMALANNPLEIVFIQLMHSITFGGYFYVGTQLTMLFIPRPYRSSGQAVYTMWGGGL

SGVIAGLFGGWLFQSFGAEIMYSIGVFFSLIGAVGFSIMWLSNRRNGYQPVVLTEMGN

MDEDR"

CDS 6490712..6491341

/gene="mobA"

/locus_tag="EFAGFIKM_05705"

/EC_number="2.7.7.77"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P32173"

/codon_start=1

/transl_table=11

/product="Molybdenum cofactor guanylyltransferase"
/db_xref="COG:COG0746"
/translation="MNTREWTGIILAGGLSSRMGTNKAMLELNGSVVLQHVTAMRPA
VSRIIVAAGPNVTYTGAMGYDCIQDHYPGKGPLAGLHAALEASDTDWNLVCACDMPLL
QTSFFDGIKKLVESHNSYSAIVPRVDGQVHPLAGAYHKRVLPDLEQRLMQDHLRVMRW
LEEIGCCYVEAEELERAGVHQVAMQMSNMNTPEEYERIRNQDSGLDSDL"

CDS complement(6491311..6492285)

/gene="rhaS_44"
/locus_tag="EFAGFIKM_05706"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01534"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaS"
/translation="MMDMRSQLEMPHHTLAHWLPIIDSNIKFYGAHSQQVPYGWAMP
EESHPGFEIMLIIEGTQESVIHGYTYTVEEGSILLIPPGFKHTNQCVSTEGMTYFSAH
FNVDDPVFTLKLMSQHSRIYAAGTADNRKMRVVLESWMGMINVSEAYTSTDKMIMQAR
MFELFALLSQAADNEPESTTSVAVSHAPAPTAMHYAGAIAEAIKQAFHAQLRTKESSV
STVKVEQIISSFGISPGYGLQVFRKVYGRSPRAYLSSLKLQEAKVLIEQPELSLGEIA
WKLGYTHLSHFSRQFKRWGTQSPLQYRNHHADASSDPVSYRSESPES"

CDS 6492531..6494534

/gene="bgaB"
/locus_tag="EFAGFIKM_05707"
/EC_number="3.2.1.23"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P19668"
/codon_start=1
/transl_table=11
/product="Beta-galactosidase bgaB"
/translation="MDKLLYGVAYYDEYMPYERLDKDIQMMKDAGINVVRIAESTWST
HEPQNGVDFDFSSVDRVLNAMHEAGIQVIVGTPTYAVPTWMVKEHPDVLATTSQGPVKY
GARQIMDITHPTYLFYAERIIRKLISRVESTHPAVIGYQTDNETKHYNAGDNVQLQFV"

KYMRNKFSSLDELNKEFGLDYWSNRINSWEDFPSVVGTINGSLGAFAKFQRQLVTNF
LAWQVGIVNEYKQEGQFVTQNFDFDWRGYSYGIQGDVDHFAASKPFDITSVDIYHPSQ
DDLTGIEISFGGDVARSTKQSNYLVLETEAQAFWHWVPYPGQLRLQAFSHLASGANMV
AYWHWHSLHNSFETYWKGLLSHDFEPNPVYIEAKTIGRDFARLSPKLVNLKKKNRVAV
LFSNEALTSIKWFGFNFTSDKNYNDVVRWVWYDELYKMNIgcdlidpsvesyteydvlv
VPALYAASDALLEKLNQFVEDGGHIVYSFKSGFANEHIKVRSTRQPGLISEACGISYN
LFVEPKHVSLRDDPFVVGEEQNIHTWMELITPTTAEVLAWYDHPHWGEYAAITQNAY
GKGKATYVGCYTSSAVIRKVLHVMKEAGVWGADQELAFPIIVKTGVNDQGNTIRYYF
NYADEATSFVNAYGEGTELLAGTPIAAAIELEPWGIRIIEQ"

CDS 6494843..6496633

/locus_tag="EFAGFIKM_05708"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MFTECYRKLIDPFKRSIRNKLILMTLLAVLPVIAMTAMAAENT

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FAQHKDFTIINDPDDPQKFHMTSMNRFEDQAQIGAISLEVKWAEFNQTLELLDSRGD

YAVYIADSTGSPVYQPNQEIQPSAEALEKLAGTKESSGFIRTAKEYVFFHSIEPSGLR

VIKIVPAHVVNESALETMKYGLVVGGLATVISVGLAALVAWRTSKPIVRLANS MKGIQ

LIKDREVVRSGRVDEIGLLEKNLHG MASRIREHIRDNYLMNLEKQT AELKALQSQIHP

HFLQNTLQMIGGMVYSQKPADSYKVIRALSEMFRYIVRAPDGLVPLQSELDQLEHYML

IQKQRFAGRLEYTLEITGELRACYIPKLSLQPIVENAFLHGLEKKQGEWKLGIEVVYE

STDVTIRICDNGVGMDAEKLTEMKSRLERLTRQADRVWSSGTSIGLVNAASRMVMHFG

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CDS 6496630..6497739

/gene="rssB_11"

/locus_tag="EFAGFIKM_05709"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00958"

/codon_start=1

/transl_table=11

/product="Regulator of RpoS"

/translation="MNKELYRVLLVDDPEWNRDILRNLGDWNELGMTVAGEAEDGEQA
IQLVKQHQPPIITDMRMPGTDGVELLQTLSGQYPQIKVIVVSGYDDFNYAKHAIRHR
AADYLLKPVNPDELNGVLAKCAKELEKVESAPESWESYPSSFAGEFSLFQQQARLRFN
DLNVQSLREWFQQQLQKLERCEINRPRQLGRVAHELQALLDELCVSNGLYERPEATAL
PPSTALASIESTIAWISTPYLLALEQLIAQRKFKNKLNLNEVKQYMEQHCMEMITLEQ
LAQIFFVSKEYLSKVFKKEYEVNVTDYVIQLRMTRAKEWVMDEQIPFKHVAEMAGYED
VSYFYRVFKKHFGVSPGEMRKGQARISGNSGSSTE"

CDS 6497887..6499167

/locus_tag="EFAGFIKM_05710"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKVWKSVASAVLVSVLLAGCGSNAGTDNGQEEASGSGTVSLKVF
VAQPRLKEHYDKYIEQFKAKEKAENIEVNVQLEMPPADNAPQILKTRLASNDAPDVF
ALHAVNEIPPFSKAGYLEDLSGQPFVDKLLDSVKPSITDAEGKIVAIPLETVSWGYYL
NKDIFEEQGLEVPITLTEMKAVVEKLKAANITPFELSYKEAWIPQLFLPLTVGALTQS
EHKDFVEKMNQDQGSFSDMKALFDIFDLVNANGTDKALEVGGDDGSAAFASGSAAMWI
QGPWFAETILKSNPDLNFGVAPMPINDNPDDTKINLSTSTSLAVSSSSKNKEVALDFV
NYILDDKDSSAFFEALKFNPIAKIHDFKSFPWVDDAQKYVSEGKAYEDPSLPQAVKDE
SGKALQGYSGQLNQQQVIDALDKAWKSYNKVNK"

CDS 6499347..6500231

/gene="melD_11"

/locus_tag="EFAGFIKM_05711"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34706"

/codon_start=1

/transl_table=11

/product="Melibiose/raffinose/stachyose import permease
protein MelD"

/db_xref="COG:COG1175"

/translation="MATNVFKKYLSELLAFTAPAFVIYAIFLLYPTFSGMFYSLTDWNG

LNRDYSFIGLGNFVELFKEDPDFLNSLWFTMKYVIFMLILQNGIALLLAVLIESRTRS

KGLFRTLFFMPNMISTIISAFMWTFIFSQVLPQLAEKLAFSFLDQQWLGDPKFSFYSI

LIVSLWNGVGYYMMIIYLAALQGVPKSLKEAAVIDGANAFQVLRNVVLPMTHTAVTICF

FLTLNGAFKVFVYVYGLTGGGPGRATQVITMNIYEEAFSNNFRYGYASAKSVVLFIV

LIFTLIQITVMKKKEVEA"

CDS 6500234..6501055

/gene="melC_9"

/locus_tag="EFAGFIKM_05712"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34518"

/codon_start=1

/transl_table=11

/product="Melibiose/raffinose/stachyose import permease
protein MelC"

/db_xref="COG:COG0395"

/translation="MQRMNLSYLIRLLILGSLVAMLPYMAVVNSFKTQGEMFQSFIA

LPTTLHWENYSDAFNKINLLGSSMNSAIVSFLGIGGIVFCASLAGYKLSRTSGRLSNL

IFFLFVASMLVPFHSMIPLTRVAKGMGVQGSTYGLALIYIGLGVNMAIFLYHGFVKS

IPRELEESAQMDGCNEFQTFQIIFPLLLPITVTIAILDFLWIWDFLLPLLMLTDVN

RYTLILSTNMLFGGEYNKEWPLILSSVLTAIPVILIYAFFQKFIMEGIAEGAVKG"

CDS complement(6501214..6502707)

/gene="norG_2"

/locus_tag="EFAGFIKM_05713"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2G1P1"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator NorG"

/db_xref="COG:COG1167"

/translation="MERSDSRLNMGWKPNPSLDLPLYRQIEAYVRQKITTGEWSAGYR

LPSQRIWAESMEVNRSTLVTALDNLAAAGLIEGRHGGGTYSISGSGWHGMAHGAMPNWN
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LNYMEPQGSLELREALSVHLQTTGIQASPDSILIVSGSLQALHLISVGLLPRGSAVLL
EKPSYLYSIHAFQSAGLKMSGIPMDDEGLHIARLEDAVQHVKDQDHISLLYTIPSFHN
PTGSVMSDHRREELMTTARTLGISILEDAAAYSDLWLDTPPPSSLKVRDQEGRVLHMG
LSKAVSPGLRLGWLVGPEPVIRRLADIKMQTDYGTSSLAQEAAALWFAEGHHVGHIER
LRPELRKRRDFMLELLQRHFRGIAKWIPAGGFYIWLQFTVSPLSIRQLFHTCLEQNV
LIHPGYLYDRLDASHIRLSYAYASPDEMERGLQCLAEAVHRLMDSGS"

CDS 6502843..6503451

/gene="argO"

/locus_tag="EFAGFIKM_05714"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P11667"

/codon_start=1

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/product="Arginine exporter protein ArgO"

/db_xref="COG:COG1279"

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CDS complement(6503660..6503974)

/locus_tag="EFAGFIKM_05715"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MMFLSAFSLYFHKFLKNFNSPISFVENLINIRYARTKEATVNIE

RSLKDVQHSIQQMEQEITSISQSSNQQAVLVTEFSEVIDQLNSVSRDLKVFIESMLLK

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CDS complement(6504161..6505162)

/gene="moaA_3"

/locus_tag="EFAGFIKM_05716"

/EC_number="4.1.99.22"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q44118"

/codon_start=1

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/translation="MELLQDSFGRIHDYIRISVTDRCNLRCVYCMPEAGMEFAPHDEI
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VVLMMKGINDDEIKDFIAMTIDQPLHVRFIEYMPIGQASDSWRKSYLPLEAVTDVCAEA
GWTVENTKGPAGNGPSRNMKIVGSEGTFLIHPVSDHFCDNCNRLRLTADGHIKACLY
WSDEYNVRRFVDDPDAMAALFLKALGTPKPNHEMALALEQKMQSHTPTVRRMSQIGG"

CDS complement(6505282..6507504)

/locus_tag="EFAGFIKM_05717"

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/codon_start=1

/transl_table=11

/product="hypothetical protein"

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QVVFSTYKKHIGQIYEDYEALIGPGLKYSRADRHSSKCLYGPYSDPLTDIGPRSSAF
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CDS 6508033..6508833

/gene="nrtC"

/locus_tag="EFAGFIKM_05718"

/EC_number="7.3.2.4"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P38045"

/codon_start=1

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/db_xref="COG:COG0715"

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WRTVRHNVLELLELGTTRKECRRISGELLEMVGLTRFADHYPWQLSGGMQQRVSIAR
ALALDPPLLLMDEPFSALEFTKEKLQLELLEIKRSTDKTFLFVTHSIPEAVFLSDRI
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CDS 6508838..6509650

/locus_tag="EFAGFIKM_05719"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MSLRFFKPGYRSWVVIWIMAVLVLWEGIAWILQLFLSPQQAASR
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LMRSCGASLTARYIKLLPSALPGLFSGMKIAAPLAVTSSIVVELMGAPDGLGVLMS
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CDS 6509647..6510585

/locus_tag="EFAGFIKM_05720"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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PIVALAPIMNNWFGDGIWSRIA VVTITMAAMAVSLFKGLTSIQPQYSDLLSGLAASR
MQFFWKLRPLPHALPSLFAGLKINMSTSIIGAIVGEFFIASQGLGYLLSDQIRLANMPL
AWSCIVIAAVLGIVLYEAVVLAEKRLIPWNRARTDY"

CDS 6510661..6511725

/gene="ribY"
/locus_tag="EFAGFIKM_05721"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A9WGD2"
/codon_start=1
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/translation="MYKTLKPGLLVLLVVTMLSACSTKSEPTAEPA AASSGGAGEA
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SQQFQVLAFMEKNGLDPKKDIELVKQGFTMDQFFNDQVDVATATIYNEFHV VLESGBK
ESDLDFVNIEDAGVGMLEDTLIAKKDWVDSNRELAVKVTRAILKGWNYAIDNQ DETVD
IVMSNVTDGSTTREHQVTMLEEIAKLIRPEGFTEQQVGSFVDESFTRTADIALNYGLI
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CDS 6511747..6513120

/gene="tpa"
/locus_tag="EFAGFIKM_05722"
/EC_number="2.6.1.77"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9APM5"
/codon_start=1
/transl_table=11
/product="Taurine--pyruvate aminotransferase"

/db_xref="COG:COG0161"
/translation="MSSVDQQPQPLGGTKEEWMEKDRKYVWHHISPHNDHPMIAVSGE
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EKLNDWLEGEYRIFFSNSGSDANEVAFKIARQYHHQNGEPTRHKFISRHRAYHGNSMG
ALGATGQAARKIKYEPLGVGFSHVPPPYCYRCPFGRNKDGCGLCATIYEEVIRWEGP
ETVAAVIMEPVITGGGMIVPPPDYMRVTQEQICQRYGVLLIVDEVICGFGRSGQKFGHQ
NYGVQPDIVTMAKGMTSAYSPLSATAVRADLYDTFREPGPDAHFRHVNTFGGNPVSCR
VALANLEILERENLVSRAEELGYLLREKLEPLLELSIVGDIRSFGFACGIELIEADGS
PAEADKVMKVLTSCKRDGILIGKNGDTPGPFANILTISPPFVTTEDELDLIAGSLLVA
LRSLDVG"

CDS 6513219..6514508

/gene="hyuC"
/locus_tag="EFAGFIKM_05723"
/EC_number="3.5.1.87"
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/inference="similar to AA sequence:UniProtKB:Q01264"
/codon_start=1
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/translation="MQTTTGKVINQLRLNERIEQLSQIGRIAETGVCRLALTPEDMDG
IIQVRLWMEKAGLTTRLDPFGNLIGRLEGADQLLPILMIGSHIDSQPYGGRYDGAIGV
LGALEAVQCLIENGIQPRMPIEIIAFCDEEGSRFNKGLFGSRGITGQLEEGELERQDK
NGVTRREALAFCSPSDFEEAIYPPGSIGSYLELHIEQGPVLEALNAPVGLVTGISG
PLWLTVTMKGMAHGASVPMGMRHDALVGSAKVIAAFDDMVREDPEAPTGTGSLRV
FPDSRNIIPEEVSFTVDLRDMEMERRNRLEARLMNILDDVSFRYGLTYSLTEDTNSEP
RYCAEPIKSVIRSSAEEIGVTLPELMSPGFHDALALSLVCDYGMIFVRSKDGISHHPS
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CDS 6514513..6515394

/locus_tag="EFAGFIKM_05724"
/EC_number="3.5.1.77"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P60327"

/codon_start=1
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/product="N-carbamoyl-D-amino acid hydrolase"
/translation="MSKISIGLIQASHEIEGSAPVEVHKEAAVQKHITLVREAAARGA
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ARVGVYICYDRHFPEGARLLGLAGAEIVFNPSATVAGTSEYLWKLEQPAHAVANGYYV
AAINRVGVEAPWNMGEFYGQSYLVDPRGRMVAIGSRDQDEVVIGEMDTEMIREVRNVW
QFYRDRRPETYEHLVSL"

CDS 6515445..6516812

/gene="gltD"
/locus_tag="EFAGFIKM_05725"
/EC_number="1.4.1.13"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P09832"
/codon_start=1
/transl_table=11
/product="Glutamate synthase [NADPH] small chain"
/db_xref="COG:COG0493"
/translation="MNSSGTTLSDYGWESRFAEMKPAMTGKEAMEESNRCLYCYDAPC
IKACPTDINIPSFISKISTGHLKGSARTIMDANPVGASCARVCPTEELCEGACVLNES
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TIYEAKPKGGLNTYGIVAFRLPESVALWEVEQVEALGVQIRYGVRIQVDIPATQLLE
QHEAIIACGMGSVPMLGIEGERLEGVYDAIELVESTKQGVPPALNGLKVAVIGAGNT
AVDAATCSVRLGAERVQMLYRRGESQMTAYAFEYTFKQEGVEFRWFTLPQRIIGDEN
GRVQAVECVKMELITPPGGGRALPVPVEGSEFMIECDTVIRAIGQHRLLPLIEAFGLR
HQWGVVEIEPHTYRTSHPQIYAAGDVIFGQGQGEAMVVSAAQQGKLAAAAMKALPGQ
VEETA"

CDS 6517340..6518635

/gene="preA"
/locus_tag="EFAGFIKM_05726"
/EC_number="1.3.1.1"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P25889"
/codon_start=1
/transl_table=11
/product="NAD-dependent dihydropyrimidine dehydrogenase
subunit PreA"
/db_xref="COG:COG0167"
/translation="MADLSINLAGIRSPNPFWLASAPPTNTGYQVQRAFEAGWGGAVW
KTLGEPINTSSRFAAVHFGGQRVAGFNNIELISDRPLEVNLREIAETKKRFPDRAVV
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WVKEVATTPVIVKLTPNITDITATARAARVGGADAISLINTINSLAGVDLDSWNTVPH
VGGKGAHGGYCGPAVKPIALNMVAECARNPEVGVPISGIGGISDWRDTAEFLMGATG
VQVCTAAMHHGFRIVEDMIDGLNDYLDEKGLSSVAELVGQTVPRYSDWGNLDLNYKV
ARINRDVCINCNKCHIACEDTSHQCIDMLTDPGSGYLEVVEEDCVGCNLC SIVCPVDG
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CDS 6518632..6520077

/locus_tag="EFAGFIKM_05727"
/EC_number="3.5.2.-"
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/inference="similar to AA sequence:UniProtKB:Q45515"
/codon_start=1
/transl_table=11
/product="D-hydantoinase"
/translation="MSTRKLIRNGVLVTASDTFEADILIEKGKITQIGIGLIPDERME
IVDAAGCYVIPGGIDPHTHLDMPFGGTVTADDFATGTTAAAFGGTTTIIDFCLTQKGR
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QFQADDGILFQTLQKAKEYGALVMVHAENGVIDLLVRQALAEGRTEPIHHALTRPSM
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IMDQPDFEGAKYVWSPPLREAAHQDVLWNALKSGQLQTIGSDHCSFNFKGQKDLGKDD
FSKIPNGGPVIEDRLSILYSEGVVKGRLTNQWVLDLCSTRASKLFGLPQKGTAVGT
DADIVIFDPSVKRVISADTHHMNVLDYSAFEGMQVQGCPVTVLCRGEYVIRDRQYAGTA
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CDS 6520077..6520304

/locus_tag="EFAGFIKM_05728"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSDHDVFEAERIAIERMIAQGYRIYAVREHLEGAHVIWGHDPDLPEEKQEQYVGTASGRKWFSHILIRQLQEQRGA"

CDS complement(6520320..6521984)

/locus_tag="EFAGFIKM_05729"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLHIQIRDMLKRPVFRKAEVLASDRALERYVRWVHIMEVPEVGDLLNGGELVLTGIGWQEGEQHGLSFLRQLIARGAAGLCMELGDHTKSQLGAMKEIAVADFP LIWFREQVRYIDITQDLHFTLIRSHQRMIAELDSLTSFNQ LLLNGDGVQP LLRLLSRTTGCAVALYPLEGEASAVPYCPPEELETRRQDWFSQRGQLEGEHITALKAYTESALDVISIPVQALDYTFADLVLMHQKLPDHDSSISIKLSDEFIIQALERCAAAIAQDWMRTKYMEEKRRYKEDMWVIDWLNHHSTKEIHEYSAVNPLLATSKATIILFDSNPAYTDSLRLQKLLIQRNIVARSVFARDNFTLYSTVLNHQIILDPLPGSQRKSSLWRCIEQLQQHEQEQTHRLFSGLFGVGHSCADLARLKDSLDSAKETLRIQKDIGVMQQPFYSNLHCYRIIASMKQSGNLDDFIEEYLGPLIRYDVEKGGQLLRTLKQYLVLCCKQETATALYIVRQTLYHRLDKIEALLGEDYILPEKRVAIELAIYAYEYIHGPIA"

CDS complement(6522338..6525574)

/gene="mdtC"

/locus_tag="EFAGFIKM_05730"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01424"

/codon_start=1

/transl_table=11

/product="Multidrug resistance protein MdtC"

/translation="MKGIINFSLNNKFAIWILTIISFAGLYSGLTMKQETIPNINVP
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IQPALEDIDGVAQVQVSGQYVKEVQLKFDQAKMAELGLTEDTVNGIVQGSSIRVPLGL
FELDKSQKAVVVDGNIIDIDDLKNLAIPVPPGGAGASAGNGASAAPQGGSGAPTSEAGQ
GTTPGSAQGTDAQEGQAAGGNASVGSPPGAANAPGIPTVKLSEIAKIEVIGQAESISR
TDGKESIGISVVKSNDA NTVDVVNAVKD KAEELQTQFKNADLTVLLDQGKPIQDSVNT
MLGKAVFGALFAILILLFLRNIRSTIISIPLSLLMALTALNMMDITLNMMTLGA
MTVAIGRVVDDSI VVIENIYRRLTLKGERLKGRELVREATREMFVPILSSTIVTIAVF
LPLALVSGMVGELFLPFALTMVFALLASLIVAITIVPMLAHTLFRKGLKNKQNHEEKP
GKMAEGYKRLLNWTL SHKLITVSI AVILLVGSFLYPPFIGASFLPEQQDKYVTITYSP
QTGALREDVEKEALVAEKWLLEQPGLEKMQYSIGGTNPLSSMGGGGGNSALFYIEYNE
DTKDFTQVKEQLVEGLKKEVTVGTWNELDMSGGLGGSGLSLSIYGDNVEQLKPVSDEI
LKLVEADKDNFEKADTTLADTYGQYTLVADQEKLSLGLTAGQLAMALSPARERPVL T
EVDIDNKTYKVYVETDDKTFNSIKEIEDET VTSPLGIEVPIKDVAKVEEGTSPNSIMQ
IDGKVVVQVTANILASDVTKASSNLQAEIDKLDLPDGVEVKFGGTTEQINDTFTQLGL
AMLAAIAIVYFVLVVTFGGGLAPFAILFSLPFTVIGIMVGLFIAGGTLDVSAMMGGLM
LIGIVVTNAIVLIDRVIHKEKEGMPTREALLEAGATRLRPILMTALATIGALLPLVTG
LEESAGIISKGLGITVIGGLISSTLLTLVIVPIVYEFLMKFKKKRIED"

CDS complement(6525608..6526555)

/locus_tag="EFAGFIKM_05731"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNPIHEMNEKKKLIITTALKLFSSKGSAA TSMQEIAELCGMSKG
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LTQGLFLSYVKIWFTEMPSLTVTKMATNLLQMMDYAAHGFLKQRPLPLIPLEDWPAWI
TELHPDSTVMRHPIHIKQM QDIAASELPAGQPKNDALETISILRQEMMEFTPRRAI
LGMMHNLNENVTAIQPLHSELQHILDAMYSRFIQADSSHT"

CDS complement(6526769..6526900)

/locus_tag="EFAGFIKM_05732"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MKKLLARMGSYTGYTLLIGMAIFYLIALVAIIILALYAFTGGN"

CDS complement(6527240..6527554)

/gene="gdnD_2"
/locus_tag="EFAGFIKM_05733"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P49857"
/codon_start=1
/transl_table=11
/product="putative guanidinium efflux system subunit GdnD"
/db_xref="COG:COG2076"
/translation="MAWMAIVGAGICEIFGVIGINGASTKKGWPYIVLMLVSFVFSFS
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CDS complement(6527554..6527895)

/gene="gdnC_2"
/locus_tag="EFAGFIKM_05734"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P49856"
/codon_start=1
/transl_table=11
/product="putative guanidinium efflux system subunit GdnC"
/db_xref="COG:COG2076"
/translation="MNRNWLYVFIGGIIIVWVSGLKHASNAWEWTLTGIAIVISFGL
IIAASKRLPVGTVYAVFTGIGTAGTVLTEMVLFGEPPRLAKVLLIGLLLCGVIGLKL
TDQQEAKGGAV"

CDS complement(6527892..6528515)

/locus_tag="EFAGFIKM_05735"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTAQSI RDAALFHFARDGYEGASLR AIADEVGIKKPSIYAHFSC

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CDS complement(6528642..6530117)

/locus_tag="EFAGFIKM_05736"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MVSLRRHTSDRKSSRGKFPYIRTGLVLLVLWLI AVMLYQTYKPL

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CDS 6530374..6531330

/gene="carH"

/locus_tag="EFAGFIKM_05737"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q50900"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional repressor CarH"

/translation="MGNKVYSIKQVAAMLGIPTVTLRAWENRYS AVTPERTESGYRMY

TEENVADLRWLKEQVELHQTNISEAVRMLKVSKLNPPEALPTPIMAPVPTMEEAYARM
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HFMTQLISQRFYQFFHLFPIYPHLPKVLALCPEGEHHQVGLLLFSLFMRKNGAEVLYL
GANTPEEGVFPIIREQKIKLVCLSITSPGLLEQCDQLIERIKNEFPHIRFVLGGKGYE
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CDS 6531596..6533146

/gene="crtN"

/locus_tag="EFAGFIKM_05738"

/EC_number="1.3.8.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q4VKV1"

/codon_start=1

/transl_table=11

/product="4,4'-diapophytoene desaturase

(4,4'-diapolycopene-forming)"

/translation="MIPNQQRKRAAVIGAGPGGLAAAMLLSGQGGEVDVYEKQPVIGG
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TALPKLDVHNTVYGILSRYFTDERLRWAFTFQSKYLGMSAWDCPGTFTILSFIEHHYG
LFHPIGGVNRIFQAMADVVEEYGGRIHTSTPVKQVIVRNGRAEGVLLENERIEADHV
VVNADFAHAVNHLFKPGVLKKYTPEKMKRKKYSCSTAMLYLGV DGEVDLP HHSIYFPE
DYRLNVDEITKHKMLSADPSLYIHNP SRLDSTLAPEGKSALYVLMPTPNLTADIDWEA
ERENVQEAMMKRMEGIPELADIRSRIEECMLFTPLDWETLDVYRGATFNMAHNLGQM
MYLRPHNEFEELKSVWLVG GGT HPGSGLPTIFESARISVRLIQEEDARTRSKPSSYVK
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CDS 6533143..6534606

/gene="crtNc"

/locus_tag="EFAGFIKM_05739"

/EC_number="1.2.99.10"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0DPE9"

/codon_start=1

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EEQTAEIERLFPGESRGFTRFMKMDTLFPAGRAAFLEAFPRKRDFFTPSTMSLMGR
LRAHKSVRKAVGDYFEHEELLDAYSLSQSLYIGGSPFGTPGIYSLLPYAEHEYGIWMVK
GGYAALPAILEQELISRGGRVVLNSEVTGLKIKNGVCEGIETAAGAENVDAIIYNGDF
PHLSGLLGQSPAVARKRKPYRPSSGCVLLYVGVDKTWEDATTHQFFLPPSLEGLQEV
FNQRRIPAKSSFYVFNPVALDETAAPQGQSVLYFLIPVPDAEGVDWDQESEALAERVL
EEAEQRGFPGLRAAIKWKKV RTPADAERDGLYGGGSFGIAPVLFQSGVYRPQPKPFPN
IKGLYAAGASVHPGGGVPIVMQSARMAVNQLMKEMGT"

CDS 6534603..6535475

/gene="crtB"

/locus_tag="EFAGFIKM_05740"

/EC_number="2.5.1.32"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37294"

/codon_start=1

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QLTDLKVTHYTTLQELEHYCYLVAGTVGEMLLPVLRDDNGAEVAMNGIALGKGMQIVN
IIRDVGEDRARVRRYVPLEIMEKHGYTEQDFEDGVVDERFIAIVHELKAAALNWFRIG
MDRLDTYPTESAFSIELAAAFYSTILHAVERNDYDVYTKRAYVSDCLKLEMLGAIVKR
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CDS 6535475..6536242

/locus_tag="EFAGFIKM_05741"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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IYQGRNRTGLSDQSVIWLKPGLWISSVIIWLGGMGVEWVGVHTHWPFGEYAYSDFFGI
HLFSVPVTLGFAWIAVVGNSALLSGGGSTWTGKLLRAVKTGFWAIVLDLVLDPVAHAR
GFWEWQAPGGFYGVPWTNYISWFIMGAFLSLFLPAMPNDRSSLLRAKWLYQLFILLFG
LLALKEGITGSFIIAAGVLLAEGSWLYDSRRKIKNV"

CDS 6536211..6536972

/locus_tag="EFAGFIKM_05742"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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SINKASASGIRTSLQYTSSELLDSGKRVWIFPQGEILHQEARPIQFRPGIGLLLRSPN
AIAVPVTLCHGMVQHDLPESMQAGPAVMEDWKALKSEEIAARLGHVLEQQLDDHRSE
LIRMGQGSPLDAIPLIRHVRSTSEKYDATRKRVNR"

CDS 6537172..6538122

/gene="crtQ"

/locus_tag="EFAGFIKM_05743"

/EC_number="2.4.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A3E0"

/codon_start=1

/transl_table=11

/product="4,4'-diaponeurosporenoate glycosyltransferase"

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YQVTKTWMEKLVVPMVMVFTIISHLPIFMIRRSSSPMFVAATGAFLLIHRSSYEASGGH
AAIQAHLVDDMSLAKAVKRAGHPVMLTDVHDVTNTRMYQNGAEVWNGYKKNMYEGMGR
KDVLLLGTMLMYTLMYIVPPLGLIIGLLMGSSMFVLYGLLGTLLGMAVKRVADHAGGQ
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CDS 6538119..6539600

/gene="crtNb"
/locus_tag="EFAGFIKM_05744"
/EC_number="1.14.99.44"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q4VKU9"
/codon_start=1
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/translation="MRGNVIIIAGFGGLSCAIQLASQGVQVTILERQKHVGGKLQQI
ERDGYHFDGRGPSTITMPSTFRSVFDHAGVAMEDYVQLYELEPRTRNIFADGTVVDLSG
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LRVRPTVKLDKLLRSYFQHPHTLAMFGRYATYVGSSPYQSPSIFAMMGHVEAEVGIYG
VKGGTCQLIEGMTRLAREKGVQIITGIEVRQIVVRNGKVAGVDTDQGFREADQVWANG
DVLSVNRLLLAPEHRKEMSDARIQKYEPSISGFVTLAGVRRQYDALLHHTVFFPERYE
LEFDHIFRDRKMPEDPTIYICYSGYSEAGMAPAGASNLFILVNAPYLSDSWNWEQQTE
RYGAFVLEQLAARGISGLNESDVLIRYTPRDIERDTLAHQGSIYGISSNSVKQTFMRP
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CDS 6539935..6541002

/gene="fni"
/locus_tag="EFAGFIKM_05745"
/EC_number="5.3.3.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P50740"
/codon_start=1
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/product="Isopentenyl-diphosphate delta-isomerase"
/db_xref="COG:COG1304"
/translation="MNEQERAGERLLPEVATGERKLEHVRLCLEENVAGEGVTSGMER
FAFRHHPLPELDFEEVHLETSFIGKKVRTPLLISSMTGGSKTTGAINERLARVANARG
WALGVGSIRAAVEQPELASTFDVRRWAPDIPVIANLGAVQLNYGFTTADFQRAVDIAG
ADMLVLHLNLTQEVEFQPEGNTNFSGLFQRIENLCRELDVPVGVKEVGFIDGVTAQRL
YEAGVSFIDVAGAGGTSWVQVEKYRNNNPVRRAAAAEFADWGIPTAECIQEVRALNPA

GALIGSGGLHTGVDAAKALALGADLAGFGRSLLESASVSDDALNERLEQVEFELRTVM

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CDS complement(6541150..6541713)

/locus_tag="EFAGFIKM_05746"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDFNYLFHQSYIDLPPPLQKSVYRSFYNLVHQDITYLLGRDHFL

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CDS 6542002..6543120

/locus_tag="EFAGFIKM_05747"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNKKKLLIGSSACLALFLSVGVAGANLGNVLQKHLVEDEAVLQ

KNINNMSNEQLIDEIDNLAATVGQPSTLAKNDSVGQNEINTLIPFVSALFERKDQLKD

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DFTLDDVGLLKEIHHEDDDILAFNGLKRLSNINVSEAYGISESILSNIEEQSPNKISA

ALRATAKYLKNESQSTLQKNTVDLEADFIDTSFKIHKSSNDEVKDSIFAISEIGSQ

KAITQIESDLVEQELKAFVDQNFITLKEILTGNPTEDIRFVVSALILPIVDLVE

PLSEVTSSISDPDLKKRSEEVIIVAQKEGISGNYKWAE"

CDS 6543150..6543755

/locus_tag="EFAGFIKM_05748"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKISRKLSLILFAIVLLGTSYTGGGTADAATGNQGYAAYRDGV

FFGFDWHAGLWDEPASNYGLPILHAPGTGKSVQWDTWSNFIDGNNFKGTYRPNTAPSS
AQRDLFVAMGRNLRQTQNISYNLGYQVYYSTGSASTYVKYDEVSSMRCDGVIEYIYEWY
SFRVYGNQTQWDVTKNDFWIREQHSGTLITPKKQVNYLTAI"

CDS 6543755..6544192

/locus_tag="EFAGFIKM_05749"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGKYKHLLMLLIVVPFTIINFSSYLKGHTPSIFQAAASILFIL

VWVYGYIMQSDKYKEYALLSTLYWLAGVILLTIGYFANSIIIPATIIWAGPVYGYR

YFLELPANLVFALVSIVIVYVSSIVGVLLGRIFKKRSVTFGEK"

CDS complement(6544376..6544807)

/locus_tag="EFAGFIKM_05750"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTHRRFSKKKIIILSAIVLVIGILAFKSLNVAIDPFRHLRITI

HNQSDYDLTNIQASLAQGDSYSTNESGSTYVFKKDIPSGVKVKFAPQLKLSGEGTVSL

EFTDSRGKTYNKMVCGYTEYLSGNSYVTVTNENVNVKEECM"

CDS 6545022..6545492

/gene="yycN"

/locus_tag="EFAGFIKM_05751"

/EC_number="2.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O32293"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0454"

/translation="MKLFPMNQEDYASFRIRSIKDFAEKVEAGTWAEERAAQQLAEES

YERYLPEGLNTPGAYLYNLVHPVDGNVGYIWFNITDNRRGKDAFLLDIVVEEAHRGKG

YGTETMKALEQAALSLGVDRIGLHVFGHNVRASSLYRKMGYEVTDLTMYKEIKG"

