

Supplementary files

Table S1. Features of sixteen whole-genome sequences of methicillin-resistant *S. aureus* strains used for the identification of vaccine candidates and drug target proteins

Strain ID	MLST Type	Clonal complex (CC)	Size (bp)	GC%	CDS	Accession No.
SA G5	ST45	CC45	2760385	32.77	2689	CP032160
SA G6	ST228	CC5	2856214	32.79	2734	RAHA00000000
SA G8	ST225	CC8	2857863	32.81	2743	QZFC00000000
SA H27	ST22	CC22	2783185	32.73	2630	CP032161
SA H29	ST8	CC8	2834624	32.65	2843	CP032468
SA H32	ST22	CC22	2786627	32.72	2657	RAHP00000000
NCTC 8325	ST8	CC8	2821361	32.9	2872	CP000253.1
CA-347	ST45	CC45	2875156	32.9	2766	CP006044.1
ST228	ST228	CC5	2783086	32.82	2654	HE579071.1
JH9	ST105	CC5	2937129	32.9	2879	CP000703.1
Newman	ST254	CC8	2878897	32.89	2854	AP009351.1
HO 5096 0412	ST22	CC22	2832299	32.8	2527	HE681097.1
Mu50 DNA	ST5	CC5	2878529	32.87	2867	BA000017.4
MRSA252	ST36	CC30	2902619	32.80	2872	BX571856.1
H-EMRSA-15	ST22	CC22	2846320	32.80	2740	CP007659
DSM 20231	ST8	CC8	2755072	32.88	2734	CP011526.1

Table S2. Subtractive genome analysis of methicillin-resistant *S. aureus* strains

Features	Number of proteins
Core-genome	1719
Non-redundant proteins	1678
Essential core-proteins	278
Essential non-paralogous proteins	98
Cytoplasmic (CYT) proteins	78
Secreted (SEC) proteins	2
Potentially surface exposed (PSE) proteins	6
Membrane (MEM) proteins	12

Table S3. Linear B-cell epitopes of 4 putative vaccine candidates of *S. aureus* determined by SVNTrip (20mers)

Protein Name	Linear B-cell epitopes	Start-End	Score
Foldase protein (PrsA)	DTMKKIGKDQIANASFTEML	45 - 64	1.000
	GEVSDVVKSSFYHIIKADK	226 - 245	0.438
	KMINKLIVPVTASALLGAC	2 - 21	0.366
	DFKDRDIKSVVEDKILNPEK	286 - 305	0.359
	YKENLRTAAYHKELLSDKIK	112 - 131	0.222
ESAT-6 machinery protein (EssA)	LTFLTASSNNGGLNIDVQQE	9 - 28	1.000
Penicillin-binding protein 1 (PBP1)	YSSNTLMMHLQDLVGADKMK	367 - 386	1.000
	TYQDKLKIEKMNLPGISLLP	146 - 165	0.603
	STFKSYGLAAAIQEGAFDPD	314 - 333	0.502
	QSIKAGNKVLPFSKVLLTD	636 - 655	0.442
	KNKIGAVLLVGLFGLLFIL	10 - 29	0.410
	AFKPIMENTLKYLNVGKSKD	573 - 592	0.403
	KGSGFVSHQSISKGQKLEK	685 - 704	0.353
	FNPETGKDFGKKWANDLYQN	289 - 308	0.343
	KDLFAVMDAKTGEILAYSQ	266 - 285	0.336
	VERYKLVAIDKKASANSKK	80 - 99	0.303
DD-transpeptidase (PBP2)	TSHKAMSDYTAYMLAEMKLG	543 - 562	1.000
	KAQEAYLSYRLEQEYSKDDI	168 - 187	0.564
	ENVMSKISSRDGEDFKRPSS	649 - 668	0.425
	YKRLFGAIGKNLTGGFGSEG	126 - 145	0.377
	WEDAKKIDLKANLVNRTAEE	268 - 287	0.372
	KNKDQQVGATILDSKTGGLV	354 - 373	0.332
	KAAEDRKNTVLYLMHYHKRI	244 - 263	0.306
	YDKNGELVKTLDNQQRHEHV	78 - 97	0.290
	FKDENLGNVLQSGIKIYTNM	316 - 335	0.286
	GFSKVKQYGENSFVGHSSQQE	623 - 642	0.263

Table S4. Drug target prioritization parameters and functional analysis of eight protein targets.

Protein Name	Protein ID*	Gene	Length (aa)	Mo. Wt. (KDa)	Structural quality MHOLline	Function
Biotin protein ligase	WP_000049913.1	<i>birA</i>	323	37.07	Very High	MF: Biotin-[acetyl-CoA-carboxylase] ligase activity. BF: Protein biotinylation
HPr kinase/phosphorylase	WP_000958224.1	<i>hprK</i>	310	34.48	Very High	MF: ATP binding Source, magnesium ion binding, phosphorelay sensor kinase activity, protein serine/threonine/tyrosine kinase activity, protein serine/threonine kinase activity. BF: Carbohydrate metabolic process, regulation of carbohydrate metabolic process
Thymidylate kinase	WP_001272126.1	<i>tmk</i>	210	24.06	Very High	MF: Thymidylate kinase activity. BF: Nucleotide biosynthesis
Phosphate acetyltransferase	WP_000774281.1	<i>pta</i>	328	34.98	Very High	MF: Phosphate acetyltransferase activity, BF: Acetyl-CoA biosynthetic process
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--L-lysine ligase	WP_000340119.1	<i>murE</i>	494	54.21	Very High	MF: UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-L-lysine ligase activity. BF: Cell cycle, Cell division, Cell shape, Cell wall biogenesis/degradation, Peptidoglycan synthesis
UTP--glucose-1-phosphate uridylyltransferase	WP_000721337.1	<i>gtaB</i>	288	32.49	Very High	MF: UTP:glucose-1-phosphate uridylyltransferase activity. BF: Enterobacterial common antigen biosynthetic process, UDP-glucose metabolic process
Fatty acid/phospholipid synthesis	WP_000239744.1	<i>plsX</i>	328	35.43	High	MF: Phosphate:acyl-[acyl carrier protein] acyltransferase activity. BF: Fatty acid biosynthetic process, phospholipid biosynthetic process
Pantothenate synthetase	WP_000163742.1	<i>panC</i>	283	31.44	Good	MF: ATP binding, pantoate-beta-alanine ligase activity. BF: Pantothenate biosynthesis

Protein ID represent the NCBI protein accession number, **MF** and **BF** represent Molecular function and biological function, respectively of the identified target proteins

Table S5. Identified druggable pocket with its volume, surface area and drug score of each target protein obtained from DoGSiteScorer.

Target protein	Volume (Å ³)	Surface area (Å ²)	Drug score	Binding site residues
Biotin protein ligase	1425.15	1648.25	0.80	SER93, THR94, GLN95, LEU96, LYS99, LN116, GLY119, ARG120, GLY121, ARG122 , ARG125 , HIS126, TRP127, SER128, SER129, SER130, GLN133, GLY134, LEU135, TRP136, MET137, SER138, SER148, MET149, ILE150, SER151, LYS152, ASN154, LEU155, ALA158, VAL175, LYS176, TRP177, PRO178, ASN179, ASP180, TYR182 , LYS187, VAL188, GLY190, PHE191, LEU192, THR193, GLU194, GLY208, ILE209, GLY210, ASN212, GLN215, ASP219, PHE220, ILE224, ARG227 , ALA228, TYR271, ASP301, GLY302, TYR303, LEU316, ILE317, SER318, ALA319, ASP320, ILE321, ASP322
HPr kinase/phosphorylase	562.79	751.65	0.77	VAL147, LEU148, ILE149, THR150 , GLY151 , ASP152, ILE155, LYS157, GLU159, THR160, GLU163, LEU226, ASN227 , ILE228, ASN229 , LYS258 , LYS259 , THR260 , ILE261, VAL263, ARG267, ASN268, VAL269, ALA270, ILE273, ALA276
Thymidylate kinase	470.78	479.38	0.73	ARG41, GLU42 , PRO43, GLY49, ILE52, ARG53, VAL56, GLU67, ALA68, MET69, LEU70, PHE71, ALA72, SER74, ARG75 , CYS95, ASP96, ARG97 , TYR98, SER101, SER102, TYR105 , GLN106 , VAL117, LEU120, ASN121
Phosphate acetyltransferase	415.87	484.65	0.77	LYS143, THR149, ILE152, PHE153, PHE154, ILE163, GLU184, LYS187, SER188, SER191, PHE192, VAL292, VAL295, LEU296, GLN297, GLY298, LEU299 , ASN300, SER301, PRO302, VAL303, ASN304, ILE321, GLN325 , ALA326, LEU327, GLN328
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-L-lysine ligase	703.09	912.87	0.85	THR115 , ALA118, THR119, HIS122, LEU123, ARG126, LYS127, TYR134, ASN138, GLY139, PHE140, GLN141, ASN143, GLU144, LYS146, THR147, GLU330, PRO331, VAL332, GLU333
UTP-glucose-1-phosphate uridylyltransferase	430.21	506.94	0.66	GLY109, LEU110 , GLY111, LEU130, ASP132, ASP133, TYR170, GLY171, PHE188, VAL189, GLU190, LYS191,

				ILE203, MET204, GLY205, TYR207, ASN226, ILE228, GLN229, LEU230, THR231, ILE234, ARG252, ASP254, GLY256
Fatty acid/phospholipid synthesis	2202.2	2922.41	0.82	MET9, GLY11, ASP12, ASN13, PRO15, ILE59, GLU60, MET61, GLU62, MET77, SER94, ALA95, GLY96, ASN97, THR98, ALA100, LEU101, ILE112, VAL115, ALA119, LEU120, VAL121, VAL122, THR123, LEU124, PRO125, THR126, ILE127, ASP128, GLY129, LYS130, GLY131, PHE132, VAL133, PHE134, LEU135, VAL137, GLN150, GLN153, LEU154, ILE157, TYR158, ILE162, ARG163, ALA207, LYS208, LEU210, MET211, GLY225, ASN226, VAL228, LEU229, ASN231, LEU232, GLU233, THR235, ALA236, ALA258, ILE259, LEU260, LYS261, LYS262 , ASP263, LEU264, ALA265, GLU266, PHE267, ALA268, LYS269, LYS270, MET271, ASP272, TYR273, TYR276, GLY277, GLY278, SER279, VAL280, LEU281, LEU282, HIS292, SER295, ASN296, LYS298, ALA299, TYR301, ALA303, ILE304, ALA307, ALA310, GLY311
Pantothenate synthetase	1400.83	1071.11	0.81	ILE28, PRO29, THR30 , MET31 , GLY32, HIS35 , GLY37, HIS38, THR40, MET41, SER55, VAL56, PHE57, VAL58, ASN59, GLN62, PHE63, TYR72, PHE92, PRO94, MET99, LEU117, GLU118, ARG122, HIS125, PHE126, VAL129, VAL132, VAL133, LEU136, TYR146, PHE147, GLY148 , LYS149, LYS150, ASP151, ALA152, GLN153, GLN154, ILE174, ASP175, ILE176, VAL177, ARG178, GLY182, LEU183, ALA184, LYS185, SER186, SER187, ARG188, ASN189, ALA200, VAL201, HIS202, LEU203, SER204, GLU242, PHE262, SER264, LEU265, ALA266, PHE269, ARG273, LEU274, ILE275, ASP276, ASN277

*Amino acid with red color represent the amino acid residues involved in H-bond formation with respective ligand.

Sequence file 1: Human_Non-Homologous_Essential_protein sequences

>10 chromosomal replication initiator protein DnaA

MSEKEIWEKVLQAEKLSAVSYSTFLKDTELYTIKDGEAIVLSSIPFNANWLNQQAIEIIQAILFDVVGYEVKPHFITTEELANYSNNETATPKETTKPST
ETTEDNHVLGREQFNAHNTFDFTVIGPGRNRFPHAAASLAVAEAPAKAYNPLFIYGGVGLGKTHLMHAIGHHVLDDNNPDAKVIYTSSEKFTNEFIKSIR
DNEGEAFRERYRNIDVLLIDDIQFIQNKVQTQEEFFYTFNELHQNNKQIVISSDRPPKEIAQLEDRLRSRFEWGLIVDITPPDYETRMALQKKIEEEKLD
IPPEALNYIANQIQSNIRELEGALTRLLAYSQLLGKPITTELTAEALKDIIQAPKSKKTIQDIQKIVGQYNNVRIEDFSAKKRTKSIAYPRQIAMYLSRELTD
FSLPKIGEEFGGRDHTTVIHAHEKISKDLKEDPIFKQEVERLEKEIRNV

>20 DNA polymerase III, beta chain

MMEFTIKRDYFITQLNDTLKAISPRITLILTGIKIDAKEHEVILTGSSEISIEITIPKTVGDGDIVNISETGSVVLPGRRFFVDIIKKLPKGDVKLSTNEQFQT
LITSGHSEFNLSGLDPDQYPLLPQVSRDDAIQLSVKVLKNVIAQTNAFVSTSETRPVLTVGNWLIQENELICTATDSHRLAVRKLQLEDVSENKNVIIPG
KALAELENKIMSDNEEDIDIFFASNQVLFKVGNVNFISRLLEGHYPTTRLPENYEIKLSIDNGEFYHAIDRASLLAREGGNNVIKLTGDDVVELSSTSP
EIGTVKEEVDANDVEGGLNKISFNSKYMMDALKAIDNDEVEVEFFGTMPKPKGDDSVTLILPIRTY