CDS 6545614..6546714

/gene="ychF"

/locus_tag="EFAGFIKM_05752"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37518"

/codon_start=1

/transl_table=11

/product="Ribosome-binding ATPase YchF"

/db_xref="COG:COG0012"

/translation="MALKAGIVGLPNVGKSTLFNAITQAGAESANYPFCTIDPNVGIV

EVPDERLDKLTENVVPKKTVPATAFEFVDIAGLVRGASKGEGLGKFLAHIREVDAIVH

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EVEVLERVKAVLYDDKPARSMELTDELLIVRDLHLLTLKPVLYAANVAEDEIGDVAN

NAYVQKVREFAAAENAEVVPISAKVEEEISELEGEDKQMFLEELGIEDSGLNLLIKAA

YKLLGLTYFTAGVQEVRAWTIRKGTKAPGAAGVIHTDFERGFIRAEVVSYYDDLVAAG

SMNGAKERGQLRLEGKEYVVNDGDVMHFRFNV"

CDS 6547353..6548420

/gene="prfA"

/locus_tag="EFAGFIKM_05753"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q8DU64"

/codon_start=1

/transl_table=11

/product="Peptide chain release factor 1"

/db_xref="COG:COG0216"

/translation="MLDKLQALADRYDKLSELLCDPDVASDNKKLREYSKEQSDLQPT

YEAYNEYKQVSQDLEAAKEMQGEKLDDREMVMKMEIDELSTRQKELDELIRVLMPLK

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VVFLINGRGAYSKMKYESGAHRVQRIPTTESGGRIHTSTSTVAVMPEAEDFDIEIHDK

DIRVDTFCSSGAGGQSVNTTKSAVRVTHVPTGIVATCQDGKSQNSNKEKALQVLRTRI

FDMKRMEEEAKISVERKSKVGTGDRSERIRTYNFPQSRVTDHRIGLTMHKLDQIMNGE
IEDILSALTIAQQTELMDRGE"

CDS 6548424..6549329

/gene="prmC"

/locus_tag="EFAGFIKM_05754"

/EC_number="2.1.1.297"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:B0B9D1"

/codon_start=1

/transl_table=11

/product="Release factor glutamine methyltransferase"

/translation="MTRAQFVMTPEQSCREAFVEASSFLEKCGVYEPQNNARLLLEHV
LGVYGAAYMMQPEPFPSEHRSRWEDAVTRKAAGEPAQYIIGSQEFYGLPFEVTPAVL
IPRPETELLVEAVLREADRVFPDGAFLAVDIGTGSGAIAVTMASLRPRWQVGAGDLSA
AALQVAARNAAANGVQIDFREGDLLAPFAGARVDILVSNPPYIPAADIAGLQQEVRDH
EPRMALDGGPDGLAPYRIMLEQLALLPAPPQIIGFELGQGQARDIAALLESAGHWPEI
IIVPDLAGIERHVLGVRTSEQVTKM"

CDS 6549415..6550635

/gene="mrdB_2"

/locus_tag="EFAGFIKM_05755"

/EC_number="2.4.1.129"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_02079"

/codon_start=1

/transl_table=11

/product="Peptidoglycan glycosyltransferase MrdB"

/translation="MLHKFKKIDYSIVFILVILMGISILSIYSTTFGRPKLEGLPKSA
VIFYILGFVVFVGMSMINYKFIKKNLYIYGVGMLLLIFVMFFGKEYYGAKGWLSIFG
VSLQPAELFKLCLIVFLSAFLARKKNRPLYFGRDVIPLSLCVLPPLLVLQNDLGNA
LSYVVILVGLLWIGNIKFTHALIGFMIAVAFIGGTQAYIHYHDEIVKFLNEIGRSHW
ADRFDPWLVPELTSRDVLWQTYNAKLAIGSGGITGKGMEGTTIQSNRVPLAYADSIF
VQIGEEFGFIGASVLLLLYFILHRLVLIALECKDRAGPYLIVGIIAMLLYQIFVNIG

PFIGLMPLTGITLPISSGGTSIMINMISMGLVMSIKVHTEENEDILGSAEQPSITDL

VMKLLRRKPSQQEQ"

CDS 6550904..6552124

/gene="ftsW_3"

/locus_tag="EFAGFIKM_05756"

/EC_number="2.4.1.129"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07639"

/codon_start=1

/transl_table=11

/product="putative peptidoglycan glycosyltransferase FtsW"

/db_xref="COG:COG0772"

/translation="MLRMLKKMDGVILFVMLLLMIISVFAIYSGTQTDANLANHHVKT

LYFYVAGFIAVLVIGLGNKYLYVKYAFYLYGLGIILLILANVLGSSINNANGWLKLGE

SFSFQPAELFKMILILFLAHLIVKRQRGTLKFWRDIVPIGCWAFIPFALVMAQNDLGN

ALGYVVILAAVFWIGNMRLKHALIALAIVGVAFFGFVKAYTFYHDEVFTFLEKIKREH

WAERIDPWLPEKATSKASWHTKNAGLAIGSGGIIGKGYLQGTSVQSGRPYTYSDSI

FVVIAEEFGFVGASVLILLYFILIHRMVLIALACRDRAGPVIIVGIIGMLLYQVFENV

GAFLGLMPLTGITLPIFISYGGTSLINMACIGVVMMSIKLYGQEEDELLMGEQQPRLS

ERLWNMLKKEKSAV"

CDS 6553044..6553703

/locus_tag="EFAGFIKM_05757"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSRRIVKQIGLIIVCLMMIIMMWEGQKTDAAVAATAIPEQSIRL

RILANSAPGDQLVKREIRDAVVAQMGEWVAELENPQSLDEARKVIREHLSEIENRVG

EELASRGLNYEYQVELGSVPFPTKLYGGTVYPAGDYEAVRITLGEGKGQNWVCVLFPP

LCFIDAGTGDALAKPSTVSAAAAEPGDAAESVQGDTPPEARFFLWDMAVKLWSWVTELF

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CDS 6553902..6555140

/gene="ywlC"
/locus_tag="EFAGFIKM_05758"
/EC_number="2.7.7.87"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39153"
/codon_start=1
/transl_table=11
/product="Threonylcarbamoyl-AMP synthase"
/db_xref="COG:COG0009"
/translation="MSRENEPVQHTSEMRDGREECDMKAPVELVTEMWDVRVLVSAEN
DHRMGNIELLDVKKGSADQQALADLQAAAACIRQGQTVAFPPTETVYGLGADARSTAAV
EAVFVAKGRPSDNPLIVHIAHRDQLDALVTEVNETAEALMAAFWPGPLTLVLPVRLGA
VSPRVTAGLDTVAVRMPDHPVALQLIAAAACPVAAPSANRSGRPSPTLASHVREDLDG
RIGGIVDGGPTGVGVESTVVQVGDDGTVTILRPGGITAEQLSAVAARVATDPALLAEG
ADGVDSPAPRSPGMKYTHYAPAGALCVVEGPPAAVAAWISAALAEAAQRGERTAVLAF
AEHAEQYRADAVFSLGDASELEEAARRLYAALRSCDEQGATYIVAEACSREGLGAAVM
NRLLKAAGNQLIQVGNQRPL"

CDS 6555316..6555876

/gene="mntP"
/locus_tag="EFAGFIKM_05759"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P76264"
/codon_start=1
/transl_table=11
/product="putative manganese efflux pump MntP"
/db_xref="COG:COG1971"
/translation="MWDVSAHVGQLVTILIMAVLGLDAFSLGIGIMKGIRLRDVLRL
ISIVTALFHIIMPLIGMYMGKYVSSLLGDITTYAAGLLVLLGGHMILNAFREGDTKL
VDHRSLLGVVLFSLSVSDSFSVGVSLGMFSSNLILTFLAFGVCGGVMSVMGLLLGRR
VSQNLGDYGEAIGGAILLAFGLLFIF"

CDS 6555935..6556507

/gene="ywle"

/locus_tag="EFAGFIKM_05760"

/EC_number="3.9.1.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:S0F332"

/codon_start=1

/transl_table=11

/product="Protein-arginine-phosphatase"

/translation="MKHILFVCTGNTCRSPMAEGLLRKLALERGIQVEVRSAGVAATS
GMPISRHAEEAVLRDHNVEGPPQSTQLSSNLVGWADLVLTLTRSHKHVMQVFPDSVHK
TYTLKEYVEDDEQVLSDVQELDSLAFATLEMKRALGQEILASERERAIEIRQRIPSFDI
SDPFGGSRDDYNIAAAEIRTALDRLLDKLG"

CDS 6556827..6557420

/locus_tag="EFAGFIKM_05761"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39157"

/note="UPF0340 protein YwlG"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTIELDSEQPGLQEQTTSILHELALAGQLGPGQIVVIGTSTSEV
AGARIGTSGAIEVAQQLLAGIREVQEEFGFDTVFQCCEHLNRALVMERSVLTRLGLTE
VGAVPVPKAGGSMASAAAYRSLTDPCLAEHVQAHAGLDIGETMIGMHLRHVAVPYRTAL
RYVGDARVTTALTRPKLIGGERAVYRMEEQPDSTFCD"

CDS 6557677..6558924

/gene="glyA_2"

/locus_tag="EFAGFIKM_05762"

/EC_number="2.1.2.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39148"

/codon_start=1

/transl_table=11

/product="Serine hydroxymethyltransferase"

/db_xref="COG:COG0112"

/translation="MEQLRKNDPAVLEAMNLELKRQQNNIELIASENIVSEAVIEAMG

SVLTNKYAEGYPGKRYYGCEHVDIVEDIARDRAKELFGAEHVNVPQPHSGAQANMAVY

LAALKPGDTVLMGNLAHGGHLTHGSPVNASGLLYNFVAYGVQEDTFLIDYDEVKAAF

KHRPRLIVAGASAYPRTIDFEKLASIANDVGALFMVDMAHIAAGLVAAGLHPNPVPHAH

FVTTTTHTKTLRGPRGGMILCRKAWAAAIDKAVFPGSQGGPLMHVIASKAVAFGEALQP

SFKTYAENVVKNAQVLAETLIAEGLNIVSGGTDNHLMLIDTRSVNITGKEAEHVLDSI

GITVNKNAIPFDPTSPFVTSGIRIGTPAATSRGMNEEAMVAIGKIIAKTLKNPKDTAK

LDEARAEVTALTDQFPLYTDLKY"

CDS 6559350..6559979

/gene="upp"

/locus_tag="EFAGFIKM_05763"

/EC_number="2.4.2.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P70881"

/codon_start=1

/transl_table=11

/product="Uracil phosphoribosyltransferase"

/translation="MGKLVICDHPLIQHKLTFIRDMRTNTKDFRELVDEVATLMAYEI

TRDVELETIDVQTPVAATQGKVISGRMLGLVPILRAGLGMLDGVVKLLPAKVGHVGL

FRDPETLQPVEYYTKLPTDVTERQLIVIDPMLATGGSAAIDVLKKRGCTQIKMMNL

VAAPEGVKAVQDAHPDVDIYVAALDDRLDDHGYIVPGLGDAGDRLYGTK"

CDS 6560036..6561193

/gene="mnaA"

/locus_tag="EFAGFIKM_05764"

/EC_number="5.1.3.14"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39131"

/codon_start=1

/transl_table=11

/product="UDP-N-acetylglucosamine 2-epimerase"

/db_xref="COG:COG0381"

/translation="MSNKIKVMTIFGVRPEAIKMAPLILELQKHPESESIVCVTAQH
RQMLDQVLEVFDIHPDYDLDMKDRQTLNEITIRVLGGLEPVLSEAKPDIVLVHGDTL
TTFVASAAFLQQIQVGHVEAGLRTWNKLSPEEMNRQLTGVLADLHFAPTDWSSSN
LAKENKSESSTYVTGNTVTDVFQYTVREDYTHPVLDDWAQGKRLVLMTAHRRESQGEPH
RNIFQAVKRIADEFEDIAIVYPVHPSPAVKEPAHAILGNHPRIQLIDPLDVVDLHNFY
PHTHLILTDSGGLQEEAPSGVPLVLRDTERPEGIEAGTLELVGTEELVYERTKA
LLTDKTLYESMSQAANPYGDGHASERIVNAILHHFGVNSERPESFHRKFKK"

CDS 6561379..6561633

/locus_tag="EFAGFIKM_05765"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MADSNKPNSSRNHDDNVWKAMGLVTAFGIEIAVLAVAGYYAGSW
LDKTIGGNGIWIASVLFLLAAGGVSIYFIKKIMGESDE"

CDS 6561626..6562003

/locus_tag="EFAGFIKM_05766"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSELTRYRRSMTVFVVMYFLMICFLAAFMPRVETIALGLALGTG
VSWINAFYLGKVRKMSDDAAEGNLKRVNLGFLTRAAFAVLGIFISMRFPQYFNTYAV
AGGLVIAQYSLLIIGIVYSRRAE"

CDS 6562049..6562867

/gene="atpB"

/locus_tag="EFAGFIKM_05767"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P09218"

/codon_start=1

/transl_table=11

/product="ATP synthase subunit a"

/translation="MHEAPIIMLGGFRLDLSVLLMLVVTGAIVFIFAVLATRRLSVEN
PGKLQNFMEWAVEFVRNLISSTMDMKKGKHFISLALSMIMFIFVGNMLGLPLVAVSEV
TDVNQAQVFGKPIVTAVEAFEKAHAKDPEAHPHVELAWWKSPADLSVTMGLALVAFL
VSHGLGLFRNTKGYLQHYFKPFALFLPINLIETASKLLTHGMRLFANIFAGEVLIATI
LKLTTFKVFGAIAAIPLLMVWQGFSGFIGAIQAFVFILMMVYISQSIETHDEH"

CDS 6562946..6563170

/gene="atpE"
/locus_tag="EFAGFIKM_05768"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P00845"
/codon_start=1
/transl_table=11
/product="ATP synthase subunit c"
/translation="MGAMALIAAAIVAGLGAFGAGIGNGMVISKTVEGIARQPEAKST
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CDS 6563284..6563772

/gene="atpF"
/locus_tag="EFAGFIKM_05769"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37814"
/codon_start=1
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/db_xref="COG:COG0711"
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CDS 6563769..6564317

/gene="atpH"
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/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P09220"

/codon_start=1

/transl_table=11

/product="ATP synthase subunit delta"

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CDS 6564334..6565848

/gene="atpA"

/locus_tag="EFAGFIKM_05771"

/EC_number="7.1.2.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5KUJ1"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0056"

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ISITDGQIFLEADLFNAGQRPAINVGISVSRVGGSAQIKAMKKVAGSLRLDLAQYREL
QAFSQFGSDLKATQARLNRGARMMEILKQGVNQPLAVEQQVVSPLYTAVKGFLDEIPT
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CDS 6565979..6566851

/gene="atpG"

/locus_tag="EFAGFIKM_05772"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5KUJ2"

/codon_start=1
/transl_table=11
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/db_xref="COG:COG0224"
/translation="MAKGMREIKRQIKSVQSTKQITKAMEMVAAAKLRKAQEKAEEAR
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FELAEFDELYICYNRFVNALTQIPTVEKLLPMETPEVTAAEGPTASYEYEPSAEAVLE
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EITEIVAGANAAQG"

CDS 6566945..6568348

/gene="atpD"
/locus_tag="EFAGFIKM_05773"
/EC_number="7.1.2.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q5KUJ3"
/codon_start=1
/transl_table=11
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/db_xref="COG:COG0055"
/translation="MNKGRVVSIMGPVVDVEFDRGGLPEILNAITITTVSESGVSVNL
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KTVTIQELINNIAQEHGGISVFAGVGERTREGNDLYHEMSDSGVINKTAMVFGQMNEP
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TLATEMGQLQERITSTKKGSVTSIQAIYVPADDYTDPAATTFAHLDATTNLERKISE
MGIYPAVDPLASSSRILSPEVVGEEHYNVAQGVKRILARYNELQDIIAILGMDELSEE
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LFVGTIEEAWEKAKTLV"

CDS 6568411..6568815

/gene="atpC"
/locus_tag="EFAGFIKM_05774"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q5KUJ4"
/codon_start=1
/transl_table=11
/product="ATP synthase epsilon chain"
/db_xref="COG:COG0355"
/translation="MSTFLLIIVTPERLVYSEQVNSITARGIEGELGILPGHIPMVTP
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CDS 6569422..6569679

/locus_tag="EFAGFIKM_05775"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDTDLTNQVNQALSTNGLVSIIVSLLCIALSWWALTNLKLDLII
RQPRGAQGRRLLHLLAILGHAVAGFVIDYLSWTQMLRNLF"

CDS 6570198..6571547

/gene="murAA"
/locus_tag="EFAGFIKM_05776"
/EC_number="2.5.1.7"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P70965"
/codon_start=1
/transl_table=11
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1-carboxyvinyltransferase 1"
/db_xref="COG:COG0766"
/translation="MMSKFIVRGGKRLTGSVKVSGAKNSVLPPIAASLLGEEGQSVII
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LDVASVGATQNIMMAATLAEGVTVLENAAKEPEIVDLANFLNGMGAIVRGAGTGVIRI"

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MHVDEFQLMNAEIKVEGRSSIITGNAKLKGAKVTATDLRAGAALIIAGLVAEGTTEVG
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CDS 6572020..6573360

/locus_tag="EFAGFIKM_05777"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKEARVQVKVPLVPRPGMQEPEGNTVSGVEKDKAAPLNLRTPVS

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QPAAAVSALLAMALLIPVILVWPRTSESPKPIAPTSSSTRTPAPAPAVPVTYPEPK

VRVYLSATGTTMNLPLEDYVTGVVAAEMPAEFRLEALKAQAIAARTFIVRRLAASDTS

GVPSPAADVTDVTNVHQVFIPPDQVKADWTRLGKAKEWEKLQQAVRESRDTVMYQGGKA

ITASFFSTSNGYTENAEDVWGNAPYLSVDSPWDKNLAPGFKQVTMTKRNEILQKLN

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DEIQITTYGYGHGVGMSQWGANGMAQEGHTATQILKHYYTGISFGQASKMLASK"

CDS 6574386..6575126

/gene="spolIQ"

/locus_tag="EFAGFIKM_05778"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P71044"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0739"

/translation="MNEQNKKTNQEETPKTTQGVPASQPSSWKRAMSKRWVFPAAYIA

AAGIILTLVWVYQGTGDKTLNSDPASGVVETGASAGTEGTAVGGEEESVEVVAKSENF

VWPVAVPSEISVVKPFYDSEASTEEHEAMVQYNDTFIPNTGVDLARGDNKTFEVKAA

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GKTLGNHLHFEVYEDGQPVNPQGYYLPEK"

CDS 6575297..6575584

/gene="spoIIID"

/locus_tag="EFAGFIKM_05779"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P15281"

/codon_start=1

/transl_table=11

/product="Stage III sporulation protein D"

/translation="MHDYIKERTIKIGRCIVETRNTVRTIAKEFGVSKSTVHKDLTER

LPEINPDLDQVKHILEYHKSIRHLRGGEATKIKYKKTSGKKREVLASAKS"

CDS 6575804..6576802

/gene="mbl"

/locus_tag="EFAGFIKM_05780"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39751"

/codon_start=1

/transl_table=11

/product="Cell shape-determining protein Mbl"

/db_xref="COG:COG1077"

/translation="MFSKDIDGLGTANVLIHVKGSGVVLDEPSVVTIERDTKRVLAV

GEEARRMVGRTPGNIVAIRPLRDGVIADEFTEAMLRHFNRVVGARSWYSHPRILICA

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RGVLTGGGALLNGLDELLSNELHVPVWVAEDPMHCVVKGTGIMLNNLDQVVKKKF"

CDS 6576906..6577790

/gene="flgG_2"

/locus_tag="EFAGFIKM_05781"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A1J3"

/codon_start=1

/transl_table=11

/product="Flagellar basal-body rod protein FlgG"
/db_xref="COG:COG4786"
/translation="MLRGLYTATAGMITQQRHDTATQNIVNMNTTGYKQVNSVSRSF
PEMLITLVGGDANLPTKRLGKLNTGVFAEESLSMNLQGTIMETGQKNDFSISNMTVN
DPQTGQPVPFDASGKFVRADGTVTFQPQAYFTVQDAEGNTGYTRDGHFEITGTGQLLS
STGSQVLDNNGQPVVLTGSVEQFKVDEQGRLVDAATGAPTGVTLGISVIDQPNQLVRQ
GNGNFSLSDANGATSRMMAAGDNVQIRQGYLEGSNVDASQATVDMNAAFRA YEANQKI
VQFYDRSLDKAVNEVGRV"

CDS 6578212..6579051

/gene="flgG_3"
/locus_tag="EFAGFIKM_05782"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A1J3"
/codon_start=1
/transl_table=11
/product="Flagellar basal-body rod protein FlgG"

/db_xref="COG:COG4786"
/translation="MNNSMISAKVSMTAIQQRLDVISDNIANVNTAGYKSKQAAFEDV
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SKVAFDENGNNLIRRGNAANATIGAQLQVVDIERPEGLVQFADNLFGLDAGLTEDDVF
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MRA"

CDS 6579064..6579288

/locus_tag="EFAGFIKM_05783"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MTETQQQNSKPEKKEVKKKKSGWRIARWFLVPILLVLALAGGMV
AGYVVLGKQDIGSVWQWSTWEHVYNLVFAP"

CDS 6579777..6580208

/gene="fabZ"
/locus_tag="EFAGFIKM_05784"
/EC_number="4.2.1.59"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9HXY7"
/codon_start=1
/transl_table=11
/product="3-hydroxyacyl-[acyl-carrier-protein] dehydratase
FabZ"
/db_xref="COG:COG0764"
/translation="MLDIKQIQEIIPHRPPFLLVDKILEIEDGKRAVGLKNVTINEPF
FIGHFPEYPVMPGVLITEALAQVGAVAILNLEGNGKIGFLAGLDNFRFRGQVVPDGT
LILEVEITRLKGSIGKKGKATARVNDKVVAEGEIMFALSDPS"

CDS 6580320..6582041

/gene="pgcA"
/locus_tag="EFAGFIKM_05785"
/EC_number="5.4.2.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P18159"
/codon_start=1
/transl_table=11
/product="Phosphoglucomutase"
/translation="MEQLSTAAAETLQQWLEDASIDEATKQELRDLQDQPKLEERFY
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MSRVDAQ"

CDS 6582259..6584280

/locus_tag="EFAGFIKM_05786"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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EMFLRTTLEDTFGVRPRFKEFMLGHPLFIVGVFAALKYRKVIFVLIIAIGQLSMVDT
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CDS 6584256..6585437

/locus_tag="EFAGFIKM_05787"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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RFWESDRKELTAAAGLKKLCSKRAVHLRFLPFHLPVDEQASRFLMEMLGDVTSKGSE
ISITEDLTPQLMLEEVSKCDLVIGMRLHSLIYAASQYVPPVGISYDPKIDQFLRLD
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CDS 6585445..6586206

/gene="tagA_2"

/locus_tag="EFAGFIKM_05788"

/EC_number="2.4.1.187"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P27620"

/codon_start=1

/transl_table=11

/product="N-acetylglucosaminyldiphosphoundecaprenol

N-acetyl-beta-D-mannosaminyltransferase"

/db_xref="COG:COG1922"

/translation="MSQTGSIPTVSIYGIPFSKLTMKETVKVLQEAVLSKQTPHQVIT

ANPIMVMAALENPAIMEVMQAAELIVPDGTGVVWAANYCGNPVAERVPGFELLHELLR

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CDS 6586622..6587749

/gene="tagO_2"

/locus_tag="EFAGFIKM_05789"

/EC_number="2.7.8.33"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34753"

/codon_start=1

/transl_table=11

/product="putative undecaprenyl-phosphate

N-acetylglucosaminy 1-phosphate transferase"

/db_xref="COG:COG0472"

/translation="MVAIFIIGFIVSMGLALALTPLVKKFAVRIGAMDTPNARKVHTR

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FMGDTGSLFLGFSLAMLSMLGFKQIAIVSFITPLIIIGVPLSDTFFAIIRRAVQRKPI
FAPDKGHLHHCLRELGFSHRQTVLIIYGIAAFFGVLAIIQSSAAMFEANWVTFVVICI
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CDS 6587915..6591868

/locus_tag="EFAGFIKM_05790"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQQKKRPLVWIMLVTMVFSLPQGLFGGAVASAAEGDPVGSNAY
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FDKDQPFTDLKVQMGQNKSSILSSNPFTGTSTATTGQVLLPYSASPNPFSPTNG
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PKKDQTLRLRLAYGNFSAGYNASYTFSPAQDITEIYYLPDYKAGEAIDSQTKLDGTK
LQTDEFFILVESSEPISTLVGEYLPTGTTKLTIDPVDTVDMKLDNQKIYKVSFGL
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TDEDANKLPITISTTLKINVIDQNQSTVTSFMPTLIPKDSRQQFINKPITQYEDDEMK
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QPATAGLPSYDITGNSDLFLARIQNLKFDVPGTHVYTLLEINSTGARTTQRLEIVREP
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DGFFGPDQPVTRQAAMMIARAMNAKLAANDSKLTATLAKSFLDSTSIDFYARPAIVA
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CDS 6592073..6592414

/locus_tag="EFAGFIKM_05791"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKPIYSRAQLGYMKAKTQFEKQAVILEKKLEDTRKTEEISQEVMEGLVQSTGFHDAYNSLVLAENELIEWSHTTMKHEKTYRENRPIDDMYLRNLNSDPNMR
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CDS 6592931..6596005

/locus_tag="EFAGFIKM_05792"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRNTSDPIKENSVMNAQGGDKKVMKKILSVALSTAMAFSMFAS
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YTGGNKLDNQKAIKLTVSGIKNSDGSKTIAQEVFTFPVDVTPSVKEVKGLGTGAFQV
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GLKVVPVESDFAVAADTEAPTVTSAKSYDLQKVEIEFNEPIRSFTRVYNGTTAKTGEV
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VNDSVKATATNKVTVKFDGILNTVDANDFAVRVGTTNYNVVLGQPTYSNNGQTIANFT
IAGDNKLNAAAPVAKFGLRVTPNTQDNLGVRVDVPAVAAGIDVIDNIKPETKDFDTNK
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CDS 6596174..6598765

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CDS 6598906..6599472

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/codon_start=1

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CDS 6599621..6599893

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/inference="similar to AA sequence:UniProtKB:P02959"

/codon_start=1

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CDS 6600149..6601351

/gene="metK"

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CDS 6601544..6605254

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CDS 6605371..6606597

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CDS 6606829..6609552

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CDS 6609600..6610760

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kinase/phosphatase DegS"

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CDS 6610765..6611490

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CDS 6611848..6612225

/locus_tag="EFAGFIKM_05802"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS 6612683..6614572

/gene="mfd_2"
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/inference="protein motif:HAMAP:MF_00969"
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HPLPVPRLIKMVTVAECIKKRNLP SALRTNIQISLKRDAQVFVFVTRIAQIEAFVNLM
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CDS 6614638..6615534

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CDS 6615851..6620362

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CDS 6620512..6620919

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CDS 6620891..6621013

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CDS 6621093..6621377

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CDS 6621389..6621892

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CDS 6621912..6623465

/gene="flgK"

/locus_tag="EFAGFIKM_05810"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P33235"

/codon_start=1

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CDS 6623490..6624410

/gene="hag"

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CDS 6624428..6624997

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CDS 6625052..6625531

/gene="fliW"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:A4ISV0"
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CDS 6625532..6625777

/gene="csrA"

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CDS 6625922..6627532

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/inference="ab initio prediction:Prodigal:002006"

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CDS 6628069..6629643

/gene="fliD"
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SFTDSNGKSLFTGSTSIATMVATINGNAKANVTAKYDEISGKLIINSKTSKTDGKADL
VGTDDDSLLELFNQKYNPVDDGPDKYKTTNAQDAKFSVNGRDYTDKSNTVTINGVQLT
LQKTTADPADPSKDIPVSITTSSDTETALQTIKSFVEDYNSLITLLNTKLDENKYRDF
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MGSYNSGGKIVLDEVVLKKALTENPQKAVDLFQGTGSEANNGIFDKLADKISGSLDSL
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MNKLSSQSSSLFSTTS"

CDS 6629673..6630065

/gene="fliS"
/locus_tag="EFAGFIKM_05818"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39739"
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/db_xref="COG:COG1516"

/translation="MIKSPYEKYRQSSVQTSTPAQLVIMLYDGAIRFVKVGLEGLNNQ
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AIGYLTDLRETWMQASKLASTQTESAHG"

CDS 6630058..6630393

/locus_tag="EFAGFIKM_05819"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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CDS 6630793..6630990

/gene="cspB_2"

/locus_tag="EFAGFIKM_05820"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P41016"

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CDS 6631411..6631974

/gene="yyvD"

/locus_tag="EFAGFIKM_05821"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P28368"

/codon_start=1

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/product="Ribosome hibernation promotion factor"

/db_xref="COG:COG1544"

/translation="MNLSIRGQQIEVTDALKDYVDKKLSRLEKYFDAPLNSDGAVTLS

TTRGLHTVEVTIPLKGIVLRAEDESDDMYASIDSVVDKLERQIRKHKTINRKFRQEG
SLKTLFVEDPTGTVATAELDADTDDDDFEVVRTKRFMLKPMDVEEAILQNMNVGHNFF
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CDS 6632623..6635265

/gene="secA_2"

/locus_tag="EFAGFIKM_05822"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P28366"

/codon_start=1

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/db_xref="COG:COG0653"

/translation="MASLELIHHITFILFVTPGQVDAISIRWCRMAATGGLFCFARKG

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ADVVKYKSIDGKFNAVVEEIVARHKNQPIVGTVSIENSERLSDMLKRRGVKHQVLNA

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VESAQKRVEGNFDFVRKVVLYDDVMNQREIYKQRREVLESENKQIVMDMIKPSI

ERIVEAHCSDDIPENWELQEVADYMNSKLLDDGSITKDDLWGKEAEIIEFLFTKVQN

KYNAREERIGEEMVREFEKVVVLRAVDSKWMDHIDAMDQLRQGIHLRAYGGTDPLREY

QFEGFEMFHQMIASIQEEVATYVMRAQIESNQERQAVVEESQISTSGEPAEKRPVKVS

DQIGRNDPCPCGSGKKFKHCHGQE"

CDS 6635602..6636621

/gene="prfB"

/locus_tag="EFAGFIKM_05823"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A6R4"

/codon_start=1

/transl_table=11

/product="Peptide chain release factor 2"

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GAGGTESQDWGQMLLRMYTRWSEKRGFKVEVLDYLPGDEAGIKSVTSLIKGHNAYGYL
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GQHINTTDSAVRITHLPTGVVTCQNERSQIKNRERAMKMLRSKLYERKIEEQKQQLD
EIRGDQSDISWGSQIRSYVFHPYSMVKDHRTSVETGNTGAVMDGDLDAFIDGYLRSQI
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CDS 6636754..6637662

/locus_tag="EFAGFIKM_05824"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MQQRSQLHNNRKKRITSLIPLNGPWRNVVDTVSIIVGSFLIAVA
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QKYSGLSYSLCVVIMDATVIIMAAFVLSLEQSLYALIGLYVTGKVIDAVEMGLGFSKV
AYIISNQTEAISKVILDDLDRGLTKLEAKGGYTDDQRTVLMVVVGQNEVPRLKALIRS
VDPGAFVIISNAHEVLGEGFKRGEHV"

CDS complement(6637942..6639390)

/gene="clsA_3"

/locus_tag="EFAGFIKM_05825"

/EC_number="2.7.8.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P71040"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG1502"
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VFGFVLYLLTGQNLTRYRLFQWKERKKLGLERIEAQLTQLHDNRTPFRNQATETSQD
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IRDALIRKAREGIKVRLLYDALGSRRVSKRFFKELREAGGLVEVFFPSKFSLINLRMN
YRNHRKIVIIDGNLGYTGGFNVGDEYLGLNSKFGYWRDTHLRIQGNVHALQTRFLLD
WNEASKQHDTPTYVPAHFPHIEGTGKIAMQIVSSGPDAETEHKNSYLMINGAKQSIL
IQTPYFIPDASVFELRLACLSGIDVRIMIPNKPDPHAFVYWATLSYIGELLKVGAKVF
IYDNGFIHAKTLIIDLVSASVGTANIDYRSFRLNFEVNAFMYDETIATLVQTFEHD
HVSREMTLDEYQKRSLIIRFKEAISRLSPIL"

CDS 6639721..6640770

/gene="argC"
/locus_tag="EFAGFIKM_05826"
/EC_number="1.2.1.38"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q07906"
/codon_start=1
/transl_table=11
/product="N-acetyl-gamma-glutamyl-phosphate reductase"
/translation="MNNKLKVAIVGSTGYGGVELIRFFQNHPLVEITSVISSSSSGES
IADGFPHLTGVIHRPLDGVDPAEIASRADLVFTATPSGVSAKLVPSTLLAAGLKVIDLS
GDFRLKDGTVYEEWYKHPAPPADLLEQAVYGMAEVYGEEVKGQNFISNPGCYPTATLL
GLIPAVEAGWIDPSTIIIDAKSGVSGAGRGTSLTNHYAEMNENLKAYKLNKHQHIPEI
EQVLGSITGTPVTFTTHLVPMTRGIMSTMYASLVGEHSDREIVDLRKYYENRPFV
RVREPGIWPSTKEVYGSNYCDIGFAVDPRTRGLTIISVIDNLVKGASGQAIQNMNLM
GWEENLGLNMTPVYP"

CDS 6640902..6642140

/gene="argJ"
/locus_tag="EFAGFIKM_05827"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q07908"
/codon_start=1

/transl_table=11

/product="Arginine biosynthesis bifunctional protein ArgJ"

/translation="MGTNVEQHTFIVVENGITVTPGGFTAGGLHCGLKKTSRNDIGAI
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LTTDLVKKEACVSVMVNGKTVTIAGAAKGSGMIHPNMATMLAFMTSDAVIGAEALQSL
LRQATNYTFNMITVDGDTSTNDMLVAMSSGYAGNEELTMEHPDWDAFAAGFTYVCQVL
AKAIARDGEGATKLVEVEVTGAVSDESAQAIKTVIGSSLVKSAMFGADANWGRIIAA
VGRAGQPVNPDVDIRLGDISVLAQSRPVVFDEELALAYLQTDTVRIVVDLHHGEGTA
TAWGCDLTYYDYVRINAAYRT"

CDS 6642459..6643298

/gene="argB"

/locus_tag="EFAGFIKM_05828"

/EC_number="2.7.2.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9X2A4"

/codon_start=1

/transl_table=11

/product="Acetylglutamate kinase"

/db_xref="COG:COG0548"

/translation="MNSTLPNKSTATEASTEKQMFVMKCGGSTLAALPESFFADLRDL
QSQGTQPVIVHGGGPAISDNLAKLGIETEFVNGLRKTTEPVLDDVEMVLAGSINKQIV
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APVGVDATGQRYNINADTAAGAVASHLGVSIRMIVTDVPGIMKNVGGEEKVLPSVSVQ
EIEDMIQTGEIYGGMIPKVRAAIIACIHGQVREVVVDGSEPQILSRVLGGEEIIGTRII
RMQ"

CDS 6643665..6644918

/gene="argD"

/locus_tag="EFAGFIKM_05829"

/EC_number="2.6.1.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O66442"

/codon_start=1
/transl_table=11
/product="Acetylornithine aminotransferase"
/db_xref="COG:COG4992"
/translation="MAKGNEQPGSGTAVAGATATGTASQTESSLFQTYARYPISLVKG
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AALLTANTCADAVFFCNSGAEEAIAIKVARRYHQVKGTDRYEVIITFAQSFHGRTLA
TLTATGQDKVKEGFLPLPAGFVTVPPLHDIPALEAAIGPNTAAIMLEMVQAEGGVYPVE
PEFVKHVRKLCDEHGLLLIVDEVQTGMGRTGKLFHEHYGIEPDVFTVAKGIGSGFPV
GAMLGKGFRLDAFTPGSHATTGGTPLASSVVIATITMLEDRLPERAAEMGKYLMS
MRNRLAGNSFVKEVRGLGLLVGIECAEPIGDIVLAGQKRGILFVSAGPNVIRLLPNLY
VSKEEIDEAVSLVATLIEEHVAAKA"

CDS 6645021..6645155

/locus_tag="EFAGFIKM_05830"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDKLEKHPDKVLTLSSLTMRVQGTGNKEAIIHDSTTDGKGSED
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CDS 6645118..6646083

/gene="argF"
/locus_tag="EFAGFIKM_05831"
/EC_number="2.1.3.3"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P18186"
/codon_start=1
/transl_table=11
/product="Ornithine carbamoyltransferase"
/db_xref="COG:COG0078"
/translation="MTAQQTEKVQKIDLRGRDFIEFTDYAEEIRYLLDLAIEIKGKQ
KSGVPFQPLKGKTIGLIFEKSSSTRTRVSFEVGMFQLGGHALFLSKNDIQLGRGETTHD"

TAKVLSRYLDGIMIRTFGHHNVTELAEHADVPVINGLSDAAHPCQVLADFQTVLEHKG
KLAGLKMVYIGDGNNMAHSLMLGAAKMGMHVAVATPEGYEPDSAVVEQARIIAQESGS
EVTVTYSAQEAAKDADIVYTDVWASMGFEEEQKIREQAFAAYQVDEELMKGAKPDYMF
LHCLPAHRGEEVSAGVIDGPNSLIFDQAENRLHAQKALMAALMSE"

CDS 6646177..6647412

/gene="argG"

/locus_tag="EFAGFIKM_05832"

/EC_number="6.3.4.5"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P59846"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0137"

/translation="MAKEKIVLAYSGGLDTSVILKWLKETYDAEIIAFTADIGQKDEL

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VDIARAEGATAIAHGATGKGNDQVRFELNAAALTPDINVIAPWRLEEFRNQFPGRAEM

IAYAEKHGIPVTASAAKPYSTDRNLLHISYESGVLEDPWFDPSADENKDMFLLSSAPE

DAPDQAEYVELEFEQGDCVALNGERLSPLQVMEQLNELGGKHGIGRVDMVENRFVGMK

SRGVYETPGGTILFTAHRKMESITMDREVMNLRDSLITRYSTLVYNGFWFAPERLALQ

ALVTESQKNVTGTVRVKLYKGNIIAGVKSPVSLYNPDIAATMEADPTQAYDQGDATGF

IRLNALRLKVNSGVEQNKN"

CDS 6647496..6648923

/gene="argH"

/locus_tag="EFAGFIKM_05833"

/EC_number="4.3.2.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9LAE5"

/codon_start=1

/transl_table=11

/product="Argininosuccinate lyase"

/db_xref="COG:COG0165"

/translation="MSERGVLTVSKLWGGFRFTKQTNHLVEEYASINFDKALAEEDIQ
GSLAHVTMLGKCGILPAEDVETIKEGLMTVLHKIGAGEVEFSVSEDIHMNIEKNLIE
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GYTHLQRAQPILFAHHL MAYVSMFQRDAERLMDSYKRINILPLGAGALAGTTFPIDRH
FVAEQLGFDGVYENSLDAVSDRDFIVEFLAAASLIMTHLSRLSEELVLSSTTEFGFVE
LDDAFCTGSSIMPQKKNPDPVELVRGKTGRVYGNLIGLLTVLKSPLAYNKMVEDKE
GMFDTVATLEGALQLFAPMIATMTVNKDRMRQAVNQDFS NATDIADFLVGEGLPFRQA
HEVIGKTVLYCIQNSKYLLDLTIDEFRQFSPLFDDRIEVLQPEAVVNARNVYGGTAS
GQVAEAIGRSEKVL EITEQWITNRG"

CDS complement(6649131..6649919)

/locus_tag="EFAGFIKM_05834"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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PALARSFFPLSDQREDNFVAGLSMGGYGAFKLALRKPDQYAAAASLSGALDMSAHMDR
NASSALQQTELQRIFGPEVAGTENDLIHLLKENQSNESPRPLLYQCCGTEDFLYEDNQ
TFRQACEQTNFELTYEEGPGEHEWGYWDAKIQDVLKWLPLQKRD"

CDS 6650194..6650817

/locus_tag="EFAGFIKM_05835"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

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DLLKEAGREQSLYALEQIMMLYVLDKLLMSGDITRQEGALLIEVMSEHYLFTGKPSE
LVLIRKMGVPSFMLVTAGTEFYFDNGVKVVL RQPMGTFMEELKLKLG"

CDS 6650832..6651560

/locus_tag="EFAGFIKM_05836"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEERNKRNDLNVAGISQTAGGNFHRVSDGMAKVNGNLDCTSME
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CDS 6651529..6652278

/locus_tag="EFAGFIKM_05837"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPRWAAVSEFKVWIWRERDGMNNNLGRSLDKKMDISIVGDGS
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DGEDGIQASGLHAKAEHIKVVGELHLSGDCQAENIKLNGRLTIAGMLSAEHITLKIMG
PSEVKEMGGSII SVKSGRLNDLFTGSKSILKAQIIEGDDIELENTEAEIVRGDKIKIG
PGCRIGTVEYRSSLQIHPQSEVLLQSNRSLD"

CDS 6652351..6653904

/gene="bmr3_4"

/locus_tag="EFAGFIKM_05838"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P96712"

/codon_start=1

/transl_table=11

/product="Multidrug resistance protein 3"

/translation="MVARKNISGLVLAGLLLSILMASMDNTIVATAMGDIVGKLGGLD
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YRAIQGIGAGALVPIAFTIMFDVVAPESRGKLGGLFGAVFGLSSVFGPLL GAYITQYA
TWEWVFYINLPLGLIAFVFIAFFYKESHQHQSQQIDWLGAVTLIGAVVCLIFGLELGG

KTFAWGSWQILGLFAGFVALALLFLFAETKAKEPIISFSMFRNRVYWSSNVIGMFSGA
AFITASVYIPIFIQGVLGKATNSGLVLLPMMLGSVVTASLGGVLMTKIKYRNIMIPT
LALLVIGLGLLTLDENSSLWTIRIYMVMVGLGVGASFSVLSNAAMNAFEPQRRGAAS
STLNFLRSLGMTMGITIFGIVQSQVFTRKMNDALAGSAAEAGGASAGGVPQGVDLTD
HALLSPELRQAIPPQVLDTITHALSSSIVQLFAWAVIPAALALVASFFMGREKMVVG
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CDS complement(6654135..6655568)

/locus_tag="EFAGFIKM_05839"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKIHLTVIVLFSILLIGSASYGLLYMYVNQPALPKDVHVGGML

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QLEEGNLWERAYARYHFPKEFSLDMSYDLRPLQEHLSPAWEKETFGTPADAVRRITAS

DKVQYIPEKGVRRIDWDTLSLIQTKLHRDFSVLNPDEKPAPLLIQVPLYTLKPEVTL

DSLREQEGIDRKIIQFSTGLGNSSEGRIHNVSAAAEAINGMILPPDATFDYEKVVRQAE

KEYGFREAPVIVNGRLTPGIGGGICQVSSTVYNAALLTGLDIIERRNHSLPVKYLPKG

LDATFASGAINFRFKNNTGKSLLIHAEVKNHQLMVKFFGTFPENVSYSLESRTIETLS

VPVKYVSSTVLPDGAQQVLQDGQPGYIVETVRTKRLDGKVVESKTITRDTYKAQNRLI

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CDS 6655823..6656509

/gene="ftsE"

/locus_tag="EFAGFIKM_05840"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34814"

/codon_start=1

/transl_table=11

/product="Cell division ATP-binding protein FtsE"

/db_xref="COG:COG2884"

/translation="MIEMQDVWKTYANGTHALQGVSVKIDRNEFVYIVGPSGAGKSTF

MKLMYREEVPTKGQISINGFNIGKLKPRKIPYVRRNIGVVFQDFRLLPRMTAFENVAF

AMEVIEAPKRHIKKRVMEVLDLVGLRSKANREPSQLSGGEQQRIAIARAIVNNPSVII
ADEPTGNLDPETSWGIMQLLDEINFRGTTIVMATHNKDIVNTMRKRVIAIESGQIVRD
QMRGEYGYEF"

CDS 6656499..6657416

/gene="ftsX"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34876"
/codon_start=1
/transl_table=11
/product="Cell division protein FtsX"
/db_xref="COG:COG2177"
/translation="MNFSTLLRHLREGFKNVFRNGWMSVASIMSIIVSLLILGVFMLL
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RERLGESADNVLSGFDVDNNPLPETIEVEVIEPETVTFVAQKIEALNEKHPEKPIMKV
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ATNTFIRWPFIEGALIGFIGSVITVGVLVFGYSQLMKTIGQDVFQMMLNLIPLGEIW
GLFGTLLIGLVGVILGSTLSIRKSLNV"

CDS 6657604..6658884

/locus_tag="EFAGFIKM_05842"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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QDQHLLDEHKADKQLVVDKKAELDVQYAEAKSLYAQKKQRKSQLNEKEAEKQVLLASY
DAKIEESEELTQEEDVLMQIASKRSALLQEKNKLREQAAAAAKAAAAAARAKAAA
KAPTRVSSDSSSEVTYSSGNGIFSRPVSGGRISGFGPRTHPITGVVGKMHAGVDFAV
PQGTSVHAASGGIVIMAEWYSGYGYTVIVDHGGGLWTLYGHLREGGFKVSKGDTVSKG
DTIAESGNTGNSTGPHLHFEVRDNGTAVNPMNYL"

CDS 6659020..6660492

/gene="ctpB"
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/EC_number="3.4.21.102"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O35002"
/codon_start=1
/transl_table=11
/product="Carboxy-terminal processing protease CtpB"
/db_xref="COG:COG0793"
/translation="MMKKRSALLLVIVGLLGGSLLTLVLMTYPGIASQATPGEGLLAS
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TVQTSYDKQMGDGSLLKITIAKWLT PNGDWIHEKGIKPDIAVDQPDYFSVAPINKEKL
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CDS 6660599..6661885

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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34375"
/codon_start=1
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/db_xref="COG:COG0265"
/translation="MLQLFIQPFYYIAVILIALIYHRQLLQERKLFHVRLQSSITQTI
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FGEITQSMLPGQKVQISSKRLMIYGAALLVFSLLAAWWSPLMVVAALIAFIGHEFLWW
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ALRMNPAFCKLEVRNHQGESKFMQRAIYEGEHHQLGVIMAPDNHEVWAIIRLSPLTLFH
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CDS complement(6661976..6662665)
/gene="lnrK"
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/inference="similar to AA sequence:UniProtKB:P94439"
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/db_xref="COG:COG2197"
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CDS complement(6662686..6663897)
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/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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CDS 6664109..6665044

/gene="lnrL_6"

/locus_tag="EFAGFIKM_05847"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94440"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG1131"

/translation="MGILEVDHVVKRYGSKLSVDHLNLSVGKGEIFGLLGPNAGKST
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PTVGIDPQSRNHILESVRTLNMKGSTIIYTSHYMEEVAAISHRVAIMDQGRIIACGTE
AELRERVASEEKVVLSTSGIIPNVVEELKLHPRVRMVDVSENTLTITLPSAQQLQDL
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CDS 6665057..6666253

/gene="lnrM"

/locus_tag="EFAGFIKM_05848"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94441"

/codon_start=1

/transl_table=11

/product="Linearmycin resistance permease protein LnrM"

/db_xref="COG:COG0842"

/translation="MNIWHICIFELRRILKIRSVVLNLFILPLLLIFILGMALSSTMG
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GITKVLGPVIAAMASASESGTANSTSI AVTNPGKTGTAYSASQYYAASMLAMFMLYS
GMTTSTSLFGERDNKTLIRLQAAPIGNGVIFAGKIAGNSLLAFLQATTIILMTYWFYG
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CDS 6666246..6667424

/gene="lnrN"

/locus_tag="EFAGFIKM_05849"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94442"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG0842"

/translation="MNSLHIAWLMIRRTLGRKMGFITLLLPCLVITGAVALFGSDQI

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CDS complement(6667523..6668365)

/gene="lafU"

/locus_tag="EFAGFIKM_05850"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q03478"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG1360"

/translation="MSRRSKRRGKRETIDHRDRWMITYADLITLLLIFFVIMYAMSNL

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QLQP"

CDS complement(6668349..6669146)

/gene="pomA_2"

/locus_tag="EFAGFIKM_05851"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O06873"

/codon_start=1

/transl_table=11

/product="Chemotaxis protein PomA"

/db_xref="COG:COG1291"

/translation="MDIATLIGIIAGIAAVISGFLWEGGQLSGLLQKTAALIVFGGTI

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CDS 6669316..6671307

/gene="uvrB_2"

/locus_tag="EFAGFIKM_05852"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37954"

/codon_start=1

/transl_table=11

/product="UvrABC system protein B"

/db_xref="COG:COG0556"

/translation="MSDIIMSDKTFEIESEFSPQGDQPAAIIELVKGVQEGKRYQTLL

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SSMLLSLRVGMEKPRNQILSRLVEIQYQRNDINFVRGTFRVRGDVVEIFPASKGEHAI

RVELFGDEIEKITEIDVLTGELIGEREHIAIFPASHFVTQEETMKVALVNIERELEER

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DERVLITTLTKKMSEDLT DY LKEVG I K V R Y L H S E I K T L E R M A I L R D L R L G V F H V L I G I
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CDS 6671493..6671954

/locus_tag="EFAGFIKM_05853"

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/codon_start=1

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/product="hypothetical protein"

/translation="MGVESAPVLTSEPSRRQWRPCRERGEAESVPVLTLEPSQRQWRP
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CDS 6672178..6675036

/gene="uvrA_2"

/locus_tag="EFAGFIKM_05854"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P63383"

/codon_start=1

/transl_table=11

/product="UvrABC system protein A"

/translation="MASDNIVIKGARAHLNKNIDITIPRDRFVVLTLGSGSGKSSLAF
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VTEIYDYLRLLFARVGHPCPDHGV EISSQTVEQMVDRI MQYPERTRLQILAPIISGR
KGEHKS VFADVSKQG FVRVRVNGELRDLSEDIQLEKNKKHTIEVVVDRI VVKDDVQAR
LADSIETALNLSGGQLLVDIMGEEELRFSSNFACPVCGFSIEELAPRMFSFNSPFGAC
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PVEDLPAEQMNKLLQGTGTEKIRFRYENDFGQRKEALVTFEGIVNNLERRYRTASEG
IREFIEGYMSAKPCGTCKGQRLKRESLAVTINDHNMAYVTSLSIGEAGRFFDSLELSE
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LYILDEPSIGLHQ RDNDRLISTLAHMRDIGNTLIVVEHDEDTMMAADYIIDIGPGAGI
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CRGDGIIKIEMHFLPDVYVPC EVCKGKRYNRETLEVKYKNRNISDVLEMTVEDATQFF
ENIPKIHRRKMQTLMDVGLGYINLGQPATTLSGGEAQRVKLASELYRRSTGKTIYILDE
PTTGLHVDDIDRLLNVLHRLVDSGESVLVIEHNLDVIKTADYVVDLGPEGGSGGGTIV
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CDS 6675375..6675587

/locus_tag="EFAGFIKM_05855"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLFAEAATASTSNFNAFDIFVILFTILIFIGVVRLLRAPKKNLF

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CDS 6675864..6677033

/locus_tag="EFAGFIKM_05856"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSVLGKKGIAILMAAVLSISVAATAGAAESKAAMQAKVVDGQVY

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DDRYNLAHGTGVIIRSNGWIVTNAHVVDGLTNPVVVTTDGNTYKITKTYSDALSDLAL

IKINAKSLKPASFASQT TVGETVIALGTPISFSLRNSATVGVISGLNRGVEATYRL

IQTDTAINPGNSGGPLVNLKGEVVGINS MKFSAVGVESLGFSIPVDTVQYIIDQFFKY

GKIKRASLGLQLEESWSAIVGLPTDDPLTITGVLSPEAKKAKIKEGDVLYSVAGTRVS

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CDS 6677077..6678972

/locus_tag="EFAGFIKM_05857"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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QDVALDADDLLQQLVQEAKQSGDTVLDREAVSKGKTPYARIIVKDVDGMLWEMRQYLS
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YGIELKIPAGWSMDNNQMIYEAKDGAYLQWRVTSKAGTTVKDWSGQLDKWMRETFTP
ESYEPIGSYTMDISGETAEVNEFRYNFGGGWQTEFDVLLQKNGYRYAEYTFPEEQIA
DRAWFERIMKSVEIDFTVADNFGQLDEDPYLTDKTKTLTRTSKRYHYSVDIPRYWTP
YSDRFEYSPVYFTFTGGFEFSIAASEDKSIEMTVSQLREAYAEATKTRKNFQLLRSEEL
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CDS 6679301..6681814

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/inference="ab initio prediction:Prodigal:002006"
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DNTPPSKEEVRELQQSFSRGFTHGFLSGTNNKELVDGTFPKSRGVYLGRVDQVLRDGV
VLKLDAPVKRGD GIVFDAGDPTQKEEGGRVYD VRRKGLKLECEAE EGWIVDVVPGRSD
VDLRRVKVGDKVWKTNDPALDKRLRQSFETEKPYRVFPVKV K VIGSPGQPLSTWWTDV
QKGTTVRIDSEMELDIAQKRPMTHELLEE QFGRLGGTVFQLEGMDVNLHGDV IIPMRE
LNNIRRQAVEQLAGERPKPPVYVKRAVDVYGDSVKPASPVARGQAELTALCRSLPQVE
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DAVLVRNTGALYFYLRHRMENPDAKHPELIGDFSLNIANHKA VELFLEAGCDWITPSY
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ASLQDRIGMSPVRVDEGCRNTVYNAVEQSGAEYLTNFMDLGVSRYRVEFLEETPEQV
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CDS 6681920..6685570

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/locus_tag="EFAGFIKM_05859"

/EC_number="3.6.4.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01821"

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/transl_table=11

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LSEQDIRELLMV"

CDS 6685828..6686706

/gene="gtaB_3"

/locus_tag="EFAGFIKM_05860"

/EC_number="2.7.7.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q05852"

/codon_start=1

/transl_table=11

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/db_xref="COG:COG1210"

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CDS 6686888..6687436

/gene="rfbC"

/locus_tag="EFAGFIKM_05861"

/EC_number="5.1.3.13"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P26394"

/codon_start=1

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/db_xref="COG:COG1898"

/translation="MKVLPLFMDGAAILEPKVYGDHRGYFMESYNEQVLHEQGIQHVF

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CDS 6687491..6688516

/gene="rffG"
/locus_tag="EFAGFIKM_05862"
/EC_number="4.2.1.46"
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/inference="similar to AA sequence:UniProtKB:P27830"
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CDS 6688513..6689394

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/EC_number="1.1.1.133"
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CDS 6689529..6690404

/locus_tag="EFAGFIKM_05864"
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RSLVDAAKEHDP SVLDRVVVQIYNEP MLETVKEVYAFPSI IYTLYATQDTEAQV VDFV
QKNDIDAVTMPEYKVNQN FVAKLNSAGSVTYVHTINDTEQVANYEKWGVYGVYSDVLT
EQELDEMNT RFAWK P"

CDS 6690520..6691215

/gene="pcrB"
/locus_tag="EFAGFIKM_05865"
/EC_number="2.5.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q81ZG3"
/codon_start=1
/transl_table=11
/product="Heptaprenylglyceryl phosphate synthase"
/db_xref="COG:COG1646"
/translation="MIDMIKQWRHVFKLDPDREITDEELDLVCM SGTDAIIVGGSSGI
TYDNTVDLMSRVRRYELPCVLEVSDLEAVVPGFDGYLIPMVLNATDSKWMIGHHQQAI
ERYGYLIPWDL LIAEGYIVLNANSTVARLTGADTDLTTGAAVAYAQA AERLLNLPIVY
MEYSGTFGDMELVGETYRQLERAHLIYGGGIDDSEKASQAAQVADTVVVG NIVYSDLT
KALETVLAVKGTI"

CDS 6691653..6694007

/gene="pcrA"
/locus_tag="EFAGFIKM_05866"
/EC_number="3.6.4.12"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34580"

/codon_start=1
/transl_table=11
/product="ATP-dependent DNA helicase PcrA"
/db_xref="COG:COG0210"
/translation="MQPVNIHDAVARLNTPQRQAVEATDGPLLIMAGAGSGKTRVLTH
RIAYLIATRKAPPWGILAITFTNKAAREMQDRVSQLVGGSQGRDIWVSTFHSMCVRIL
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EQYEKQAGDYFEGIVAKIYKMYQKKLRANNSLDFDDLIMQTIQLFKEVPEVLDFYQKK
FQYIHVDEYQDTNRAQYMLCRMLADSHHHICVVGSDSQSIYRWRGADISNILNFEKDY
PEASTILLEQNYRSTSNILNAANEVIGLNTGRKPKKLWTDKEGGSKIKVYRADSEHDE
GYFVTSEISKNVKNGKSYQNHAILYRTNAQSRVIEEILIKSDIPYQIVGGIKFYDRKE
IKDILAYLRLLSNPDDDISLTRIINVPKRSIGDTTVAKLAAAAGERGISIFRVLQVVD
DLGFAGRTRNALVEFYDMIAALHQMVEYLSVTELTEKILEMSQYRLEMQNENTLESRA
RLENIEEFLSVTMEFEKNNEKTLVSFLTDLALIADIDSMNDDEEDQSDAVTLMTMHS
AKGLEFPVVFIVGMEEGVFPHSRAFMDEELEEERRLAYVGITRAEEQLFLSCAQMRT
LFGRTTANPPSRFLDEIPDELKEDTSMARDRYRRGSSGGGSYGGRGLGSSGGSNFGGG
TKLFDHQSKSGSSATSSTPTSRVTTSVSRPTYSTPSSASKPAASNGEAGFKAGDKVQH
GKWGTGTIVAVKGTGNDTELQIAFPAPVGVKRLLAGFAPITKVE"

CDS 6694296..6696317

/gene="ligA"
/locus_tag="EFAGFIKM_05867"
/EC_number="6.5.1.2"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P15042"
/codon_start=1
/transl_table=11
/product="DNA ligase"
/db_xref="COG:COG0272"
/translation="MDPMHRMEQLVTELNQHNHYQYYTMDQPQISDKEYDLLYDELVTL
EQESGMVLPDSPTQRVGGELLKGFTPHRHLSSLWSLDKAQNIEQLRSWNTRVLKLIND
YNSKNPDTPLEPGYVIELKFDGLTLNLTYTNGELVQASTRGNGTVGEGILAQVRTIR
SVPLKIPYTSGTIEVQGEIMNLSVLDRYNETAAEPLKNARNAAAGALRNLPKATAE"

RRLNAYFYNVGYSDDIQFANHQQMMDFLRENRFKVNPSITYFHEFDDVMEQLAAIQEN
RGQLDYLIDGAVIKITDMRTREVLGYTDKFPRWAVAYKFEAEETTTVLNAVWVNVGRT
GKVTPLARVEPVELAGVTVQNCTLNNVGDIERKNLKFALGTRVFIRRSNDVIPEILGK
VTEESDGEEIVFPEQCPACGFPLEQRG AHLFCNNRLACKPQTVARISHFASRDAMDIE
TFSEKTAIQLYDDLNVREPADLYTLQFDDLVLKLERFGEKKANNLIAALELSKDRDLAS
FLYSLGIPNTGKSTTRMLADHYRDLHAIMNATVEELVELPDVGGIVAESIVNFFADPF
TQAAIEKMLNLGVKAQAPEAPAVAVVEDSFFSGKTVVLTGTLHQLTREEATQRLEALG
AKVTGSVSKKTDLVIAGEKAGSKLTKAHD LGIPTIEDEDELVRLNLPQG"

CDS complement(6696452..6697744)

/gene="msrP_2"

/locus_tag="EFAGFIKM_05868"

/EC_number="1.8.5.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01206"

/codon_start=1

/transl_table=11

/product="Protein-methionine-sulfoxide reductase catalytic

subunit MsrP"

/translation="MILAITGLMLVGGFWREILGIGRWLKWLHIIVGLAMLAPVYY

LILAGKHWKQLRNRPWQRVNTIFVLALLVGWLLSGIVLWQFKLAGPRWSNAALLIHD

LTWVGLPYIIYHSITRTKWLDKDPARRAVKTTTTSTRTQNTADPSDSRSDEKETPAAIS

SSQFDRSSERDPLKSEERPQPLYTRRTFIRSAVGVGLAVTLGPTFISWVGRNLKIDNS

IDSMLENDPNRMVPLPQPLSASSPPIGGGAEGHFRVYTVTPIPSFSNANWSFRIDGLV

ERAQVWNWEQFVKLARTVQVSDFHCVTGWSVYKNTWEGISLAHLLKQAGVKPEAHSVK

FYSGDGVYTDAILDQAQMEDIMVAVMHDGKPIPADLGGPVRLVIPQMYAYKSVKWLN

RIELIDSEHIGYWEERGYDKDAWLTGASQRIPNNLSGS"

rRNA 6698467..6700017

/locus_tag="EFAGFIKM_05869"

/product="16S ribosomal RNA"

tRNA 6700129..6700204

/locus_tag="EFAGFIKM_05870"

/product="tRNA-Ala"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Ala(tgc)"

rRNA 6700417..6703340

/locus_tag="EFAGFIKM_05871"

/product="23S ribosomal RNA"

rRNA 6703425..6703536

/locus_tag="EFAGFIKM_05872"

/product="5S ribosomal RNA"

CDS 6703718..6704893

/gene="eis"

/locus_tag="EFAGFIKM_05873"

/EC_number="2.3.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01812"

/codon_start=1

/transl_table=11

/product="N-acetyltransferase Eis"

/translation="MEIQKLTVDDEFEPAMALSEYAFQVAMSEEQKEKRRSQFSSQDIW

GVYEDGQLGAKLHIIPFQTYIHGRSFEMGGIAGVATWPEYRRKGWVAGLLKHALEEMN

RNKQISISFLHPFSFGFYRKYGWETYVEFKRYKVPTAHLPPKKATPGTIRRGDPGLSIL

KEVYSAYAERYNGTLVRDDARWENSVLVNGTSQKAVYYDETDAAGYLLYEVKENKFT

IKEIYLNEEARQGLWTFIANHDSMIQEVTLQAPASDTLAFQLDNPRIQQEIVPYFMA

RIVSVEQFISQYPFASQDSPVQIVLQVEDTYAPWNEGVWQLNVAMNGTASIWKTSPEI

NDDQTIKVDIQSLTAVLMGYRRPTEMARIGRINGPNTAIKALEQAIPERETYLLDFF"

CDS 6705355..6705816

/gene="ctsr"

/locus_tag="EFAGFIKM_05874"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C3W947"

/codon_start=1

/transl_table=11

/product="Transcriptional regulator CtsR"

/translation="MRNISDIERYLKSIHESPEGMVEIQRNDLADQFSCVPSQINY
VISTRFTLEKGYLVESKRGGGGYVRIQRIELPAQSALHNHLHHSIGEEIGQTAAEGLI
YQLEEARFLSKREAGLMRAAVSREVILVKLPYRDQIRARMLKAMLISLLGK"

CDS 6705848..6706372

/gene="mcsA"
/locus_tag="EFAGFIKM_05875"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37569"
/codon_start=1
/transl_table=11
/product="Protein-arginine kinase activator protein"
/db_xref="COG:COG3880"
/translation="MLCQECNKRPATLHFTKIVNGEKTEFHICESCAREKGEMIPGTA
GGFSIHNLLSGLLDFDPAGKSGSAGTPPAKALQCEECGMTYSQFSKIGRFGCSSCYKY
FDSRLDPLFKRVHGNSTSHVGKVPARAGGRIKVKRQIADLKRELQESIAQEEFEEAAQI
RDQIRGLEKGIAQE"

CDS 6706401..6707471

/gene="mcsB"
/locus_tag="EFAGFIKM_05876"
/EC_number="2.7.14.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37570"
/codon_start=1
/transl_table=11
/product="Protein-arginine kinase"
/db_xref="COG:COG3869"
/translation="MPNLRFTEKALSDWMRSDAADSEIVISSRVRIARNLQHVPFPML
ASNEQSEEVNLKLSEVLQYDDVHAFGDFHTLDLIDIDELDKRVLVEKHLISPSLANES
RNGAVILSEDESVSIMINEEDHLRIQCLYPGFQVKEAWEKASAIDDAFEAHVDYAFDD
RRGYLTSCPTNVGTGVRASVMMHLPALVMTQQIGRILTAVSQVGLTVRGIYGEGSEAM
GNLFQISNQITLGQTEQEVIENTLHGVVLQMIGHERTARERLITDSRLRITDRVMRSYG
ILSHAAIVDSKEAAQRLSDVRLGVLDGLDGLSITVMNELNVMTQPGFLQKTFGEDMR"

TDERDIYRAQLIRDTINAAKQS"

CDS 6707543..6710119

/gene="clpC"

/locus_tag="EFAGFIKM_05877"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37571"

/codon_start=1

/transl_table=11

/product="Negative regulator of genetic competence

ClpC/MecB"

/db_xref="COG:COG0542"

/translation="MPIDFIRSTAANKNDMKNNTTVISLHDPRFIQNHGGAGDMMFGRF

TERAQKVLALAQEEAVRLGHNNIGTEHILLGLIREGEGIAAKALIGLGLGLEKIQDEV

ETLIGRGQEQPTNIAYTPRAKKVIELSMDEARKLGHTYVGTEHILLGLIREGEGVAAR

VLNNLGISLNKARQQVLQLLGSSEAVSSHNGTPANVSTPTLDSLARDLTAYARENNLD

PVIGRSKEIERVIQVLSRRTKNNPVLIGEPGVGKTAIAEGLAQKIIANEIPETLRDKR

VMTLDMGSVVGAGTKYRGFEFEDRLKKIMDEIRQAGNIVLFIDELHTLIGAGGAEGAIDA

SNILKPALARGELQCIGATTLDEYRKYIEKDAALERRFQPITVDQPSPEEAIQILHGL

RDRYEAHHRVKITDEAIVQAVKLSDRYITDRFLPKAIDLIDEAGSKVRLNSYTIPP

NLKQLESRLDIRKEKDAAVQSQEFEKAAALRDTEQKIREELDVTKNQWKEKQGRDSE

VTPEDIAQVVASWTGIPVNQLKEEETQRLMNLESILHERVIGQDEAVKSVSRAVRRAR

AGLKDPKRPMGSFIFLGPTGVGKTELARALAEAMFGDENAVIRIDMSEYGEKHSTSRL

VGAPPGYVGYYEGGQLTEKVRKPYSVLLDEIEKAHPEVFNILLQVLEDGRLTDSKG

RVVDFRNTLIILTSNVGAEAIKRNSTLGFTAVVDAGADYDNMKGKVMDELKKSFRPEF

LNRIDEIIVFHSLEEKHIAEIVTLMSEELRKRLLEHEVDFELDNAKSFLAKSGFDPA

YGARPLRRAIQKHIEDKLSEELLTGNVTKGDSLLIDEENGALSVTKKDVVPSNEEIE

TK"

CDS 6710392..6711759

/gene="radA"

/locus_tag="EFAGFIKM_05878"

/EC_number="3.6.4.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37572"

/codon_start=1

/transl_table=11

/product="DNA repair protein RadA"

/db_xref="COG:COG1066"

/translation="MAKVKTKFQCTECGYEAPKWYGKCPGCQSWNSMVEETETVVKTQ
GRNSPLFDSKDKPLIIDIDSGQEPRVQTGIGELNRVLGGGIVPGSLVLVGGDPGIGK
STLMLQTSHALTHSGLRVLYVSGEESVKQTKLRADRLGALSAELYVLCETNMERVEEA
VDQIQPHFLVIDSIQTVYLPEVTSAPGSVAQVRECTSRFMRIAKGRGIATVLVGHVTK
EGAIAGPRMLEHMVDCVLYFEGERHHHTYRLLRAVKNRFGSTNEIGIFEMGEDGLREVG
NPSELFSLERPLGVAGSTVVASMEGTRPLLVELQALISTTHFPSRRMATGVDLHRLN
LIIAVLEKRMGMFLQTQDAYLNVAGGVRLDEPAVDLAVAVCIASSLRDVPTKPDDVIF
GEIGLTGEVRAVSRAEQRVKEAAKLGFKRVILPEKSLKGWKHPRGIQLIGVNTVADAL
AVALD"

CDS 6711773..6712849

/gene="disA"

/locus_tag="EFAGFIKM_05879"

/EC_number="2.7.7.85"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q6HPT4"

/codon_start=1

/transl_table=11

/product="DNA integrity scanning protein DisA"

/translation="MKDMSQLDNMNELLRLIAPGTPFREGLENVLRAKTGALLVVGYS
PEVMEVVDGGFSINCDSPNYLYELAKMDGAILSEDLKRILYANTQLIPDSSISSSE
TGIRHRTAERVAKQTGKLVVSISQRRNIITLYQGTLRYSLKEIGVILTKANQAIQTLE
KYKAVLTQSLTNLSASEFEELVTIPEVVNVIQRTEMVMRIKTEIKRYIHELGNRGLI
SMQMEELVGTTEEEAWLLYKDYARDDSDDKIREIIVGLKRLSDDELDAHHIVRLLGY
PSSAATSEDSVAPRGFRVLNKPRLPNVIIHNLVDQFEQLPHVIMATIEELDEVDGIG
EVRARTIKEGLKRLQEQMFIQRQM"

CDS 6712895..6713626

/locus_tag="EFAGFIKM_05880"

/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MLTRFIPNLFTLGNLFLGMMAILLAIDGNYSLAAIMVIVAMLLD
GLDGRVARALNAQSEFGKELDSLSDMVSFGAAPALIIFMVSFQDSMPILAWIATAAFP
ICGAIRLARFNVRPGIPGYFTGLPIPAAGGVLATLSLFNKDIGPVSMMIATLLLSYLM
VSSLKYPNFKKVGLPRKAIWIAPWVVLFAIAVAVIFPEQLSKLIFIPLVLYALYGMKH
NVRTAASRSRAKKRKDEKSSRPSDR"

CDS complement(6713754..6714194)

/locus_tag="EFAGFIKM_05881"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MAYNEFNSYPEVSGKMSTLSLQAFQDQVSELLLRHRSLIDVLSK
TGQAGASVNRAVSKAITECGCIELHATKQKYAPESDIAQTKGLLETHVEGELCENCRE
VISSELGRNLFYMSALCNLLDINMEEVVNHESQKCSTLGMFNLS"

CDS 6714323..6715408

/gene="yacL"
/locus_tag="EFAGFIKM_05882"
/EC_number="3.1.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q06754"
/codon_start=1
/transl_table=11
/product="putative PIN and TRAM-domain containing protein
YacL"
/db_xref="COG:COG4956"
/translation="MWKKGILTFTGLCGAWFGYTAYHLAGKSVPWMAEWIQSAGLLGA
GISTLLGAVMFMVAVCNIGGTLMADRLHSGIDSLAKVPMNELAAGAAGTVAGLLVALLL
YPVVGWMGTAGEVLQVALTVISAYCGYTLAMAKKDDLGAFWMSGRWGHPEVDEDRRME"