>DNA gyrase A subunit

LKEELLMAELPQSRINERNITSEMRESFLDYAMSVIVARALPDVRDGLKPVHRRILYGLNEQGMTPDKSYKKSARIVGDVMGKYHPHGDSSIEYAMV
RMAQDFSYRYPLVDGQGNFGSMGMDGAAAMRYTEARMTKITLELLRDINKDTIDFIDNYDGNEREPSVLPARFPNLLANGASGIAVGMATNIPPH
NLTELINGVLSKNPDISIAELMEDIEGPDFPTAGLILGSGIRRAYETGRGSIQMRSAVIEERGGRQIVVTEIPFQVKNKARMIEKIAELVRDKKID
GITDLRDETSRLTGVRVVIDVRKIDANASVILNNLYKQTPQTSTFGVNMIALVNGRPKLINLKEALVHYLEHQKTVVRRRTQYNLRKAKDRAHILEGLRI
ALDHIDEIISTIRESDDTKVAMESLQQRFLSEKQAQAILDMRLRLTGLERDKIEAENELLYISELAILADEEVLQLVRDELTEIDRFDDRRTEI
QLGGFENLEDEDLPIEEQIVITLSHNNYIKRPLVSTYRAQNRGGRGVQGMNTEEDFVSQVLTLSTHDHVLFFTNKGRVYKLGVEVPELSRQSKGIP
VVNAIELENDEVISTMIAVKDLESEDNLFVFATKRGVVKRSALSNFSRINRNGKIAISFREDELIAVRLTSGQEDILIGTSHASLIRFPESTLRPLGRTAT
GVKGITLREGDEVVGLDVAHANSVDEVVVTENGYGKRTPVNDYRLSNRGGKGKITATITERNGNVVCITVTGEEDLMIVTNAGVIIRLDVADISQ
NGRAAQGVRLIRLGGDDQFVSTVAKVKEDAEDETNEDEQSTSTVSEDGTEQQREAVVNDETPGNAIHEVIDSEENDEGRIEVRQDFMDRVEEDI
QQSSDEE

>SAEMRSA100160 DnaB-like helicase

MDRMYEQNQMPPHNEAEQSVLGSIIIDPELINTTQEVLLPESFYRGHQAQHFIFRAMMHLNEDNKEIDVVTLMQDLSSEGLNEAGGPQYLAEIESTN
VPTRNVQYYTIDIVSKHALKRRLIQTADSIANDGYNDELELDAILSDAERRILESSRESGDFKDIRDLVGLQVYETAEELDQNSGQTPGIPTGYRDL
QMTAGFNRNDLIILAAARPSVGKTAFAFNIAQKVATHEDMYTVGIFSLMGADQLATRMICSSGNVDSNRLRTGTMTEEDWSRFTIAVGKLSRTKIFI
DDTPGIRINDLRKCRRLKQEHGLDMIVIDYLLQIQQSGSRASDNRRQEQVEISRTLKALARELECPVIALSQLSRGVEQRQDKRPMMSDIRESGSIEQ
DADIVAFLYRDDYYNRGGDEDDDDGGGFEPQTNDENGEIEIIIAKQRNGPTGTVKLHFMKQYNKFTDIDYAHADMM

>SAEMRSA100180 response regulator protein

MQMARKVVVVDDKEPIADILEFNLKKEGYDVYCAVDGNDVLDLIYEEEPDIVLLDIMLPGRDGMVEVCREVRKKYEMPIIMLTAKDSEIDKVLGLELG
ADDYVTKPFSTRELIAVRKANLRRHYSQPAQDTGNVTNEITIKDIVIYPDAYSIKKRGEDIELTHREFELFHYLSKHMGMQVMTREHLLQTVWGYDYFG
DVRTVDVTIRRLREKIEDDPSPHEIVTRRGVGYFLQQHE

>SAEMRSA103150 DNA-binding protein

VSELSKSEDQRITKTKYEQIKQIDISDIKPNPYQPRKTFDENHLNDLADSIKQYGILQPIVLRKTVQGYIVVGERRFRASKIAGLYKYSIIKDLTDEDM
MELAVIENLQREDLNAIEEAESYQRLMTDLKITQQEVAKRLSKSRPIYANMLRLLHLPKKIADMVKDGRLTSAHGRTLLAIKDEQQMLRLAKRVVKEK
WSVRYLENHVNELKNVSSKSETDKVDITKPKFIKQQRQLREQYGAQVDISIKKSVGKISFEFESQDDFVRRIIEQLNRKYGK

>SAEMRSA103210 putative single strand DNA-binding protein

MLNRVVLVGRITKDPYRTTPSGVSVATFTLAVNRTFTNAQGEREADFINCVFRRQADNVNNYLSKGLAGVDGRLQSRNYENQEGRRVFVTEV
VCDVSVQFLEPKNAQQNGGQRQQNEFQDYGGGFGGQSGQNNNSYNSSNTKQSDNPFANANGPIDISDDDLFP

>NWMN 0446 thymidylate kinase

LRMNKMSAFITFEGPEGSGKTTVINEVYHRLVKDYDVIMTREPGGVPTGEEIRKIVLEGNDMDIRTEAMLFAASRREHLVLKIPALKEGKVVLCDRY
IDSSLAYQGYARGIGVEEVRALNEFAINGLYPDLTILNVSAEVRERIIKNSRDQNRDLQEDLKFHEKVIIEGYQEIHNESQRFKSVNADQPLENVVE
DTYQTIKYLEKI

>SAEMRSA104210 conserved hypothetical protein

MIYETAPAKINFITLDTLFRNDGYHEIEMIMTTVDLNDRLTFHKKRDKRIVVEIEHNYVPSNHKNLAYRAAQLFIEQYQLKQGVTSIDKEIPVSAGLA
GGSDAAATLRGLNRLFDIGASLEELALLGSKIGTDIPFCIYNKTAICTGRGEKIEFLNKPSSAWVILAKPNLGISSPDIFKLINLDKRYDVHTKMCYEAL
NRDYQQLCQSLSNRLEPISVSKHPQIDKLKNNMLKSGADGALMSGSGPTVYGLARKESQAKNIYNAVNGCCNEVYLVRLLG

>SAI7S6 1003710 50S ribosomal protein L25

MRMASLKSIIIRQKQTRSDLKQLRKSGKVPVVYGYGTKNVSVKVDEVEFIKVIREVGRNGVIELGVGSKTIKVMVADYQFDPLKNQITHIDFLAIN
MSEERTVEVPVQLVGEAVGAKEGGVVEQPLFNLEVTATPDNIPEAIEVDITELNINDSLTVADVKTGDFKIENDSAESVTVVAPTEEPTTEEIEAM
EGEQQTTEEPEVVGESKEDEEETEE

>SAEMRSA104350 conserved hypothetical protein

MLNSNGWHVDDHIVAVSTGIDSMCLLYQLNDYKDSYRKLTCLHVNHGVRASIEEARFLEVYCERHHIDLHIKKLDLSHSLDRNNSIQNEARIKR
YEWFDMMNVLEADVLLTAHHLDDQLETIMYRIFNGKSTRNKLGFDELSKRKGQYIYRPLLAVSKKEIKQFQERYHIPYFEDESNDKNKYVRNDIRN
RIIPAIDENNQLKVSHLLKLKQWHDEQYDILQYSAKQFIQEFVKFDEQSKYLEVSRQAFNNLPNSLKMVVLDCLLSKYYELFNISAKTYEWFQFSSK
KAQFSINLTDKWIQIAYGKLIIMAKNNGDITYFRVQTIEKPGNYIFNKYRLEIHSNLPKCLFPLTVRTRQSGDTFKLNGRDGYKKVNRLFIDCKVQQWV
RDQMPIVLDKQQRIIIVGDLYQQQTIKQWIIISKNGDE

>SAI7S6 1003810 Dihydropteroate synthase

MTTKKIMGILNVTPDFSDGGKFNNVETAINRVKAMIDEGADIIDVGGVSTRPGHEMVTLEEEELNRLVPVVEAIVGFDVKISVDTRSEVAEACLK
GVDMINDQWAGLYDHRMFQIVAKYDAEIIIMHNGNGNRDEPVVEMLTSLAQAHQAKIAGIPSNKIWLDPGIGFAKTRNEEAEMARLDELVA
TEYPVLLATSRKRFTKEMMGYDTPVERDEVTAATTAYGIMKGVRAVRVHNVELNAKLAKGIDFLKENENARHNL

>SAEMRSA104630 transcription antitermination protein

MSEEVGAKRWYAVHTYSGYENKVKNLEKRVESMNMTEQIFRVVPIEEENQVKDGKAKTTVKKTFPGYVLVELIMTDESWYVVRNTPGVTGFV
GSAGAGSKPNPLPEEVRFILKQMGLEKKTIDVELEVGEQVRIKSGPFANQVGEVQEIEDKFKLTVLVDMMFGRETPVEVEFDQIEKL

>SAEMRSA104650 50S ribosomal protein L1

MAKKGKKYQEAASKVDRTQHYSVEEAIKLAKETSIAINFDAVEVAFRLGIDTRKNDQQIRGAVVLPNGTGKSQSVLVFAKGDKIAEAEAGADYVG
EAEYVQKIQQGWFDVDFVATPDMMGVEVGLGRVLGPGLMPNPKTGTVTMDVKKAVEEIKAGKVEYRAEKAGIVHASIGKVSFTDEQLIENFN
TLQDVLAKAKPSSAKGTIFYKSAVATTTMGPGVKIDTASF

>SAEMRSA104660 50S ribosomal protein L10

MSAIEAKKQLVDEIAEVLNSVSTVIVDYRGLTVAEVDLRSQLEAGVEYKVYKNTMVRRAAEKAGIEGLDEFLEGTPTAIATSSEDAFAAAKVISGF
AKDHEALEIKSGVMEGNVITAEVKTGSLPSHDGLVSMLLSVLQAPVRNFAYAVKAIGEQQEESAE

>SAEMRSA105160 putative phosphate acetyltransferase

MADLLNVLDKLSGKNVIVLPEGEDERVLTAATQLQATDYVTPIVLGDETKVQSLAQKLNLDISNIELINPATSEFKAELVQSFVERRKKGATEEQAQ
ELLNNVNYFGTMLVYAGKADGLVSGAAHSTGDTVRLPQIIKTKPGVSRSTGIFFMKIGDEQYIFGDCAINPELDSQGLAEIAVESAKSALSFGMDPK
VAMLSFSTKGSASDDVTKVQEAVKLAQQKAEEKLEAIIIDGFEQFDAIIVPGVAEKAPGAKLQGDANVVFPSLEAGNIGYKIAQLGGYDAVG
PVLQGLNSPVNDLSRGCSIEDVYNLSIITAAQALQ

>SAEMRSA106090 putative undecaprenol kinase

MFIIELIKGIILGVVEGLTEFAPVSSTGHMILVDDMWLKSSEFLGSQSFTFKIVIQLGVSFAAAWVFRERFLEILHIGKHKHVEGENDQQRSKPRRLN
LLHVLVGMVPAGILGLLDFDIEEHLFSVPTVMIGLFGAIYMIADKYSKVNPNQTVDDQINYFQAFVIGISQAVAMWPGFSRSGSTISTGVLMKLN
HKAASDFTFIMAVPIMLAASGLSLLKHYQDIQADIPFYILGLAFTVGLIAIKTFLHLINKIKLIPFAIRIVLVIFAILYFGFGIGKI

>SAEMRSA106580 ribonucleoside-diphosphate reductase beta chain

MIAVNWNTQEDMTNMFWRQNISQMWWETEFKVSKDIAWKTLSAEQDTFFKALAGLTGLDTHQADDGMPLVMLHTTDLRKKAVYSFMAM
MEQIHAKSYSHIFTTLLPSSETNYLLDEWVLEPHLYKSDKIVANYHKLWGKEASIDQYMARVTSVLETFLFFSGFYPLLAGQKMTTSGEIIK
ILLDESIGHVFTGLDAQHLRNELSESEKQKADQEMYKLLNDLYLNEESYTKMLYDDLIGITEDVLNVYKYNKALSNLGFEPYFEEREFPNIIENALDT
TTKNHDFSVKGDGYVLALNVEALQDDDFVFDNK

>SAEMRSA106640 putative UDP-N-acetylenolpyruvoylglucosamine reductase

VINKDIYQALQQLIPNEKIKVDEPLKRYTYTKGGNADFYTPTKNEEVQAVVKYAYQNEIPVTVLGNGSNIIIEGGIRGIVISLLSDHIEVSDDAIIAGS
GAAIIDVSRVARDYALTGLEFACGIPGSIGGAVYMNAGAYGGEVKDCIDYALCVNEQGSGLIKLTKELELDYRNSIIQKEHLVLEAAFTLAPGKMTET

QAKMDDLTERRESKQPLEYPSGVSFQRPPGHFAGKLIQDSNLQGHRIGGVEVSTKHAGFMVNVNDNGTATDYENLIHYVQKTVKEKFGIELNREV
RIIGEHPKES

>SAEMRSA106790 preprotein translocase SecA subunit

MGFLSKILDGNNKEIKQLGKLADKVIALEEKTAITLDEEIRNKTQKFQTELADIDNVKKQNDYLDKILPEAYALVREGSKRVFNMTPTKVQIMGGIAIH
KGDIAEMRTGEGKTLTATMPTYLNALAGRGVHVITVNEYLSSVQSEEMAELYNFLGLTVGLNLNSKTTEEKREAYAQDITYSTNNELGFDYLRDNM
VNYSEDRVMRPLHFAIIDEVDSILIDEARTPLIISGEAEKSTSLYTQANVFAKMLKQDEDEKYDEKTKAVHLTEQGADKAERMFKVENLYDVQNVQDVI
SHINTALRAHVTLQRDQVDMVVDGEVLVDQFTGRTPMPGRRFSEGLHQAIEAKEGVQIQNESKTMASITFQNYFRMYNKLAMGTGTAKTEEEEF
NIYNMTVTQIPTNKPVRNDKSDLIYISQKGFDAVVEDVVEKHKAGQPVLLGTAVETSEYISNLLKRGIRHVDVLNAKNHEREAEIVAGAGQKGA
VTIATNMAGRGTDIKLGEGVEELGGLAVIGTERHESRRIDDQLRGRSGRQGDGDSRFYLSLQDELMIRFGSERLQKMMSRLGLDDSTPIESKMVS
RAVESAQKRVEGNNFDARKRILEYDEVLRKQREIYNERNISIIEEDSSQVVDAMLRLSTLQRSINYINTADDEPEYQPFIDYINDIFLQEGDITEDDIK
KDAEDIFEVWAKIEAAYQSQKDILEEQMNEFERMILLRSIDSHWTDHIDTMDQLRQGIHLRSYAQQNPLRDYQNEGHLEFDIMMQNIIEEDTCKFI
LKSVVQVEDNIEREKTTFEAKHVSADGKEKVKPKPIVKGQVGRNDDPCGSGKKFKNCHGK