EHKILDTSVIIDGRIADICKTGFIEGTIVPEFVLEELQHIADSSDLLKRNRRGLD
ILNKIQKELDVKVLIIYEGDFEEISEVDSKLVKLAKVLQGKVVNTDFNLNKVCELQGV
VLNINDLANAVKPVVLPGEEIMVQIIKDQKEHGQGVAYLDDGTMIVVEGGREYIGMMM
EVLVTSVLQTSAGRMIFAKPKLLEKAQ"

CDS 6715491..6716186

/gene="ispD"

/locus_tag="EFAGFIKM_05883"

/EC_number="2.7.7.60"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q06755"

/codon_start=1

/transl_table=11

/product="2-C-methyl-D-erythritol 4-phosphate
cytidyltransferase"

/db_xref="COG:COG1211"

/translation="MDKGWGVVIVAAGRGRMGTTESKQFLLLQDKPVFIHTLEVFAA
LDEIREMVLVTGAADVERCQDWVKEYQLDSRVVRVIPGGKERQHSVHKGLEALGTDWVL
VHDGVRPFVNHEQIKGCMAAAISGGGA AVLAVPVKDTIKQVNAEGVVTATPDRSSLWS
IQTPQAFRLSSLLSAYESAEQDGLGTDDAMLAERQGMSVKVVEGNYTNIKLTPEDL
QYATFLLGGEKKR"

CDS 6716183..6716659

/gene="ispF"

/locus_tag="EFAGFIKM_05884"

/EC_number="4.6.1.12"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q06756"

/codon_start=1

/transl_table=11

/product="2-C-methyl-D-erythritol 2,4-cyclodiphosphate
synthase"

/db_xref="COG:COG0245"

/translation="MIRVGQGFDVHQLVEGRPCIIGGVVTIPYEKGLLGHSADADVLLHA

ISDAILGAVALGDIGKHFPDTPDFKADADSLKLEHVVWLKDRGYKLGNIIDSTIIAQ
KPKMAPYIPQMAEVIKALEADVTQVNVKATTEQLGFPRGEGIAAQSVVCLVRV"

CDS 6716693..6718150

/gene="gltX"

/locus_tag="EFAGFIKM_05885"

/EC_number="6.1.1.17"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P99170"

/codon_start=1

/transl_table=11

/product="Glutamate--tRNA ligase"

/translation="MSTDIRVRYAPSPTGHLHIGNARTALFNYLYAKHNNGKFIIRIE

DTDVKRNIAGGEESQLKYLKWLGIWDESIDVGGEYGPYRQTERLDLYRKYTQELLDK

GLAYRCFCTEEELEQEREEQSARGETPRYSGKHRDLNPEQISAFEAEGRVASIRFRVP

EERTYTFDDMVKGITISFNSKESGDFVIVKKGDIPTYNYAVAVDDHLMKISHVLRGEDH

ISNTPRQLMIYEALGWEPQFGHMTLIVNENHKKLSKRDESVIQFIEQYDQLGYLPEA

MFNFISLLGWSPGEEEEIFSQEQLISIFDTKRLSKSPAVFDTHKLAHLNNHYIKHADP

ERIAEMAIPHLQKAGRISSELSAEQKEWAYTLVHLYQEQMNSASDIVELSEVFFRSNL

ELESEGEAVLAEQVPTVLKAFADKVQASEEFTPSKMAALIKEVQKETGFKGKQLFMP

IRVALTGQTHGRDLNQTIVLLGRDVTIERLLAQVK"

CDS 6718689..6719348

/gene="cysE"

/locus_tag="EFAGFIKM_05886"

/EC_number="2.3.1.30"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q06750"

/codon_start=1

/transl_table=11

/product="Serine acetyltransferase"

/db_xref="COG:COG1045"

/translation="MFKKIRSDIQAVFENDPAARGWFEVVFTYSGLHAIWAHRMAHFL

YKRRWFSVARFISQVSRFMTGIEIHGPATIGNRLFIDHGMGVVIGETCEIGDDVVIYQ

GVTLGGTGKEKGKRHPTIGNNVVISSGAKVLGSFSVGDQCNIGANSVVLKEVPSNSTV
VGIPGRIVKQDGRRVDRLSQQLPDPVDSLGRGMQKELERLQEEVRTLQNARENETVRD
T"

CDS 6719391..6720791

/gene="cysS"

/locus_tag="EFAGFIKM_05887"

/EC_number="6.1.1.16"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q06752"

/codon_start=1

/transl_table=11

/product="Cysteine--tRNA ligase"

/db_xref="COG:COG0215"

/translation="MTLQIYNTMSRTKEEFVPQEPGKVKMYVCGPTVYDYIHIGNARP

VIFFDTVRGYLEQTGHEVNYVVNFTDVDDKLIRKAEQLGTDVPHVAEKFIAAYYEDLE

GLGIPKASSNPRVTENMPLIIDFIRELVEKGFAYENGGDVYRTGKFSEYGKLSKQNL

QELQFGIRVGVDERKEHPEDFVLWKAAPGEIYWSSPWGDGRPGWHIECSAMAREYLG

DTLDIHGGGQDLQFPHHECECAQSEVLTGKPLANYWMHNGFIRIDNEKMSKSLGNGVL

VKDLRNQYKREAIRYFMLSTHYRNPLNFTDDTMEQAQNSVDRIANAVGNLNRHNAV

VDQDITAEFAARLDQIRQQYHEKMQDDFNTPDAITAMFEWAGEANQLLQQEVVNAADI

RALLELFSELNAVLRIYTDAPELLDEEVERLIEERVEARKSKNWARADEIRDELSAR

GILLEDTAQGMRRRK"

CDS 6720788..6721267

/gene="mrnC"

/locus_tag="EFAGFIKM_05888"

/EC_number="3.1.26.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01468"

/codon_start=1

/transl_table=11

/product="Mini-ribonuclease 3"

/translation="MSEGHPNTPKQQEQVTEGGWFPYPPSRPARLIPPIALAYIGDAV

YEAVRQYLLSKANMRPNHLHRSATGLVSAKAQSRILTTIEDELTEEERDVRQGRNA
KSGSVPKNADVLEYRHATAFECLIGYLYSSGHHDRMIELIGLGIEHAEQQSPSPTKK"

CDS 6721311..6722057

/locus_tag="EFAGFIKM_05889"

/EC_number="2.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A794"

/codon_start=1

/transl_table=11

/product="Putative TrmH family tRNA/rRNA
methyltransferase"

/translation="MEEEWIAGKHSVTEALRSGRTINKIWIADTAQKHLTQPIISEAK
KLGIVIQHVDKRKLDQTPGIQHQQGVVAQAAPYAYVEVEDILAAAKAKNEHPFLILLD
EIEDPHNLGSILRTADCTGAHGVIVPKRRSAAVTVTVSKTSAGAVEYVPVARVSNLGQ
TIDRLKEEGVWVVGTDVTAHEGVFGNGVFTGPVALVIGNENKGMGRLIREKCDVLIKL
PMQQGQINSLNASVAAGVVMYEVLSRQAQE"

CDS 6722063..6722584

/gene="yacP"

/locus_tag="EFAGFIKM_05890"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37574"

/codon_start=1

/transl_table=11

/product="putative protein YacP"

/db_xref="COG:COG3688"

/translation="MADSRDVLLVDGYNMIGDWPELTCLAESGLEEARNRLLFRLADY
QAFSGRRVIVFDAYLVPGLGKSFTQSKVQIYFTKEKETADECIERLVRELSMRRRQI
YVATSDMVEQHVIFGQGALRVSAARELLIEVEQNEKELKKRLEEDQAKTTRNTIGGKLS
PDVLKEFERWRRE"

CDS 6722756..6723400

/gene="sigH"

/locus_tag="EFAGFIKM_05891"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P17869"

/codon_start=1

/transl_table=11

/product="RNA polymerase sigma-H factor"

/db_xref="COG:COG1595"

/translation="MSVDLKDIMLSKYDYQSDDEDIVEAFREGESALEFLINKYRN
FV
RAKARSYFLIGADREDIIQEGMIGLYKSIRDFFKGDKLASFKAFAELCITRQII
TAIKT
ATRQKHIPLNSYVSLDKPIYDEESDRTLDDVICGTQVSDPEELIINQEEFV
GLEDKMS
EILSDLERKVLMLYLDGRSYQEIAVDLDRHVKSIDNALQRVKKLEKYLEVR
DN"

CDS 6723872..6724063

/gene="secE"

/locus_tag="EFAGFIKM_05892"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00422"

/codon_start=1

/transl_table=11

/product="Protein translocase subunit SecE"

/translation="MKRSFKSLISFFSESWAELKKVRWPNRKELTNYTLIVLGT
VVVM
TLFFWVIDIGISFVIEAI"

CDS 6724085..6724618

/gene="nusG_2"

/locus_tag="EFAGFIKM_05893"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q06795"

/codon_start=1

/transl_table=11

/product="Transcription termination/antitermination
protein NusG"

/db_xref="COG:COG0250"

/translation="MEKRWYVVHTYSGYENKVKANLEKRVESMGMEDKIFRVL
VPMEE
EUVNKDGGKKKTVMRKVYPGYVLVEMVQTDDSWYVVRNTPGVTGFGSTG
SGSKPTALL"

PEEEVQILKHMGMVEPKKIEFDLKESVRIKVGPFANFVGSVEEILVDKSKLKVHVN

FGRETPLELEYTQVEKI"

CDS 6724687..6725112

/gene="rplK"

/locus_tag="EFAGFIKM_05894"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q06796"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L11"

/db_xref="COG:COG0080"

/translation="MAKKVIKVMVKLQIPAGKANPAPPVGPALGQAGVNIMAFCKEFNA

RTADQAGLIIPVEISVFEDRSFTFITKTPPAVLLKVAKVEKGSGEPNKKKVATVKR

DAVRQIAETKMPDLNAADVESAMRMVEGTARSMGITIED"

CDS 6725208..6725900

/gene="rplA"

/locus_tag="EFAGFIKM_05895"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q06797"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L1"

/db_xref="COG:COG0081"

/translation="MAKHGKKYLEAAKLIDSEATYEPSEAVELVKKAAATAKFDETIEA

AVRLGVDPRKQDQAVRGVVVLPHTGTQTRVLVFAKGDKAKEAEAAGADYVGDADMIN

KIQQGWFEFDVCVATPDMMSEVGKLGRLGKGLMPNPKAGTVTFDVTKAVQEIKAGK

IEYRLDRAGQIHAPIGKASFSEQLNENFKALMEALNRAKPAAAKGVYLNVSLSSTM

GPGARVNAAAFR"

CDS 6726140..6726643

/gene="rpU"

/locus_tag="EFAGFIKM_05896"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P42923"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L10"

/db_xref="COG:COG0244"

/translation="MANAKVIQAKQESVDAVTAKLRESVTTVVVDYRGLNVAQVTELR

KQLREAGIEFQVLKNSLLRRAAAAELTELDVLTGPTAIAFSVDDVVAPAKILNDFA

KKNDALCLKGAVVEGRVIGVEEVKALAEPLSRDGLLSMLLSVLQAPVRNFALAVKAVA

EKEEQGA"

CDS 6726716..6727075

/gene="rplL"

/locus_tag="EFAGFIKM_05897"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P02395"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L7/L12"

/translation="MSKEQILEAIKGMTVLELNDLVKAIEEEFGVTAAAPVAAAGAVA

SAEAEQSEFDVILTSAGASKINVIKAVREITGLGLKEAKELVDNAPKALKEKVAKEEA

EAVKAKLEEAGASVEVK"

CDS 6727172..6727792

/gene="rsmC"

/locus_tag="EFAGFIKM_05898"

/EC_number="2.1.1.172"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39406"

/codon_start=1

/transl_table=11

/product="Ribosomal RNA small subunit methyltransferase C"

/db_xref="COG:COG2813"

/translation="MSNHYYSDKPQVAHRRATEAVLRGFSLRFVTDAGVFSKSGIDY

GSRVLIDAIELPSGAHVLDVGCYGPMLTAAKLVPDGHVTMIDINERAVELSRENAK

ANGINNVTVLQSNLLAEVKKQDFDVILTNPPIRAGKETVHTIFEQAHRHLKVGGSLWI
VIQKKQGAPSAKAKLESLFGRVEEVTKDKGYRIFKAVKSEEVSTKS"

CDS 6728188..6731733

/gene="rpoB"

/locus_tag="EFAGFIKM_05899"

/EC_number="2.7.7.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37870"

/codon_start=1

/transl_table=11

/product="DNA-directed RNA polymerase subunit beta"

/db_xref="COG:COG0085"

/translation="MAGHLVQYGRRTRRSYARINEILEVPNLIEIQKSYDWFLEEG
REMFQDISPIQDFTGNLILEFIDYSLGEPKYTVDDAKERDVTYAAPLRVKVRLINKET
GEVKEQEVFMGDFPLMTNTGTFIINGAERVIVSQLVRSPSVYFSTKVDKNAKKTAT
VIPNRGAWLELEMDAKDVVYVRIDRTRKIPVTVLLRSLGFGTDAEILDLLGNDEYIRN
TLDKNDTDSTEKALIEIYERLRPGEPPTLDNAKSLVARFFDPKRYDLANVGRYKMNK
KLHIKNRFLNQRLAESLDAETGEIIAEAGQMVDRLRLDEIMPYLEKSVGFRTYHVG
NVLDANDVPMQTIIDVFSPTEDGKVVKLIANGIIDKSVKNVTPADISSISYFLNLLQG
IGSTDDIDHLGNRRRLRSVGELLQNQFRIGLSRMERVVRERMSIQDANVITPQALINIR
PVIASIKEFFGSSQLSQFMDQTNPLGELTHKRRLSALGPGGLTRERAGMEVRDVHPSH
YGRMCPIETPEGNIGLINSLSFARVNEYGFIEAPYRWVDPKTGIVTEQIDYLTAE
EDNYVIAQANAKLNEDGTFEEEEIIVRYNKQSDNLTMPSERVDYMDVSPKQVVSAT
ALIPFLENDSDNRALMGSMQRQAVPLLPKAPLVGTGMEHKAADSGVCIVSDYDGI
IERSSANEIWWRRVEEVDGQEVKGDIVKYKLHKFMRSNQGTCINQRPIVKRGA
AVKAGDILADGPSTEMGELALGRNVVAFMTWEGYNYEDAILLSEKLVKEDVYTSIH
IEEYESEARDTKLGPEEITRDIPNVGEEALRNLDERGIIRIGAEISAGDILVGKVTPK
GVTELTAEERLLHAIFGEKAREVRDTSLRVPHGTDGIVVDVKVFTRENGDELPPGVN
QLVRVYIAQKRKISEGDKMAGRHHGNKGVARILPEEDMPFLPDGTPVQIVLNPLGVPS
RMNIGQVLEVHLGMAAMQLGIHVATPVFDGAKEYDVFDTMEEAGMQRNGKTVLYDGR
TGEEFEREVTVGVMHMIKLAHMVDDKIHARSTGPYSLVTQQPLGGKAQFGGQRFGE
MEVWALEAYGAAYTLQEILTVKSDDVVGRVKTYESIVKGENVPEPGVPESFKVLIKEL
QSLGMDVKIL

SEDEQEIEMREMDDDDAASDKLSLNLEGTEVGAE"

CDS 6731846..6735460

/gene="rpoC"

/locus_tag="EFAGFIKM_05900"

/EC_number="2.7.7.6"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37871"

/codon_start=1

/transl_table=11

/product="DNA-directed RNA polymerase subunit beta"

/db_xref="COG:COG0086"

/translation="MLDVNNFEYMKIGLASPEKIRSWSRGEVKKPETINYRTLKPEKE

GLFCEKIFGPTKDWECHCGKYKRVRYKGVVCDRCGVEVTRAKVRRERMGHIELAAPVS

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KYGYGFHAGMGAEAVKLLQDLIDKEFLKEELRTAQGQRRNRAIKRLEVIEAFRN

SGNKPEWMIMDVLPVIPPELRPMVQLDGGRFATSDLNDLYRRVINRNNRLKRLLDLGA

PDIIVQNEKRMLQEAVDALIDNGRRGRPVTGPGNRPLKSLSHMLKGKQGRFRQNLLGK

RVDYSGRSVIVVGPYLKMYQCGLPKDMALELFKPFVMKELVNKGLAHNIKSARKKVER

VSPEVWDVLEEVIKEHPVLLNRAPTLHRLGIQAFEPILVEGKAIRLHPLVCTAYNADF

DGDQMAVHVPLSAEAQAEARILMLASGNILNPKDGKPVVTPSQDMVLGSYYLTMDNKE

EKGTGMILRTVNEAVSAYQRGTAGLHARVAIPVKALGKTSFTEEQQEGMLLTTVGKII

FNEIFPASFPYINDATRANLYQGTADHSFVYEKGADLREAIMNAPLAGGVGKEYLGS

IARCFEIIYHTTETAVILDKIKQLGFTYSTRAGITVAVSDVIVPPEKFEILRKSEEKAQ

IVTNQYRRGLITNEERYDRIIDIWSKSKDDITEILMKSMDRYNSIMMMVDSKARGNKS

QITQLGGMRLMANPSGRRIELPIKSNFREGLTVLEYFISTHGARKGLADTALRTADS

GYLTRRLVDVAQDVIVRDDDCGTDKGFTVSRIQDGKEVIEDLYDRIEGRYCFETLRHP

ETKEIIVGRNELIDSDKAEAIKAGITKLQIRSVLSCRASHGVCKKCYGRNLATGKHV

EIGEAVGIIAAQSIGEPGTQLTMRTFHTGGVAGDDITQGLPRIQELFEARNPKGQATI

SEIDGVVKEIREAKDRREIEIQGEAESKVYAVTYGSRVRVSEGAEEVEAGDELTDGSID

PKEMLRIKGIRGVQNYILQEVQRVYRNQGVINDKHVEVMIRQMLRKIRIVDAGDTTL

LPGSFVDMHEYERANKIAILSDKEPAVAKPILLGITKASLETDSFLSAASFQETTRVL

TDAAIKGVQDQLLGLKENVIIGKLIPAGTGMHRYRSIKFAEPEDGQSSVEELEPVSD

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CDS 6735665..6735916

/gene="rplGB"

/locus_tag="EFAGFIKM_05901"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P46350"

/codon_start=1

/transl_table=11

/product="Ribosome-associated protein L7Ae-like protein"

/db_xref="COG:COG1358"

/translation="MSNEKALQDAHVKIGTKQTMRMVQTGMASEVYVAEDSDPQLTSK

IIALCEQHNVKCTKVDTMKNLGKACGIGVGAAMAAVVKS"

CDS 6736067..6736489

/gene="rpsL"

/locus_tag="EFAGFIKM_05902"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P21472"

/codon_start=1

/transl_table=11

/product="30S ribosomal protein S12"

/db_xref="COG:COG0048"

/translation="MPTINQLVRKGRQAKVEKSKSPALQKGFNALKRESTNISAPQKR

GVCTRVGTMTPRKPNSALRKYARVRLTNRLEVTAYIPGIGHNLQEHSVVLIRGGKVKD

LAGVRYHIVRGALDTAGVNNRMQARSKYGAKRPKAKKA"

CDS 6736577..6737047

/gene="rpsG"

/locus_tag="EFAGFIKM_05903"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P21469"

/codon_start=1

/transl_table=11

/product="30S ribosomal protein S7"

/db_xref="COG:COG0049"

/translation="MPRKGPVTKRDVLPDPLYNSKLVTRLINRIMIGGKRGVAQSILY

NAFKLIQERTGNDPMEVFEEAAIKNIMPVLEVKARRVGGANYQVPIEVKPERRTALGLR

WLVNYSRNRGEKTMEERLAAEIIDASNNTGASVKKREDTHKMAEANKAFAHYRW"

CDS 6737097..6739175

/gene="fusA"

/locus_tag="EFAGFIKM_05904"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80868"

/codon_start=1

/transl_table=11

/product="Elongation factor G"

/db_xref="COG:COG0480"

/translation="MAREFSLKNTRNIGIMAHIDAGKTTTTTERILFYTGRTHKIGEVB

EGAATMDWMEQEQRGITITSAATTAAWKGHRVNIIDTPGHVDFTVEVERSLRVLDGA

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AIQLPIGAENDFKGIIDIVAQKAHMYKDDLQGDIEEVEIPAFAADQVEELRNELIERV

AELDEELTMKYLEGEEITIDEIKTVLRKGVVDVKIFPVICGSSYRNKGVQLMLDAVID

YLPAPTDVASITGHLEDGTEAIRKSSDEEPFSALAFKIMTDPYVGKLTFFRVYSGVLQ

SGSYVLNATKNKRERIGRILQMHANSRQEITVVYSGDIAAAVGLKDTGTGDTLCDEKN

PVILESMNFPDPVIEIAVEPKKADQDKLGVALGKLTEEDPTLRAHTDEETGQTILAG

MGELHLDIIIDMRREFKVETTVGKPQVAYRETFRAPARVEGKFVRQSGGRGQYGHVW

VEFEPLEPGTGSQFESKVVGGSVPREYIQPALSGIEEQMKNQVIAGFPLVDVKATIVD

GSYHDVDSNEMAFKIAGSMALKAADKCKPVLLPIMKVEVTVPEEYMGDVMGMLNSR

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EIVAKTKGTE"

CDS 6739271..6740461

/gene="tuf"

/locus_tag="EFAGFIKM_05905"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P33166"

/codon_start=1

/transl_table=11
/product="Elongation factor Tu"
/db_xref="COG:COG0050"
/translation="MAKAKYERNKPHVNIQTIGHVDHGKTTLTAAITTVLSKTYGGAA
IAFDQIDKAPEERERGITISTSHVEYETDTRHYAHVDCPGHADYVKNMITGAAQMDGA
ILVVSAAADGPMPTREHILLSRQVGVPYIVVFLNKCDMVEDEELLELVEMEVRDLLNE
YEFPGDDTPITRGSAREALANPDGEWAQKIIEMFKEIDTYIPLPERQTDKPFLMPVED
VFSITGRGT VATGRVERGTVKVGEIEIVGITEETKKS SVTVGVEMFRKLLDSAQAGDN
IGALLRGVDRTQIERGQVLAKPGSVKPHTEFTAQIYVLTKEEGGRHKPFFTGYRPQFY
FRTT DVTGIINLPEGTEMVMPGDNITVTVSLISPIAIEEGTKFSIREGGRTVGAGSVA
SIQK"

CDS 6740898..6741206

/gene="rpsJ"
/locus_tag="EFAGFIKM_05906"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P21471"
/codon_start=1
/transl_table=11
/product="30S ribosomal protein S10"
/db_xref="COG:COG0051"
/translation="MAKQKIRIRLKAYDHRILDQSAEKIVETAKRSGAGVSGPIPLPT
EKQIITILRAVHKYKDSREQFEQRTHKRLIDIVNPTPQTVDALMRLDLPSGVDIEIKL
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CDS 6741253..6741876

/gene="rplC"
/locus_tag="EFAGFIKM_05907"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42920"
/codon_start=1
/transl_table=11
/product="50S ribosomal protein L3"
/db_xref="COG:COG0087"

/translation="MKAILGKKLGMTQVFTPEGNVVPVTVIEAGPCVVLQKKDIENDG
YEAIQIGYSKKKEKNANKPEAGHAKKANTAPKRYVREVRGINIAEYEVGQELKADIFA
EGEFVDVTGISKGKGFAGVIKRWGQSTGPM SHGSR YHRGPGSMGSIQANRV PKGR LP
GHMGHDTITIQRLVVKDAERNVLLVKGSI PGPKNSLIRVKETVKK"

CDS 6741902..6742525

/gene="rplD"
/locus_tag="EFAGFIKM_05908"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P28601"
/codon_start=1
/transl_table=11
/product="50S ribosomal protein L4"
/translation="MPKVS VYNVDGSQVGEVELND AVFGIEPNQH VLYDAVLMQRASL
RQGTHKVKGRSEVRGGGRKPWKQKGTGRARQGSIRSPQWKGGGIVFGPTPRSYAYKLP
KKVRR LAIKSALSSKVL DNDIIVLDALTLPKTK EFAAILS NLKVGRKALIVAPSYD
DNVALSARNIPGVKFVAADGINVLDVLSHDKLIITKEAVQKV EEVLA"

CDS 6742525..6742815

/gene="rplW"
/locus_tag="EFAGFIKM_05909"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42924"
/codon_start=1
/transl_table=11
/product="50S ribosomal protein L23"
/db_xref="COG:COG0089"
/translation="MKDPRDIVKRPIITERTADMMNDLK YVFEVDIRANKTEIKKAVE
AIFNVKVKNVNLT RVPAPKPKRYGRYSGYTSEWK KAFVTLTKDSKTLEFFETV"

CDS 6742846..6743676

/gene="rplB"
/locus_tag="EFAGFIKM_05910"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P04257"

/codon_start=1
/transl_table=11
/product="50S ribosomal protein L2"
/translation="MPIKKYKPTSPARRNMSVSTFEEITNQPEKSLAPLSKQAGRN
NQGKITVRHHGGGHHKRKYRIIDFKRTKDGPGRVATIEYDPNRTSNIALIHYADGEKR
YIIAPKGLKVGDDQVFSGPESDIKIGNALPLENIPVGTVIHNIELKPGKGGQLVRAAGT
EAQLLGKEEKYVSVRLSSGEVRRILKVCRTIGSVGNQDHELIKIGKAGRSRWLGKRP
EVRGVVMNPNDHPHGGGEGRAPIGRKSPMSPWGKPTLGKTRKKNKASDKYIIRRTK
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CDS 6743748..6744026

/gene="rpsS"
/locus_tag="EFAGFIKM_05911"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P66494"
/codon_start=1
/transl_table=11
/product="30S ribosomal protein S19"
/translation="MGRSLKKGPFIDGYMLKKVEEMEASGKKNVIKTWSRRSTIFPQF
IGHTFGVYDGRKHVPVYVTEDMVGHKLGEFAPTRTYKGHTADDDKTRR"

CDS 6744062..6744394

/gene="rplV"
/locus_tag="EFAGFIKM_05912"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P42060"
/codon_start=1
/transl_table=11
/product="50S ribosomal protein L22"
/db_xref="COG:COG0091"
/translation="MEAKAHAKFIRIAPRKAQLVVDLIRGKQVGEAVAILRHTPKSAS
PIVEKLLNSAIAANAEHNYSLDVNNLVISQAYVNQGPTMKRFRPRAMGRASRINKRTSH
ITLVVSEK"

CDS 6744410..6745075

/gene="rpsC"
/locus_tag="EFAGFIKM_05913"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P23309"
/codon_start=1
/transl_table=11
/product="30S ribosomal protein S3"
/translation="MGQKVNVPVGLRVGIIRDWESKWYAGKDFGDLLMEDVRIREFLKN
KLKDSALSRVEIERAANRVNVTIHTAKPGMVIGKGGSEVENLRNQITKIAGGKKVHIN
ISEIKNQDLDAVLVAESIAQQLERRVSFRRALKQAIQRTMRSGAKGIKTQVGGRLGGA
EIARSEGYSEGTVPLHTLRADIDYGTAEAHTTYGLIGVKVWIYRGEVLPTAKKQAAKE
GGN"

CDS 6745078..6745512

/gene="rplP"
/locus_tag="EFAGFIKM_05914"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P14577"
/codon_start=1
/transl_table=11
/product="50S ribosomal protein L16"
/db_xref="COG:COG0197"
/translation="MLVPKRVKHRKQQRGHMKGQAKGGTTLNFGHEYGLQATEPAWITN
RQIEAARIAMTRYIKRGGKWWIKIFDPDKPITQKPLEVRMGSGKGNVEKWWAVVKPGKI
MFELAGVP EEIAREAMRLAAHKLPIKTKFVKREELGGEANES"

CDS 6745502..6745699

/gene="rpmC"
/locus_tag="EFAGFIKM_05915"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P04457"
/codon_start=1
/transl_table=11
/product="50S ribosomal protein L29"

/translation="MKASEFRNLTSAEIEQKIAGFKEELFNLRFQLATGQLDNPTRIR

DVRKEIARAKTIIRERELGIG"

CDS 6745748..6746014

/gene="rpsQ"

/locus_tag="EFAGFIKM_05916"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P12874"

/codon_start=1

/transl_table=11

/product="30S ribosomal protein S17"

/db_xref="COG:COG0186"

/translation="MSEERNARKVQTGKVVSDKMDKTIVVAVETYKKHNLVHKRIKVT

KKFKAHDEENTAKIGDTVKIMETRPLSKDKRWRLTEIVEKAVII"

CDS 6746050..6746418

/gene="rplN"

/locus_tag="EFAGFIKM_05917"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P12875"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L14"

/db_xref="COG:COG0093"

/translation="MIQPFTRLTVADNSGAKELMCIRVLGGTGRRTAQIGDLIVCSVK

QATPGGVVKKGDVVRAVVVVRTKRSVRRKDGSYIGFDENAAVVVKDDRSRGRTRIFGPV

ARELRDKDFMKIVSLAPEVI"

CDS 6746458..6746811

/gene="rplX"

/locus_tag="EFAGFIKM_05918"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0CI78"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L24"

/db_xref="COG:COG0198"

/translation="MPRVKKVLESHNNKLHVKKEDTVMVISGKDKGKKGRVIAAYPRE
NRVLVEGVNMVKKHQKPNQQNPQGGIIEKEAPIHVSNMHIDPKSGKVTRVGYKVLDN
GKKVRVAKRSGEIID"

CDS 6746844..6747386

/gene="rplE"

/locus_tag="EFAGFIKM_05919"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P12877"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L5"

/db_xref="COG:COG0094"

/translation="MASRMKERYLQEIAPALMQKFNYTTVMQVPKIEKIVINMGVGDA
VQNSKVLDSAVNDLQLIAGQKPVITRAKKSAGFKLRENMPIGAKVTLRGERMYFFLD
KLLNVTLPVRVDFRGVSSNAFDGRGNYTLGLKEQLIFPEIEYDKVDKVRGMDIVITT
AKTDEESRELLTQMGMPPFVK"

CDS 6747460..6747645

/gene="rpsZ"

/locus_tag="EFAGFIKM_05920"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54798"

/codon_start=1

/transl_table=11

/product="30S ribosomal protein S14 type Z"

/translation="MAKTSMKVKQQRTPKFKVRAYTRCERCGRPHSVLQKFKICRICF
RELAYKGQIPGVKKASW"

CDS 6747678..6748076

/gene="rpsH"

/locus_tag="EFAGFIKM_05921"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P12879"

/codon_start=1

/transl_table=11

/product="30S ribosomal protein S8"

/db_xref="COG:COG0096"

/translation="MTMSDPIADMLTRIRNANTVRHETVEMPASTMKKQIADILKREG
FIRDAEVIDDNKQGIIRVFLKYGQNNERVITGLKRISKPLRVYTKSNEVPRVLGGLG
IAIISTSKGIMTDKEARQSKSGGEVVCYVW"

CDS 6748107..6748649

/gene="rplF"

/locus_tag="EFAGFIKM_05922"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P46898"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L6"

/db_xref="COG:COG0097"

/translation="MSRIGRKPIVPSGVDITLDNTVITVKGPKGTLTRELHKDMKVT
VENNEITVVRPSDNKTHRSLHGTTTSVVNNMVSGVTEGFAKSLELVGVGYRASKSGDK
IVLNVGYSHPEITPEAGIEFEVPSNTKIIVRGIDKERVGAYAAKIRSVREPEPYKKG
GIKYEGERIIRKEGKAGKKK"

CDS 6748767..6749135

/gene="rplR"

/locus_tag="EFAGFIKM_05923"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P46899"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L18"

/db_xref="COG:COG0256"

/translation="MITKPDKNKARLKRHLRVRKKIQGTAARPRLNVFRSGKHYAQI
IDDVAGVTIASASTVDKELSTDIKNGASVESARKVGELVAKRAKDKGVSNI VFDRSGY

LYHGRIAALAEAAAREAGLEF"

CDS 6749163..6749660

/gene="rpsE"

/locus_tag="EFAGFIKM_05924"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P21467"

/codon_start=1

/transl_table=11

/product="30S ribosomal protein S5"

/db_xref="COG:COG0098"

/translation="MRVDPNTLELTERVVNINRVAKVVKGGRRFSFSALVVVGDNNGW

VGAGIGKAGEVPDAIRKGIEDAKKNLVHVPLVGTSIPHLVTGKFGAGRVLLKPASEGT

GVIAGGPVRAVLELAGVGDILTKSLGSSNSMNMVNATLEGLSRLKRAEDVAKLRGKSV

EELLG"

CDS 6749674..6749859

/gene="rpmD"

/locus_tag="EFAGFIKM_05925"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P02431"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L30"

/translation="MAKLEITLVRSLIGRPETQRTTVKTLGLRKINSKVVQNDNPAIR

GMINKVSHLVAVKEVEA"

CDS 6749903..6750343

/gene="rplO"

/locus_tag="EFAGFIKM_05926"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0A0F6"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L15"

/translation="MKLHELSPSPGSRKERKRLGRGPSSGTGKTSGRGHKGQNSRSGG
GVRPGFEGGQNPPLYRRLPKRGFVNPTKEYAVVNTEDLNSFAAGTEVTPEFLMTNGVV
KNAKSGIKILNGDVTVKLTVKANKFSQSAIEKIEAAGGTTEVI"

CDS 6750343..6751641

/gene="secY"

/locus_tag="EFAGFIKM_05927"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q7A468"

/codon_start=1

/transl_table=11

/product="Protein translocase subunit SecY"

/translation="MFKTLKNIWRVEDLRKRVLFTLFVLIYRIGSFVPVPGVNKDVF
EATNSAGKEVFGLLNTFSGGALFQFSIFALGIVPYITASIIQVLLSMDVIPKLAEWAK
QGEQGKKKSAQLTRYLTIGLALIQAFGTSIGFNRLYNTMVPNATFADYILIAIVLTA
GTSFLMWLGEQITEKGIGNGISILIFAGILSTVPNIIKQTIESDFIQPDQLFMNILKG
VIIAIVIVLIIIGVIYIQQAIRKIPVQYAKRVVGNKMYGGQNTHIPLKINAAGVIPVI
FASLLMFPTIIANFWADRLWAQWIGQNLTHKPLGMLLYVVMIFGFTFFYTFVQMNP
QQMADNMKKNGGYIPGIRPGKATEKYLTRVMTRLTMAGAMFLAVISVLPVILGALSGL
PQSAQIGGTSLIVIGVALDTMKQIESQLIKRHYKGFINK"

CDS 6751732..6752376

/gene="adk"

/locus_tag="EFAGFIKM_05928"

/EC_number="2.7.4.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P27142"

/codon_start=1

/transl_table=11

/product="Adenylate kinase"

/translation="MNILFMGPPGAGKGTQADVIVKEFGIPHISTGDAFRLAIKQGTP
IGMKAKEYMDQGLLPDDVTIGIVEERLQQPDCREGFLLDGFPRTLSQAEALDGILDR
LNSGLDHVINLKVDRNKLLARLTGRRICKNCGSTYHVFNPPKQEGICDKCAGELYQR
SDDNEESVGTSLDEYINKTAPLLTFYETKGLLRQMNGEQDIDQVSQEIVSLLRG"

CDS 6752380..6753132

/gene="map_4"

/locus_tag="EFAGFIKM_05929"

/EC_number="3.4.11.18"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P19994"

/codon_start=1

/transl_table=11

/product="Methionine aminopeptidase 1"

/db_xref="COG:COG0024"

/translation="MIIGKSETELGLMREAGRIVAETHRLAEHIAPGITTGELDHMA

DQYIRSQGAVPSFKGYNGFPASVCASVNEELVHGFPGKRKLNEGDIVTFDIGAQYQGY

HGDSAWTYPVGRISSEARRLLDVTEASLYAGLALVKPDVRLFTISHAIQKYIEDEGFS

VVREYVGHGIGTDLHEEPQIPNYGLPDRGPRLKAGMVLAIEPMVNVGRRYVKTLEDNW

TVVTVDGKLCARFEHTVAVTPDGMEIFTKLNA"