>SAEMRSA106860 HPr kinase/phosphatase

MLTTEKLVETLKLDLIAGEEGLSKPIKNADISRPGLEMAGYFSHYASDRIQLLGTTELSFYNNLLPKDGRAGMRKLRPETPAIIVTRGLQPPEELVEAA
KELNTPLIVAKDATTSLSMRSLTTFLEHALAKTTSLHGVLDVYGVGLITGDSGIGKSETALELVKRGHRLVADDNVEIRQINKDELIGKPPKLIHLEIR
GLGIINVMTLFGAGSILTEKRIRLNINLENWNKQKLYDRVGLNEETLSILDTEITKKTIPVRPGRNVAVIEVAAMNYRLNIMGINTAEFSEERLNEEIIKN
SHKSEE

>SAR081prolipoprotein diacylglycerol transferase

MGGIVFNIDPVAFNLGLPSVVRWYGIHIVGILLGYFVAQRALVKAGLHKDTLVDIIFYSALFGFIAARIYFVIFQWPYYAENPGEIIKIWHGGIAIHGGLI
GGFIAGVIVCKVKNLNPFQIGDIVAPSILAQGIGRWGNFMNHEAHGGPVSRAFLEQLHLPNFIIENMYINGQYYHPTFLYESIWDVAGFIILVNIRKH
LKLGETFFLYLTWYSIGRFFIEGLRTDSLMLTSNIRVAQLVSLILLISILIVYRIKYNPPLYSKVGALPWPTRKVK

>SAEMRSA107480 conserved hypothetical protein

MAKKAPDVGDKYGFHDDDSIFRSERGLTENIVREISNMKNEPEWMLDFRLKSLKLFYKMPMPQWGGDLSELNFDITYYVKPSEQAERSWDE
VPKEIKRTFDKLGPEAEQKYLAVGSAQYSEVYHNMKELEEKGIIFKDTDSALQENEELFKKYFASVVPADNKFALNSAVWSSGFSIYVPKNIK
LDTPLQAYFRINSENMGQFERTLIIADEGASVHYVEGCTAPVYTTSSLHSAVVEIIVHKDAHVRYYTIQNWANNVYNLVTKRTFVYENGMEWVDG
NLGSKLTMYKPNVCVLLGEGAKGSTLSIAFAGKGQVQDAGAKMIHKAPNTSSTIVSKSISKNGGKVIYRGIVHFGRKAKGARSNIECDTLILDNESTDT
IPYNEVFNDQISLEHAEKVSKVSEELFYLMRSGISEEEATEMIVMGFIEPTKELPMEYAVEMNRLIKFEMEESIG

>SAEMRSA108480 UDP-N-acetylmuramoylalanine-D-glutamate--2,6-diaminopimelate ligase

LDASTLFKKVKVVRVLSLEQIDITDTSRTAREGSIFVASVGYTVDSHKFCQNVADQGCKLVVNKEQ
SLPANVTQVVPDTRLVASILAHTLYDPSHQLVTFGVTGTNGKTSIATMIHLIQRKLQKNSAYLGTNGF
QINETKTKGANTTPETVSLTKIKEAVDAGAESMTLEVSSHGLVLGRLRGVEFDVAIFSNTLQDHLDFHG
TMEAYGHAKSLFSQLGEDLSKEKYVVLNNDDSFSEYLRVTPYEVFSYGIDEEAQFMAKNIQESLQGV
FDFVTPFGTYPVKSPYVGKFNISNIMAAMIAVWSKGTSLETIIKAIVENLEPVEGRLEVLDPSLPIDLIID
YAHTADGMNKLIDAVQPFVKQLIFLVGMAGERDLTKTPEMGRVACRADYVIFTDPNPANDDPKMLTAE
AKGATHQNYIEFDDRAEGIKHAIDIAEPGDTVVLASKGREPYQIMPGHIKVPHRDDLIGLEAAYKKFGGG
PVDQ

>SAEMRSA109190 conserved hypothetical protein

MKQLHPNEVGVALGGLGEIGKNYAVEYKDEIVIDAGIKFPDDNLLGIDYVIPDYTYLVQNQDKIVGL
FITHGHEDHIGGVFLLKQLNIPIYGGPLALGLIRNKLEEHLLRTAKLNEINEDSVIKSKHFTISFYLT
THSIPETYGVIVDTPGKVVHTGDFKFDTPVGKPAKIAKMAQLGEEGVLCCLSDSTNSLVPDFTLSERE
VGQNVDKIFRNCKGRIIFATFASNIYRVQAVEAAIKNNRKIVTFGRSMENNIKIGMELGYKAPPETFI
EPNKINTVPKHELLILCTGSQGEPMMAALSRIANGTHKQIKIIPEDTVVFSSSPIPGNTKSINRTINSYK
AGADVHSKISNIHSTGHGSQGDQQLMLRLIKPKYFLPIHGEYRMLKAHGETGVECGVEEDNVFIFDIGD
VLALTHDSARKAGRIPSGNVLDGSGIGDIGNVVIRDRKLLSEGLVIVVVSIDFNTNKLSSGPDIIISRG
FVYMRSGQLIYDAQRKIKTDVSKLNQNKDIQWHQIKSSIIETLQPYLFECTARKPMILPVIMKVNEQK
ESNNK

>SaurJH9 1173 cell cycle protein

MTEYMKNFRSILRYIGKTSKFIDYPLLVTYIVLSLIGLVMVYSASMVPATKGTLTGGIDVPGTYFYNRQLAYVIMSFIIVFFIAFLMNVKLLSNIKVQKGM
IITIVSLLLLTLVIGKDINGSKSWINLGMNLQASELLKIAIILYIPFMISKMKMPRVLSKPKLILSPIVLALGCTFLVFLQKDVGQTLILLIILVAIIFYSGIGVNVK
LRFGIPAVLGFLVVFVIALMAGWLPSYLTARFSTLTDPFQFESGTGYHISNLLAIGNGGVFGKGLGNSAMKLGYLEPHTDFIAICEELGLIGLLVI
TLEFFIVYRAFQFANKTSSYFYKLCVGIATYFGSQTFVNIGGISATIPLTGVPLPFISFGGSSMISLSIAMGLLLIVGKQIKVDQQRKKQQKQVDIRRF
N

>SAEMRSA109800 putative glutamate racemase

MNKPIGVIDSGVGGLTVAKEIMRQLPNETIYLGDIGRCYPGRPGEQVKQYTVIEARKLMEFDIKMLVIACNTATAVALEYLQKTLSPVIGVIEPGA
RTAIMTTRNQNVLLGTETIKSEAYRTHIKRINPHVEVHGACPGFVPLVEQMRYSOPTITSIVIHQTLKRWRNSESDEVILGCTHYPLLYKLIYDYFG
GKKTVISSGLETAREVSALLTFSNEHASYTEHPDHRFFATGDPHTITNIIKEWLNLSVNVERISVND

>SAEMRSA110140 penicillin-binding protein 1

MAKQKIKIKKNKIGAVLLVLGLLFFILVLRISYIMITGHSNGQDLVMKANEEKYLKNAQQPERGKIYDRNGKVLAEDEVRYKLVAVIDKKASANSKK
PRHVVDKKETAKKLSTVIDMKPEEIEKRLSQKKAQFIEFGRKGTNLTYQDKLIEKMNLPGISLLPETERFYPNGNFASHLIGRAQKNPDTGELKGALG
VEKIFDSYLSGSGSLRYIHDIWGYIAPNTKKEKQPKRGDDVHLTIDSNIQVFVEEALDGMVERYQPKDLFAVVMDAKTGEILAYSQRPTFNPETGKD
FGKKWANDLYQNTYEPGSTFKSYGLAAAIQEGAFDPDKKYKSGHRDIMGSRISDWNRVGVGWEIPMSLGFTYSSNTLMMHLQDLVGADKMMSW
YERFGFGKSTKGMFMDGEAPGQIGWSNELQQKTSFSGQSTTVTPVQMLQAQSAFFNDGNMLKPWFVNSVENPVSKRQFYKGQKQIAGKPITKDT
AEKVEKQLDLVNSKSKSHAANYRIDGYEVEGKTGTAQVAAPNGGGYVKGPNPYFVSFMDGAPKKNPKVIVYAGMSLAQKNDQEAYELGVSKAFK
PIMENTLKYLVNGKSKDDTSNAEYSKVPDVEGQDKQKVIDNSAKSLEPVTIGTGTQIKAQSIKAGNKVLPKSVLILLTDGDLTMPDMTGWTKEDV
IAFENLTNIKVNKSGSGFVSHQSISKQQLTEKDIDVEFSSENVDSNSTNNSDSNSDDKKKSDSKTDKDKSD

>SAEMRSA110150 phospho-N-acetylmuramoyl-pentapeptide-transferase

MIFVYALLALVITFVLVPLIPTLKRKMFQGSIREEGPQSHMKKTGTPTMGGLTFLLSIVITSLVAIIFVDQANPIILLFVTIGFGLIGFIDDIIVVKNNQ
GLTSKQKFLAQIGIAIIFVLSNVFHLVNFSTSIHIFTNVAIPLSFAYVIFVWQVGFSAVNLTLDGLDGLATGLSIIGFTMYAIMSFVLGETAIGFICIM
LFALLGFLPYNINPAKVFMDGTGSLALGGIFATISIMLNQELSLIFIGLVFIETLSVMLQVASFKLTGKRIFKMSPIHHHFELIGWSEWKVVTVFWAVG
LISGLIGLWIGVH

>SAEMRSA110160 UDP-N-acetylmuramoylalanine--D-glutamate ligase

MLNYTGLENKNVLVVLGAKSGYEAALLSKLGANVTVNDGKDLSDQAHAKDLESMGIVSVSGSHPLTLLDNNPIIVKNPGIPYTVSIIDEAVKRGKIL
TEVELSYLISEAPIAVTGTNGKTTVTSLIGDMFKKSRLTGRLSGNIGYVASKVAQEVKPTDYLVTELSSFQLLIGIEKYKPHIAITNIYSAHLDYHENLENY
QNAKKQIYKNQTEEDYLICNYHQRVIESEELKAKTLFSTQQEVDGIYKDSFVYKGVRIINTEDLVLPGEHNLNLAVALACILAGVPIKAIDSLTTF
SGIEHRLQYVGTNRTNKYYNDSKATNTLATQFALNSFNQPIIWLCCGLDRGNEFDELIPYMENVRAMVVFQGTAKAKFALGNSQGSVIEANNVE
DAVDKVQDIIEPNDVLLSPACASWDQYSTFEERGEKFIERFRAHLPY

>SAEMRSA110170 putative cell division protein

LMDDKTKNDQQESNEDKDELELFRNTSKRRQRKRKATHFSNQNKDDTSQQTDFDEIYLINKDFKKE
ESNDENNDSSASHANNNNIDSDTSDNIENEDYRYNQEIQQNESNGIAVDNEQPQSAPEQNSDSNDEET
VTKKERKSKVTQLKPLTLEEKRLRRKRQKRIQYSVITILVLLIIVLIMFSPLSKIAHVNINGNNHVS
TSKINKVLGVKNDSRMYTFSKKNAINDLEEDPLIKSVEIHKQLPNTLVNDITENEIALVKYKGGYLL
ENGKLLKGSNDVKINDAPVMDGFGKTKEDDMIKALSEMTPVRRYIAEVYAPSKNKQSRIELFTTDGLQ
VIGDISTISKMKYYPQMSQSLSDSSGKLKTRGYIDLSVGASFIPYRGNTSSQSESDKNVTKSSQEENQ
AKEELQSVLNKINKQSSKNN

>AA076 0589 cell division protein FtsA

MEEHYVVSIDIGSSSVKTIVGEKFHNGINVIQTGQTYTSGIKNGLIDDFDIARQAIKDTIKKASIASGVD
IKEVFLKLPITGEVYDESNEIDFYEDTEINGSHIEKVLGIREKNDVQETEVINVFPIRFIVDKENEVS
DPKELIARHSLKVEAGVIAIQSILINMIKCEACGVVDVLDVYSDAYNYGSILTATEKELGACVIDIGED
VTQVAFYERGELVDADSIEMAGRDIITDDIAQGLNTSYETAKEVKHQYGHAFYDSASDQDIFTVEQVDSDE
TVQYTQKDLSDFIARVEEIFFEVFDVLQDLGLTKVNGGFIVTGGSANLLGVKELSDMVSEKVRHTPS
QMGIRKPEFSSAISTISSIAFDELDDYVTINYHDNEETEDVIDVKDKDNESKLGGFDWFKRKTNNKDT
HENEVESTDEEIQSEDNHQEHKQNEHVQDKDKKEESKFKKLMKSLFE

>SAEMRSA110190 cell division protein FtsZ

MLEFEQGFNHLATLKVIGVGGGGNNAVNRMIDHGMNNVEFIAINTDQALNLSKAESKIQIGELTRGLG

AGANPEIGKKAEESEREQIEDAIQGADMVFTSGMGGGTGTGAAPVVAKIAKEMGALTVGVVTRPFSFEG
RKRQTQAAAGVEAMKAAVDTLIVPNDRLDIVDKSTPMMEAFKEADNVLRQGVQGISDLIAVSGEVNLD
FADVKTIMSNQGSALMGIGVSSGENRAVEAAKKAISPLLETISIVGAQGVLMNITGGESLSLFEAQEAAD
IVQDAADEDVNMI FGTVINPELQDEIVVTIATGFDKPTSHGRKSGSTGFGTSVNTSSNATSKDESFTS
NSSNAQATDSVSERTHTTKEDDIPSFIRNREERSRTRRR

>SAEMRSA110290 lipoprotein signal peptidase

MHKKYFIGTSILIAVFVIFDQVTKYIATTMKIGDSFEVIPHLNITSHRNNGAAWGILSGKMTFFFI
TIILIALVYFFIKDAQYNLFMQVAISLLFAGALGNFIDRILTGEVVDIFDTNIFGYDFPIFNIADSSLT
IGVILIIALLKDTSNKKEKEVK

>SAEMRSA110540 conserved hypothetical protein

LKTGRIVKSISGVYQVDVNGERFNTKPRGLFRKKKFSPPVVDIVEFDVQVQINIEGYIHQVYERKNELKRPP
VSNIDTLVIVMSAVEPNFSTQLLDRFLVIAHSYQLDARVLVTKDKTPIEQLEINELLKIYENIGYETE
FIGNDDDRKKIVEAWPAGLIVLSGQSGVGKSTFLNHYRPELNLETNDISKSLNRGKHTRHVELFERQNG
YIADTPGFSALDFDHIDKDEIKDYFLELNRYGETCKFRNCNHIKEPNCNVKHQLEIGNIAQFRYDHYLQL
FNEISNRKVRY

>SAEMRSA110620 putative fatty acid synthesis protein

MVKLAIDMMGGDNAPDIVLEAVQKAVEDFKDLEILFGDEKKYNLNHERIEFRHCSEKIEMEDEPVRAIK
RKKDSSMVKMAEAVKSGEADGCVSAGNTGALMSAGLFIVGRIKGVARPALVVTLPTIDGKGFVFLDVGAN
ADAKPEHLLQYAQLGDIYAQKIRGIDNPISLLNIGTEPAKGNLSLTKSYELLNHDHSLNFVGNIEAKTL
MDGDTDVVVTDGYTGMMVLKNLEGTAKSIGKMLKDTIMSSTKNKLAGAILKKDLAEFAKKMDYSEYGGSV
LLGLEGTVVKAHGSSNAKAFYSAIRQAKIAGEQNIVQTMKETVGESNE

>SAI7S6 1009020 UMP kinase

VSSLLVYVYTIHDREDKKMAQISKYKRVLKLSGEALAGEKGFGINPVIKSVAEQVAEVAKMDCEIAVI
VGGGNIWRGKTGSDLGMDRGATADYMGMLATVMNALALQDSLEQLDCDTRVLTSIEMKQVAEPYIRRAIR
HLEKKRVVIFAAGIGNPYFSTDTTAALRAAEVEADVILMGKNNVDGVVSADPKVNKDAVKYEHLETHIQML
QEGQLQVMDSTASSFCMDNNIPLTVFSIMEEGNIKRAVMGEKIGTLITK

>SAEMRSA110920 ribosome recycling factor

MSDIINETKSRMQKSIESLSRELANISAGRANSNLLNGVTVDYYGAPTPVQQLASINVPEARLLVISPYD
KTSVADIEKAIIAANLGVNPTSDEGEVIRIAPALTEERRKERVKDVKKIGEEAKVSVRNIRRDMDQLKK
DEKNGDITEDELRSGETDVQEATDNSIKEIDQMIADKEKDIMS

>SAEMRSA110970 DNA polymerase III PolC-type

LAMTEQQKFKVLADQIKISNQLDAEILNSGELTRIDVSNKNRTWEFHITLPQFLAHEDYLLFINAIEQEF
KDIANVTCRFTVTNGTNQDEHVYKFGHCIDQTALSPKVKGQLKQKLIMSGKVLKVMVSNDIERNHFDK
ACNGSLIAFRNCGFDIDKIFETNDNDQEQNLASLEAHIQEEDQSARLATEKLEKMKAEKAKQQDNNE
SAVDKQIGKPIQIENIKPIESIEEYKVAIEGVIFDINLKLKSGRHIVEIKVTDYTDLSVLKMFTRK
NKDDLEHFKALSVGKVVRAQGRIEEDTFIRDLVMMMSDIEEIKKATKKDKAEKRVFHLHTAMSQMDGI
PNISAYVKQAADWGHAPAIATDHNVVQAFPDAAHAAEKHGKMIYGMGMLVDDGVPIAYKPQDVVLKDA
TYVVFDEVTTGLSNQYDKIELAAVKVHNGEIIDKFERFSNPHRLSETIINLTHITDDMLVDAPEIEEV
LTFEKEWVGDAIFVAHNASFDMGFIDTGYERLFGFPSTNGVIDTLELSTINTEYKGHGLNFLAKKYGVE
LTQHHRAIYDTEATAYIFIKMVQMQKELGVLNHNINKLSNEDAYKRARPSHVTLIVQNQQGLKNLFKI
VSASLVKYFYRTPRIPRSLDEYREGLLVGTACDEGELFTAVMQKDQSQVEKIAKYDFIEIQPPALYQD
LIDRELIRDTELEIYQRLIHAGDTAGIPVIATGNAHYLFEHDGIARKILIASQPGNPLNRSTLPEAHF
RTTDEMLNEFHFLGEEKAHEIVVKNTELADRIERVPIKDELYTPRMEGANEEIRELSYANARKLYGED
LPQIVIDRLEKELKSIINGFAVIYLIQSRLVKKSLDDGYLVGSRGSGVGSFVATMTEITEVNPLPPHYI
CPNCKRSEFFNDGSGVSGFDLPDKTCETCGAPLIKEGQDIPFETFLGFGDKVDPIDLNFSGEYQPNAHN
YTKVLFGEDKVFRAGTIGTVAEKTAFGYVKGYLNDQGIHKGAEIDRLVKGCTGVKRTTGQHPGGIIVVP
DYMDIYDFTPIQYPADDQNSAWMTTHDFHSHIDNVKLKLDILGHDDPTMIRMLQDLGIDPKTIPVDDKE
VMQIFSTPESLGVTEILCKTGTFGVPEFGTGFVRQMLEDTKPTTFSELVQISGLSHGTDVWLGNQAQEL

IKTGICDLSSVIGCRDDIMVYLMYAGLEPSMAFKIMESVRKKGKGLTEEMIETMKENEVPDWYLDSCCLKIK
YMFPAHAAAYVLMMAVRIAYFKVHHPLYYYASYFTIRASDFDLITMIKDKTSIRNTVKDMYSRYMDLGKK
EKDVLTVLEIMNEMAHRGYRMQPISLEKSQAFEFIEGDTLIPPFISVPGLGENVAKRIVEARDDGPFLS
KEDLNKKAGLSQKII EYLDELGSLPNLPDKAQLSIFDM

>SAEMRSA111050 putative riboflavin biosynthesis protein

MKVIEVTHPIQSKQYITEDVAMAFGFFDGMHKGHDKVFILNEIAEARSLLKAVMTFDPHPSVVLNPKRK
RTTYLTPLSDKIEKISQHDIDYCVVNFSSRFANVSVEDEFVENYIIKNNVKEVIAGFDFTFGKFGKGNMT
VLQEYDAFNTTIVSKQEIENEKISTTSIRQDLINGELQKANDALGYIYSIKGTVVQGEKRGRTIGFPTAN
IQPSDDYLLPRKGVYAVSIEIGTENKLYRGVANIGVKPTFHDPNKAEVVIEVNIFDFEDNIYGERVTNVW
HHFLRPEIKFDGIDPLVKQMNDKSRKAYLLAVDFGDEVAYNI

>SAI7S6 1009170 DNA translocase FtsK

VRQLAQAKKKSTAKKKTASKKRTNSRKKKNDNPIRYVIAILVVVLMVLGVFQLGIIGRLIDSFFNYLFGY
SRYLTYLVLATGFTYYSKRIPKTRRTAGSIVLQJALLFVSQVLVHFNSGIKAEREPVLSYVYQSYQHS
HFPNFGGGVGLGFYLLELSPVLSLFGVCITILLCSSVILLTNHQHRDVAKVALENIKAWFGSFKNEKMS
ERNQEKQLKREEKARLKEEQKARQNEQPQIKDVSDFTEVPQERDIPYGHTEENESKQCQPSRKRVFDA
ENSSNNIVNHQADQQEQLETEQTHNSVESENTIEEAGEVTNVSVVPPVPLTLNQPQKQKATSKAEVQRKGQ
VLENTLKDFGVNAKVTQIKIGPAVTQYEQPAQGVKVSIVNLHNDIALALAAKDVRIEAPIGRSAVGI
EVPNEKISLVSLEVLDEKFPSSNNKLEVLGRDISGDPITVPLNEMPHLLVAGSTGSGKSVCSINGIITSI
LLNAKPHEVKMLMIDPKMVLELVNYPHLLIPVVTNPHKAAQALEKIVAEMERRYDLFQHSSTRNIKGY
NELIRKQNQELDEKQPELPYIVVIVDELADLMMVAGKEVENAIQIRITQMARAAAGIHLIVATQRPVSDVIT
GIKNNIPSRIAFAVSSQDTSRTIIGTGAELKLGKGMVYVNGDSSQTRIQQAFGLSDQEVQDVVNYVV
EQQQANYVKEIEPDAPVDKSEMKSSEDALYDEAYLFVVEQQKASTSLLQRQFRIGYNRASRLMDDLERNQV
IGPQKGSKPRQVLIDLNNDEV

>SAEMRSA112010 putative membrane protein

MMIIVMLLSYLIGAFPSGFVIGLFFKKDIRQFGSGNTGATNSFRVLGRPAGFLVTFDLIFKGFITVFF
PLWLVPVHADGPSTFTFTNGLIVGLCAILGHVYPVYLKFQGGKAVATSAGVVLGVNPILLILAIIFVVL
KIFYVSLASIVAAICCVIGSLIQDYILLVVSFLVSIILIRHSNIARIFRGEPEKIKWM

>SAEMRSA112200 tryptophan synthase beta chain

MNKQIQTEADELFFGEYGGQYVPETLMPAIELKKAYKEAKADPEFQRELYYLSEYVGRATPLTYAAS
YTESLGGAKIYKREDLNHTGAHKINNALGQALLAKRMGKKKLVAETGAGQHGVASATVAALFDMELVVF
MGSEDIKRQQLNVFRMELLGAKVVAVEDGQGTLSDAVNKALQYVWVSHVDDTHYLLGSALGPDPPFTIVRD
FQSVIGKEIKSILKKEGRLPDAIVACIGGGSNAIGTFYPIKDDVALYGVAAAGQGEDTDKHALAIGKG
SPGVLHGTKMYLIQDEGGQVQLAHSISAGLDYPGIGPEHSYYHDIGRVTFENASDTQAMNALINFTEKHEG
IIPAIESAHALSYVERLAPTMSEKEDIIIVVTISGRGDKDMETIRQYMAERGLAND

>SAEMRSA112560 aspartokinase II

MVTRSVLKFGSSVSDFTKIKRIAEMLKERVNQDEQLIVVVSAMGNTTDQLMTNVSTLTAKPKQELALL
LTTGEQQTVSYSMLVNDIGVNAKAMTGYQAGIKTIGHHLKSKIAQINPQTFEQAFQENDILVVAGFQGI
NEHQELTTLGRGSDTTAVALAVSNQIPCEIYTDVDGVYATDPRLLPKAKRLDIVSYEEMMEMSALGAGV
LETRVELAKNYNIPLYLGTLSNVKGTWIMSNEEILEKKAVTGVALDKHMMHVTISYPLPDNQLLTQLF
TELEEGAVNVDMISQIVNLDGLQLSFTIKDSDFHQISMILETLKNQYALAYKINEHYVKISLIGSGMRD
MSGVASKAFLTLIENNIPFYQTTTSEISISYVIDDFNGQQAVEKLYDAFNI

>SAEMRSA112570 aspartate semialdehyde dehydrogenase

MTKLAVVGATGLVGTKMLETNLNRKNIPFDELVLFSARSAGQEVFEQEKTYTVQELTDARASEHFDYVLM
SAGGGTSEHFAPLFEKAGAVIDNSSQWRMAEDIDLIVPEVNEPTFTRGIIANPNCSTIQSVVPLKVLQD
AYGLKRVAYTTYQAVSGSGMKGKKDLAEGVNGKAPEAYPHPIYNNVLPIDVFLNGYTKKEEQKMIDETR
KILNAPDLKVTATCARVPVQDSHSVEIDVTLDEKATAEDIKALFDQDDRVLVDNPNENNEYPMAINSTNK
DEVFVGRIRRDDSLNTFHVWCTSDNLLKGAALNAVQVLEQVMRLKGAN

>SAEMRSA112590 dihydrodipicolinate reductase

VKILLIGYGAMNQVRVARLAEKGHEIVGVIENTPKATTPYQQYQHIADVVDADVAIDFSNPNFLPLDE
EFHPLVAVTTGEKEKLLNKDELSQLNMPVFFSANMSYGVYALTKILAAVPLDDFDIELTEAHNNKKV
DAPSGTLEKLYDVIVSLKENVTPVYDRHELNEKRQPDIGIHSIRGGTIVGEHEVLFAGTDETIQITHRA
QSKDIFANGAIQAAERLVNKPNGLYTFDNL

>SAEMRSA112600 putative tetrahydrodipicolinate acetyltransferase

MVQHLTAEEIIQYISDAKKSTPIKVYLNNGNFEGITYPESFKVFGSEQSKVIFCEADDWKPFYEAYGSQFE
DIEIEMDRRNSAIPKDLTNTNARIEPGAFIREQAIIEDGAVVMMGATINIGAVVGEGTMIDMNATLGGR
ATTGKNVHVGAGAVLAGVIEPPSASPVIIEDDVLIGANAVILEGVRVGKGAIVAAGAIVTQDVPAGAVVA
GTPAKVIKQASEVQDTKKEIVAALRLND