CDS 6753143..6753451

/locus_tag="EFAGFIKM_05930"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNSQSNPQLGQLVKIRKGRNADQAAVIVAIADSKFVYIADGDKR

KFDQPKKKNLLHLELQPMISSEVVNSLNESGRVTNGKLRYAVHSFLESTNIQAEEKGD

"

CDS 6753455..6753670

/gene="infA"

/locus_tag="EFAGFIKM_05931"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P20458"

/codon_start=1

/transl_table=11

/product="Translation initiation factor IF-1"

/db_xref="COG:COG0361"

/translation="MAKEDVIEEGTVLEPLPNATFKVELENGHQILAHVSGKLRMHF
IRILTGDKVVVQLSPYDLTKGRITYRK"

CDS 6753823..6753936

/gene="rpmJ"

/locus_tag="EFAGFIKM_05932"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P20278"

/codon_start=1

/transl_table=11

/product="50S ribosomal protein L36"

/db_xref="COG:COG0257"

/translation="MKVRPSVKPICEKCKVIRRKGNVMVICENPKHKQKQG"

CDS 6753957..6754325

/gene="rpsM"

/locus_tag="EFAGFIKM_05933"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P20282"

/codon_start=1

/transl_table=11

/product="30S ribosomal protein S13"

/db_xref="COG:COG0099"

/translation="MARISGVDLPRDKRVEIALTYIFGIGKTTSQKILSTTGINPDTR
VRDLTEDEVGKLRESIDKEVKVEGDLRREISLNILRLTEIGCYRGVRHRRGLPVRGQR
TKTNARTRKGPVRTVANKKK"

CDS 6754345..6754740

/gene="rpsK"

/locus_tag="EFAGFIKM_05934"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P66357"

/codon_start=1

/transl_table=11

/product="30S ribosomal protein S11"
/translation="MAKPKKVVRTKRRDRKNIESGVAHIRSTFNNTIVTITDPHGNAI
SWASSGGLGFRGSRKSTPFAAQMAAETAAKAAMEHGMKAVEVMVKGPAGREAAIRSL
QAAGLEVNLIKDVTPVPHNGCRPPKRRRV"

CDS 6754877..6755821

/gene="rpoA"
/locus_tag="EFAGFIKM_05935"
/EC_number="2.7.7.6"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P20429"
/codon_start=1
/transl_table=11
/product="DNA-directed RNA polymerase subunit alpha"
/db_xref="COG:COG0202"
/translation="MIEIEKPKIETVDVNDGTYGKFVVEPLERGYGTTLGNSLRRIL
LSSLPGAAVSSVQIDGVLHEFATVPGVMEDVTEVILNLKALSLKIHSDDEEKVLEIDAE
GEGAITAGDIRADSDVEILNPDLHIATLGPGRSLHMRIFANRGRGYVQADRNKRDDQP
IGVIPVDSIFTPISRVNYAVENTRVGQVTNYDKLTLEVWTDGSIRPEEAVSLGAKILT
EHLMLFVGLTDEAKDAEIMVEKEEDKKEKVLEMTIEELDLSVRSYNCLKRAGINTVQE
LTTKTEEDMMKVRNLGRKSLEEVQEKLEELGLGLRTEE"

CDS 6755856..6756221

/gene="rplQ"
/locus_tag="EFAGFIKM_05936"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P07843"
/codon_start=1
/transl_table=11
/product="50S ribosomal protein L17"
/translation="MAYQKLGRNSSARKALFRDLVTDLFLYERIQTTEAKAKEVRSIA
EKLITKAKKGDHARRQVAAYVRRETIDGEQDAIQKLFSELSGRYAERPGGYTRILKL
GPRRGDAAPMVYLELVDRA"

CDS 6756396..6757154

/gene="truA"
/locus_tag="EFAGFIKM_05937"
/EC_number="5.4.99.12"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q5SHU9"
/codon_start=1
/transl_table=11
/product="tRNA pseudouridine synthase A"
/db_xref="COG:COG0101"
/translation="MTLTYDGTAYFGFQVQPGGNTIQDHLEDAIRALTGEKVKITGSG
RTDAGVHARRQIFNFPTESQIPIERWCIALNSRLPSDIVVIDAIEVSADFHSRYAAKK
KTYRYTVNANQFPDVFNRRLLQYHHHAKLDILAMQEGLRHFITYDFTSFASRKSQKEN
HVRSVYEAWMEVDRSMCRDHPRDQGVIIHYVSGNGFLQHMVRIIVGTLLEIGEGKRKA
SDVPMIAACNRSAAGPTAVSCGLMLWDLEYKKD"

CDS 6757360..6757797

/gene="rplM"
/locus_tag="EFAGFIKM_05938"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P70974"
/codon_start=1
/transl_table=11
/product="50S ribosomal protein L13"
/db_xref="COG:COG0102"
/translation="MRTTYMAKPNEVERQWHIIDAEGKTLGRLASEAAALIRGKHKPQ
FTPHVDTGDFVVIINAEKIVLTGKKMQGKKYYRHSMHPGGLKVTTAEEMVKNKPERML
ELAVRGMLPKTRMGEEKMKLRLKAYRGTEHPHAAQKPEVYELRG"

CDS 6757817..6758209

/gene="rpsI"
/locus_tag="EFAGFIKM_05939"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P21470"
/codon_start=1

/transl_table=11
/product="30S ribosomal protein S9"
/db_xref="COG:COG0103"
/translation="MAQVQYYGTGRRKHSVARVRLVPGEGRIVINKRDINEYFGLETL
KLIVKQPLNLTETLNNDVVLVIAHGGGISGQAGAIRHGISRALLKADPEYRASLKKAG
FLTRDPRMKERKKYGLKAARRAPQFSKR"

CDS 6759011..6759703

/gene="cysH"
/locus_tag="EFAGFIKM_05940"
/EC_number="1.8.4.8"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P94498"
/codon_start=1
/transl_table=11
/product="Phosphoadenosine phosphosulfate reductase"
/db_xref="COG:COG0175"
/translation="MNLLEKEELARTKAELEHASPEDIIRYAIETFPNITFACSFGA
EDVVLVDMVQKISPSTDIFYLDTFHFKEYETRDKMQENYNLEFVRVSPKITPEEQA
AQHGEELWKSDPNGCCNIRKVEPLTRILSQYDAWITGIRRDQAPTRANSKKVEYDSKF
GLMKFNPIAHWTTEDVWQYIRDNNVVYNPLHDQNYPSIGCEHCTRQVMPGEDPRAGR
SGNDKTECGLHK"

CDS 6759727..6760896

/gene="sat"
/locus_tag="EFAGFIKM_05941"
/EC_number="2.7.7.4"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34764"
/codon_start=1
/transl_table=11
/product="Sulfate adenylyltransferase"
/db_xref="COG:COG2046"
/translation="MTSILPHGGTLVQRIVQGEEREQLLQDSKNLSSLLINTWTISDL"

DLIGVGAFSPLEGFLNEEDYLSVISRMRLADGTVWSIPITLAVDDKQAASLQIGELVK
LVGDQDGVTYGLLEVQSIYQVDQGEEARRVFKTDDPEHPGVKKLLERPATYVGGPIQV
LNRPKPSKFEEFYDPADTRKIFQEKGWKTVVGFGQTRNPVHRAHEYIQKSAMEIVDAL
FLNPLVGETKSDDVPADVRMKSylvllenYYPADRAFLGVFPAAMRYAGPREAIFHAM
VRKNYGCTHFIVGRDHAGVGDDYGYEAQEIFTNFTAEELGITPLFFEHSFFCTKCGN
MASSKTCPHDKEHHMALSGTKVRGLLRDGGQCPPPEFTRPEVAEVLIEGMAEQVRS"

CDS 6760965..6761720

/locus_tag="EFAGFIKM_05942"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRKNMGKHFVWIRLKTIKRVMLSLCLLAMLVAVMSYELPSAKT

SGYWSLPMAGKVIAIDAGHGPDGGAVSKQGVIEKDINLSIALYVRDYLQQAGALVVM

TREIDTDLAESDTKGYSKRKTEDLKQVRRIEDKQADLFISIHMNSVPSNRWGAQVF

YTTNHPDNEGLANLLQQEMVRNLENTDRIAKTVNTVYLLQALKIPSALVEVGFLSHPE

EARMLADEAYQRKVAASIYNGILRYSSGERPKS"

CDS 6761800..6762900

/gene="saIA"

/locus_tag="EFAGFIKM_05943"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P50863"

/codon_start=1

/transl_table=11

/product="Iron-sulfur cluster carrier protein"

/db_xref="COG:COG0489"

/translation="MLSKEQILELLQPLQEPQLGVSLTELEWVRDIMVKENHVALTIV

TLENRPEDTTALSDAARNLLSQRGLKDVHIRVRAASEHDRESLSMGQPDDEPDRDEVL

VKGHAAGLDGHELLSPESGVRFIASGKGGVGKSTVTNLAALARQGKKVGLIDAD

IYGFSVPDMMGIEEYPVVEDGVIQPIERFGVKVMSMGFFIRENNPVIWRGPMLGRMLR

QFFTDVQWGELDYMLLDLPPGTGDVALDVHQMLPQSKEIIVTTPHATAAFVAARAGAM

AIQTDHELLGVVENMAYYECGSCGEKDYVFRGGGGRLAESLHTSLLAQIPLGTPDNH

PSEPDFSPSVYKADSRIGAIYDEVAQSIESKF"

CDS complement(6762986..6763735)

/gene="gerD"

/locus_tag="EFAGFIKM_05944"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P16450"

/codon_start=1

/transl_table=11

/product="Spore germination protein GerD"

/translation="MKRPLWQLCCVVLGLSVMLAGCGSDQSSSPQGSYKEMKTMVVD

ILKSDEGKKAVEEALTGQSSSSGSSGSEEGGGSGGASGSIGMKMLMPVQSSEQIRIAV

KDTITAPEYKKEFEKIMTDPQFAGEFAKVINAQSKQLHMQLIKDPTYQKSVGDIMKSP

EVSKMFMDMTKTPDYRKQTMVTMQEVMQNPLFRMEVLTLLKKVVQDELQPKVESGGQQ

GKEQGGQEGQGQEGSDGGDGGSGDSGGGGGS"

CDS 6763861..6764493

/locus_tag="EFAGFIKM_05945"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNLRRWFFLFWTALLIGAAGALGTGLIMMLVNGEKTNGLNDFLL

YLLILFGSGVMISVYSQMGGFFAYLILNYMGKGVFPKRGWQIVQIVLTVLALLDVMFLR

LFVGGDRERISDIVLGIILAAAIVTAYVKVKLTHISALVPTLFFMIAVTIVETIGVL

RIDVNAATIFIVVPLLLCNAYQMLILHRLVDVSTNQSVSGKAEQLKESRA"

CDS complement(6764592..6765368)

/locus_tag="EFAGFIKM_05946"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNSFYVFSGKKIKRYLIVLVAIFAIGIYLERGNVSVFSEEAP

SAVYSVPTEKKVIALTFDISWGDKRTEPILKVLQENKVQKATFFLSSPWSKTHPEIVT

AIKEAGYEIGSHGHRHENYSSLTEEEIRKEISTAHSILTDLTGKEPKLLRLPNGDFDK
RVLQVANSINYQVWQWDTDSLWKNPGVQTIVDRVVSKAHPGDIVLLHASDSSKQTHE
ALPVIIDKLKNQGYEFVTVSELLNHSSVEGKEVRDQASGQ"

CDS 6765491..6766108

/locus_tag="EFAGFIKM_05947"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLKFSTFLKDLGSIRGALIWSVVLFAVGIGAGWVSTGPLEELL

NQIGGLREVSEERLEQGGNVQWNFFLFIFFNNAIKSVLVIYAGIFFGILPVIFLLINGM

VLGFVHHTTMNYGASFYDIVVKGLLPHGIIIPVIIIACAFGLKFGGLVIKSLAQLGS

DKRNTMGTRWKAFMNRTLASFVVVILLVAAIESTLTYTLVRG"

CDS 6766262..6766492

/locus_tag="EFAGFIKM_05948"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLGMLFNEKECKELDYVLRKELDEMLFDLSDNRDLQEIYAIAS

RYKTVFRMYARFAPPKELSKYARGGKLKSKP"

CDS 6766492..6766626

/locus_tag="EFAGFIKM_05949"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLKLVIYSIYSSGSEVRLFIAGAVPLNHENVKLLRGSYFLSKKG

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rRNA 6766975..6768525

/locus_tag="EFAGFIKM_05950"

/product="16S ribosomal RNA"

rRNA 6768686..6768797
/locus_tag="EFAGFIKM_05951"
/product="5S ribosomal RNA"

tRNA 6768837..6768913
/locus_tag="EFAGFIKM_05952"
/product="tRNA-Ile"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Ile(gat)"

tRNA 6768936..6769011
/locus_tag="EFAGFIKM_05953"
/product="tRNA-Ala"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Ala(tgc)"

rRNA 6769224..6772145
/locus_tag="EFAGFIKM_05954"
/product="23S ribosomal RNA"

rRNA 6772293..6772404
/locus_tag="EFAGFIKM_05955"
/product="5S ribosomal RNA"

tRNA 6772492..6772567
/locus_tag="EFAGFIKM_05956"
/product="tRNA-Asn"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Asn(gtt)"

tRNA 6772571..6772643
/locus_tag="EFAGFIKM_05957"
/product="tRNA-Thr"
/inference="COORDINATES:profile:Aragorn:001002"
/note="tRNA-Thr(ggt)"

tRNA 6772654..6772725
/locus_tag="EFAGFIKM_05958"
/product="tRNA-Glu"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Glu(ttc)"

tRNA 6772733..6772808

/locus_tag="EFAGFIKM_05959"

/product="tRNA-Val"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Val(tac)"

tRNA 6772818..6772892

/locus_tag="EFAGFIKM_05960"

/product="tRNA-Gln"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Gln(ttg)"

tRNA 6772902..6772977

/locus_tag="EFAGFIKM_05961"

/product="tRNA-Lys"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Lys(ttt)"

tRNA 6772983..6773067

/locus_tag="EFAGFIKM_05962"

/product="tRNA-Leu"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Leu(tag)"

tRNA 6773075..6773149

/locus_tag="EFAGFIKM_05963"

/product="tRNA-Gly"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Gly(gcc)"

tRNA 6773157..6773233

/locus_tag="EFAGFIKM_05964"

/product="tRNA-Arg"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Arg(acg)"

tRNA 6773248..6773323

/locus_tag="EFAGFIKM_05965"

/product="tRNA-Pro"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Pro(tgg)"

tRNA 6773336..6773406

/locus_tag="EFAGFIKM_05966"

/product="tRNA-Gly"

/inference="COORDINATES:profile:Aragorn:001002"

/note="tRNA-Gly(tcc)"

CDS complement(6773642..6773980)

/locus_tag="EFAGFIKM_05967"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKGTTIIASVLLVAAMAGPAAADGQMSKGMDTNTNGSRVRSYQ

DTNYMDRANTNLNMDGNYRNNGDYRTNSVRANATTTNRDNGMDWGWLGLLGLLGLAGM

RKRVTDHNER"

CDS 6774561..6777353

/gene="ppc"

/locus_tag="EFAGFIKM_05968"

/EC_number="4.1.1.31"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9RNU9"

/codon_start=1

/transl_table=11

/product="Phosphoenolpyruvate carboxylase"

/db_xref="COG:COG2352"

/translation="MTETMVTASKSQSNNLLRRDVRFLGNILGEVLVHQGGTELLDIV

EKIRETSKSLRAEFLPELYAEFKTMIQELDSNDRHQVIRAFAIYFQLVNIAEQNHRIR

RKRDYERSAGNAVQPGSIEKAVQDLKERGLSHTEVEEILDDLSEELVMTAHPTEAMRR

VILDIHKRISEDMSLDNPTLTREREQLREKLLNEVITLWQTDELDRKPTVLDEV
NGMYFFHETLFHVLDPVYQELERCLNKFYDPDHDWHVPTYLRFGSWIGGDRDGNPSVTS
DVTWQTLLMQRKALREYQRIMIELMGHLSFSTNIIHVSELVQSIEQDRNSVTLKKV
DIWRNEKEPYRIKLAYMIAKLNNVLNKLQGPDRYHSAQDLIDELMIIDRSRHHFA
DYVADTTIRKMIRQVELFGFHTAALDVRQHSKEHENAMSEILAKMNIVEDYARLTEDG
KIDLLARLLDDPRPLTSPYHQYTEGTKECLDVFRITKRAQNEFGNGCITSYLISMTQG
ASDLLEVMMVFAKEVGLFTKGHNQDVVSTLQAVPLFETIDDLHAASDIMQKLFNLPVYR
ASVKGRNELHEIMLGYSNSKDGGVVTANWELRVAMNAITAVGNEHGVKLFHGRGG
ALGRGGMPLNRSILAQPPHTIGGGIKITEQGEVISSRYSLQGIAYRSLEQATSALITA
ALNGLEPQESASERHWDSSIKEISEVSLTKYQDLIFRDPDFFTFKESTPLPEVGELN
IGSRPSKRKNSDKFEDLRAIPWVFAWTQSRYPWPAWYAAGTGLQSYQDKEENLVVLK
EMYASFPFFRTLIDTVQMAVAKADLVIAKEYSAMTSNKEARDRIYQIEAEFKLTKE
ILKITGEAEILDDVPVIQESIRLRNPYVDPLSYMQVQLSELDRMRERGEDDTELLRE
VLLTINGIAAGLRNTG"

CDS 6777597..6778181

/gene="sigW_6"

/locus_tag="EFAGFIKM_05969"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q45585"

/codon_start=1

/transl_table=11

/product="ECF RNA polymerase sigma factor SigW"

/db_xref="COG:COG1595"

/translation="MSGGIRVDNLENRLIKLVKGDQRAFAEIVELYKDKLFHLAYRM
LNNRHEAEDVVQETFLRVFRNMEKYDPNQKFSTWIYRIATNLCIDRLRRKKPSYSLDA
ELNDQEGSDGYAMLPSSDRTPESALLSETQTLIREAIDSLPAKYKSMILRYLQDLS
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CDS 6778182..6778352

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CDS 6778318..6778932

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CDS 6779247..6780083

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CDS 6780076..6781569

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CDS 6781641..6782981

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CDS 6783730..6785562

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CDS 6786367..6787650

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CDS 6788346..6803336

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CDS 6803503..6806811

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CDS 6806801..6808627

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CDS 6808624..6810357

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CDS 6810440..6829333

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CDS complement(6829698..6830348)

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/locus_tag="EFAGFIKM_05982"

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/inference="similar to AA sequence:UniProtKB:P81102"

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/db_xref="COG:COG0778"

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GYDTNPMAGYDKGQIAEAFGLDKERFQPVMLISIGKAAKDGYPYRLPVETITTWV"

CDS 6830478..6830843

/gene="merR1"

/locus_tag="EFAGFIKM_05983"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P22853"

/codon_start=1

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/product="Mercuric resistance operon regulatory protein"

/translation="MKISEVANHVNLPISTIRYYEKIGIIPDEHMLRDHNNYRIYAQS
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CDS complement(6830893..6831567)

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CDS complement(6831589..6832470)

/gene="cynR_2"
/locus_tag="EFAGFIKM_05985"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P27111"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator CynR"
/translation="MEIRQMENFITVCEELHFTRAAEKLGISQPTLSQQIRGLEDELG
VPLFDRVGKKIVMTQAGTLFLEHCVQMIRHLQNTQDALAEFRNDQGRRLVIGVLPDDL
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EEYVLVSENHDWAERSSIEIQELRDIQTMFPEGFTGRELV DGYCRKYGFTLNTIME
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CDS 6832640..6833821

/gene="yycB_3"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P37482"
/codon_start=1
/transl_table=11
/product="putative transporter YycB"
/db_xref="COG:COG2807"

/translation="MKFFYIVLALILASLNLRPPITSISPLMSTIQNDLGLSGMTASL
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CDS complement(6833859..6834827)

/locus_tag="EFAGFIKM_05987"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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IHEKFMSALSDKQRQDIENIQHRVYFQHQTEQIRDSAHLEFLLMAAVQNIVIQITYANQ
RRSSDQRSSSANTNIRTIQPIALYARKGYWYCQAYDLHKQAYRVFRCDRIISAETTEI
EPLTHVKELYSQDAQSLWKPSEQAIPFKCLMDEAGIELFQQEHFPSMQIIEKMGHMYL
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CDS 6834915..6835358

/locus_tag="EFAGFIKM_05988"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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CDS 6835588..6836112

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/locus_tag="EFAGFIKM_05989"

/EC_number="5.1.3.33"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:A1YPR3"

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CDS 6836585..6837505

/gene="bdIA"

/locus_tag="EFAGFIKM_05990"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9I3S1"

/codon_start=1

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/db_xref="COG:COG0840"

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ELMSSISYISEVSTSNRATLTHLQEQAGSIQGVVRTIREISSQTQLLALNAAIEAHA

GEFGRGFDIVAKEVKKLSAMVESSINEIRDSVTGITKEIGNITGGTKKVEEYVEQSQK

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CDS 6837520..6839367

/locus_tag="EFAGFIKM_05991"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MVPNTGTAFFCCSVHKKTGIIIVIKRGHNTWEYLQLCHAEKCWGG

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YTEGLVDQDLVDDHLITPLMLEGVPLLKQEGFLHPDNAHLLSAYLQDQLLPVSLVEE
TKSLQELAVGVLFGKNALLVDGLPSALLIGAHNIKS RGMNEPLSEGLLRGPRIGFTEQ
LSDNTGILRRYGSDQSLFIKKFEVGSRIKKDLAIAYIQDIADPNLVAEVCKRIEEMDM
DSMLESgyVEQLIEDSTLSPFQQVLNTERPDRVMGALLEGRVAILLDGTPFVLIVPVT
FSMLLQSPEDYYERWIPGTFLRVLRFMAAMLALLAPALYISFISFHPGLIPTKLVTI
IETRTGVPFPSIIEVLIMELSIEILREAGIRLPKPIAPAMGIVGGLIIGQAAVQAGII
SQFLVIVVAVTAISSFTIPVYSAGLTRILRFSAMFSAAILGLYGVVMFFLLVCTHLA
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CDS 6839406..6840506

/gene="yndE_3"

/locus_tag="EFAGFIKM_05992"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O31809"

/codon_start=1

/transl_table=11

/product="Spore germination protein YndE"

/translation="MNDSQGKLTQTQTVVIIVNYMLGAGILTLPRTTSKAVGTPDVWI

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MSWGIFISTTIYLITVVMVIGSLSLDGIKTRTWPTLDLVRSEIQLIFERFESLLL

IWIMQIFSTTAITHYCASVGIRDLFRTKKIKGIMYGLLPFIYVTAMMPKTVDDTFALG

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CDS 6840503..6841705

/gene="gerBC_3"

/locus_tag="EFAGFIKM_05993"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39571"

/codon_start=1

/transl_table=11

/product="Spore germination protein B3"
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SHHRA LDVLT SQDPSRIPAFYLTGITNNSYLSNKILDPVLLSKLDAQMQSGSSFLLQN
VLNSDGEDKFSGGSIFDGKTTKFIGELSQTDLEGLSWLKPKEHGGVLKTHNKQGFTVV
YEMKNKKT VIPKVVGNDISFHVKVDSEGWLMEDWRAPEEEEEKGAYLRELEKEFAELA
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TNP GSSTE"

CDS 6841970..6843382

/gene="rocC"
/locus_tag="EFAGFIKM_05994"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P39636"
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VPLNALLISMVGGALALLSSIIAPGT VYITLV SISGLAVVAVWMSISASQYMFRRQYI
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CDS 6843360..6844418

/gene="mmuM"
/locus_tag="EFAGFIKM_05995"
/EC_number="2.1.1.10"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q47690"

/codon_start=1

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/product="Homocysteine S-methyltransferase"

/db_xref="COG:COG2040"

/translation="MTQAQQTNPSEQILREHPVMILDGALATELEQHGCDLDDPLWSA
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AQARDDVWAEVQSGLVERESSTGQLVEAPSVRSGNVENITDRTGDREADSLRLRPIIA
GSVGPYGAYLADGSEYVGHYGVSDETLVEFHRPRMAALLEAGADILAFETIPSLQEAK
VLVDLLKEFP HAYAWLSFSLKDGT SISEGTPLEVCAQTFGSEPQIAAIGLNCAPMEVV
TEAVGILSSASDKPVIVYPNSGETYDAVTKTWSGQGT CGSMSDASEQWVAAGAKIIGG
CCRTTPHQIGALAKKWRR"

CDS complement(6844506..6846908)

/locus_tag="EFAGFIKM_05996"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAVMFKLSLSYLSRNKIQNALIALLLLLSTLLVSTAIVILANTG
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HIPNIYLYMFNTPPPPWGVDELIFSSGKPDTVPEQGSVWIPTSMANAYHISVGDITGF
KTGSSTLELNVSGIVIDVPYGAFFSSTARVWMNPTDYQHDLATLAGNENRMMGIHFND
YSMNSVYWERYNRETGIPFLESKMEFEAIASFYLIINQVIGFIMIFMGVVMLSIALMT
IGFTIADAILANYRTIGILKSLGLTSRKITIGTYVIQYALISIVAIIPGLALSIWISKW
IINISVSSLRVGNQNIPVQGLDAAILAGVLLFTLVILFTVLYAKKARSIQPVQAIRYG
MSETDHSRRAGKMNSPLAHWIGFTRLPTAVLGFRHVFKN TKSSVLTILLTTMASSVL
VLGYVLLTSINGIEQTA AKWGYDNANIAAVVVNKS NFPKAELEHVLAQDSRISNVGWQ
GNTTGVISPE SLAAVEGQSISL NLSVLDGSYQELGFETLKG VNPQHTNEIAIGVSVAK
TSDKDLGDLIDIYIEGEKRTFLITGIYQAIANMSVSGRITIDAMRSVNP DYSEFDDIF
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TFIIIFSTCRINIRKESRTYGIYKSLGMTSRQIRLSLTMGMFILSSVGAILGIFGVY
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CDS complement(6846911..6847669)

/gene="lolD_2"

/locus_tag="EFAGFIKM_05997"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P75957"

/codon_start=1

/transl_table=11

/product="Lipoprotein-releasing system ATP-binding protein

LolD"

/db_xref="COG:COG1136"

/translation="MSKKVIIRARNLCKTYNSGSEQHHAIRNVLDLIYEGETVIMGN

SGSGKSTLLYLLSGLDQITAGEVYFRDQRIDAYSEREMSNFRTRRIGYIYQSINLVPD

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LINSPDIIFADEPTGSLNMEHGTAVLDTLTDLNRKGQSVVMVTHDIKAACRADRLIYI

LDGKIGGILEFNTYDKHQIQDREAIIFALVTGKE"

CDS complement(6847771..6849213)

/gene="sasA_26"

/locus_tag="EFAGFIKM_05998"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"

/codon_start=1

/transl_table=11

/product="Adaptive-response sensory-kinase SasA"

/translation="MSLNSWSKRWLLTTLGLLIIIVLSILVLSMMLLQDRNSGESNLS

LNQVRLKVNPLLLALEQNHQHLNEQNIREDIRSTARETGVLITYLNLDGKVILSSDPI

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QQPMTFPVILISALMLLSLILSLFLFWMKRKLDKHLSPHQLKQHAESILKGNYEK

IQYNRNDELLEVYAMFDLMRTEIKHMSEQRIQQEQAQKELITNISHDIKTPITTIKAY

IEAIEEGLCNDQETLMEYMGVMRTHTDKTARLVEDLLVHALQELGQISVETHEMYSGP

ILETMLKPIEHVVLTKGLIYKGPYIPNVLIAIDPTRIEQVISNLAANALKHTAPGDT
IHIDMELESGHLKVTIADSGQGIRVQDMPFVFQRYFRGQASHAEQRVQEGTGLGLSIC
QSIIEAHGGHISFTSKEGQGTFRFYLPIC"

CDS complement(6849234..6849935)

/gene="walR_7"

/locus_tag="EFAGFIKM_05999"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37478"

/codon_start=1

/transl_table=11

/product="Transcriptional regulatory protein WalR"

/db_xref="COG:COG0745"

/translation="MLTHQRKVLIEDESDISRILRDYLTRNQYEAAVAATGQDGLQI

MELIQPDYIILDIMLPDMDGIEVCREIRRRNNIPILILSARGSDTDKVLGLGFGADDY

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VLKTVWGVGYKLNYE"

CDS complement(6850172..6851002)

/gene="rhaR_44"

/locus_tag="EFAGFIKM_06000"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01533"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaR"

/translation="MDTLETSLICDYSYHYKAFTHNMKGELQTYLFRLQTEGSCKVY

VQDKEFRMTSGDLLLLKPGDDYHLVVDEPHKEGRLSSGDYYLFCEGSWIENWWKRQHR

STVSRIGLDDKLISLWRNMLLEKRRGPLEENAELKDALLRGLCLYIDRAIKENIQTDR

AVSSALKLKRFIGEHATVTFKLEEAARYAGLSLSRAVRLFKEHYNQTMIQYAIEIRLN

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CDS 6851201..6851977

/gene="iole_5"
/locus_tag="EFAGFIKM_06001"
/EC_number="4.2.1.44"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01672"
/codon_start=1
/transl_table=11
/product="Inosose dehydratase"
/translation="MKKLNIGLQLFTLRDETAADFRGTLRKVAALGYEGVEFAGYGDI
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AEGWTKLFAELQQYGAEAAKQGLIFGYHNHDFEFHGQVGDANAFDAMFAQTSPEAVKV
EMDVCWVQFAGQNPPIEYIKQYAGRLPLLHLKDFSKDEQGQMKTLELGQGSVDLPAVIE
GATNAGVEWLIVEQDVCQNPPLSVSNSYNWLKENYLNQF"

CDS 6852033..6853052

/gene="afr_2"
/locus_tag="EFAGFIKM_06002"
/EC_number="1.1.1.292"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q2I8V6"
/codon_start=1
/transl_table=11
/product="1,5-anhydro-D-fructose reductase"
/translation="MSKIKVAVFGCGAIAERRHIPEYAANENVLVAFADPVVERAEK
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EEGEQMIEAAKNGVYLMVGHNQRLMPPHVKAKEILDSGKLGKVLNFRTSFGHPGPEG
WSVDGAESWFFRKEEAIMGAMGDLGVHKSDFIYLLNDEVSEVAGFISTLHKEGTKVD
DNATCLLRMKSGAIGTLVASWTQYRAGDNSTVLWCENGVMKIGTVEGDEVIVELTNGT
VETYKVGAMATNEKQVPSGVDAFVESIVTQTTPAISGEEGLRSLQVILAAFESEKTG
QIVKL"

CDS complement(6853322..6854269)

/gene="yhdN"
/locus_tag="EFAGFIKM_06003"

/EC_number="1.1.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P80874"

/codon_start=1

/transl_table=11

/product="Aldo-keto reductase YhdN"

/db_xref="COG:COG0667"

/translation="MEYIEIAGAGKRVSRLIKGTDYFVHNAYDKAATNMDAFLSIGGN
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LERLQTDHVEMYALHRDDPNTPTVSVILEALNEHIESGKIGAIGASNWTWQRLEEANAY
AAANGLKGFTFSSPNLSLAKANEPFWEGCVSADAETLAWHEQTKLPLLSWSSQARGFF
TGRFTPEVRDNEDLVRVYFYSDDNWERLHRAEQLANSKKTSPIQIALAYVLNQTFPTCA
LIGAQNQAELLSCDEGSRLTTPAEIAWLDLGSDVPAGI"

CDS complement(6854290..6855294)

/locus_tag="EFAGFIKM_06004"

/EC_number="1.1.1.384"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:B3TMR8"

/codon_start=1

/transl_table=11

/product="dTDP-3,4-didehydro-2,6-dideoxy-alpha-D-glucose
3-reductase"

/translation="MNSVQKLRWGILGSASIAVESVIPGLQQSELNQVTAIASRDEDK
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ALTEQEAQEMVQACADAGVHLAEAFMYRHHPRYEQIRDIIASGEIGEIRGMHSTFSFN
NSNASGNVRFRRDWGGGALYDIGCYSISVARLLLGQEPSAATVIGMFSPEDHQVDMMA
SGLLEFDNHVGVTFDSSMWAAFRNTLEVLGSDGIIIVPSAFISGQDRSSNFYVTAGGE
RREIEVPQVNHYSLQGDDMARAVLQGKGLRFAPSDAVANMKVLEACLRSAEERTRITL
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CDS 6855413..6856252

/gene="rhaR_45"

/locus_tag="EFAGFIKM_06005"

/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01533"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional activator RhaR"
/translation="MMRQTVLLTLQDIPYFCYPESVGHYMDHVQHAVLREAGALNNFN
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YMIERGLHRNLLWTLRQRSSWEEAHLALLTEAEQNTMLRPAQLSTLYAVLAEFVQHA
VPLKSTRTTSKAESRVLALLPQMQQEACQPFLQDWADLAGVSSYYFCKMFKSAVEMT
PMEFITRSLQMAKQWLLERPTANIGQIAEEAGYPNASYFNRQFMAHEGMTPTDYRGL
YHN"

CDS 6856359..6856766

/gene="nsrR"
/locus_tag="EFAGFIKM_06006"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01177"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional repressor NsrR"
/translation="MKYSKATNYALHTMLHLVSTAPEQLVSVHQLAELQKVSPYLSK
ILTKLVKAGMIESTSGANGGYRLSRKNPDPSFLEIIHAIEGQASLFECSQNHNAGCLI
QQVMVQAEEEMESFLNNKKMSELASQMKGASL"

CDS 6856932..6857381

/gene="baiE"
/locus_tag="EFAGFIKM_06007"
/EC_number="4.2.1.106"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P19412"
/codon_start=1
/transl_table=11
/product="Bile acid 7-alpha dehydratase"
/translation="MSQSTITGLEQLLALENIRNTKARYCRYIDTKQWDTLGDFVAPD"

AVADFSTEGNPIPVLTGRDITVQVFRDLVDVAVTVHHVHSAEVEFVSENEAKVIS PME

DWVTFPEGNENKSFHGFHGHYHETFVKIDGQWYIKHTSLKRLRLDLFE"

CDS complement(6857584..6858963)

/gene="ribZ_2"

/locus_tag="EFAGFIKM_06008"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q180E3"

/codon_start=1

/transl_table=11

/product="Riboflavin transporter RibZ"

/translation="MNNTATASSGERTGIQEGLIVSLLGFTVVLVVMNTMMFNLALPK

IAAEFMLTSVASSWIVTGYSIVFAISSITFSRLSDFIPIRTLFTTGLTLLGAASVLGF

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VIGGSITQFLGWHDLFIVTGLTLFLIPVFFKLLPRETPQKGSFDLLGAVLLAIGTTGV

LLFLTSRQWYTLVIGAAALLFWLRIRRAADPFVQPALFKDKKYMMLSSLGIVSYINN

FSTLFLLPQILAHLYGLTPAQSGLVIFPGAVVSMLLSNRIGRMIDRHGNTLLLKFAPW

LLLAAGLFALFADNNIYAIMAVYVLLSVGFSSLTTSVSNELSGNLTMDQVGAGMGLF

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KVTKTSHQI"

CDS 6859169..6859492

/locus_tag="EFAGFIKM_06009"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKILHHPQVSDIELSSVLYALSDPTRLGIVAEAAARSGEQPCSHF

HAPVVKSTMSHHIRTLREAGVIRVRVQGTQHFLTLRSDDLETRFPGLLQPLLQAAQAS

STDPS"

CDS 6860080..6861000

/locus_tag="EFAGFIKM_06010"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSNMHRIHWFDEQIRGGRFPNSSWLAREFEISRRQAQRDIEYMA
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FSLCPLKMISQFNADYVVGYEADPVQQVAIRLEGIVHVSILDERFEYRSDALLGGWEE
PLPVRKPFVAEIRLKLQHMDLWQGYRIRARQDQIYSIEFYDTDAFLQHFLVSEWEEL
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CDS 6861029..6862027

/locus_tag="EFAGFIKM_06011"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAENILDNLVMKRESKSYVDSLHAILTHTGQFQGSKVVLGYTG
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WVRRSIDEGTGVIYWIPEFGVIHGYDDSDRIFYVQDGWSKEPQILLYDNFGLNFTGFW
YCQVFGDQVRIPEQQMLLESLRLAIEDWDTPYRLLPDQNIASGKKAYDVWVEALRSGD
FDESGAGYILESFCHSRTEIRMYLQGVIRGIWNELDQTCAYYQLGTLIDQMKGIVQQ
ENRRVLRSDTTEDLAQVLVKAKVLEEQAIDYFRVISRKYPDRKRSTIPRWGAHSAR"

CDS 6862052..6862864

/locus_tag="EFAGFIKM_06012"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MMATKVVLQDWIQSPQAVNFADECRSWSGVSAYTDALYRILLHK
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FEPTFPLYQKHALLDIKASIDRGVGAILWHDQFVIVTGYDDAERVLFICESKGNEIIR
LPYDSFGRNSTPYWYYQILEACAPIDLWEVCKESLIQAVYKWETHDYMLPPQDYACGA
AAYAAIAAALQSGTYDAEQAATVLFAIMPNQDWIFPLMLQDLSICPFKWTRS"

CDS 6863315..6863506

/locus_tag="EFAGFIKM_06013"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MVHNPETIQECIEHARQRLYQIASQYPELWHPEVIRQSMVLDEL
INEYNNATRGRRTISNQLKS"

CDS complement(6863552..6864430)

/gene="ycjP_6"
/locus_tag="EFAGFIKM_06014"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P77716"
/codon_start=1
/transl_table=11
/product="Inner membrane ABC transporter permease protein
YcjP"
/db_xref="COG:COG0395"
/translation="MYHKTTGYRIFNGFNLFIAAVSILCILPLVHILAVSFSGKAAA
SANLVTLPIDFTVDAYTKTFGNSNFLSALWISVQRTVLGTLLSMTLVFLTAYPLSKE
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NFFRNVPKELEEAAFIDGANHITLTKIYLPVSMPIATISLFTMVGQWNSWFDGLIY
MNDASKYPLATLMQTIIVQQDFSNMNV DATQLQNMSQRTVNAAQIFIGALPILLVYPF
LQRFFVKGIVLGAVKE"

CDS complement(6864465..6865430)

/gene="yteP_38"
/locus_tag="EFAGFIKM_06015"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:C0SPB3"
/codon_start=1
/transl_table=11
/product="putative multiple-sugar transport system
permease YteP"

/db_xref="COG:COG4209"

/translation="MAIEQPLTTNTPVRKMTPHPRKRTRWNFKRTWPLHMLLPVLL

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NQVLAAAGVEPIFFLGDGDWFRVTVVVSDVWKEFGFGTIVFLAALAGINPALYEASEV

DGATRLRQTLHITLPALVPMIIVVGTLSLGNILNAGFDQIFNLNPLVYEKGDIIDTF

VYRMGILNGKMSFATAVGLFKSFVAMFLVISAYRMAYKIANRYRIF"

CDS 6865704..6867464

/locus_tag="EFAGFIKM_06016"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKFTVFAKTVILLICLLVPILLLYTYANQANVDMVVEEKQQSSL

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FAYLTQSFNHMAEQIQELIEKVYEERIRSREATLKHLSQINPHFLYNCLFYIKNMTQ

LGNREAVIAMSLSLGDYYRYITRGENDMTTVEEEIRLLDHYLSIQQMRTNRLTYEIAV

PQQMLLLHIPRLLIQPIVENAVIHGIEPMEGSGHVVTGMVPEHIEGRKYTRYSLFV

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SVEIRWFEEEQPHDESDGRG"

CDS 6867439..6869031

/gene="rhaS_45"

/locus_tag="EFAGFIKM_06017"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01534"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional activator RhaS"

/translation="MMNLMVVDDDEHSAVESIAVSIPWREHGIGQVFKAYSVKEALEHM
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FPDQVPQLYHQAVSALRKQAEAGKGLHLNAAAGTNGATLKSAALEYPPGLTTLLEAG
RMEDAHRKIDQIFAELSNSVFPEHVYVAFHYLAAAFSYMAHREGRQLAEVLGEQYQQL
LKDGYGISLRSLETWTRSVMQQWAESANDTGQDAGSTLIRQVQQWIDHHLGEDLSLQV
IAGEVHLHPVYLSKMYKQSTGEGISDYIIRSRMERAVHLLKHTAMKIYEVGQEVGYNN
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CDS 6869152..6870804

/locus_tag="EFAGFIKM_06018"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MYRKMMTALLAITMVAVTACSSGAKEEPAKEAAAPLALQDGKYE
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GNGKKDITYGLTVGMKNALNTWMTESGWIFGMYNTMPGQWNDAGDGTLYGSIQPGVKE
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ATYKAIALPTGPTGESHQHGSGASNGVVLINKDMANPEIFFTYQNYLFDNFANPEVGS
EFEHGFAQGQYDYDIVDGKVVGEAEVKDGVSPKTYTITYDGARIPNLMMDTLAE
LAKGKEPETPFKNTKIANKEPVFAAEVVVANKDNAIKSKFTGAPTETMKMKQDAIDKLE
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CDS complement(6871172..6871414)

/locus_tag="EFAGFIKM_06019"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSYSKYFPLENYLNQVSITLTAELEEILGFTLPPTAYNREQWW

VNNSNNHTQALSWLNAGWKVENVILGKNVTFVRCES"

CDS 6871701..6873419

/locus_tag="EFAGFIKM_06020"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTLYDQAMEEMITTIHEWFDEQEKRDDLESVVKRTTLQMGIFN

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CKANDVFALMTIHIRKEGAGAYQQALTFITHLLKQGFPSYKIKLKSSVKRYLPIKGL

AKSDTHRIFANALEYPELHPLLEEYAREAIQEFEFYEDTEGEKSCMPGSYATFGLGLV

DEQYFPLVEYYMGEVDDEHQLIQDKFIAAFLEKQGVTAQAIPALVASLRRSTDLSLKLK

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LQVAGK"

CDS 6873510..6874562

/locus_tag="EFAGFIKM_06021"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="METLRRNMWQGLNARDKEAWMRKLVRQLPDAMVYEGLETFERFG

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PWGDSFDYTMRLKHFGSLEGVDEIVDGSAAETASSRVEEKDDRPYDLEMPNFFGVQFAG

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DAMMYRRVIRLAELAL"

CDS 6874598..6875254

/locus_tag="EFAGFIKM_06022"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MANNKRSPYDDSPYVIYTVDGIRLSAGILVLFFLNVFLLIPVF
SVPFQSLYTYILLPPLGFMNTWAIALIAAPRRQLQNYVLFGRGVFGIVCSVGFMVIIQK
FAYGILGLSTPWYAIGSFVYGFVAFVQYVKFRLRKLQPPQRKKGDKSTDVPGATITM
ITGGAYLLANISLAFVTQQTAVVLMCVYIMLAFVVFHFIMDLHRYYWLRQIMNKAES
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CDS complement(6875377..6876483)

/locus_tag="EFAGFIKM_06023"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKNMKKSVATMMVLGMLTGATGVFAGTQLEKISAYLNHGISF
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MKVDVSPRDYSDGYTSKDVKLSNGVIAKWYTPDQTGMLTFKLDDRYVTLSSPDHKLSQ
AQLQQVAVSVQKANSNNDQGITAFADVNYSKQQLDNIRKAFKFDGFTTAYAPQHMVA
GDTFISVGAGGDGVNFVFNRMNVTVSPKDYSFSYDGKTVKLPNGVSAKWYTPDQTDML
TFKLDDRYVTLSSPNNQLTHTQLEQMAVSVQKVK"

CDS complement(6876674..6876880)

/locus_tag="EFAGFIKM_06024"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MTWLPPYVLIVGIALFGGIATMIIGNSKANQTSNPEYDRRTKQNL
SKLSYVYVGAIVLGFGGLILYLFN"

CDS 6877210..6878838

/locus_tag="EFAGFIKM_06025"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKMKMKKFIAPVLSLTLLMPGIAGAAAAPQTPMTIMKASVNTPA
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AAAKQALQVHEDLVQKVFDEYVAGDYADAYKAYREGFKEMFDVSKALSTAITTQMPEK
FENTKADTKAADLRSALNHLASEHFALSALQMSEQYDGRTAASNALITAEAGNTADFK
AAIASVYGNDGANAFEKIWVTNHVNAQSDYVKAVKNNDATARA AVEKRIDGFTTEFAT
FLDSATAGKLPKAAGQQALTTHENQVQNVLDQYAAGNYGASYTTNREGFKVMFGVGQA
LGNAIVTQFNDKFQEPATPAPAPEMTTVWMQLNSKMLKINDKTTNMDTTPVLWKNTTY
IPLRFLSEGIGATVKWDKKAQQVTVMAGDDTLEFWVNNNVMEVNGVKKNVGATVFNK
DGRTQVPLRFIAELLNWDVKWAQKDGSITLTKSM"

CDS 6879027..6879476

/gene="bdbC"

/locus_tag="EFAGFIKM_06026"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00287"

/codon_start=1

/transl_table=11

/product="disulfide formation protein"

/translation="MSTSSKSERPERNVDTRLFVAWAVSVIATGGSLYFSEIKGFLPC
DLCWYQRIFMYPLTILLGIAYFKDDVGITKYVLP LSFVGGGISLYHVTIQRIFSATGN
AVACGKVP CYTDYLNWFGFITIPLLALIAFIIIVMLWGIGKTPKSS"

CDS 6879496..6879939

/locus_tag="EFAGFIKM_06027"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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KAKVNEEVALQIKLTQGEQPVNDADHVQFQVWNEQDEPEAPSFQGMMSAAEELESRG
TKAVSIGDGIYEVKHAFQEPGVYVVQAHVTSGAMHTMPRTKVTVE"

CDS 6880110..6881597

/locus_tag="EFAGFIKM_06028"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
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LINSFRVQMIPTYIVTLVLFITLIIQLMKSYRGDRYVQSVRRPNRLSRIKMTLILILL
LAFSAGSIILTWLLPAFTMPEPTGTYAIGTFSQHLVDESREETKTPEAGDKRELMINV
WYPVDQEEAAQGLPLEHYPSELGEAISLVFGIPSQVFSYLDTIPTHVQGAEMSAVQSK
YPVLLFSPGIRSARFQSMTMIIEELVSHGYIVVGIDHPYTSAQVTFPDGRAVSQADPE
FATSAELYQYNVEGIGIRADDASFVLNLTQWNSHDPNQLLQGNLDLDHVGMGHSYG
GATTAEALAQDDRFKAGLSLEGGFWGEVSTTALKQPFMYIMSGGTAKSLDPEATAKDK
VFYPEFEPDLDRVMLNSLNDTYLTVENFFHQSFDTISLISPKMFARGMTPEHNVDIT
RSYALAFFDRYLKGKEQPLLQGSSAQFPEATYDATYTKIRNEQTQ"

CDS 6881624..6882025

/gene="cueR"
/locus_tag="EFAGFIKM_06029"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q93CH6"
/codon_start=1
/transl_table=11
/product="HTH-type transcriptional regulator CueR"
/db_xref="COG:COG0789"
/translation="METMTRGTLAKRTGVSMATLRYIEDSGILPAPRRSSNGYRVYTE
DYLVIKIKFIKDAQLLGYSLKEIQETLQLLSQEDMEKDTLKTIVRERIADIQTHIDHLE
QMQUIHLARLLHTPEDDIDNYIQSFRVQKKEP"

CDS 6882192..6882326

/locus_tag="EFAGFIKM_06030"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MRDLQGFVSDYIKGKKHLHLEIGVITKGDIEYHSLGNPQKKS
VY"

CDS complement(6882336..6882488)

/locus_tag="EFAGFIKM_06031"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MIKTIKIERKKPPTESAEVHPQVLSVGGVFFSLHHGFQYFIPTG
SSGMSG"

CDS complement(6882485..6883162)

/gene="astE"
/locus_tag="EFAGFIKM_06032"
/EC_number="3.5.1.96"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00767"
/codon_start=1
/transl_table=11
/product="Succinylglutamate desuccinylase"
/translation="MLVTKHVLLASTVHATPYFIVRGMMPGPVMFITSGVHGNETASM
AAAQKLADDIATGRHAIQRGLLIIVPRVNQQAYAKKIRGKPD LNRTFPRRMSGKAKHP
LAAAVFQLAREHRADWWLDLHEANGLSQLSSRVLGQTLITNPGSRTIRACRRVIERMN
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LREASMS"

CDS complement(6883259..6884233)

/gene="btuD_19"
/locus_tag="EFAGFIKM_06033"

/EC_number="7.6.2.8"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01005"

/codon_start=1

/transl_table=11

/product="Vitamin B12 import ATP-binding protein BtuD"

/translation="MNMITARHLQKEFKTPVIREGRFSGRLTFSREYVSKEAVRDIS
FDIGPGEFVG YIGPNGAGKSTTIKMLTGILHPTSGEVRLDGMNPHQDRRRTVGRLGVV
FGQRSQLWWDLPVKDSYDILAEMYGVRAEDKKRLSQFAELLDLESFWATPVRKLSLG
QRMRADLAASMLHDPELLFLDEPTIGLDVNAKRNIRQFLRTLNETFGKTILLTTHDMD
DIEQLCSRVMVINHGQLTYDGTISSLRETIGLPTLIRVTFRGAFHIPDVVSSAIHITG
MEGQIVTVEVNRKEWSTMDTLKQLEHWGEIEDVEMKEPDFEDIIHRVY"

CDS complement(6884250..6885050)

/locus_tag="EFAGFIKM_06034"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKRTSWFNLYKMLIRTSIRSRMQYKFNFIMASVLAALIQUISEFL
MVALVLHKFGAIGWSLHEIGYLFAIMTSLKTLYRTFGNEVHHLEKYL VNGELDQLLT
RPMPVLLALLPQNFRIMAGEVLQGGFILCWSLAGMMHSGQIGWIAIPFSLFIILTGA
VILFSIGLATATLGFWTTRIEELQTITEDAARTAAQYPLTLYPKWMSGILLTVIPVGFV
NYIPSLYLLRGEAGAWILVAVAAVAVLSLAASLRFWQFGMTKYQSTGS"

CDS complement(6885047..6885823)

/locus_tag="EFAGFIKM_06035"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLYFTLASKAYSRNLQYRGAHMVHNLASAMFGYMYACLWIGIGA
DHTLGEYGTQGMISYIAFTQSSLWISGFLTNGLGIPLSVRTGQIALDLMPVHLFTHL
MAREWGQIAYQFVYKSIPIYLLFSIVFSLHWPSDVSTLFYAALGLAGAA YLSICMNYI

IGATSMWTTESWLHWGNHAMMNLLAGFFIPLEWLPNWLEQLAWISYPFLLYVPTRI
YLGFEFGSLLWGTLLWCVFMTLICLAITQVLRRKVEVQGG"

CDS 6886129..6886980

/gene="degV_2"

/locus_tag="EFAGFIKM_06036"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P32436"

/codon_start=1

/transl_table=11

/product="Protein DegV"

/db_xref="COG:COG1307"

/translation="MKKIAWVTDSTSTLDPVFAEQNHIVPLRIVFGEECYRETDDI

TSEMFYEKLAEASRASSSQPPIGEFIELYESLKDKYDEIITHCSTELSGTLHTSMQA

AEIAGVTVTAIDSKAGAYPHREMIMQGLEWQKQGCSAAEIKVNIEQMIDNMSFYLIPA

SLQHLHRSGRVSGTQLIISQLLKIHLRLFEEGKVVVNEKIRTFKRTKERMLDMLKLD

MEKVKHVCIMHANNQEEAVTIKKQIAALLPRLKTEIMPFIPVVSIHAGAGTIGLCWIH

SENGYRE"

CDS 6887133..6887849

/gene="walR_8"

/locus_tag="EFAGFIKM_06037"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37478"

/codon_start=1

/transl_table=11

/product="Transcriptional regulatory protein WalR"

/db_xref="COG:COG0745"

/translation="MLSHRLLLVEDDRSISEMVGPPYLEKEGYDVTYAYDGLEAERQFS

QSQPGYDLVILDLMLPRKSGMDVLQTIRAVSLVPVLILSAKDGEVDKALGLGFGADDY

LSKPFSLIELTARIKAAIRRANYTTPPVAEVAKDQRIHIGGLVVDMETYEVEGTPV

KLTSKEFGILKLLVTHPGKVFTKAQIYASVWNDHYYGDENIINVHMRRLREKLEADPS

DPQYIKTLWGIGYKLEAEQG"

CDS 6887846..6888778

/gene="sasA_27"
/locus_tag="EFAGFIKM_06038"
/EC_number="2.7.-.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01837"
/codon_start=1
/transl_table=11
/product="Adaptive-response sensory-kinase SasA"
/translation="MTLIFAITTGILAIIVIGLWMRLRKRTQHLSYIHQKILAILDQG
TFERLLVFNSDDQVSRLKDMNQLLDHAHRAKAGYANQEKEMRNMLSNISHDLKTPLT
VVLGYSETLLHSPSLTDQERKIMTEKIQDKAQEVLRLIHSFFDLAKLESGDTELVLSR
VNISELCRLKMLSFYEMLTNLGLHVELEIPDGDIFVQANEEALDRVLDNLITNGMKYG
AEGKVLGLSLDHSIGGPVTLQIWDQKGKIPSEHSRVFERMYTLEDSRNRLYQGSGLG
LTITKRLLIERMGGSIHLHSPHQRTVFSVTLKAW"

CDS 6888905..6889828

/gene="bcrA_3"
/locus_tag="EFAGFIKM_06039"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q5WNX0"
/codon_start=1
/transl_table=11
/product="Bacitracin transport ATP-binding protein BcrA"
/translation="MNYIARTIDVTKVYEGVEVVSNNMNIKQGEIYGFLGPNGAGKT
TIMKMLTNLVKPTSGEIELFGEKLTPTS YEVLKRMGSIIEYPFFYDRLSAGENLELHC
EYMGFYNNKIIDNTMEMVGLKDTGKKPVKDFSLGMKQRLGLARALITPELLILDEPI
NGLDPVGIREMRDLFKRLSNEYRITLLVSSHILGEIEQIADTVGVIRGGRLVEEVSM
SIRGSQNEYIELQAVDIRKATYVIEHQLGLSNYKLVDDRTLRIYDPGIIPSELNTKLI
QHGEIESISKRAHSLEEHFMKLVKGDEDVA"

CDS 6889821..6890519

/locus_tag="EFAGFIKM_06040"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLKLIRLEMRKHRFVRNFAGAGIANIAVLLFLIMIGFVDVGAED
YAYGDYQTAFMIIDTFVRATFIIFAGALLSKLWISEYRNKTMNVMFTYPIQRHKIAA
KLIIVFGFTFVMIMVTDLLMGSLLLIVNHFYSFIPGSLTNQDILGLLVKYSMSSLSAA
CMALIPLFFGMRKHSVTTTMVSSILLVLIVCSGFNGSEVSIHSLIIPLTLGAIGIWI
ASMSMVRLETKDVN"

CDS 6890625..6891437

/gene="pdxK"

/locus_tag="EFAGFIKM_06041"

/EC_number="2.7.1.35"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P39610"

/codon_start=1

/transl_table=11

/product="Pyridoxine kinase"

/db_xref="COG:COG0351"

/translation="MTIPKTLTIAGSDTSGGAGIQADLKTQELGVYGMTVLTTVVAM
EPETWDHQVFPVELNVVEAQLRTVLDGIGFDAMKTGMLGSVDIIELVAKHIRRSGLPQ
IVIDPVMVCKGTDEVLQPENTAMIEFLLPGADLVTPNLFEASQLAKSGPIRSKEQME
AAAAAIHAHGSKHVLIKDRGVISPGKAMDLLYDGTNYEWFADVVGSGYTHGAGCTTS
AAITAGLARGLSVKEAVREGKAFVTKAIAGGFPLNRFVGPTLHVAHRLEQQR"

CDS 6891532..6891720

/locus_tag="EFAGFIKM_06042"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MASFFMRIFIKISNFWLILIVYIMGAFQNMCGHMNDTWNRYVII
RNLKRRVGHDQNSASGGR"

CDS 6891689..6892369

/gene="srrA_5"

/locus_tag="EFAGFIKM_06043"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9L524"

/codon_start=1

/transl_table=11

/product="Transcriptional regulatory protein SrrA"

/db_xref="COG:COG0745"

/translation="MIRTVLLVEDESRIREIVADYFIKEQWNVIEAEHGVQALELLAL
HEVDLVILDVLMPEMDGWTLCGHIRSQSTVPIIMLTARSEDDDKIHGFQLGVDDYVTK
PFSPRVLVARAETLMKRVEGAFGREQGVIRFGQVTLDPWARRLEKDGIEVELAPKEYD
LLLYLVRNAGIVLSRDAILNRIWGFDFEGDSRVVDTHIKKLRSKLGDEAKCIRTVIGT
GYRFEAEA"

CDS 6892366..6894114

/gene="rcsC_21"

/locus_tag="EFAGFIKM_06044"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00979"

/codon_start=1

/transl_table=11

/product="Sensor histidine kinase RcsC"

/translation="MRRNGVTMKLFLVMAGCLVLLYGTTVFAQLVWFDPFYQHQQVSS
MKKKLSKFEQQYSNGHWSDLQLAKETGKFMRQNSHLVILTNKGRLVNDPFIHITLLQE
DGSHVKVSLSLFINSENAGWITSHLKYGQELTVRGPASGSMVYPFKIQDATSAAWGTE
SFQESIEPVKEWSGVLTEVVLNPLATWSQRQGLLVQALDSRFPLSTEDQLALANGKML
NEEWMDSWSGVRNVITIAPVHRSGPEQQILIFSLTSLQEMREANEATRLFYAYFGIGAF
ILILLALLLSRIVTKPLLALNHVAKKMSTLDFTVKSPIRRNDEIGSLSNSLNALSGT
LGQTLLEELRQANTQMRTDMEMKQEIEQRQRKFFADASHEKTPISIIKGYSEGLKDGW
SESKRERYIEIIADEAIKMETMVEEMLDLVRLESSAVQLNTDAVALADMIEDIAGRLG
PQLKDKGLDVVLVSTTEQTVEGDRSKLEQVIFNIMMNAIRHAIPHTDITIEISRREGF
VHISIENKGEQIAEAERQYIWERFYRVERSRNRKMGGTGLGLAIAKQILDHGCYSGV
ENTPDGVRFYIIFPKA"

CDS 6894136..6894681

/locus_tag="EFAGFIKM_06045"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKSLPSILTLGNLSSGMLAVIMAIHGEFALAVMMIWWAMFFDLF
DGYAARKLHCEGEFGKSLDSLADVVSFGTAPVLILYLNSMIEVSVLGMALTALFPICG
ALRLARYNCQKTASSGFVGMPTFAGGLMSFFALWSPYFTHGVAYLVIIVLSGLMVSQ
IRFPSLKQVLASHEKDIVEPK"

CDS 6894695..6895180

/locus_tag="EFAGFIKM_06046"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEFAKEFIGQYGYFAIYGLLALGVIGMPIPDEVMMTFVGYLASI
SVLDYSVSIIVSFGGAFTGGLLSYMIGKKAGRPLVEKYGKWVG VNAKRFSRVESWFLK
YGYWSIILGYFIPGIRHLMCCFSGISKMAIGRYVVVSGIGAFVWCVVFISIGFYVGVL
T"

CDS complement(6895395..6896585)

/gene="gerN"

/locus_tag="EFAGFIKM_06047"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q9KI10"

/codon_start=1

/transl_table=11

/product="Na(+)/H(+)-K(+) antiporter GerN"

/db_xref="COG:COG0475"

/translation="MEFILVLALILIFTKLAGDLSVRLGQPSVLGKLIVGVILGPALL
GWVQQSDFVHYMAEIGVLLLMIAGLETDLQLKKNWKAFAVAVGGVILPFIGGYGS
AIAFGMSQTHALFFGLLFCATSVSISVQTLKDMNQLSSREGTTILGAAVVDDVLVVVL

LAVMMSLLGTGAGDVSIGLLIGKLLFFVIIFAAGWWLVPRVMKWMAPLRVTETVITT
GLIICFLFSYFAEWMGVAGIIGAFAAGIAISQTKFKHEVETKIEPIAYGIFVPVFFVS
IGLNVTFDGVGSQIWFIVVISLIAIVTKLIGGGAGARLTGFDRSSSIAIGAGMISRGE
VALIIASTGLASGLLDSEYFTSVVIMVIVTTLVTPPLLKITFARKKGEKQVERGIEES
HLSG"

CDS 6896802..6896939

/locus_tag="EFAGFIKM_06048"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGAGLDLSENGRKGAIFYSGAQRFLFRVLSLNSPELPRYNDIEHR
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CDS 6896960..6897532

/locus_tag="EFAGFIKM_06049"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGKNNKGEPNIPSPTSNNKFAGIITISILANVIILLFFAPSI
GYKGDVTFDITVLPFRNAVFNSTFIFLLAALIAIKRNVKLHKRFILAAFSTLLFL
VTYLTFFHYLSPETSKYGGEGIIIRSIYFFILITHSILAALIVPLALFTLVWGWTNQLKK
HRKIARWTMPIWLYVSSTGVVVYLMMAPYY"

CDS 6897606..6898349

/gene="gpmA_4"

/locus_tag="EFAGFIKM_06050"

/EC_number="5.4.2.11"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q3JWH7"

/codon_start=1

/transl_table=11

/product="2,3-bisphosphoglycerate-dependent

phosphoglycerate mutase"

/translation="MYRVVLIRHGQSMWNVENRFTGWTDVDLTTDGYAEARKAGKIMK
EQGFDFDYAYASVLKRSIRTLALDEMDLMWIPITKTWKLNERHYGALQGLNKQQTAL
LKYGEDQVKEWRRSVNVSPALDETDDRYVQDLDDKYKRLGCTIPFTENLMDTSKRVLE
YWNAEIKPMVSAGKRVLISAHGNTLRSLVMHLDQLSEADVMALNIPTGIPLVYELDED
LHPIGHFYLTADGSTYKHEEMTHVATPSD"

CDS 6898523..6898696

/locus_tag="EFAGFIKM_06051"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKRRGIIMTAIGAGVTYLMRNKQARDKLFSTVSGMMKNSNSSS
NGTSKTRPRVEVK"

CDS 6898876..6899784

/gene="yajO_6"

/locus_tag="EFAGFIKM_06052"

/EC_number="1.1.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P77735"

/codon_start=1

/transl_table=11

/product="1-deoxyxylulose-5-phosphate synthase YajO"

/db_xref="COG:COG0667"

/translation="MKKNRLGTSELMVSEIGLGCM SLGTEM EPAMGLIHEALDHGVNL
LDTADLYDEGRNEEIVGQAIKRRDQVIVATKVGNNRRLPGKEGWSWDPSKAYIKQAVH
ESLKRLQTDYIDLYQLHGGTLDDPIEETIEAFEELKKEGLIRYYGISSIRPNVIREYV
KRAAIVSVMNQYSIADRRAE E EVLPLLEQKGISVIARGPVASGVLADSGSAKADKGYL
NYTPEQLYTIRQGLSRLVTDQRSMAQTAIRYALSHPAVA AVPGASSREQLLHNIAAS
NSPELTAAEIQEIRELSPANLYKQHR"

CDS 6899870..6900196

/gene="ydbP"

/locus_tag="EFAGFIKM_06053"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P96611"
/codon_start=1
/transl_table=11
/product="Thioredoxin-like protein YdbP"
/db_xref="COG:COG0526"
/translation="MERIQSEQQYLDTINS DGFTVIKFDTTWCPDCKNLDRFIGDVID
QHTDKTFYALDAEKFQPF AEENGVRGIPSLLVFQNGKKVAHLHSKWAKTPAQISEYLE
TLESKV"

CDS 6900421..6900603

/locus_tag="EFAGFIKM_06054"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKNEIFEEMHQLSHND DRRYRLLMIGVKQLLQEQKENRYNLRER
LKSRRKKHRNFQVKEWY"

CDS complement(6900885..6901727)

/gene="uppP_2"
/locus_tag="EFAGFIKM_06055"
/EC_number="3.6.1.27"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P60932"
/codon_start=1
/transl_table=11
/product="Undecaprenyl-diphosphatase"
/db_xref="COG:COG1968"
/translation="MLSPAFQGGRELDI ISSIIMGII EGLTEFLPVSSTGHMILTAHL
LGLSEDNESVKTFEVVVQLGAVLAVV VLYWNKFIDMFRFTGGSRPYSRRLNLGHIFLA
MVPAAVIGLVFRDWIKAHLFGPETVLYSLVIGGILMIVAERWSRKSGRITTHDVDDIS
YKQAFVAVGIFQILALWPGFSRSGSTISGGLFAGVSRVAAA EFTFLVSVPI MIGATGYD"

LYKSIDHLNGSDFPIFAIGFIAAFIVAMLAIKTFLSILKKLSLTVFAVYRFVLAAVFF

IILM"

CDS 6901909..6902541

/gene="acrR"

/locus_tag="EFAGFIKM_06056"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ACS9"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional regulator AcrR"

/db_xref="COG:COG1309"

/translation="MTKINGLEPGEERRDQIIRIAMERFATQGYHQTAKISDIVREAGV

AQGTIFYWHFKSKEAIASEIVLTGKEELLESIGQGYRKDAGSVEDMVKASERLFTDLFL

FAAQNRYFMELLLKGIVTEESVQRLVEETRNAVETAFRHNMERAIELGMLPKGMDVPL

RAALLVSMIEGMISRWLFGSDELHSKFSAMTASSLAAEAASFIFYGLLGT"

CDS 6902658..6903509

/gene="fliY_2"

/locus_tag="EFAGFIKM_06057"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AEM9"

/codon_start=1

/transl_table=11

/product="L-cystine-binding protein FliY"

/db_xref="COG:COG0834"

/translation="MNNTYGSKTRKGWSLTAILLMTVLVLSACGSKATDGGSTNGAQA

SNELEQIKSAGVIKVGMMGTYPYNFLNDKKEMDGYDADIAREVAKRLGVEVEFVSQE

FSGLTPSLQAKKLDIISQMTITDDRKKVLDFSDPYITNQVKIIVKEDNNDITKLEDF

KGKTIGVGLGTNDESYLRNEVLPKVGDFTIKTYDDVISSLKDLNAGRIDATINNMYAL

KPIVDANGLNIKAVGEAIKSDQAGIAVRKDNPELVAAALNDALKGMKDDGTYNTIFKKW

FGEEPAQ"

CDS 6903542..6904186

/gene="yecS_3"

/locus_tag="EFAGFIKM_06058"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AFT2"

/codon_start=1

/transl_table=11

/product="L-cystine transport system permease protein

YecS"

/db_xref="COG:COG0765"

/translation="MELVFENIPFLKGAYYTLVTVISMFFAFIIGVLVAIARLKGP

MWLRRIARFYVSIMRGTPLLVQLFVIYYGLVDYGVTLGSLTAACLGLSLNAGAFSLSET

FRGAIQAVPKGQTEAAYATGMTPAQAMRRIIFPQAVRIAIPPMGNTFIGMLKETSLVA

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CDS 6904203..6904949

/gene="tcyC"

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/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

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/codon_start=1

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CDS 6905228..6905650

/gene="yhfA"

/locus_tag="EFAGFIKM_06060"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ADX1"

/codon_start=1
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/db_xref="COG:COG1765"
/translation="MNVTTVWKGKRAFTSEGPSGYAVGMDATAAYGGDSKGATPMELL
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CDS 6905977..6907767

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/locus_tag="EFAGFIKM_06061"
/EC_number="2.7.11.1"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00637"
/codon_start=1
/transl_table=11
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LGDLNVTSRIDGNDEIGQLSRQFNVMVKSINELMTQVVEATEQNNQLEIAQKEIKLKM
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CDS 6907760..6909358

/gene="cheB_22"
/locus_tag="EFAGFIKM_06062"
/EC_number="3.5.1.44"
/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00099"
/codon_start=1
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/translation="MYKVFLVDDEPSIREGLTTIIEWEKYGFQVIATAASGREISR
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KL FKNHTGEYFNAFLDKVRMEKAKELLDEGLKVHQVAARVGYANVDYFHGKFKKYVGE
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CDS 6909534..6912443

/gene="lacZ_6"
/locus_tag="EFAGFIKM_06063"
/EC_number="3.2.1.23"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_01687"
/codon_start=1
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DGASDWHWYHLVNGTPAICLDTLPGVEPLIEVDHFHRAKRLAYAFEAKVGKGKILIS
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CDS 6912722..6913705

/gene="yteP_39"

/locus_tag="EFAGFIKM_06064"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SPB3"

/codon_start=1

/transl_table=11

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permease YteP"

/db_xref="COG:COG4209"

/translation="METLTKKASANRSSDPKPLKNRRNGIWDRMKQQKYLYLMSLP

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GGIINDLLVGLNIIDQPIQFMAKGNLFWYIVTASDMWKETGWNAAIYLAATIDNEL

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EVL DLYALNYGLNMGRFSYGTAGIFNSVVSILLFTANGLFKKFTKESIM"

CDS 6913721..6914623

/gene="araQ_36"

/locus_tag="EFAGFIKM_06065"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94530"

/codon_start=1

/transl_table=11

/product="L-arabinose transport system permease protein

AraQ"

/db_xref="COG:COG0395"

/translation="MANKAFNATRGDKLFDIFNILAMTMVLVVTLYPFLNVLAISLNN

STDTVRGGIYLWPREFTLQNYKTIFQYDGLLQGLQISILRTLVGTVLGLISSSMIAFT

LSRPDFGLRK FVSTTLALTM YFSGGLIPVYILMRDLNLIGTFWVYVLPGMISAFNVFI

IRSFIDGLPYSLQESAKLDGANDFTIYYRIILPLCKPVLATIALFLAVGQWNAWFDTY

LYNGSKAHLTTLQYELMKVLQSTQQGSGAGR N ANDMAQQMTQISPESIKMAITIVVTV

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CDS 6914810..6916498

/locus_tag="EFAGFIKM_06066"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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QDSFIQKTDQYKSKIASGRVLGVIDQDWGYSDAENALKSAGKDEATYSHFPVTLSEDI

KDHAYQDPGFVSGWGVGITTSNPDPVRTIKFFDYLA SEEGQVLMNWGIEGKQYEVKDG

KRVIPADILDQKTNNAAVFQKETGIGLYTNMSGHYGDGVKDSTDNYTTNFPEQIVAA

YSDAEKETLKAYGATTWKDLFPSEDEFPIKPWGAAYNLPTPGDSNYNVIFKKTQDIIR

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CDS 6916874..6918577

/locus_tag="EFAGFIKM_06067"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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NMGVDNVSFDATGGFEIQQRVLKELGYPEVKTLEDYENVLRITYYKHPIDGQPTIPL
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NEGLLDKDTFVQKDDQYKSKIASGRVLGLIDQEWNYGEAENALKSSNGGDKTYAHFSV
SLNKDIVDHTFQPTGFDGYGIGITSAKDPVRIIKFMDWLASEEGQVLRNHWGVEGQHY
QVENGKRIIPDDVQDRKTDNSAFTKESGIGMYNVFSARYGDGVKDATDNYYTTNFPE
QIQAGYTAAKETLKYGITTWKDFYPSEDDLKLKDWGAAYNMPVPSD TDYNVTFQKT
QDIVRKRIPEAILAKSENFDSVYDSLLAELDKAGAVEMEKQYTVWIKERVALWTGKDV
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CDS 6918900..6920597