>SAEMRSA112810 putative UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide)pyr ophosphoryl-undecaprenol N-acetylglucosamine transferase

MKKIAFTGGGTGVHVSVNLSLIPTALSQGYEALYIGSKNGIEREMIESQLPEIKYYPISSGKLRRYISLE
NAKDVFVKVLKGLDARKVLKKEKPDLLFSKGGFVSPVVIAAKSLNIPTIIHESDLTPGLANKIALKFAK
KIYTTFEETLNYLPKEKADFIGATIREDLKNGNAHNGYQLTGFNENKKVLLVMGGSLSGSKKLNSIIRENL
DALLQQYQVHIHTGKGLKDAQVKKSGYIQYEFVKEELTDLLAITDVTISRAGSNAIYEFLLTRIPMLLVP
LGLDQSRGDQIDNANHFADKGYAKAIDEEQLTAQILLQELNEMEQUERTRIINNMSYEQSYTKEALFDKM
IKDALN

>SAEMRSA113110 penicillin-binding protein 2

MTENKGSSQPKNGNNGGKSNSKKNRNVKRTIIIGFMIIAFFVLLGILLFAYYAWKAPAFTEAKLQ
DPIPAKIYDKNGELVKTLDNQGRHEHVNLKDVPKSMKDAVLATEDNRFYEHGALDYKRLFGAIGKNLTGG
FGSEGASTLTQQVVKDAFLSQHKSIGRKAQEAYLSYRLEQEYSKDDIFQVYLNKIYSDGVTGIKAAKY
YFNKDLKDLNLAEAYLAGLPQVPNNYNIYDHPKAAEDRKNTVLYLMHYHKRITDKQWEDAKKIDLKANL
VNRTEAERQNIIDTNDQSEYNSYVNFVKSELMNNKAFKDENLGNVLQSGIKIYTNMDKDVQKTLQNDVDNG
SFYKNKDQQVGATILDSKTGGLVAISGGRDFKDVVNRNQATDPHPTGSSLKPLAYGPAIENMKWATNHA
IQDESSYQVDGSTFRNYDVKSHGTYSIDALRQSFNIPALKAWQSVKQNAAGNDAPKKFAAKLGLNIEGDI
GPSEVLGGSASEFSPTQLASAFAAIANGGTYNNAHSIQKVVTDRGETIEYDHTSHKAMSDYTAYMLAEML
KGTFTKPYGSAYGHGVSGVNMGAKTGTGTGYAETYSQYNLPDAAKDVWINGFTPQYTMSVWMGFSKVKQY
GENSFVGHSSQEQEYPFLYENVMKISSRDGEDFKRPSSVSGSIPSINVSGSQDNNTNRSAGGSDTSAN
SSGTAQSNNTNRSQQSRNSGGLTGIFN

>SAEMRSA113140 conserved hypothetical protein

MDKYQLKARPVVIRRELDHYSIDLGLDEQDLVILLKLIYASETSNKQPSIELLQKGSTMQPRDITMVIQN
LIQRELLELQVQKDEEGRFTEYMNLDPFEEKLSHLKQSQMETKEQNSKEFKQLFRVLEDTFARPLSPY
EIELTNQWIDVDKHDTAIIQAALDEANSLNLSFKYMDRILLNWKKNNVKTIDDSRKIREKFNKPKMTHT
VKTVPKFDWLNENLDGK

>SAEMRSA113270 chorismate synthase

MRYLTSGESHGPQLTVIVEGIPANLEIKVEDINKEMFKRQGGYGRGRRMQIEKDTVEIVSGVRNGYTLGS
PITMVVTNDDFTHWRKIMGAAPISDEERENMKRTITKPRPGHADLVGGMKYNHRDLRNVLERSSARETAA
RVAVGALCKVLEQLDIEIYSRVVEIGGIKDKDFYDSETFKANLDRNDVRVIDDGIAQAMRDKIDEAKND
GDSIGGVVQVVENMPVGVGSYVHYDRKLDGRIAQGVVSINAFKGVSFGEFGKAAEKPGEIQDEILYNT
ELGYYRGSNHLGGLEGMSNGMPIIVNGVMKPIPTLYKPLNSVDINTKEDFKATIERSDSCAVPAASIVC
EHVVAFEIAKALLEEFQSNHIEQLKQKQIERRQLNIEF

>SAEMRSA113370 cytidylate kinase

MKAINIALDGPAAGKSTIAKRVASELSMIYVDTGAMYRALTYKYLKLNKTEDFAKLVDQTTLDTLYKAD
KGQCVIDNEDVTDFLRNNVDVTQHVSYVASKEPVRSFAVKKQKELAAEKGIVMDGRDIGTVVLPDADLV
YMIASVEERAERRYKDNQLRGIESNFEDLKRDIARDQYDMNREISPLRKADDAVTLDTTGKSIEEVTDE
ILAMVSKIK

>SAEMRSA114480 biotin carboxyl carrier protein of acetyl-CoA carboxylase

MNFKEIKELIILDKSTLTINIEDTKGKVTLLKKEKETEITPQISQMPVEAAAMPMPQVQSTDSNKTEA
PKPTSDNHKTINAPMVGTFYKSPSPDEEAYVQVGDTVSNETTVCILEAMKLFNEIQAEISGEIVEILVED
GQMVEYGQPLFKVK

>SAEMRSA114490 putative elongation factor P

MISVNDFKTGLTISVDNAIWKVIDFQHVKPGKGSFVRSKLRNLRTGAIQEKTFRAGEKVEPAMIENRRM
QYLYADGDNHVFMDNESFEQTESSDYLKEELNYLKEGMEVQIQTYEGETIGVELPKTVELTVTETEPGI
KGDATGATKSATVETGYTLNVPLFVNEGDLIINTGDGSYISRG

>SAEMRSA114580 putative shikimate kinase

MNHDKSPIILIGFMGTGKSTIGKYVADEQNLSFIDIDSYIEEKYKLTIPFISKHGEQYFRNLEFTCLQE
CINTADIIATGGGIIIEEAFNFKLNQKNIIWLDCNIDIYSRINDDPHRPNANNKTIMQLNDLYCSRIL
RYNEIAFKKFDHLLSISEIYYELLNLIKASDQY

>SAEMRSA114820 DNA primase

LRIDQSIINEIKDKTDILDLVSEYVKLEKGRNYIGLCPHFHDEKTPSFTVSEDKQICHCFGCKKGGNVFQ
FTQEIKDISFVEAVKELGDRVNVAVDIEATQSNVQIASDDLQMIEMHELIQEFYYYALTKTVEGEQAL
TYLQERGFDTALIKERGIGFAPDSSHCHDFLQKKGYDIELAYEAGLLSRNEENFSYYDRFRNRIMFPLK
NAQGRIVGYSGRTYTQGEPKYLNSPETPIFQKRKLLYNLDKARKSIRKLDEIVLLEGFMDVIKSDTAGLK
NVVATMGTTQLSDEHITFIRKLTSNITLMFDGDFAGSEATLKTGQHLLQQGLNVFVIQLPSGMDPDEYIGK
YGNDAFTTFVKNDKKSFAHYKVYKDEIAHNDLSYERYLKELSHDISLMKSSILQQKAINDVAPFFNV
PEQLANEIQFNQAPANYPPEDEYGGYDEYGGYIEPEPIGMAQFDNLSRQEKAERAFKLHLMRDKDTFLNY
YESVDKDNFTNQHFYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLSLEQYNLNDEPYENEIDDYV
NVINEKGQETIESLNHKLREATRIGDVELQKYYLQQIVAKNKERM

>SAEMRSA115060 conserved hypothetical protein

MSDNIVAIYGDVPVELVEKQSAEISQFLKSDRDDFNFKYNLYETEIAPIVEETLTPFFSDKKAILVKN
AYIFTGEKAPKDMAHNVQDLIEFIEKYDGENLIVFEIYQNKLDERKKLTCTLKKHARLKKIEQMSEEEIK
KWIQSKLNENFKDIKRDALDLFIELTGINFNIVSQEIEKLILFLGDRPTINKQDVNQIINRSLEQNVFLL
TEYIQRKKEQAIHLVKDLITMKEEPIKLLALITSNYRLFYQCKILSQKGYSGQQIAKTIGVHPYRVKLA
LGQVRHYQLDELLNIIDACAETDYKLKSSYMDKQLILELFILSL

>SAEMRSA115130 conserved hypothetical protein

MKKIVLYGGQFNPIHTAHMIVASEVFHELQPDEFYFLPSFMSPLKKHNNFIDVQHRLTMIQMIIDELGFG
DICDDEIKRGGQSYTYDTIKAFKEQHKSLEYFVIGTDQYNQLEKWKYQIEYLKEMVTFVVVNRDKNSQNV
ENAMIAIQIPRVDISSTMIRQVSEKSIQVLVPKSVENYIKGEGLYEH

>SAEMRSA115170 conserved hypothetical protein

MGLVRKFFMPNSYVQSIFQIDLKLDKGVKGIITDLNTLVGWDVKEPTERVKAWFKEANEKGITITIV
SNNNESRVASFQHLIDIFIKARKPMGKAFDKAITKMNIRPDQTVVIGDQMLTDVFGGNRRGLYTIMVV
PVKRTDGFITKFNRLIERLLRHFSKKGYITWEEN

>SAEMRSA115280 transcription elongation factor

MENQKQYPMTQEGFEKLERELEELKTVKRPEVVEKIKVARSFGLDSENSEYDAAKDEQGFIEQDIQRIEH
MLRNALIEDTGDNNVVKIGKTVTFVELPGDEEESYQIVGSAESDAFNGKISNESPMAKALIGKGLDDEV
RVPLPNGGEMNVKIVNIQ

>SAEMRSA115540 putative protein-export membrane protein

VKKSSRIIAFLLLVLLFAGMAATYKSVIKNVNLGLDLQGGFEVLYQVDPLNKGDKIDKKALQSTAQTLE
NRVNVLVGVSEPKIQVEEPNRIRVQLAGVTDQNEARKILSSQANLTIRDAEDKVKLSGSDIKQGSQAKQEFK
QETNQPTVTFKVKDKNKKFKVTETEEKRDNVMVVWLDFFKKGDSYKKEAQKKNPKFISAASVDQPINSDS
VEISGGFGKGQEGVKKAKQIAELLNAGSLPVDLKEIYSNSVGAQFGQDALDKTVFASFIGVALIYLFMLGF
YRLPGLVAIIALTTYIYTLVAFNFISGVLTLPLAALVLGVGMAVDANIIMYERIKDELIRGRTIKQAF

SKANKSSFLTIFDSNLTIVIAAAVLFFFGESSVKGFATMLLLGILMIFVTAVFLSRFLLSLLVSSNIFKN
 QFWLFGVKKNRHDINEGVDVHDLKTSFEKWNFVKLAKPLIGVSILIVVGLVILYIFKLNLDGIDFSSGT
 RVDFQSKQAITQQKVEQVVKDSGLKADQIQINGKDNKVATVQFKDDLTRAQDNKLSDNKSKFGDTPQIN
 TVSPIIGQELAKNAMLALYASIGIIIVSLRFEWRMGLSSVLALLHVDVFIIVAFSLFRIEVDLTFIAA
 VLTIVGYSINDTIVTFDRVRENQKVKVITTEQIDDIVNRSIRQTMTRSINTVLTIVVVVAILFFGAP
 TIFNFTLALFIGLISGVFSSIFIAVPLWGIMKKRQLKKSPPKHKLVVYKEKKSNDKILV

>SAEMRSA115590 Holliday junction DNA helicase RuvA
 MYAYVKGKLTHTLYPTHVVVETAGVGYEQTPNSYRFQKQLDHEVLIHTSLIVREDAQLLYGFSSEEEKDM
 FLSLIKVTGIGPKSALAILATSTPNEVKRAIENENDTYLTKFPGIGKKTARQIVLDLKGKVKITEEDSDS
 LLQVDATSTVQDQFVQEAMLALEALGYSKRELAKVEKTLNKNKYDSVDEAVKAGLQLVVS

>SaurJH9 1738 bacterial translation initiation factor 3 (bIF-3)
 VYKEERVYFYTSSFLGANFVKILEVSTIAKDQQTQINDKIRAKELRLIGQDGEQIGVKSREALEMAERV
 DLDLVVAPNAKPPVARIMDYGKFFEQKKKEKEMKKKQKIINVKEIRLSPTIEEHDFQTKLKNGRKFLT
 KGDKCKVSIRFRGRAITHKEIGQRVLEKYADECKDIATVEQPKMDGRQMFIMLAPTAEK

>SAEMRSA115950 chromosome replication initiation/membrane attachment protein
 MGRQAFEFGLRPKDQFVQMQLHFDLNTNHLEVLNRLYTPLIGTQAVGLYHFMQTQFVKESHNETLILSHYIF
 MNELKINLLEFRQQMDLLEAIGLLKAFVKHDEQETQFVYQLIQPPSAHLFFNDPMLSIFLYSEVEHRRFH
 ELKKYFEYQQIDLSEFKQVTRQFTDVFKVPSTKIDIDTSDIPINEPYQGIDLSNESFDFEMLRQMLGKHF
 ISQDIVTKDAKRLITQLATLYGLTADGMKHVILNSITSGQQLSFEEMRKQARSYYLMEHENQMPKLQVKS
 PVTSSSTGKSSEVNPKPQSDWEFELLEQTSPIDMLASWSEPTISQKTMVEELIEREKMSFGVINILLQ
 FVMLKEDMKLPKAYILEIASNWKKGKIKTAKEAYNYAKKVNQPKNEGSSGNYQKRGSYGQRNRISKEKT
 PKWLENRDKPSEEDSAKDNSVDDQQLQEQDRQAFDLKLSKKWEEDSQ