/locus_tag="EFAGFIKM_06068"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

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GVDNVTFDATGGFEIQQRVLKELGYPEVKTLEDYENVLRAYYEKHPIDGQPTIPLTL
NADDWKIMITVTNPAFQATGAPDDGEYYIDPETYEAKLHYKRPEEREYFRWLNKMYNE
GLLDKDAFVQKDDQYKSKIASGRVLGLIDQEWNYQEAENALKSSGKDDATYAHFSVSL
NDEIVDHTFQPAFGDGYGIGITSAKDPVRIIKFMDWLASDEGQVLRNHWGIEGEHYNV
EDGKRVIPDDVQDRKTDNSNFSKETGIGMYNVFSARYGDGVKDSTDNYYTTNFPEQI
VAGYTAAKETLKYGITTWKEFYPAEEDLPVKDWGAAYNMSVPSGTDYEVTFQKTQD
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CDS 6920788..6923169

/locus_tag="EFAGFIKM_06069"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSQHNNQTKINRLWYQQPAKRWEEALPIGNRLGGMVYGGTADE
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LTADQKGAVSVSVTLDSPHPYRVETSGDALTMFSRCPSHVESNYFRDHPESVLYEEDR
GTAYAVRVAFTASGDQVKVSNLEGKLIHQGADQVVFYLAATS FESYDVL PVKDHLVL
EEECKEMISKATTHGAEALRDRHIQDYSALFN RVSIDLGV SANAELPTDERLQAYQTG
QQDPGLEALYFQYGRYLLMASSRPGSQPANLQGIWNHQVEPPWHSDYTININTEMNYW
PAEVCNLSECHEPLFDMLTDLSTN TGRRTARILY GARGWTAHHNVDIWRTTPTGGDAS
WAFWPMGGVWLTSHLWEHYQFTGDQRFLEERAYPIMKEAALFCLDWLVEGPDGYLVTI
PSTSPENKFLTDAGEARSISMASTMDMTLIRELFSRCIEAAKQLNIDESLASEWSEAL
EKLYPFQIGSEGQLLEWFKDFAESEPGHRHVSHLYGLYPGEQINRVHTPELLEASRVS
LERRISQGGGHTGWSCAWLINLYARLLDGSQAHQFVRTLLARSTHPNLFDDHPPFQID
GNFGGTAGIAEMLLQSHLNLHLLPALPELWTQGRVEGLRARGGYTVGITWADNKLVS
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CDS 6923186..6924547

/gene="bglA"

/locus_tag="EFAGFIKM_06070"

/EC_number="3.2.1.21"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P22073"

/codon_start=1

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WLT FN EPWCIAFLSNLLGIHAPGNKDLQTSINVAHGLLVAHGKAVQSFRRLGTTGQIG
IAPNVCWAEPYSKSPEDQAACDRSIALNTDWFLDPIYKGSYPQFMVDWFAEAGATVPI
QEGDMEIISQPIDLLGINYYTMGINRFNPEAGALQSEEVDMGLTKTDIGWPVESRGLY
EFMHYLQKYGNVDVYITENGACINDDLENGKINDDRRISYYEQHLAQIHRIINDGINL
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NPQ"

CDS 6924908..6925171

/locus_tag="EFAGFIKM_06071"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MASKTAMVSQLERKDKNMRRAVLTMTVLAWVALITGVVMCLINL
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CDS 6925490..6926464

/gene="cyoA"

/locus_tag="EFAGFIKM_06072"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0ABJ1"

/codon_start=1

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/product="Cytochrome bo(3) ubiquinol oxidase subunit 2"

/db_xref="COG:COG1622"

/translation="MNKKPRSLIRIIIPVVLTLVTIALIVWPMLAGGQYVVLDPKGPI
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TLNIPADRPVKFELTADSPMNSFWIPQLGGQIYMSGMAMTLYLQADHEGKYWGSGAN
FTGEHFGEMRFDVNATSDDEDFDNWVAEVKQSSQALTTEGYAALAEPGTSNVAYYSAFP
EGLFQNIIVTKYVIDGNGAHSKHGSSNEASGAIQNSTDKSNQDEDKSAN"

CDS 6926486..6928456

/gene="qoxB"

/locus_tag="EFAGFIKM_06073"

/EC_number="1.10.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:E0TW66"

/codon_start=1

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FTTHGTIMILFMAMPFMFGLFNVIVPLQIGARDVAFPFLNSLSFWLFFLGAMLFNLSF
VIGGSPDAGWLSYPPLSELSSHSPGVGQNFYIWGIQISGIGSLATGINFLVTIIKMRAP
GMRWMKMPMFTWSVFSTCIILFAFPILTVTALLFLDRFAGAHFFTLDLGGNPMMYI
NLIWMWGHPEVYIVVLPAGVFSEIVSTFSRKKLFGYKSMVFAMLIISFLSFFTWAHH
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KLGKWAFTWNIGFYVCFMPQYAVGLMGMTTRRLSTYGWDTGWWELNFVSTIGAFLMGV
GFLFQVAQIADGIRKYKTLKASADPWDGRTLEWSIPSPAPEYNFAITPRGDDIDEWWE
EKERRAKGIYPPEQPLEPIHMPKNSAIPFIMSSFWFVAGFGFVFGWLWMAILGLAGVG
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CDS 6928457..6929077

/gene="cyoC"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0ABJ3"
/codon_start=1
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/db_xref="COG:COG1845"
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WLIVTAVLGASFIALEVYEFIELIHEGFSFTTSAASGAFFTLVGTHGLHVSLGLIWM
GLMFQLKKRGITDVTRGKINVISLYWHFLDVVWIFLLSIVYLMGVM"

CDS 6929078..6929407

/gene="cyoD"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0ABJ6"
/codon_start=1

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/product="Cytochrome bo(3) ubiquinol oxidase subunit 4"

/db_xref="COG:COG3125"

/translation="MAEHNSHDSHSHEQHGSLKSYVIGFILSVVLTIIPLVVVLNDMM
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LNNAVAH"

CDS 6929633..6930616

/locus_tag="EFAGFIKM_06076"

/EC_number="1.3.1.103"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q59I44"

/codon_start=1

/transl_table=11

/product="2-haloacrylate reductase"

/translation="MKARVIRYYRFGEPSEVLCMEEKDVIPPGPGELSVRMYARPINP
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TLDRHTIIVPNDIDHSASQLYINPVTAWLICTEVLKLTYGDTLIVNAGGSAIGRIFA
QISKIYGFKLIALTRDDRHTAELYRLGAVSVINTTKELLQARITELTEGYGTDAAVDC
IGGTDGEQLVNCLKPNGTVISVGLLSGITPLWHEVTRGTQVHVKLFWLKHWVERCSQE
RWEQVFHEVMELVRAGRLVMTNIGTTYELTNVQQAIEAAESGIGGKVLLQ"

CDS 6930689..6931261

/gene="bioY_2"

/locus_tag="EFAGFIKM_06077"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q2KBP7"

/codon_start=1

/transl_table=11

/product="Biotin transporter BioY"

/db_xref="COG:COG1268"

/translation="MKIKDMMFTAIAAAVIAVLGLLPPIPLPFPITVQTLGVMLA
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CDS 6931340..6932149

/gene="ecfA1_2"

/locus_tag="EFAGFIKM_06078"

/EC_number="7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q1GBJ0"

/codon_start=1

/transl_table=11

/product="Energy-coupling factor transporter ATP-binding
protein EcfA1"

/db_xref="COG:COG1122"

/translation="MIHFSNVTFGYANRATMLNDINLHIRSGEYVAFAGRNGAGKSTI
ARLMNGLLLPTTGQVTFNDYVTSNEDDLIIRQRIGMIFQNPENQIVASTVFEDIAFG
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DESTSMLDPEGKDQIALLMGELYKQGITIVTITHDLEEIAASSRVIVLDQGDICYDGS
PEALFQGEYWRFPGITAPFIVEAREALNRKGLHSSSALTLEDLVDDLCKLH"

CDS 6932134..6932997

/gene="ecfA2"

/locus_tag="EFAGFIKM_06079"

/EC_number="3.6.3.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q03PY6"

/codon_start=1

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/product="Energy-coupling factor transporter ATP-binding
protein EcfA2"

/db_xref="COG:COG1122"

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KDISFGPKNLGWSAEKVRSTCLDALHMGVGLDESFCNRSPFELSGGEKRRVAIASVLAM
NPEVLILDEPTVGLDSEGKEQLMELFCSWQKEQGSTIIMVTHDMETVAEYAEVVIIFE"

RGQVQRHTTPLQLFTEYQVELKDMGLKLPKALQLVEAINVKLNVELQLESVKKEWILS

YIADFFQRKEL"

CDS 6933000..6933803

/gene="ecfT_2"

/locus_tag="EFAGFIKM_06080"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q03PY7"

/codon_start=1

/transl_table=11

/product="Energy-coupling factor transporter transmembrane
protein EcfT"

/db_xref="COG:COG0619"

/translation="MSLSQSFIIGQYVHRNSIIHRLDPRAKLVI AFLFMLSVM LLNSW
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SIYEEGVKAGNIAIRIILLV IASLLT LTKLGD LAQAIEDLLKPAKRLGVPTQEFA
LMISWTIRFIPILLNETDNVMKAQRARGVRFNSGNIVRRLQSFIPIVPILL LAFQKA
ESASLAVEARGYSPGMNRTQLRTL SFKKLDYQVLIISIFCFALL LALRK"

CDS 6933812..6935551

/gene="yerA"

/locus_tag="EFAGFIKM_06081"

/EC_number="3.5.4.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O34909"

/codon_start=1

/transl_table=11

/product="Putative adenine deaminase YerA"

/db_xref="COG:COG1001"

/translation="MRIYPTNLHEYHRLISVSKGDQPATMWFRQASYLNVYTGEVEQA
NIYLSGSRIAYVGAKELPTSDQTQVVELEKGHVVVPGYIEPHAHPCQMYPYTWGEAL
LQKGTVLSINDNLSLLTFLGTEALS FIEKLEETSHH MFLWWCNIDRPDRADPMTMDKW
LQHNLVIQSGELTEWPKLLANDEV LVEQLYLTKAHHGMRAEGHLPGVSYEKISTMAAA
GITADHEALHAEDVLRRLKAGLYASLRYSIRPDLPHLLKGMKGDSRFNMNRMMLTSD

GPSPNYVERTSCASMIKICMEKGISVADAYRLATLNPAVYYGLDEDLGGIAPGRLACL
NVLTSSINEPDPLHVLQRGEEVVQNQRRVVEPDEAEIRTWLRSTFSPSRRTIVNLRDQM
ETRTDIGIELVNDVITQSYHFDPRAGLETDENWMTLMDVNGSWMINTRIKGLACGIKA
LASTYNASNDTLLLGRSLSAMREASQELELRGEGILVYFVDGEQLYIPLPLSGAMGLE
SVASIGASVDQFNEKMRIHGYRFGDPLYSLFLTASHLPHIRVSDKGLYLVKTGEIVL
QATPLVNTVRKVK"

CDS 6935548..6937053

/gene="yhfT"

/locus_tag="EFAGFIKM_06082"

/EC_number="6.2.1.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O07619"

/codon_start=1

/transl_table=11

/product="putative acyl--CoA ligase YhfT"

/db_xref="COG:COG0318"

/translation="MMLLADAIRIHASQNPEKTAIFDDARQISYAELYHGIKLAANTI
LATEEDFEADELPLVGLLMNSAMMIEYFLAATKIGMCAAVFDPKWSDANLTEVINEC
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GTTGRPKGYLRSQRSWIESFAYARETFVHDAGDHVLAPGSLVYSLTYACIQTLYIGG
TFHLTSKFRAEYVLETLATHAVTHLYLVPTMFEALYKAFMASDSVTALSSVRSLISSG
DKWSPESKRKVKEVFENAGLYEFYGASELSFVTVLDPEGNRYKPDSIGKPFAGVQVSI
REAVSTEATEGTVGQLFVKSPMIFAGYYGSEEETSQVVHGEWATVGDLATRDSEGYLY
LVGRKKNMIISGGLNIYPEEIEKLLLTLEGIEEVIVVGVPDVYWGQKV TALIKLRMGS
KVSDDGIVSLCRRELATYKCPKEIIRVDAFPYTTSGKISRTKLNELLKIKI"

CDS 6937050..6938228

/gene="thlA"

/locus_tag="EFAGFIKM_06083"

/EC_number="2.3.1.9"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P45359"

/codon_start=1

/transl_table=11
/product="Acetyl-CoA acetyltransferase"
/db_xref="COG:COG0183"
/translation="MNNMLIPVILSAKRTAIGKYGGMFKEIPPEILAAEVIQAILSEI
PIPPGDIDDVLLGNAVGGGGNIARLSALQAKLPVEVPGVTIDRQCGSGLEAIHLAARL
IQSGAGEVYLAGGVESTSRAPWRLEKPLSLYGSVVPQVITRTRFSPEWIGDPDMGKAA
NNVAKKYGVTRMDQDEYALSSHRKAISSIQSGRFDNEIVPLSIPEGNQLRIIHTDECP
RANTTLAKLAALPPVFEPDGTVTAGNACPLNDGAAIVLIMSMGKALSLGLTPLMKFID
SMAVGVDPNYLIGIPVPAVTKLLSRNRFAMEDIDLVEFNEAFASQVLASLRELHIPTH
IVNVGGGALALGHPFGASGAILVTRLFNEMRHIKGARGITTLGIGGGIGLASLWEKCE
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CDS 6938242..6939099

/gene="fabG_13"
/locus_tag="EFAGFIKM_06084"
/EC_number="1.1.1.100"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P99093"
/codon_start=1
/transl_table=11
/product="3-oxoacyl-[acyl-carrier-protein] reductase FabG"
/translation="MLLEGQVAVITGSSRGIGRATAIRMAQEGAKVIVINGVQEGGVWD
VVQMIRDQGGTAIGVVESVASMAGGERIISEALREFGKIDILVNNAGVVHDKMAHKMS
ETEWDLVLNSHLKGAFACIRSALPGMRERREGSIINMISVAGLTGMIGQLNYSAAKAG
LIGMTWTLSELESYGINVNAVAPAARTDMTPYIERAKQTAETQGESFPEYWKVGSP
EDVAELMLSLCLPRCRRVTGQIFSVNGGKIGVWSPPEHRIVATQSSRENGWEAGELFE
QLLSTYVKV"

CDS 6939140..6940348

/locus_tag="EFAGFIKM_06085"
/EC_number="2.4.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P9WFR1"
/codon_start=1

/transl_table=11
/product="PGL/p-HBAD biosynthesis glycosyltransferase"
/db_xref="COG:COG1819"
/translation="MKKKRIFIGMMAGMGRVNRCLPIALKLREMGHEVAFTIWGNAGV
AMEQMGFTYIPIVIPAPKGQVFHPNFKDMNHFLSMMGYSDPVYMRDELEARLRVTIG
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GALVEYGLPETDNILTFLAGNLALLPSIPDFDPVQFGKLPVPIEYIGPVVWRDTNETG
MPANWLMKSDNDRRPRVFVYTSRLVEWGVESGGHIFREAVRALGNTSTELLIATGFNP
LEGDSVEVPPNVHFTSYVSGVMAAEHSDVMIHHGGHGGSCMTTILTGTPSLVIPTWAER
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RAAELIRRL"

CDS 6940367..6941599

/gene="setA"
/locus_tag="EFAGFIKM_06086"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P31675"
/codon_start=1
/transl_table=11
/product="Sugar efflux transporter A"
/translation="MKSLLVLRSPALLLSVCIFFIGLGYGLTLPFMPLFGVERAGM
NPLSLGIFMACGSLSGIIISTLFSRLSDKRPVRKWIIVGSCVSASVGYVFYANTDSYI
VLMLVSCTFMAMSFSAFPQLFALAREVVEREASEDTVVMVAVLRALVSLAWILGPVMA
SFIIYQFSYTGLFLVSLMYMLVAIFVLMIRAQESREPGGGTELSSDSVRSFKRLLMA
PQIVFSLLAFAFELANTMGGIVTPLYVTQELQGGKLDVGMISGVNAALQVPTMIILG
ILAKRFGSITVMKCAGLFGVVYFSLFWFTQSGWQIIAIQIFSAIFIAIVLGVGMTFFQ
DLVPMKMTGTATTLYNNANIIGSMGGGLLAGAVGNFYFGFKIVIACSAALAFGLFVLLLV
PNANKEVVRHVGGDTYES"

CDS 6941589..6942725

/locus_tag="EFAGFIKM_06087"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/translation="MKASVILSHNQKEVIQACLSSLSRQRLCEGDQYEVVVIDNGSI
DGTGEMIGRLTYDFPIRYNYIPSTEQSSRAAARNKGITIANGDVIVFLDGDQLAGPDF
IYEHLRVHKLAEGLVIGFRRYLGEESIDITSLNPGWVHAAITSSEADERFQLMERFS
ENGSAFRTAWHLSFSCNFSVNREVLIRSGMFDEGFKGWGLEDSSELGYRLQQAGGTFVL
NKKALTFHIFHPSEFDENRYDGWKTNLDYFLECHPMFEVQAQNILKEFFDPEIRKSWW
DCYIRFEKVVRAHQGYEGDRLPVSIIVVYAEGPELIQTISAEAAHREVLVIDKTPSSD
LDILCQCINEKFDVLYYKYPSEDQLIDLHYQYAVRGIVKHEIFK"

CDS 6942780..6943949

/gene="acdA"
/locus_tag="EFAGFIKM_06088"
/EC_number="1.3.99.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P45867"
/codon_start=1
/transl_table=11
/product="Acyl-CoA dehydrogenase"
/db_xref="COG:COG1960"
/translation="MNFELTEQQKQIQSAARHFVDELLIPLELLRNEREGRPGIEL
RQIRDLQQAKTQGLWGIETPEEYGGANLGTVTSALLKMELGRTCIPFVFGGEADNIL
YLCNETQQNKYLLPVIAGERQSCFAITERSAGSDASRIQMRAERVADGWVLNGEKVFI
TNGNEADFAIVFAVTDVQAEPGKGITCFLVDRDMGWTSEPIPTMGGDKSPSVLTFNQV
FVPNGNVLGEEGQGLTTAMQWISRGRWWIPAI AVGASGRLIHMAIDYVKERSTFGEQL
ASRQSIQWMIADSAVELEALKWLVLYTAWRVEQGLDARHHATMSKLYGAGRAN DIVDR
VLQIFGGIGYSKDLPIERWYREMRVWRIFEGTDEIQRMIISRNLLKGHVRI GEWD"

CDS complement(6943946..6944839)

/locus_tag="EFAGFIKM_06089"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDYQSWIGVPTPTKKMVITTDQIVQFTQGFPEEFRPDARSIPLT"

FPMIWWQQTHLPWMELPGKIMIHGQQSFTYERKLKYDAALFYRIELANVRETTGSLGK
IQLLDCTMKVTDVMKQPVLVTNTTLILLDSPALQPSYSELEPVYPQYPSEIYYQWDGK
HRLSSGELLFDACLGITSSMLIAYAAASSDNNPIHLDVLKAHEAGAPRRIAQGMLIG
GMIGNRLKMLGLDNWILCDIKYRFRSPVMEGDVVRVLVSVINTDNLSHLACSITVYIE
HRAGVPSDLLAYEGSARYTAR"

CDS 6945033..6945872

/gene="kduI"

/locus_tag="EFAGFIKM_06090"

/EC_number="5.3.1.17"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q46938"

/codon_start=1

/transl_table=11

/product="4-deoxy-L-threo-5-hexosulose-uronate

ketol-isomerase"

/db_xref="COG:COG3717"

/translation="MENRYAAHPNEVKTYDTSRLREEFLMEQLFATDELVTYSHVDR

YIVGTAVPESKDITLEVNLKDIGNFFLERREIGIINVGGHGTVTADGQGYEIGAKEC

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TIYRYIHQGEGGIQSCQLVMGITELDKGNMWNTMPAHTHNRRSEVLYWNLPEdGVVF

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DLK"

CDS 6945957..6946718

/gene="glcR_3"

/locus_tag="EFAGFIKM_06091"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94591"

/codon_start=1

/transl_table=11

/product="HTH-type transcriptional repressor GlcR"

/db_xref="COG:COG1349"

/translation="MMNPLKRHEKIMEALLERQEVTVSDLSELLQVTGKTVREDLDKL

ESMGLLVRVHGGAMLAQNDQYGILNSRGVTEKHHPEKTEIAERALAYIRPGDIVALDG
GSTTLEMAKRLDNQPLTVVTNDLFIIAELTKKEQVRLVPPGGARVRNMLVGDDTAAFI
SSLNIHKAFISTTALHPEFGLSIYTGDLVPLKKAMISASQQVYGVDHYKFGQFALRT
FAQCSELDYIISDSRLDEETAALYEQSGVTVDYQS"

CDS 6946796..6947548

/gene="kduD"

/locus_tag="EFAGFIKM_06092"

/EC_number="1.1.1.127"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P37769"

/codon_start=1

/transl_table=11

/product="2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase"

/translation="MNPFDLSGQVALVTGTSGGLGQGMAIGLAEAGADVVLVSYSKPA

ATASAIEALGRKAYMIEADLSREDELSAVFEQALAFQGRIDILVNNAGIIRRTPAADH

AVQDWHHDVIGLNLNTVFFLSQLAGRHMIERGSGKIINIASMSLYQGGINVPGYTASKH

GVAGLTKALANEWAGKGIQINGIAPGYMETDNTTQIRADENRYRDITARIPAGRWGTP

EDLKGPVVFLLASAASDYLNGHVLNVDGGWMAR"

CDS 6947586..6948431

/locus_tag="EFAGFIKM_06093"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKLGILAHTFGKQPTAQLAQTIADNGFNSVQLALAKALSDVDSS

NGKLSPGLANEIGDQFAQRGVKIAVLGCYINPIDPDPVTRRADIDRFKEHLRYARDFG

CSMVATETGGLDTYQDTHPDGYEEKAWSVLKETVEELAEAEKVGVAHAAIEPVSTHTL

HTHEHMTRLFEEIPSSNLGMLFDPCNLIKQPHAADQGAFLREVMESLYQRMIVIHAKD

VAFDAQGEKYNPVPGAGILDYPLFFELLKTYKPHIDISLEGVTAAEAVPAAKHLREVW

SAVRV"

CDS 6948670..6949977

/locus_tag="EFAGFIKM_06094"

/EC_number="2.5.1.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q9WZY4"
/codon_start=1
/transl_table=11
/product="O-acetyl-L-homoserine sulfhydrylase"
/db_xref="COG:COG2873"
/translation="MSNERELSFETLAIHAGQEIDPTTNARAVPLYQTTSYGFKDTEH
AANLFGKLEFGNIYTRLNPNPTDVFQRIAALEGGAGALATASGQAATFSLLNIAGA
GDEIVSSASLYGGTYNLFSTTLPKLGLDVKFVDSSDPENFRAAITEKTKALYAETIGN
PKGNVLDIEAVAAIAHEHGIPLVDNTFSPYLLRPIEHGADIVVHSATKFIGGHGTS
IGGVIVDSGKFDWKASGKFPGLTEPDSSYNGVVYTEAVGPIAYIIKARVQLLRDLGAT
ISPFNSWLLLQGLETLHLRVERHSSNALAVAEFLEKHEDVSWVSYAGLPSHGSYELAQ
KYLPRGQGAILTFGIKGGADAGRKLIESVKLFSHLANVGDSKSLIIHPASTTHAQLTE
DEQTAAGVNPSELIRLSVG TENIQDIIYDLEQAIKASQGASVGA"

CDS 6950398..6952413

/gene="zosA"
/locus_tag="EFAGFIKM_06095"
/EC_number="3.6.3.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O31688"
/codon_start=1
/transl_table=11
/product="Zinc-transporting ATPase"
/db_xref="COG:COG2217"
/translation="MHAIHQPLHRQKQAEQRLSQTPGPNRGRKPDFRAMLQNKEMQSA
LGSGLLMLIAWGTAPYFGTLSIMLYIVAYAVGGWTKAKEGIETLVKDRDLVDNLLMIA
ASLGAAAIGYWNEGAMLIFIFALSGALESYATERSHKDISSLLALKPETALRIEDGQM
NLVAIDDLQPGDLLLVKPGELIPADGVVYRGSSFINQSSITGESLPVDKVAGDEVYAG
TVNGEGALYVEVTKSAEGSLFGKIIKMVEEAQAEVPDSQRFMERFEGIYAHIVVGVT
LVIAGTPLLLAWTWNEAFYKAMVFLVVASPCALVSSIMPVILSAMSSSARRGILFKGG
AHMENMARTRVVAFDKTGTLTMGTPQVTDIITAEHVDRVKLLGAVAAIENLSMHPLAR"

AIVDQANKENITLQEAHVQALTGWGIEGTVNDVVWSIGKTNVMESLQSEKIKDANVD
DSDEHGANHVKISSEWGDVCSRLEGEKTVSAVMADGELVGLIAMRDTVRPQAAAAVK
KLEAMGVKVAMLTGDRARSASVIARETGVSVMVYADLLPEDKVKQVQALRKQYGPVLMV
GDGVNDAPALAAATVGMGMGLSGSGTALEVADAVLMNDNIEEIAWVIGQARRAQRTVK
QNMCFAITVILALIAGNFLQDVALPLGVVGHEGSTILVILNGLRLLR"

CDS 6952546..6953355

/locus_tag="EFAGFIKM_06096"

/EC_number="3.1.1.2"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P22862"

/codon_start=1

/transl_table=11

/product="Arylesterase"

/translation="MGRYVQVEPNVKVYVEDIGETPVVFLHGWPVNYKMFYQLNVL
PNHGIRAIIDFRGYGLSDKPSTGYDYDRMADDVRAVIDDLELKDAVLAGFSMGGAI
VHYMSRHKHGHVSKLALLSAAAPVFTQREGYPYGLTPEQLNEQIIEPIFADRPKLLET
FGGMFFAKKHSQPFMDWFHALGMEASSYGTIRSAIALRDEDLRGDLSSIQVPTAILHG
KKDEICPFEEAEQMHQGIASSQLIAFEESGHGAFYDELEKFNSELIRFIQS"

CDS complement(6953479..6954210)

/gene="zupT"

/locus_tag="EFAGFIKM_06097"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00548"

/codon_start=1

/transl_table=11

/product="Zinc transporter ZupT"

/translation="MNDALIGSFISAMSTGLGAVPILFMRKISHRLRDILLAYAAGIM
TSASVYNLIPEALGQSNLFVLAFGIMLGSLVLLVLEMKIPHVDLENPEKMPFKIETKA
FMIIAAITMHNLPGLSVGVSYASSDENLGNLIAFSIGLQNAPEGFLVALFLVNQNIG
RFKALGIATLTGAVEIITAMIGYTLSSLVAGLVPYGLAFAAGAMMFIVYKELIPESHG
DGNARVATMSFLLGLITMIGLTELF"

CDS 6954467..6955408

/gene="trxB_4"
/locus_tag="EFAGFIKM_06098"
/EC_number="1.8.1.9"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P9WHH1"
/codon_start=1
/transl_table=11
/product="Thioredoxin reductase"
/db_xref="COG:COG0492"
/translation="MYKSIIGTGPAGLTAAIYLARANLNPLVIEGPQPGGQLTTTTE
VENFPGFPDGIMGPELMDNMRKQAERFGAEFRTGWVNNIDMSERPFKIQVEGMGELVS
ETLILSTGATAKYLGIPEETNVGRGVSTCATCDGFFFRNKEIIVIGGGDSALEEASF
LSRFGSKVTLVHRREELRGSKIMQDRARSNEKVEMALNRTPLEVLADNGVTGLKVLN
NETGEEVIPASGVFVAIGHTPNTGFLGGQITTDEHGYILTPGTSETNIPGVFACGD
VQDTRYKQAITAAGSGCMAAMDTEKYIESLEHSAVVL"

CDS 6955470..6955700

/gene="nrdH"
/locus_tag="EFAGFIKM_06099"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:Q48708"
/codon_start=1
/transl_table=11
/product="Glutaredoxin-like protein NrdH"
/db_xref="COG:COG0695"
/translation="MENVIVYTSTNCPNCKSVKTFLADKGISYEERNIETSDEFAQQV
WDMGVRAVPLTVIGEHRILGMNKTQFAKALDA"

CDS complement(6955840..6956037)

/locus_tag="EFAGFIKM_06100"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

/translation="MTYVDTSDISAQMFVTVLLFLIVLAPLFSLGILRLFQSKKKAGF

MYMLSGLLVYVVFQTFMSIFF"

CDS complement(6956185..6957351)

/gene="nagC_2"

/locus_tag="EFAGFIKM_06101"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P0AF20"

/codon_start=1

/transl_table=11

/product="N-acetylglucosamine repressor"

/db_xref="COG:COG1940"

/translation="MKITGDQMLVKKINKSIVLDTIRRHAPLSRARVSEVTGLNKATV

SNLVADLISDDLQVEIGPGESSGGRKPLMLLFRGTSGYAVGLELSVTHLKGLLDLEG

HIITEYAVTLKHHDVSSVLEQLKLAACKLIEAAPSPHGVIGIGIGVPGMVDEAGTVL

FAPNLGWEEKVALRSMLEEEFELPVTIDNEANAGAHGELNFGAGIGVRHMIYISAGMGI

GSGIMVDGELYKGAWGYAGETGHMSIEAEGLPCSCGNRGCWELYASEKAYEHPDHQLK

LPAHITRELIHYAEQGHAEVQELYNTIGRKLIGITNIVNSFNPERIIIGGPLSEAGP

WIETALKQVVEERTLPYHRRSLQIEWAALGSRSTRVGAAYSQISQFLGKIRVSV"

CDS 6957550..6958866

/gene="xylA_2"

/locus_tag="EFAGFIKM_06102"

/EC_number="5.3.1.5"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P54273"

/codon_start=1

/transl_table=11

/product="Xylose isomerase"

/translation="MAYFESVNKIAFEGKDSKNPFAFKHYNPEEVVAGKSMEEHFRFG

MAYWHTLTAGGSDPFGAETAVRSWDKYSGLDLAKVRVEAAFEFLEKMNLPPFCFHDVD

IAPEGNNLREFYSNIDTIVDLIEDHMKSSGKLLWNTANMFSNPRFMFGAASTCNADV

YAHAAAQIKKGLEVGKRLGAENYVFWGGREGYDTLLNTDMQLEQDNIARMFHMAVDYA

KEIGFDAQFLIEPKPKEPTKHQYDYDAATSIAFLQKYGLDKHFKLNLEANHATLAGHT

FDHEIRVARTNGMLGSLDANQGDM LGWDTDEFVDMYDATLTMYEVLKNGGIGRGGV
NFDAKVRRGSF EADDLFLAHIAGMDTYAKGLKVA AKLIEDRVFDDFIEKRYSSFSEGI
GADV VAGKATLASLA EYALNNESPRKNQSGRQELLRAQLNQYILAD"

CDS 6959151..6959411

/locus_tag="EFAGFIKM_06103"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSIKVSFITNDESRSLDQSFCYENEYVLLVSYPCVSRIMHAKRS

EQKGPEEAKRSHLSPDFTLAKGYKGNPGVMAIRGFSDHEVTT"

CDS 6959463..6960956

/gene="xylB_4"

/locus_tag="EFAGFIKM_06104"

/EC_number="2.7.1.17"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P35850"

/codon_start=1

/transl_table=11

/product="Xylulose kinase"

/db_xref="COG:COG1070"

/translation="MSYVIGVDLGTSAVKTVLVNREGKVAFEASEAYPLYQPKAGYSE

QNPEDWVEQTIVSLRKLLEVSGVQPSEIEGLSFSGQM HGLVLVDAEGKPLRNAILWND

TRTTAQCRRIEKVLDGKLLSIARNRALEGFTLPKILWVQENEP ELLQQASLFLLPKDY

VRYRLTG DYAMDYSDAAGTLLLDVAGKQWSNEIAEAFELPISLC PRLVESFEVGTLL

PEIADQTGLAAATKVYAGGADNACGAIGAGILSEGQTMCSIGTSGVVLSYEERKD LDF

EGKVHFFNHGEKDAFYIMGVTLAAGYSLSWFKDTFAADKSFDVLLQGIDQIPAGS NGL

LFTPYIVGERTPHPDANIRGSFIGMDAGHKLEHFGRVMEGITFSLRESIDILRGAGK

TVNEVISIGGGAKNEAWLQM QADVFNATIVKLESEQGPAMGAAML AAYGCGWFPSLQE

CATAFIRPAKSYEPNPETVAVYDRLFALYQEVYQGTRSLNDRLAEYR"

CDS 6961179..6961895

/locus_tag="EFAGFIKM_06105"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDGHEEHERPHITLSMIVRNEENRYLRQALERHRPWIDRAVIID

DGSTDGTVALCRELLDGIPLVLVENAASRFADEVSLRKQQWEETVATNPEWILNLDAD

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WKEQYESILDQEPRLLAWFE"

CDS 6961907..6964048

/locus_tag="EFAGFIKM_06106"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSTLKKDPLRKSQEESQPQIEPNSQEKEDQNEKQHESANENQKE

SQINHRPSRRSDNSLETRQSEEHEAFEQERILIASPIRQTTPVLREFLDSLHALERTT

VKTDYLFVDDNVEEAASNILHEFVLQHEGTVIQADEHGSGSPDNKGVYSKDEGGHYWQ

DEQIWRVAGLKNRILQYARHNHYDAVFLIDSDLVLHPRTLEQLVSSGKDIVSNIFWTR

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SLDPDVDSVTMDYNLSFTADGKVAYSLRRNRLVRRDRQFRWIGAVHEYLA VAGNLLHS

DIAVTHKKDKEYTDRNLRIYRKKEQAGEEFGPRDLYYFGNELKDHGQHEDAVKYYEKF

LDTGLGWVEDQIACQKIADCEAALERPEQEVTALFRSFAYDLPRAEICCRLGGYFAD

REDYRKALFWYEQATRAVRPDDPMVVLNEAAWTWMPHLQLCVCYDRMGNRAKAREHND

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CDS 6964296..6964922

/gene="kdgA_2"

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/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P50846"

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/db_xref="COG:COG0800"

/translation="MNLTEVLLESRLVAIVRGISREAAVTAGQGMTSGGIRLMEVTLN

TPGAHDIIADWRERHEGKAYVGAGTVLNVQMAKEAVAAGAQLVSPNVDSLVEIYAVE

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CDS 6965092..6966018

/locus_tag="EFAGFIKM_06108"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKAKTMIGGMLAVALTAGGLWKA AVKSQTPKKIPITLTPMPF

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MYDVRSHGASDPVRAASAYLFRDDLLAALRYTTARPEIDADAIGVLGHSLGGLGTILA

VTEGIPVSAVITDSMP SQFEVIVSSELRRRRLPLFPLAQLIPRIWFWRLGESLKS YRQ

RDPVIMLNERRRG MQLPMLMVHSGDNFIPPSELEYFMSKADPPVEHLWVNSGGHSCS

EEDPAFWDTVIPFLKTHVQGQKKSNDSSIASS"

CDS 6966245..6968638

/locus_tag="EFAGFIKM_06109"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSLNWKFNLR LKMFATKATTAAMATLLLASQTPGFAGSASAAQA

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ATPEQLPADVKPAISYEEAKALYLEEFKLILAYSRYGGYGMNGGQVIPAGVNLAYMPT
RDENSIYGNYEALDANTGEWKLLYGDTSSATKAEPDILGHVAEAALRNMTQHGVLLA
DEQGRVFPDRVITRGDWFNYLARAINPNMDLYYSGDGGDKLYADVTPDSPYYKAVRAL
IDQRWLAGADPEQNLNPQEEMTREELAVLLVRILRYEKLAGFYTLPSDLPNIADASAI
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CDS 6968840..6969967

/locus_tag="EFAGFIKM_06110"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MGKNGKRIITILLAGCLIAVALPRTVDLDQLYAASGTSDISTAT

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YDTSKKYTAYDGLVTGSTVCQGYSLAYRMLERVGIDNRIVEGTAGGQLHAWNIVNL

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CDS 6970131..6974642

/locus_tag="EFAGFIKM_06111"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MRKKVSIVIIALLLVQTMMQGWIFTPTMHAQDELTNLPASAISD

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WKVQYNYNQQEILQTNAWIEDRFD TAKQQLINNSVKVYQVDINASGAASNRTLINPNE
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ANNSGNVSTKAGLVDPADYELNVEGNTFTFTFKKDIHTAFILEYQSYINADHGARIEN
KVEFAGQSSSVIGEGNQSGIKVSLAGAGGGASTGLGKIRIYKVSDAGVLLEGAIFAIY
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GKTIEFKD TDIAFEIKNKKIRQGFELSKVDAVDSSKTLKGATFELYSKDGATREKIDE
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AGGKLVVTKVNAKDKSVLSGIEFELRDRSNIVIDTKVTDLNGVIEFDGLDYGSYTLVE
TKAEGFVIEQPETLVSIK PETQITIENKKNDRSVKLIKTNAGRTQHLQGAVFELRAQ
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VPFEITNIQTEAVVVEKTNQAIPVSGGGTSGPYNPGTPTTGVTDPDEKPVTPPEPGTPN
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FRRRQQLQR"

CDS complement(6974769..6975410)
/gene="srtA"
/locus_tag="EFAGFIKM_06112"
/EC_number="3.4.22.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0DPQ5"
/codon_start=1
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/translation="MKKFSILLVLLGILIISFPFLRETYDWQQTRVMNDLEQLQNGL
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KVAATHLVETTSIGNKGNAAIAAHRAHKKGRLFNRLVELQIGDSMEVTLADRTIIQYK
VDQISVVEPTDLSVLEDPLGLGQVLTITCDPLVNPTHLIVRAIAVKPNVTGT"

CDS complement(6975645..6977126)

/gene="lysP"

/locus_tag="EFAGFIKM_06113"

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/inference="similar to AA sequence:UniProtKB:P25737"

/codon_start=1

/transl_table=11

/product="Lysine-specific permease"

/db_xref="COG:COG0833"

/translation="MQDRSNPTTTTGPSLKKGLRARHMTMIALGGSIGTGLFLASGTA
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FAIIKVATVIIFLAVGVLMIFGIMGGEAVGFSNFTIGDAPFHGGFFAVLGVFMAAGFS
FQGTELIGVAAGESENPRENVPRAIRQVFWRILIFYILAITVISLIIPYTHPNLLKGD
LENIGVSPFTLVFEKAGLAIAASVMNAVILTSVLSAGNSGMYASSRVLYALARDGKAP
RFLGKLNKKGIPMNALLTTAVGMLAFLASLFGDGIVYTWLLNASGMCGFITWLGIAI
SHYRFRRAYVAQGRDLSLDPYRARWFPGPIFAFVLCIIVIIGQNYQAFTGDQIDWSG
AIVAYLSVPLFLVLWLGYKWIKTKKVPLQECDFTPTESPSDK"

CDS complement(6977609..6978751)

/locus_tag="EFAGFIKM_06114"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MNIVSIEPTSPNTMMLHLDERLEDGIRKTYTLDNERSAPAFIR
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FGEAQVFVQFFRGVPMQIRVKAGVKEERISLDRFVKAVTEVASATMIKERKLSYGV
RYGELPDIAREVEQELEAAYPPERLEQVIKQAIHGTKEEFVERRRELDGAELEEL

RNEDWNVRYAAFDGMEPTAERLPLVAHALHDNKMQIRRLAVVYLGDIRTPEAMELLYE
ALQDSSPAVRRTAGDTLSDIGDPAATPAMTATLSDKSKLVRWRAARFLYEVGTEEAQ
ALRVAADDPEFEVSLQAKMALERIESGEQAAGTVWQQMAGRNNKKEE"

CDS 6978994..6979413

/locus_tag="EFAGFIKM_06115"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEPITVLSDGKRHIAYENIIQLFRNWIEDSTSGSAIETHRGSWE

NARYCIVDYQVAEEAVSAANAI RAFMPQLPLLITDFQALIRKRHLQQITGTGEMKMI

LWNEQDPNQLIKDIENWFHSSSIHKSEIAIPPILSMR"

CDS complement(6979462..6980160)

/gene="regX3_5"

/locus_tag="EFAGFIKM_06116"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P9WGL9"

/codon_start=1

/transl_table=11

/product="Sensory transduction protein regX3"

/db_xref="COG:COG0745"

/translation="MTIKVLLIEDEKNLADMI AFFLEEEGYITERVHHAREALLFPQ

FQPDIVVTDLMLPEMDGNDLVEAFRQHSTVPILMISASTMLNDRRLALHNGADDFLCK

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YIKTVWGTGYKYVI"

CDS 6980503..6983349

/gene="sasA_28"

/locus_tag="EFAGFIKM_06117"

/EC_number="2.7.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_01837"

/codon_start=1
/transl_table=11
/product="Adaptive-response sensory-kinase SasA"
/translation="MDRIKARQMLDWLVKLRIPWIGTSILIILGSLSTIFPFTLFYG
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AGIVVDFWITTGEHKSRTGTIPLTRIAFKYVAFVVFVSLVLLSADSRRLGQMND
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TLQAGDYLDMDRFRLLKSRDNLFLSSSANIHYSVDLNLHWKQASFIYEAEMTRLTPYRVFI
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FRNGKMEWPTSHVTEVQILIGNLRKMADVLLLEQFEQIRHDKLTLEDRVIERTELKENS
EEVKRAIIESSIDAIIVDSSGLIVEFNPEAERMFGLRREEVILHKDAPSLFQGASCK
EIKNLLERFEYVEGKRYTIVEEISGIRRDGSVFPIEYKIVEIQLGKNETLYNLFIKDI
TERTRAEDRVRHALALEKLNSSELFNEKIAIQEQRDISEQFIESVREGLVMSDRSGTI
TIVNRRIEEMFGLGDFMGRSIEDLAQAIDTMVLTDNLFNLMEQTRAFLNGETAFIETEF
IFNNVDKSVFSLYMKQMDVPGKNHGFLLVFRDRTGEERLDRMKNELISVVSHEL RTPV
ATIMGYVELMMMYDL PANQQREFMQTISSEGKRLSSLLDDVLDIQRLDNEGMYHMTY
VPLVELVEGVAEQWNMKS AQRIYVHTFNGDFFAYADQNRMVQVLHNLVGNVAVKYSPGA
DRIDITLWEEEEWLCLDVRDYGIGIAEQEKDMLFNKFYRVDNSDHRQIGGTGIGLYIS
RKIVEDHKGTLT FISA PDKGSTFKVRLPKQDVLV"

CDS 6983566..6983670

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/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MFRKQEKTLIIVCLVAAVVVLYAVVKSIIIRIMSY"

CDS 6983735..6985081

/gene="ythA_2"
/locus_tag="EFAGFIKM_06119"
/EC_number="1.10.3.-"
/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:C0SP90"
/codon_start=1
/transl_table=11
/product="Putative cytochrome bd menaquinol oxidase
subunit I"
/db_xref="COG:COG1271"
/translation="MSSLDPVLLSRILTGLTLFVHIIFASIGVGVPLMIALAEWRGLR
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FAFFIEAIFLGIYLYTWDRFKKKYTHMLLLIPVALGSSASAIFITTVNSFMNQPGFT
LINGIMKDIHPAAMLNPATPTKVSHVLASSYTLSAGILAGIAAFSLLRGRDHVYYKK
ALKLTTVSALVFAISTVMIGDSSGKFLAKYQPEKLAAAEWHFKTMKEAPLVYGGILDE
NNEVKYAIEIPYALSILAGNRPDTEVKGLEEFADLRPPLSIHYMFDLKVTTGVILM
IPVLYVLRRWLPGRKPYPKWLLLIGIVLLGPLAMIAIELGWMFAEVGRQPWILRGYMKV
AEAATTSTSVGWMLVLFILLYLILCFSCIRVLSKLFRNKEAEKELESLEGGIVH"

CDS 6985078..6986112

/gene="ythB_2"
/locus_tag="EFAGFIKM_06120"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O34505"
/codon_start=1
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/product="Putative cytochrome bd menaquinol oxidase
subunit II"
/db_xref="COG:COG1294"
/translation="MSFEIAGIAILWTFLFGYLIVASIDFGAGFFSFYSILTGHENKI
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TNPYTWSVLLALVSVLYISAMFLSYAKRAGDEPAYEVLREYALLWSLPTIFASFLA
FLQINKQNPAHFEQMVNISWMFIASFICFVIAVSLVWWSKYLGWCFVAVMLQFAFAWY
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VRGNSGKKKG"

CDS 6986109..6986318

/locus_tag="EFAGFIKM_06121"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MSLFMHPNMFLLMTPLLDPLSTEGVTGIPGITGLSFFETFTIMY
APPLIIAAAIVFLFIYLAVYKNPKD"

CDS 6986390..6987427

/locus_tag="EFAGFIKM_06122"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P9WKP3"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/db_xref="COG:COG2220"
/translation="MPKIRYNNIDNVSTDKTLKEFKQWREQRRSKVKDYSYTVPKHPP
ELDYLHANRDDTSITWIGHSTFFIQYYGLNIVTDPVWAEKMGFQRRLGAPGIPIQDIP
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LGGVKITFVPAQHWTRRTLFDNTSHWGGYVLESNHSATTSAAESVATTSNQDESSTE
SGKNDTSGGPPVLYFVGDTGYFQGFKTIGERFDIGVTLMPIGAYDPEWFMTSQHVTP
EALQGFVESGSQLMVPMHYGTFKLADDTPEALDRLEVERERLGIGKERIRVLGHGET
LRIHHEEGKQG"

CDS 6987643..6989268

/gene="ybiT_3"
/locus_tag="EFAGFIKM_06123"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P0A9U3"
/codon_start=1
/transl_table=11
/product="putative ABC transporter ATP-binding protein
YbiT"
/db_xref="COG:COG0488"

/translation="MISTSGITLRYGKRALFEDVNIKFTPGNCYGLIGANGAGKSTFL
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KVRVLLAQALFGRPNNLLLDEPTNHLDESISQWLENFLMDYEGTVIVVSHDRHFLNKV
CTHIADIDFGKIQMYVGNDFWYESSQLALALQRDANKKKKEEKIKELQAFIQRFSANA
SKSKQATSRKKTLDKITLDDLPSNRKYPFINFKPEREAGKQLLTVDRIDKSIDGVKM
LNDVSFVVKGDKIAFVGPNNGNAKSLFDILMGETEADSGEYTWGITTTQAYFPKDNS
QYFDGVDMTLVDWLRQYSKDQDETYLRGFLGRMLFSGEESQKKASVLSGGEKVRCMLA
KMMQTGANALILDEPTNHLDESITALNNGMIDFDGTMFLTSHDHQFIQTIANRIIEI
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CDS complement(6989382..6989570)

/locus_tag="EFAGFIKM_06124"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSENNEPKKVSLQDAIRQKLAQKKEQANSQSSAYFEGGPKAM

KSQNNKKPNNQRRRTGGS"

CDS 6989823..6990710

/gene="mneS_2"

/locus_tag="EFAGFIKM_06125"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P46348"

/codon_start=1

/transl_table=11

/product="Manganese efflux system protein MneS"

/db_xref="COG:COG0053"

/translation="MNAYEEIRKGERGAWVSIVAYLVLSAFKLICGYLFASSALLADG

FNNLTDIVASIAVLIGLRISQKPPDSDHAYGHFRAETVAALVASFIMAMVGLQVLVEA

VRSWYEGAFVAPNLWAAAVAVVCAVVMLGVYRYNNRLAKQINSQALMAAAKDNRSDAW

VSIGAAVGIIGAQFGLPWLDKVAIAVGLLICKTAWEIFRDSTHRLTDGFDQKELTDL

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CDS complement(6990802..6991341)

/locus_tag="EFAGFIKM_06126"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MKKIVSFAAALTLMGSMAAAAGAEAAVTGTVTPETGTEVTTTPT

TTTTPAVEVNKPAVEVNKPAVETVEGTAETVTGTTTDTTGAEGTSTTTETPATTDDK

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CDS complement(6991714..6991878)

/locus_tag="EFAGFIKM_06127"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MLKWSVLFLIALVAGIFGFFGIVEAAASIAKVLFFIFVVLFI

SLITGRSRMR"

CDS 6992099..6992608

/locus_tag="EFAGFIKM_06128"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MIYQISVALIAVAFAVLVFFLIRTLKSAQGSLDNVSQTLQEVQK

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MAKFQTKRNNAEQTKHAEAVHVTAPPATSTDRTLQSYEATYNGEAKGGKNWMKYIDVA

ANVWQRMRK"

CDS 6992680..6993210

/locus_tag="EFAGFIKM_06129"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MKLLLVMFSPFSVQPAAVPAAHDMQWTAMEEKASEVTLAVD
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GSQEIEGIDLFDDTVS"

CDS 6993305..6993649

/gene="yflT"
/locus_tag="EFAGFIKM_06130"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P80241"
/codon_start=1

/transl_table=11
/product="General stress protein 17M"
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KGKVLVIAKKKD"

CDS 6994182..6995351

/gene="cheB_23"
/locus_tag="EFAGFIKM_06131"
/EC_number="3.5.1.44"
/inference="ab initio prediction:Prodigal:002006"
/inference="protein motif:HAMAP:MF_00099"

/codon_start=1
/transl_table=11
/product="Protein-glutamate
methylesterase/protein-glutamine glutaminase"
/translation="MRILIVDDNPTNVIIIIEILKKENYRDIVTASSAMEMFEVLGIG
EESNELRPRPSDIDLILLDMMMPEDMGIEACSIVQKFENLKDIPIIMVTAIGDSKKLA
EALDAGASDYVTKPINKVELMARIRLALRLKQEKDWHKERDQRIQDELKLAAMVQNAV
LSPAIRDPLFQVHAIYKPSFELAGDLYSWYPLGEGRYGVLLLDMMGHGISSSLFTMFI"

ASVLKDTVTTYVDPEKVIQELNRRFNQLHLEKQLVQYYFTAIYLVVDTRMKRIDYVNA
GHPPALFFRNDGSVTTFDSVCCPVGLFDKMDIEPQTIHYEGDGHIALYTDGLLEAVQG
GQEEQHEFLIEKLTGSHQWNEAAMQAMFFDDEIPQERDDDKCLVWITLDKGAGDE"

CDS 6995348..6999073

/gene="rcsC_22"

/locus_tag="EFAGFIKM_06132"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00979"

/codon_start=1

/transl_table=11

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/translation="MKIRNKLLIGFTALMAILIVLTFVSYERLNSSNQIDQMYQERY

LKVRFTSAARGEVNDIAKVLANLLLNPNNSTGAADADLKEMKDRGDRNLVEVRNRANS

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SRYQDQEIDTEIKDANAAYTRAVQITISIMIAGLLLALGVILWVLP SITRGLNTV SMM

INSFGKG RYRTIRRIQVKSTDEIGQIASVFKDVSSDLEEKLEIERAYVQAQQDQNWMS

SNIARVPELLRGIGSIRQISQMFISEFTPVLGAQLGVVYLIDEEKHPDELRRYGAYAF

EENEDVGKEMYRIGEG LIGQAALDMTP IILENTPEDYVHIGSASGSTRAAGIMIYPVV

FEDELIGVVEVASFEGF NELHKQLFTQLIMNLGVILNNVRRRLRVEELLRESQALTEE

LQVQSEELQTQQEELRRSNENLEEQT EALKRSEELLQRQQEELEHFNT ELIAKTRALE

EQVREVEEKND EIEKTKTQLEQQATQLSMTSKYKSEFLANMSHELRTPLNSLLILSQL

LSENKGGNLTDKQQEYAQTIYMSGADLLKMIDEILDLSKVDAGKMDIN YETVRMEELT

SFVQQNFGPMANKKELNLNIDFSDLP EWVYTDSHRVKQILRNLLSNAFKFTNRGSVS

LIGRRMKPEELPGYMNTNQEYLGFSVKDTGIGIPSDKTDLIFEAFQQVDGTT SRKYGG

TGLGLSISRELARLLGGAIQVESSEGE GSCFTLYLPDNHEEEALGEEGASREAAVSLE

DLYEKSIEARTMLSSHQSILSPDPERSVGTDLSPHTPDVTQIEDDRENLMEGDKILL

IIEDDVNF AHILMDMARGRGFKALVALQGDKGLEMARQYLPDAIILDIQLPVM DGWTI

LGELKSSSATRHIPVHVISVIDDMKQGLMMGAIAYLKKPSSKDSL DKAFSHIKSYTEN

QLKRLLIVEDDEIQRKAIIE LIGHDDVAITAVSTGSEALNELHSQRYDCMVLDLMLTD

MTGFELLDQIRDDEYLN DLPIIYTGKELDSKEEMKLRKYAESIIIKDVKSPERLLDE

TTLFLHRVEANLPEDKRRILQKLHNKETLFEGKKILLVDDDIRNVFALSSVLEGYRMD

VTFAENGREALEILDKNPEFDLVLMDDMMPEMDGYEAMTRIRQIPQFEKLPIIALTAK
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CDS 6999160..7000032

/gene="cheR_2"

/locus_tag="EFAGFIKM_06133"

/EC_number="2.1.1.80"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P31105"

/codon_start=1

/transl_table=11

/product="Chemotaxis protein methyltransferase"

/translation="MTPWEPTETGADLVRMPQDEERELIEIELLEGMRHLYGYDFRN

YALPSLKRRIWHHAHAEGVKSISGLQERVLHDRSAFDRFVQNLSIPVTEMFRDPSLFR

MFREQIIPILRTYPYIRIWHAGCSTGEEVYSMAIMLHEEGLYDKARIYATDMNDRSLQ

QAKEGVYGIEKMKLFTTNYLEAGGTRAFSEYYTAKYNSVIFHPFLRKNIIFAEHNLAT

DRSFNEFNVIFCRNVMIFYNDELNRNHVHGLFHESLSHFGILVLGSKESIHFTEFSDTY

EPLDRIEKIYRKIK"

CDS 7000049..7001725

/gene="rcsC_23"

/locus_tag="EFAGFIKM_06134"

/EC_number="2.7.13.3"

/inference="ab initio prediction:Prodigal:002006"

/inference="protein motif:HAMAP:MF_00979"

/codon_start=1

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EAEIAANAKTEFLAMMSHEIRTPMNGVIGMVDLLMETELREDQKEYADIVRRSADALV

TVINDILDFTKMESGKMELEEHFELVSCIREVLGLFAAEAGKKNLELDYFLEDVPE

LIYGDMARLRQVLLNLIANAIKFTDQGGVYLIVSVNGEKDGQMALEFAVKDTGIGIAS

DKVDRLFQPFSQLDTSMTKRYGGTGLGLAICKTLVEMMGQIYLDTTEQRGATFVFTI
QAKRYVETELVQRNGEEKPTDVKNENKYPTVLIVDDHPINQKLMAIMLGKLGLLSDIA
EDGQSALDMVNGSRYPYDYVFMDLQMPVMDGLECTRRIRESLSQSNQPIIIAMTANVM
EGIQQRCAIAGMDDYISKPVKMGNVKQKIAQFQKQRQMLDPGPSAMNQAN"

CDS 7001811..7002149

/gene="rsbV"

/locus_tag="EFAGFIKM_06135"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P66838"

/codon_start=1

/transl_table=11

/product="Anti-sigma-B factor antagonist"

/translation="MNTNKNEKFNARTETQDGVCTVYLTGELDLSVAPDFRLVMEPLV

DNKEQDLVINMKELKYIDSTGIGILLSVLKARHGMEARFEVQEVPAQIQKLFDMTGIA

KFFVTQKNSQ"

CDS 7002168..7002620

/gene="rsbW"

/locus_tag="EFAGFIKM_06136"

/EC_number="2.7.11.1"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P17904"

/codon_start=1

/transl_table=11

/product="Serine-protein kinase RsbW"

/db_xref="COG:COG2172"

/translation="MNAEVQRVTNLNLPATADFVDIVRLNLYGVASKMGFSYEDIEDMK

VAVSEACNNSVLYAYSHEGGMVEVVFEVDGETLSIIVKDEGASFENTNPAVSRAGLHD

KELTEAQIGGLGFYLMQALMDDVSVESETGKGTKVVLVKRLARSEEKV"

CDS 7002617..7003390

/gene="sigB"

/locus_tag="EFAGFIKM_06137"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P06574"

/codon_start=1

/transl_table=11

/product="RNA polymerase sigma-B factor"

/db_xref="COG:COG1191"

/translation="MNEKVTPPESMSEAIGLIWEYQQTQDNEIATVLIRKYEPMKMA
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WYIQVPRRIKEKGALVQHAIDELTVKLERSPGVNEIAEYLDLTAEETIEVLAGECYH
YVSLDSPLSQDDSAATLGELISADVNDYDSVEKRMDLQQALGQLKEQEQVLILAFQD
GQSQRAIAQKLGVSQMSVSRIQKRATEKLKQIMSNASML"

CDS 7003522..7004553

/gene="corA_3"

/locus_tag="EFAGFIKM_06138"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P40948"

/codon_start=1

/transl_table=11

/product="Magnesium transport protein CorA"

/db_xref="COG:COG0598"

/translation="MIVNQIKLEARRDKLSCSDDWQWWDWVAPDTSMKNALEELTEV
FPDMRYWLYKIPEVESNYLSVRFVNGKEPVIFGSLLYAVKNERDDKRQDNQMFFYVDR
NNLVTLNMDDNTRGIMKTDERAHLQQCSEARDGMFVLFRAILHYYHVGMDHFEMNLR
DLERKMESRNARTLMDQILAAARFELLYWSNLFIPYSELMAAAHEAYLDEINENRYFQQ
LQHRVERMERLFSHYEKEIDTLISIDNAISGVRGNEIMKTLTIVTAVFIPATAAGAIW
GMNFENLPFIDKSWGVLVLVVIILSMISMYVWLMMKGWTGDLLKVSSQPSAEETEK
KGATEKRKG"

CDS complement(7004574..7004939)

/locus_tag="EFAGFIKM_06139"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSKVTINGNTPITGGTPAQQYDTSEHPFELRHEVKRLNTRLDQI
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PIVGQYIADLLGYIEDYKN"

CDS complement(7005024..7005431)

/locus_tag="EFAGFIKM_06140"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

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/translation="MNKAEEQYPVQTGSTFAKGIFIGLLGAAAALLFAPKPGRELRG
DLSEKVGIVTDRTKEVATVVGDKASELAKTVSSKTS DIAKTVNQGRNDVMDSVRKASA
DVANEASRASDEVAAASVEAKEDARKELNSTSL"

CDS complement(7005496..7005753)

/locus_tag="EFAGFIKM_06141"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MWGIIISIMMAVIIGLIGDALAGHNMPGGIIGAMIAGFAGAWLG
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CDS complement(7005888..7006589)

/locus_tag="EFAGFIKM_06142"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MPRKTYSSASFSTPGTLLRPLLNWGLAGLALSASVVFILAGLG
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QRSPRFVVG YALTGSFAMMWILNTLLKEFFRRSRPELDHLLVHGYSPSGHAMISM
GFYGM LFVIWAIERQRHNSSGVWLPVLCGISFIFLIGLSRIMLG VHYPTDVFTGFTAG
LAWIFCMVKGIKQSR"

CDS 7006768..7007787

/locus_tag="EFAGFIKM_06143"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/product="hypothetical protein"
/translation="MESALLIKEYRAGVMECAHYGHISITDEYGRIVYSAGDPYFRAF
TRSSAKPFQAIPGIRAGIASHYGLSAQEIAIMSSSHRSEPEHIRVLEQLSGKIGLGEE
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PVQREILETFADLAGIEEKEIELGTDGCGFPVFSPLSALS NAYLKLACPDLIADSS
RTAVETITSAMNEYPLMVGGTERVDSVLLEDNNIVAKGGFKGVFGFGLKKERLGITFK
VLDGSEEEWAFITQSILRQIGYSNERTIARLAEVFPSDIRNDAGTLVGHADSEFILHS
LEDSV"

CDS 7007926..7008651

/locus_tag="EFAGFIKM_06144"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P9WI85"
/codon_start=1
/transl_table=11
/product="Putative quercetin 2,3-dioxygenase"
/db_xref="COG:COG1741"
/translation="MIKVVTSEERHTSDRGWIHSEFSFSFADYDDPSNAHFGCLLAHN
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ETNPSADEPVRFLQMWFLPSERMLKPSYTNRRIEPQEHLNRLCPIVSGQGEGSEGAL
PISQDVTCYLSHLESGKKLMYPQHEDRRTHLFLISGHVEIHCSDGNFNLKPGDAARIR
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CDS complement(7008715..7008939)

/locus_tag="EFAGFIKM_06145"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:O35019"
/note="UPF0435 protein YfkK"
/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDLTQATAANMEYMIEAIKTKLRMASGAAMQASSFPLEKYEDLF
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CDS 7009098..7009655

/locus_tag="EFAGFIKM_06146"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MAAYKREMRHQGREVRKGVPAENLVLFFKNIVQLHSPAEIFV
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ACLGPKQAVGTYILSNNPLIPAQSVGGKLPPVGQYSVAAVVNANGPRPYSILQMTSLH
FVMGMSRTIADAAIEAWKWRQTFHS"

CDS 7009716..7010507

/gene="catD_2"

/locus_tag="EFAGFIKM_06147"

/EC_number="3.1.1.24"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P00632"

/codon_start=1

/transl_table=11

/product="3-oxoadipate enol-lactonase 2"

/db_xref="COG:COG0596"

/translation="MEKVMCDGTTICYAEQKGGEALILLHGYCGSSSYWDEVVPELAR
SYRCIVPDLRGHGKTDAPVGSYTIEQMGNVDLQLMDELNVEKAVLLGHSMGGYIALSI
AQRHPERLNAFGLIHSTAYPDSEEAKEKRLRAVSTIQTEGIVNFVDGLVPGLFAPEHV
ESLSKHVTRVKEIGYQTAPQGAVGAALAMRERPDRRDVLSATPLPVLLVAGEKDAVIP
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CDS 7010779..7011483

/locus_tag="EFAGFIKM_06148"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1
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/product="hypothetical protein"
/translation="MFRKDYLLRMMEEMTEAIGKVFTLKQQRKHTEALSELDELMRRQ
FGMNLSLLNSLPAEDVIEMFRFRGMIEVDNLQQAARLIEEEAYIQEKAKVEGIDDQE
RMDAEDDALIRLMRSLHFYLYALNHGANPKLLDAPERVEGVGLTKEYELPARTERQL
ALYREQQGGRYDQAENSWYRLLQLGAEPVSYRDDVQAFYERLSPLTDEQLEQGGLPRN
EVEEGLAELSRQEMNS"

CDS 7011589..7012827

/locus_tag="EFAGFIKM_06149"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/translation="MDSLRLKIQDIFEQNSLITATWSQLRRRDNVSYTKVQVKPVTLK
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VSILTKSASKTAVDLSHNRKKQYVLEEGVPVSFLVELGIMNEEGRVLARKYDKFRQIN
RFLEMVQDVIPHLPEGRPLTIVDFGCGKSYLTFALYHYLSVQQRRSLKIIGLDLADV
IEHCNDLANRLHYGDLKFLVGDIADYDELNEVDMVVTLHACDTATDAALEKAVRWGAS
VILSVPCQHELFQVEASVMNPLLSHGILKERFSALATDGIRAKLLDLMGYKTQLLE
FIDMENTPKNILRAVRGQAGEVTEMWNEYTAFRDFIHADPYLERACADLLPGDGKQA
NGKSNSSKENVQDSANCDLC"

CDS 7013019..7015631

/locus_tag="EFAGFIKM_06150"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
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LCNGDSKGSRDSTYNREDTYNKDDTYKKDDTYKKDDKNNPNGAIQTDASGSFSQILRC
KRYSGSGWTVGLGILSIVLLLAGCLSRGLYYSADLYPVILIAAGSTLIMIVLFLVGIR
LEKEQEQQGRKQVPLSPVHWLGNNERMVWRMIRIQGILRVLWPLGMMTCFGVHAWAG"

SVSKQGSMDELLRWSLLGMFTLLTAILATRTDGARWLTCGWQMAGGLLVLSGILAVCG
ILPLPYGVMRTADPEISSAGARLGGLLQYPNAYGAIVGMYALERLTAAARVIARPVPA
GRLIAAVLPLMPAQAAALLSESARGAWLATGCAAVAAFALQRRGARLPLLLAMAAPLAC
AAWLYRQLAAAQLAPAPVPGLLALAGAWAAAALLGTLLLCRLWHSGAAKAPRAAALTAI
VLGAAAAALMAVASTADRLAAGVGTGVSRLQMWRDAHQLWTEAAWLGHGGDTWRNMFR
AIQSSPYVGGEVHNGLLDLALDTGMIGIVLVAGWFLTLRSIFHFARQLMPSVLVFVL
HGAMDFDWSFTLFWMLFIWLGAWATAALKTETEGVQRSGGTVEYTPIRSELGSKLRKS
RSLFLRYLPTQSHPSAVPMRSFFHIFQRVTARLIRVSTVMILFWIGGTVWLTSRYTV
AEVQYRQAMSEPDGTPAQKVHLMALQYNPNRSDIVISLARSLPGREVESLLLNSLSH
FRMHPQIYIELGRLAAQFGEGQQAGEYFEQAIALNRYDGIGQSVALYWMEQAARREW
AGFTDRARQTAAAGVQMYERYQLLAEVEEAGNVRNDRRFVLEEHPGYGENLRRIASA
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CDS complement(7016285..7016632)

/locus_tag="EFAGFIKM_06151"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

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YVSPERMKQAEDYYYGKVITNLLWIGENRDNRKKLCEWWNADVSAEIAAMWEVDVEPL

KEAFQHAFGGYRL"

CDS 7016793..7017407

/locus_tag="EFAGFIKM_06152"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MDFIHNLVSQLFDWIQSLGYFGIMLGLMMEIIPSEIVLAYGGFL

VSQGNINFFGAMIFGTVGGVIAQLFIYWIGRYGGRPILERYGKYILIQKKHIDHSEEW

FRKYGTGVIFTARFVPVVRHAISIPAGITKMHAGKFILLTTLAVIPWTALFIYLG MIL

GDQWKHIDEKAAPYVMPILLVALALMIVYVLIKWMNARKKKKGSV"

CDS 7017410..7017979

/locus_tag="EFAGFIKM_06153"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MGKPNLSHKFGKGLPPKDFIESMTKNQSEFQANYDSFTWSNEED

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RQEIGKRYGEGTESHAAIIRELRELISGY"

CDS 7017986..7018615

/locus_tag="EFAGFIKM_06154"

/EC_number="3.-.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:Q5XD24"

/codon_start=1

/transl_table=11

/product="putative metallo-hydrolase"

/translation="MLNIRTFSLGPLQTNAYLLQGDDSGKAVIIDPGMNPGLLKAIQ

DLEIEAILLTHAHFDHMGGVDEIRKLKGCPVYLHDLESDWLTPKLNGLNWQATPPL

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CDS 7019224..7019469

/locus_tag="EFAGFIKM_06155"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MEKTRVIPLNQRVEYPIIEENRRILESGKRETGTERALIHNPVS

TNEVVKSQQNIWASRVLRNGARNQPWFDKLQDYRNQV"

CDS 7019572..7020102

/gene="sigY"

/locus_tag="EFAGFIKM_06156"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:P94370"

/codon_start=1

/transl_table=11

/product="RNA polymerase sigma factor SigY"

/db_xref="COG:COG1595"

/translation="MIKAAELEEVRRAVSGDDSAALAALLQRYYTFVYKYLKVTMDAN
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AVRRFRWQLETRNEEWTDVMDAMTRLTPEHRVAVLLKHYYGYGYDEIGEMLGIPAGTV
KSRTAYGLRQLRKELE"

CDS 7020105..7020440

/locus_tag="EFAGFIKM_06157"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/translation="MSRSDDAQEQEVVERLQQHMKVLDDAFEPTSIPSLGSLEAQVRE
RKQIRRRANWIEMICFWLVGLFAITFGALFFVSAPALYLGIQALGTAVAVILAVIWAG
RRRKEVHHE"

CDS 7020433..7020663

/locus_tag="EFAGFIKM_06158"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

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/product="hypothetical protein"

/translation="MNKMHYSLDEISPLWLTLGIFLLVQGTWIFQDARRRGRFPWLW
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CDS 7020796..7021179

/locus_tag="EFAGFIKM_06159"

/inference="ab initio prediction:Prodigal:002006"

/codon_start=1

/transl_table=11

/product="hypothetical protein"
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EEEEETANDVMSQADFIKQVNLRAWI"

CDS 7021385..7021672

/gene="gatC"
/locus_tag="EFAGFIKM_06160"
/EC_number="6.3.5.-"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P68808"
/codon_start=1
/transl_table=11
/product="Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase
subunit C"
/translation="MSISNNDVQHVAKLARLNLTAEEEEQTLTGQLNAILKYAEKLNEL
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CDS 7021700..7023157

/gene="gatA_2"
/locus_tag="EFAGFIKM_06161"
/EC_number="6.3.5.7"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:UniProtKB:P63489"
/codon_start=1
/transl_table=11
/product="Glutamyl-tRNA(Gln) amidotransferase subunit A"
/translation="MSLFEQSLPELHNKLHAKELSVSDLVDQAYQNIGAHDCKVKAYL
ALDEEQARARARQLDDRVLVS GEEKGLLFGLPVGIKDNIVTNGLR TTCGSQFLRN FDPV
YDATVVEKLKAADTVTIGKLN MDEFAMGGSNENSSFS PVRNPWALDRVPGGSSGGSAA
AVAAGEAYFTLGSDTGGSIRQPASYCGVVGLKPTYGLVSRFGLVAFASSLDQIGPLTK
NVEDSAYVLQAIAGYDAKDSTS AKVEIPDYLSGLTG DVKGLRIAVPKEYIGEGVDPQV
KETVLSALKVLEGLGATWEEVSLPHTEYAVATYYLLASSEASSNLARFDG VRYGVRAD
NPDNLLDLYHQSR SQFGPEVKRRIMLGTYALSSGYDAYYLKAQKVRTLKQDFDNV

FAKYDVIIGPTAPTTAFKLSQVDDPLTMYLNDILTIPVNLAGVPAVSIPCGFSDGLP

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CDS 7023184..7024623

/gene="gatB"

/locus_tag="EFAGFIKM_06162"

/EC_number="6.3.5.-"

/inference="ab initio prediction:Prodigal:002006"

/inference="similar to AA sequence:UniProtKB:O30509"

/codon_start=1

/transl_table=11

/product="Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase
subunit B"

/db_xref="COG:COG0064"

/translation="MSASKYETVVGLEVHVELHTNSKIFCGCSTAFGAPPNTHTCPVC

LGHPGVLPVLNRQAVDYAMKAAMALNCTIADVSKFDRKNYFYPDSPKAYQISQFDQPI

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