>SAEMRSA116120 DNA polymerase III alpha subunit
 MVAYLNIHTAYDLLNSSLKIEDAVRLAVSENVDAITDTNVLYGFPKFYDTCIANNIKPIFGMTIYVTN
 GLNTVETVVLAKNNDGLKDLYLQSSSEIKMNALEHVSFELLKRFSNNMIIIFKNVADEHRDIVQVFDSDHED
 TYLDHRSVLVQGKIKHVVQNCYQTRQDADTISALAAIRDNTKLDLIHQDEDFGAHFLTENEIQQLDVNQ
 EYLTQVDVIAQCNALKYHQSLLPQYQTPNDESAKKYLWRVLVTQLKLELNYDVYLERLKYEYKVTN
 MGFEDYFLIVSDLIHAKTHDVMVGPGRGSSAGSLVSYLLGITTIDPIKFNLLFERFLNPERVTMPDIDI
 DFEDTRRERVYQVQEKYELHVSIGIVTFGHLLARAVARDVGRIMGFDEVTLNEISSLIPIHLGITLDEA
 YQIDDFKKFVHRNHRHERWFSICKKLEGLPRHTSTHAAGIIINDHPLYEAPLTKGDTGLLTQWTMTEAE
 RIGLLKIDFLGLRNLSIIHQILTQVKKDLGINIDIENIPFDDQKVFELLSQGDGTTGIFQLES DGVRSVLK
 KKKPEHFEDIVAVTSLYRPGPMEEIPTYITRRHDPKSVQYLPHLEPIKNTYGVIIYQEIMQIASTFA
 NFSYGEADILRRAMSKKNRAVLESERQHFIEGAKQNGYHEDISKQIFDLILKFADYGFRAHVSYSKIA
 YIMSYLKVRYPNYFYANILSNVIGSEKKAQMIEEAKKQGITILPPNINESHCYKPSQEGIYLSIGTIK
 GVGYSQSVKVVVDERYQNGKFDFFDARRIPKRVKTRKLEALILVGAFDAFGKTRSTLLQAIDQVLDGD
 LNIEQDGLFDILTPKQMYEDKEELPDALISQYEKEYLGFYVSQHPVDKKFVAKQYLTIFKLSNAQNPKP
 ILVQFDKVKQIRTKNGQNMFAVTLNDGIETLDGVIFPNQFKYEELSHNDLFIVSGKFDLRKQQRQLII
 NEIQTATFEEQKLAFQAKIIRNKSHIDAFEEAIKATKENANDVVL SFYDETQKMTTLGYINQKDSMF
 NNFIQSFNPSDIRLI

>SAEMRSA116260 putative septation ring formation regulator
 MVLYIILAIIVIIIAVGVLFYLRSNKRQIIIEKAIERKNEIETLPFDQNLQSLKLNKGETKTKYDAMK
 KDNVESTNKYLAPVEEKIHNAEALLDKFSFNAAQSEIDDANELMDSYEQSYQQQLEDVNEIALYKDNDE
 LYDKCKVDYREMKRDVLANRHQFGEAASLLETEIEKFEPRELYEVKADGNYVQAHNHIAALNEQMKQL
 RSYMEEIPELIRETQKELPGQFQDLKYGCRDLKVEGYDLHVKVDSTLQSLKTELSFVEPLISRLELEEA
 NDKLANINDKLDMMYDLIEHEVKAKNDVEETKDIITDNLFKAKDMNYTLQTEIEYVRENYIYINESDAQSV
 RQFENEIQSLISVYDDILKEMSKSAVRYSEVQDNLQYLEDHVTVINDKQEKLNHLIQLREDEAEADNL
 LRVQSKKEEVYRRLLASNLTSVPERFIIMKNEIDHEVRDVNEQFSEPIHVKQLKDKVSKIVIQMNTFED
 EANDVLVNAVYAEKLIQYGNRYRKDYSNVDKSLNEAERLFKNNRYKRAIEIAEQALESVEPGVTKHIEEE
 VIKQ

>SAI7S6 1012790 UDP-N-acetylmuramate--L-alanine ligase

MSKEFYIMTHYHFVGIKSGMSSLAQIMHDLGHEVQGSIDIENYVFTEVALRNKGIKILPFDANNIKEDMV
VIQGNFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVMNGDKKTSFLI
GDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKDINDVDFDAFQEMAHNVKKGIIAW
GDDEHLRKIEADVPIYYYGFKSDDDIYAQNIQITDKGTAFDVYVDGEFYDHFSLPQYGDHTVLNALAVIA
ISYLEKLDVTNIKEALETFGGVKRRFNETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPH
TFSRTQAFLENEAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVVL
FMGAGDIQKLQNAYLDKLGKMAF

>SAEMRSA116620 putative polysaccharide biosynthesis protein

MSEKEMVRGTFILITISILITKVLGVLFIPFNYLIGGQENMAPFTYAYAPYNIAIAVATAGVPLAASKY
VAKYNAIGAYKVSQKFYKSSFIVMSITGVLGFLVLYFLAPYISELTARNVHDKNGWSVDDITWIIRIS
MVVIFIPVLATWRGIFQGYKSMGPTAVSEVTEQIARVIFILIGSYLVNLFVDFGSILLANGIATFAAAVGA
IIGIFTLWYYWRKRKHNDRMVESDYTDIDVSYGKMYEIIAYSIPFVIVSLNYPLFNLVDQFTHNGALS
LVGIPSQLQDIFFNMLNMSTNKIVMIPTSLSAGFAVSLIPYITKTFAGRLHEMHQIRTSIGVLMFITV
PASIGIMALAQLFTVYGYDPIVLGHDPNHGSRLLFYAPVAILISLVSATASMLQGIDKQKLTVYVI
LASVVIKALNYPILMLFHTPGAILSTSIALLFAIGCNFYILKKYAKFKFSYSWIHFKAIFLYSFIMMLG
VELVFFLANLFLEPTKLGYLIILGVTGILYGTITIKTRLADEFLEIPEKLRVRVFLR

>SAEMRSA116750 riboflavin biosynthesis protein

MQFDNIDSALMALKNGETIIVVDENRENEGDLVAVTEWMNDNTINFMAKEARGLICAPVSKDIAQRDL
VQMVDNDSIDFGTQFTVSIHDVDTTGISAYERLTAKKLDPSEAKDFNRPGHLFPLVAQDKGVLARN
GHTEAAVDLAKLTGAKPAGVICEIMNDDGTMAKGQDLQKFKEKHQLKMITIDDLIEYRKLEPEIEFKAK
VKMPTDFGTFDMYGFKATYTDEEIVLTKGAIRQHENVRLHSACLTGDFHSQRCDCAQLESSMKYINE
HGGMIYLPQEGRGIGLLNKLRAYELIEQGYDVTANLALGFDEDLRDYHIAAQILKYFNIEHINLLSNN
PSKFEGLKQYGIDIAERIEVIVPETVHNHDYMETKKIKMGHLI

>SAEMRSA116760 riboflavin synthase alpha chain

MFTGIVEIGVVKSVQIRQSVRTIEIEAHKITADMHIGDSISVNGACLTVIDFNQTSFTVQVIKGTENKT
YLADVKKRQSEVNLERAMSGNGRFGGHFVLGHVDELGTVSKINETANAKIITIQCQSHINNQLVKQGSITV
DGVSLTVFDKHDNSFDIHLIPETRRTILSSKKLGDKVHLETDVLFKYVENILNKDKDQLSVDKLRAFGF

>SAEMRSA117370 ferrochelatase

MTKKMGLLVMAYGTPYKESDIEPYTDIRHGKRPSEELQDLKDRYEFIGGLSPLAGTTDDQADALVSAL
NKAYADVEFKLYLGLKHISPFIEDAVEQMHNNDGITEAITVVLAPHYSSFSVGSYDKRADEEAAKYGIQLT
HVKHYYEQPKFIEYWTNKVNETLAQIPEEEHKDVLVVSASLPGKGLIEKNNDPYPQLEHTALLIKEQS
NIEHIAIGWQSEGNTGTPWLGPDPVQDLTRDLYEKHQYKNFIYTPVGFVCEHLEVLYDNDYECKVVCDDIG
ANYRPMKMPNTHPLFIGAIVDEIKSF

>SAEMRSA117980 conserved hypothetical protein

MHELTIIYHMSDKLNLYSDIGNIILRQRAKKRNKVNVEINETEGITFDECDIFFIGGSDREQALAT
KELSKIKTPLKEAIEDGMPGLTICGGYQFLGKKYITPDGTELEGLGILDYTESKTNRLTGDIVIESDTF
GTIVGFENHGGRTYHDFGLGHVTFGYGNDEDEKKEGIHYKNLLGTYLHGPIPKNYEITDYLLEKACER
KGIPFEPKEIDNEAEIQAKQVLIDRANRQKKS

>SAI7S6 1014340 Putative PF08353 domain protein

LRNFFEVALSCYNDAAGNLRKHMQRQWTAIHLAKLARKASRAVGKRGTDLPGQIARKVDTDLVRKLAEQV
DDIVISGTNGKTTTSLNIGHTLKANNIQUIHNNEGANMAAGITSAFIMQSTPKTKIAVIEIDEGSIPRV
LKEVTPSMVMFTNFRDQMDRFGEIDIMVNIAETISNKGILLNADDPFVSRLKIASDTIVYYGMKAH
AHEFEQSTMNESRYCPNCGRLLQYDIHYNQIGHYHCQCGFKREQAKYEISSFDVAPFLYLNINDEKYDM
KIAGDFNAYNALAAYTVLRELGLNEQTIKNGFETYSDNGRMQYFKKERKEAMINLAKNPAGMNASLSVG
EQLEGEKVVYISLNDNAADGRDTSWIYDADFEKLSKQKQIEAIIVTGTRAEELQLRLKLAEEVPIIVERD
IYKATAKTMIDYKGFTVAIPNYTSLAPMLEQLNRSFEGGQS

>SAEMRSA118290 manganese-dependent inorganic pyrophosphatase

LTMAKTYIFGHKNPDTDAISSAIIMAEFEQLRGNSGAKAYRLGDVSAETQFALDTFNVPAPELLTDDLGDG
QDVILVDHNEFQQSSDTIASATIKHVIDHHRIANFETAGPLCYRAEPVGCTATILYKMFRERGFEIKPEI
AGLMLSIIISDSLLFKSPTCTQQDVKAAEELKDIKVDIQKYGLDMLKAGASTTDKSVFLLNMDAKSFT
MGDYVTRIAQVNAVDLDEVLRNKEDLEKEMLAVSAQEKYDLFVLVTDIINSKILVVGAEKDKVGEAF
NVQLEDDMAFLSGVVSRRKKIVPQITEALTK

>SAV2051 similar to glycoprotein endopeptidase

MNKLRRQLSMNSLLIDTSNQPLSVALMQNDEVLAEITTDKQNHVSQVLMPAISQLFEQSKIAKQQLDAII
VAEGPGSYTGLRIGVTAKTLAYALDVKLYGVSSSLKALAATIDHTDKLLVPVFDARRQAVYTGFQWQNG
QLVTILEDQYMSIEALRAFLEDLNQPFYIYGKDTIKLQDELQGEVIAQLPNASVMYQLIDKPTDVHTFTP
KYHKLAEERNWINSQKNN

>SAEMRSA119600 conserved hypothetical protein

MNEKHNIGESTLIKINNLDENMQAMFLVEQLKSGDLILLNGDLGAGKTTLTQFIGKALGVRRTINSPTF
NIIKSYRGKNLKHMHMDCYRLEDSDLEDLGFDEFEDQAITVIEWSQFIKDLLPSTHLSINISTISENTRQ
IELFAQGEHYEQIKEAIIHEFAAH

>SAI7S6 1015240 Alanine racemase

VGITGGSNMDSKYRSAYMNVDLNAVASNFKVFSTLHPNKTVMMAVVKANAYGLGSVKVARHLMENGATFF
AVATLDEAIELRMHGITAKILVLGVLPKADIDKAIQHRVALTVPSKQWLKEAIKNISGEQEKKLWLHIKL
DTGMGRGLIKDNTYQEVIEIIQQYEQLVFEGVFTHFACADEPGDMTTEQYQRFKDMVNEAIKPEYIHCQ
NSAGSLLMDCQCFNAIRPGISLYGYYPSEYVQKVKVHLKPSVQLIANVVQTKTLQAGESVSYGATYTAT
DPTTIALPIGYADGYLRIMQGSFVNNGHQCEVIGRVCMDQTIVKVPDQVKAGDSVILIDNHRESPQSV
EVVAEKQHTINYEVLNLSRRLPRIYHGDGQRFVTNELLK

>SAEMRSA119910 putative UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase

MINVTLKQIQSWIPCEIEDQFLNQEINGVTIDSRAISKNNMLFIPFKGENVDGHRFVSKALQDGAGAAFYQ
RGTPIDENVSGPIIWVEDTLTALQQLAQAYLRHVNPVKVIAVTGSNGKTTTKDMIESVLHTEFKVKKTQGN
YNNEIGLPLTILELDNDTEISILEMGMSGFHEIEFLSNLAQPDIAVITNIGESHMQDLGSREGIAKAKSE
ITIGLKDNFTFIYDGDPELLKPHVKEVENVKCISIGVAADNALVCSVDDRTTGISFTINNKEHYDLPIL
GKHNMKNATIAIAGVHELGLTYNTIYQNLKNVSLTGMRMEQHTLENDITVINDAYNASPTSMRAAIDTSL
TLTGRRILILGDVLELGENSEMHISVGNYLEEKHIDVLYTFGNEAKYIYDSGQQHVEKAQHFNKDDMI
EVLTSDLKAHDRVLVKGSRGMKLEEVNALIS

>SAI7S6 1015360 D-alanine--D-alanine ligase

VILLRFKDKANSINNRTKSILYIKVANPDISLEENEMTKENICIVFGGKSAEHEVSILTAQNVNLNAIDK
DKYHVDIIYITNDGDWRKQNNITAEIKSTDELHLENGEALISQLLKESSSGQPYDAVFPLLHGPNGEDG
TIQGLFEVLDPYVGVNGVLSAASSMDKLVMMKQLFEHRLPQLPYISFLRSEYEKYEHNILKLVNDKLNYP
VFKPANLGSVSGSKCNNEAELKEGIKAFQFDRKLVIEQGVNAREIEVAVLGNDYPEATWPGEVVKDV
AFYDYKSKYKDGKVQLQIPADLDEVDQLTLRNMALEAFKATDCSGLVRADFFVTEDNQIYINETNAMPGF
TAFSMYPKLWENMGLSYPELITKLIELAKERHQDKQKNKYKID

>SAEMRSA119990 putative membrane protein

MKKKALLPLFLGIMVFLAGCDYSKPEKRSGFFYNTFVDPMKNVLDWLGNLLNDNYGLAIIILVLVIRII
LLPFMLSNYKNSHMMRQKMKVAKPEVEKIQEKVKRARTQEEKMAANQELMQVYKKYDMNPIKSMGLCLPM
LIQLPIIMGLYFVLKDQLVDGLFKYPHFLWFDLGRPDIIWITIIAGVLYFIQAYVSSKTMPEQRQMGYMM
MVISPIMIIWISLASALGLYWSVSAFLVVQTHFANIYIEKVAKKEVQPFIEAYEREHNGGSNKKGKN
TQVVSKKKKK

>SAEMRSA120080 putative UDP-N-acetylglucosamine 1-carboxyvinyltransferase

MDKIVIKGGNKLTGEVKVEGAKNVLPILTASLLASDKPSKLVNVPALSDVETINNVLTTLNADVITYKKD
ENAVVVDATKTLNEEAPYEYVSKMRASILVMGPELLARLGHAIVALPGGCAIGSRPIEQHIKGFEALGAEI

HLENGNIYANAKDGLKGTSHLDFPSVGATQNIIMAASLAKGKTLIENAAKEPEIVDLANYINEMGGRT
GAGTDTITINGVESLHGVEHAIIPDRIEAGTLIAGAITRGDIFVRGAIKEHMASLVYKLEEMGVELDYQ
EDGIRVRAEGLQPVDIKTLPHPGFPTDMQSQMMALLLTANGHKVVTETVFENRFMHVAEFKRMNANINV
EGRSAKLEKGSQQLGAQVKATDLRAAALILAGLVADGKTSVTELTHLDRGYVDLHGKQLGADIERIN
D

>SAEMRSA120140 putative ATP synthase delta chain

MVKVANKYAKALFDVSLDTNNLETINQELTVINEAVKDKIEQLKMVDSNPTQTAEQRRELINGVFTDINP
YIKNMMYVLADNRHISLIADVFKAQSLYNGHYNQDFATIESTYELSQEELDKIVKLVTQQTLSKVIVD
TKINPDLIGGFRVKVGTTVLDGSRNDLVQLQRKFRRVN

>SAEMRSA120150 putative ATP synthase subunit b

VTETANLFVLGAAGGVWGTIVVQVLTFFVLLALLKKFAWGPKLDVMDKRERDINRDIDDAEQAKLNAQK
LEEENKQKLKETEEVQKILEDAKVQARQQEQEIHEANVRANGMIETAQSEINSQKERAADINNQVSE
LSVLIASKVLRKEISEQDQKALVDKYLKEAGDK

>SAEMRSA120170 ATP synthase subunit a

MDHKSPLVSWNLFGDFIVFLSSILMILVTAFLVFLAIICTRNLKKRPTGKQNFVEWIFDFVRGIIEN
MAWKKGGQFHFLAVTLILYIFIANMLGLPFSIVTKDHTLWWKSPTADATVTLTLSTTIILLTHFYGIKMR
GTKQYKGYVQPFWPLAIINVFEEFTSTLTGLRLYGNIFAGEILLTLAGLFFNEPAWGWIIISIPGLIV
WQAFSIFVGTIQAYIFIMLSMVYMSHKVADEH

>SAEMRSA120330 putative tagatose-bisphosphate aldolase

MPLVSMKEMLIDAKENGYAVGQYNNLEFTQAILEASQEENAPVILGVSEGAARYMSGFYTIVKMVEGL
MHDNLITIPVAIHLHDGSSFEKCKEADAGFTSVMIDASHSPFEENVATTKKVVEYAHEKGVSEAEELGT
VGGQEDDVVADGIIYADPKCEQELVEKTGIDALAPALGSHGYPYKGEPLGFKEMEEIGLSTGLPLVLHG
GTGIPTKDIQKAIPFGTAKINVTENQIASAKAVRDVLNNDKEVYDPRKYLGPAREAIKETVKGKIEFG
TSNRAK

>SAEMRSA120690 putative membrane protein

MDFSNIFFQNLSTLKIVTSILDLLIVWVYLLITVFKGTAKIQLLKILVIVIGQQISMILNLTATSKLF
DIVIQWGLALIVIFQPEIRRALEQLGRGSFLKRYTSNTYSKDEEKLIQSVSKAVQYMAKRRIGALIVFE
KETGLQDIETGIAMDSNISQELLINVFIPNTPLHDGAMIIQGTKIAAAASYLPLSDSPKISKSLGTRHR
AAVGISEVSDAFTVIVSEETGDISVTFDGKLRRDISNEIFEELLAEHWFGRFQKKGKGV

>SAEMRSA121190 putative cobalt transport protein

MKNKLIIGRYLPINSFVHLDPRAKLMFVFLFIILIFFCHSPLTYLWVFALILFFMRLAKIQLWFLIKGL
TPIFFLIFTLMMHIFLTGGYVLVEWHGITIETNGILEGLYISRLIGIVMIATIMTLSTSPIDLTDAF
ERLLAPLKMFKLPVHQLSMIMSIALRFIPTLMDELDKIILAQKSRGSEISSGNIATRIKSFIPLLVPLFI
SAFQRAEELAVAMEVRGYDANVQRTSYRQLKWQLRDTLSLIMIIPFIIILFVLKYSKV

>SAEMRSA121290 preprotein translocase SecY subunit

MIQTLVNFFRTKEVRNKIFFTLAMLVIFKIGTYIPAPGVNPAAFDNPQGSQGATELLNTFTGGGALKRFSI
FAMGIVPYITASIVMQLLQMDIVPKFSEWAKQGEVGRRLNNVTRYLAISLAFIQSIGMAFQFNYYLKGA
LIINQSIMSULLIALVLTAGTAFLIWLGDQITQFGVGNISIIIFAGILSTLPASLIQFGQTAFVGQEDT
SLAWLKVGLLLVSLILLTVGAIYVLEAVRKIPYAKKQTAQRLGSQATYLPKVNAGVIVFVIFAMAFF
LLPRTLTLFPYDKEWAQNIANAANPSSNVGMVVYIVLIIIFTYFYAFVQVNPEKMADNLKKQGSYVPGIR
PGEQTKKYITKVYRLTFVGSIFLAVISILPATKFMGLPQSIQIGGTSLLIVIGVAIETMKSLEAQVS
QKEYKGFGR

>SAEMRSA121370 50S ribosomal protein L5

LNRLKEFNTEVTENLMKKFNYSVMEVPKIDKIVVNMGVGDAVQNSKVLDAVEEELITGQKPLVTKA
KKSJATFRLREGMPIGAKVTLRGERMYEFLDKLISVSLPRVRDFQGVSKAFDGRGNYTLGVKEQLIFPE
IDYDKVSKVRGMDIVIVTTANTDEEARELLANFGMPFRK

>SAEMRSA121430 30S ribosomal protein S3

VGQKINPIGLRVGIIRDWEAKWYAEKDFASLLHEDLKIRKFIDNELKEASVSHVEIERAANRINIAIHTG
KPGMVGKGGSEIEKLRNKNLALTDKKVHINVIEIKVDLDARLVAENIARQLENRASFRVQKQAITRA
MKLGAKGIKTQVSGRLGGADIARAEQYSEGTVPPLHTLRADIDYAHAEADTTYGKLGVKVWIYRGEVLP
NTSGGGK

>SAEMRSA125010 putative pantoate--beta-alanine ligase

MTKLITTVKEMQHIVKAAKRS GTTIGFIPTMGALHDGHLTMVRESVSTNDITVVSFVNPLQFGPNEDFD
AYPRQIDKDLELVSEVGADIVFHPAVEDMYPGELGIDVKVGPLADVLEGAKRPGHFDGVTVVNKLNFIV
MPDYAYFGKKDAQQLAIVEQMVKDFNHAVEIIGIDIVREADGLAKSSRNYYL TEQERQEA VHLSKSLLA
QALYQDGERQSKVIIDRVTEYLESHISGRIEEVAVSYSQLVEQHEITGRIFISLAVKFSKARLIDNIII
GAE

>SAEMRSA125020 putative 3-methyl-2-oxobutanoatehydroxymethyltransferase

LKTVSQLIDMKQKQTKISMVTAYDFPSAKQVEAAGIDMILVGDSLGMTVLGYESTVQVTLADMIHHGRAV
RRGAPNTFVVVDMPIGAVGISMTQDLNHALKLYQETNANAIAEGA HITPFIEKATAIGIPVVAHLGLTP
QSVGVMGYKLQGATKEAAEQ LILDAKNVEQAGAVLVLEAIPNDLAE EISKHLTIPVIGIGAGKGTGQV
LVYHDM LNYGEHKA FVKQFADF SVGVDGLKQYDQEVKSGAFPSEEYTKKKIMNEVNNND

>SAI7S6 1018940 Hydroxymethylglutaryl-CoA reductase

MSMQSLDKNFRHLRSRQKLQQLVDKQWLS EDQFDILLNHPLIDEEVANSLIENVIAQ GALPVGLLPNIIV
DDKAYVVPMMVEEPSVVAASYGAKLVNQ TGGFKTVSSERIMIGQIVFDGVDDEKLSADIKALEKQIHK
IADEAYPSIKARGGGYQRIADTFPEQQLSLKVFDTKDAMGANMLNTILEAITAFLKNESPQSDILMS
ILSNHATASVVKVQGEIDVKDLARGERTGEEVAKRMERASVLAQVDIHRATHNKGVMNGIHAVV LATGN
DTRGAEASAHAYASRDGQYRG IATWRYDQKRRLIGTIEVPMTLAIVGGGTVLPIAKASLELLNVDSAQ
ELGHVVAAVGLAQNFACRALVSEGIQQGHMSLQYKSLAIVVGAKGDEIAQVAEALKQEPRANTQVAERI
LQEIRQQ

>SAEMRSA121230 DNA-directed RNA polymerase alpha chain

MIEIEKPRIETIEISDAKF GFVVEPLERGYGTTLGNSLRILLSSLP GAAVKYIEIEGVLHEFSAVDN
VVEDVSTIIMNIKQLALKIYSEEDKTEIDVRDEGEVTASDITHSDSEILNPELKIATVSKGGHLKIRL
VANKGRGYALAEQNNTSDLP IGVIPVDSLSPVERVNYTVENTRVGQSSDFDKLTLDVWTNGSITPQESV
SLAAKIMTEHLNIFVGLTDEAQNAEIMIEKEEDQKEKVLEMSIEELDLSVRSYNCLKRAGINSVQELADK
SEADMMKVVRNLGRKSLEEVKYKLEDLGLGRKED

>RK77 010475threonylcarbamoyl-AMP synthase

VHSFLLYIMINKKGVIKLDTKIWDVREYNEDLQQYPKINEIKDIVLNGGLIGLPTETVYGLAANATDEEA
VAKIYEAKGRPSDNPLIVHIHSDQLKDFTYILDAPVEKLMQAFWPGPISFILPKPGYLCRKVSGGLSS
VAVRMPSHSVGRQLLQIINEPLAAPSANLSGRPSPTTFNHVYQDLNGRIDGIVQAEQSEEGLESTVLDCT
SFPYKIARPGSITAAMITDILPNSITHADYNDTEQPIAPGMKYKHYPNTPLTIITDIESKIGNDGKDW
SIAFIVPSNKVAFIPSEAQFIQLCQDDNDVKQASHNLYDVLHSLDENENISAAYIYG FELNDNTEAIMNR
MLKAAGNHIVKGCEL

>SAEMRSA115480 histidyl-tRNA synthetase

MIKIPRGTDILPEDSKKWRYIENQLDELMTFYNYKEIRTPIFESTDLFARGVGDSTDVVQKEMYTFKDK
GDRSITLRPEGTA AVRSYIEHKMQGNPNQPIKLYNGPMFRYERKQKGRYRQFNQFGVEAIGAENPSVD
AEVLAMVMHIYQSFGLKHLKLVINSVGDMASRKEYNEALVKHFEPVIEHFCSDCQSR LHTNPMRILDCKV
DRDKEAIKTAPRITDFLNEESKAYYEQVKAYLDDLGIPIYEDPNLVRGLDYTHAFELMMDNPNYDGA
ITL CGGGRYNGLLELDGPSETGIGFALSIERLLALEEEGIELDIEENLDLFIVTMGDQADRYAVKLLN
HLRHNGIKADKDYLRKIKGQMKQADRLGAKFTIVIGDQELENNKIDVKNMTTGESETIELDALVEYFKK

>SAEMRSA112890 dihydrofolate reductase type I

MTLSILVAHDLQRVIGFENQLPWHLPNDLKHVKKLSTGHTLVMGRKTFESIGKPLPNRRNVVLTSDTSFN

VEGVVDVIHSIEDIYQLPGHVFIFFGGQTLFEEMIDKVDDMYITAIEGKFRGDTFFPPYTFEDWEVTSSVEG
KLDEKNTIPHTFLHLIRKK

>SAEMRSA110440 putative flavoprotein

MKKILLAVTGGAAYKADLTSLTQSGYEVRLMLTNHAQKFVTPLAFAQISRNAVYTTDTFIEENPSEIQ
HIALGDWADAIIVAPATANTIAKLSVGIADDLVTSTLLATETPKFIAPAMNVHMYENKRTQQNINILKED
GYHFIEPGSGFLACGYVAKGRMEELQIVSVIDAHFQNSNRLANSSFDKRALVTAGPTIEVIDPVRVFS
NRSSGKMGYAI AEALNRNGAIVTLVAGPTTLEDPKDIEVIHVQSAEEMFEQVTSRFDEQDIVVKAASVSD
YTPVDVLEHKMKKQDGLSVSFKRTKDILKYLGEHKTSQYLIGFAAETEDIENYAQQKLRRKNADVIIISN
NVGDMSIGFSSDDNELTMHFKNNEKVNKKGKVVLAQILDELETRWQ

Sequence 2: Non_cytoplasmic_localized_proteins_(PSE_MEM_proteins)

>SAEMRSA106090_putative_undecaprenol_kinase

MFIIELIKGIILGVVEGLTEFAPVSTGHMILVDDMWLKSSEFLGSQSAFTFKIVIQLGSVFAAAWVFRE
RFLEILHIGKHKHVEGENDQRRSKPRRLNLLHVLVGMVPAGILGLLFDFFIEEHLFSVPTVMIGLFVGA
IYMIIADKYSKVNPKQTVDQINIFYQAFVIGISQAVAMWPGFSRSGSTISTGVLMKLNHKAASDFTFIMA
VPIMLAASGLSLLKHQDIQIADIPFYILGFLAAFTVGLIAIKTFLHLINKIKLIPFAIYRIVLVIFIAI
LYFGFGIGKGI

>SAEMRSA106730_putative_glycosyltransferase

MVTLLLVAVTMIVSLTITPVIASIKRLNLVDKPNFRKVHTKPIVSMGGTVILFSFLIGIWIGHPIETEI
KPLIIGAIIMYVLGLVDDIYDLKPYIKLAGQIAAALVAFYGVITIDFISLPMGTTIHFGFLSIPITVIWI
VAITNAINLIDGLDGLASGVSAIGLITIGFIAILQANIFITMICCVLLGSLIGFLFYNFHPAKIFLGDSG
ALMIGFIIGFLSLLGFKNITIIALFFPILAVPFIDTLFAMIRRVKKQGHIMQADKSHLHHKLLALGYT
HRQTVLLIYSISILFSLSSIILYVSPPLGVVLMFILIFSIELIVEFTGLIDNNYRPILNLISRKSSHKE
D

>SAEMRSA110140_penicillin-binding_protein_1

MAKQKIKIKKNIKIGAVLLVGLFGLLFFILVLRISYIMITGHSNGQDLVMKANEEKYLVKNAQQPERGKIYD
RNGKVLAEADVERYKLVAVIDKKASANSKKPRHVVDKKETAKKLSTVIDMKPEEIEKRLSQKKAFQIEFGR
KGTNLTYQDKLIEKMNLPGISLLPETERFYPNGNFASHLIGRAQKNPDTGELKGALGVEKIFDSYLSGS
KGLSRYIHDWGYIAPNTKKEKQPKRGDDVHLTIDSNIQVFVEEALDGMVERYQPKDLFAVVMDAKTGEI
LAYSQRPTFNPETGKDFGKKWANDLYQNTYEPGSTFKSYGLAAAIQEGAFDPDKKYSGHRDIMGSRISD
WNRVGVGWEIPMSLGFTYSSNTLMMHLQDLVGADKMKSWEYERFGFGKSTKGMFDGEAPGQIGWSNELQQKT
SSFGQSTTVTPVQMLQAQSAFFNDGNMLKPWFVNSVENPVSKRQFYKGQKQIAGKPITKDTAEKVEKQLD
LVVNSKKSHAANYRIDGYEVEGKTGTAQVAAPNGGGYVKGPNPYFVSFMDAPKKNPKVIVYAGMSLAQK
NDQEAYELGVSKAFKPIMENTLKYLVNKGSKDDTSNAEYSKVPDVEGQDKQAIDNVSASLEPVTIGTG
TQIKAQSIKAGNKVLPKSVLLLTGDLTMDMTGWTKEDVIAFENLTNIKVNKLGSGFVSHQSISKGQK
LTEKDIDVEFSSENVDSNSTNSDSNSDDKKKSDSKTDKDKSD

>SAEMRSA110150_phospho-N-acetylmuramoyl-pentapeptide-transferase

MIFVYALLALVITFVLVPVLIPTLKRMMKFGQSIREEGPQSHMKKTGTPTMGGLTFLLSIVITSLVAIIFV
DQANPIILLFVTIGFGLIGFIDDIIVVKNNQGLTSKQKFLAQIGIAIIFVLSNVFHLVNFSTSIHI
PFTNVAIPLSFAYVIFVWQVGSNAVNLTLDGLDGLATGLSIIGFTMYAIMSFVLGETAIGIFCIIMLF
ALLGFLPYNINPAKVMFGDTGSLALGGIFATISIMLNQELSLIFIGLVFVIETLSVMLQVASFKLTGKRI
FKMSPIHHHFFELIGWSEWKVVTVFWAVGLISGLIGLWIGVH

>SAEMRSA110290_lipoprotein_signal_peptidase

MHKKYFIGTSILIAVFFVIFDQVTKYIIATTMKIGDSFEVIPHFLNITSHRNNGAAWGILSGKMTFFFI
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IGVILIIIIALLKDTSNKKEKEVK

>SAEMRSA112010_putative_membrane_protein

MMIIVMLLSYLIGAFPSGFVIGKLFKKDIRQFGSGNTGATNSFRVLGRPAGFLVTFIDFKGFITVFF
PLWLPVHADGPSTFFTNGLIVGLCAILGHVYPVYLKQGGKAVATSAGVVLGVNPILLILAIFFVVL
KIFKYVSLASIVAAICCVIGSLIIQDYILLVVSFLVSIILIRHRSNIARIFRGEPEKIKWM

>SAEMRSA112810_putative_UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide)pyr_o-phosphoryl-undecaprenol_N-acetylglucosamine_transferase

MKKIAFTGGGTGVGHVSVNLSLIPTALSQGYEALYIGSKNGIEREMIESQLPEIKYYPISSGKLRRYISLE
NAKDVFVKLGILDARKVLKKEKPDLLFSKGGFVSPVVIAAKSLNIPTIIHESDLTPGLANKIALKFAK
KIYTTFEETLNYLPKEKADFIGATIREDLKNGNAHNGYQLTGFNENKKVLLVMGGSLGSKKLNSIIRENL
DALLQQYQVIHLTGKGLKDAQVKKSGYIQYEFVKEELTDLLAITDTVISRAGSNAIYEFLLRIPMLLVP
LGLDQSRGDQIDNANHFAKGYAKAIDEEQLTAQILLQELNEMEQUERTRIINNMSYEQSYTKEALFDKM
IKDALN

>SAEMRSA113110_penicillin-binding_protein_2

MTENKGSSQPKKNGNNGGKSNSKKNRNVKRTIIKIIGFMIIAFFVLLLGILLFAYYAWKAPAFTEAKLQ
DPIPAKIYDKNGELVKLTLDNGQRHEHVNLKDVPKSMKDAVLATEDNRFYEHGALDYKRLFAGIGNLTGG
FGSEGASTLTQQVVKDAFLSQHKSIGRKAQEAYLSYRLEQEYSKDDIFQVYLNKIYSDGVTGIKAAKY
YFNKDLKDLNLAAEAYLAGLPQVPNNYNIYDHPKAAEDRKNTVLYLMHYHKRITDKQWEDAKKIDLKANL
VNRTAEERQNIDTNQDSEYNSYVNFVKSELMNNKAFKDENLGNVLQSGIKIYTNMDKDVQKTLQNDVDNG
SFYKNKDQQVGATILDSKTGGLVAISGGRDFKDVVNRNQATDPHTGSSSLKFLAYGPAIENMKWATNHA
IQDESSYQVDGSTFRNYDVKSHGTYSIYDALRQSFNIPALKAWQSVKQNAAGNDAPKKFAAKLGLNYEGDI
GPSEVLGGSASEFSPTQLASAFAAIANGGTYNNAHSIQKVVRDGETIEYDHTSHKAMSDYTAYMLAEML
KGTFFKPYGSAYGHGVSGVNMGAKTGTGTGYAETYSQYNLPDNAAKDVWINGFTPQYTMSSVWVGFSKVKQY
GENSFVGHSSQEQEYPQLFYENVMKISSRDGEDFKRPSSVSGSIPSINVSGSQDNNTNRSAGGSDTSAN
SSGTAQSNNNTRSQQSRNSGGLTGIFN

>SAEMRSA115170_conserved_hypothetical_protein

MGLVRKFFMPNSYVQSIFQIDLDKLVDKGVKGIITDLNTLVGWDVKEPTERVKAWFKEANEKGITITIV
SNNNESRVASFQHLIDIDIFKARKPMGKAFDKAITKMNIRPDQTVVIGDQMLTDVFGGNRRGLYTIMV
PVKRTDGFITKFNRLIERLLRHFSKKGYITWEEN

>SAEMRSA115540_putative_protein-export_membrane_protein

VKKSSRIIAFLLLVLLFAGMAATYKSVIKNVNLGLDLQGGFEVLYQVDPLNKGDKIDKKALQSTAQTLE
NRNVNLGVSEPKIQVEPNRIRVQLAGVTDQNEARKILSSQANLTIRDAEDKVKLGSDDIKQGSQAKQEFK
QETNQPTVTFKVKDNKFKKVTETEEKSRDNDVMVWLDFFKKGDSYKKEAQKKNPKFISAASVDQPINSDS
VEISGGFGKGQEGVKKAKQIAELLNAGSLPVDLKEIYSNSVGAQFGQDALDKTVFASFVIGVALIYLFMLGF
YRLPGLVAIIALTTYIYLTAVAFNFIISGVLTPGLAALVLGVGMAVDANIIMYERIKDELIRIGRTIKQAF
SKANKSSFLTIFDSNLTTVIAAAVLFFGESSVKGFATMLLLGILMIFVTAVFLSRFLLSLLVSSNIFKN
QFWLFGVKKNRHDINEGVVDHDLKTSFEKWNFVKLAKPLIGVSILIVVGLVILYIFKLNLDGIDFSSGT
RVDFQSKQAITQQKVEQVVKDSGLKADQIQINGKDNKVATVQFKDDLTRAQDNKLSDNKSKFGDTPQIN
TVSPIIGQELAKNAMLALIYASIGIIIVSLRFEWRMGLSSVLALLHDVFIIAIFSLFRIEVDLTFIAA
VLTIVGYSINDTIVTFDRVRENQKVKVITTEQIDDIVNRSIRQTMTRSINTVLTIVVVVAILFFGAP
TIFNFTLALFIGLISGVFSSIFIAVPLWGIMKKRQLKSPKHKLVVYKEKKSNDKILV

>SAEMRSA116620_putative_polysaccharide_biosynthesis_protein

MSESEKEMVRGTFLITISILITKVLGVLFIPFNYLIGGQENMAPFTYAYAPYNIAIATAGVPLAASKY
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MVVIFIPVLATWRGIFQGYKSMGPTAVSEVTEQIARVIFILIGSYLVNLNVDGSSILLANGIATFAAAVGA
IIGIFTLWYWRKRKHNIDRMVESDYTDIDVSYGKMYKEIIAYSIPFVIVSLNYPFLNLDQFTHNGALS
LVGIPSQLQDIFFNMLNMSTNKIVMIPTSLSAGFAVSLIPYITKTFAGRLHEMHQIRTSIGVLMFITV
PASIGIMALAQPLTFVYGYDPIVLGHDPNHGSRLLFYAPVAILISLVSMTASMLQGIDKQKLTIVYVI

LASVVIKALALNYPLIMLFHTPGAILSTSIALLFAIGCNFYILKKYAKFKFSYSWIHFACIFLYSFIMMLG
VELVFFLANLFLEPTKLGYLIIILGVTVGILYGTITIKTRLADEFLGEIPEKLRRRVFLR

>SAEMRSA117460_putative_peptidyl-prolyl_cis-isomerase
MKMINKLIVPVATASALLGACGASATDSKENTLISSKAGDVTVADTMKKIGKDQIANASFTEMLNKILAD
KYKNKVNDKKIDEQIEKMQKQYGGKDKFEKALQQGLTADKYKENLRTAAYHKELLSKIKISDSEIKED
SKKASHILIKVSKSKSDEGLDDKEAKQKAEIQKEVSKDPSKFGEIAKKESMDTGSAKKDGEVLYLKG
QTDKDFEKALFKLDGEVSDVVKSSFGYHIIKADKPTDFNSEKQSLKEKLVQKQKPNKLLTDAYKDLL
KEYDVDFKDRDIKSVVEDKILNPEKQGGAGGQSGMSQ

>SAEMRSA119930_putative_membrane_protein
MNYSSRQQPDKHWLRKVDVVLVATIAVLAIKSVLLINSAMGGGQYSANFGIRQIFYYLGAIFAGIIMFI
SPKKIKHYTYLLYFLICLLIGLLVIPESPIPIINGAKSWYTFGPISIQSEFMKILILALARVVSRLH
NQFTFNKSFQSDLLFFKIIGVSLVPSILILLQNDLGTTLVLAIIAGVMLVSGITWRILAPIFITGIVG
AMTVILGILYAPSLIENLLGVQLYQMGRINSWLDPTYSSGDGYHLSLKAIGSGQLLGKGYNHGEVYI
PENHTDFIFSVIGELGFIGSVLILFLIFHLIRLAAKIEDQFNKIFIVGFVTLVLFHILQNIGMTI
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>SAEMRSA119990_putative_membrane_protein
MKKKALLPLFLGIMVFLAGCDYSKPEKRSFFYNTFVDPKMNVDWLGNLLNDNYGLAIIILVLVIRII
LLPFMLSNYKNSHMMRQKMKVAKPEVEKIQEKVKRARTQEEKMAANQELMQVYKYDMNPIKSMGLCLPM
LIQLPIIMGLYFVLKQDLVDGLFKYPHFLWFDLGRPDWITIAGVLYFIQAYVSSKTMPEQRRQMGYMM
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TQVVSKKKKK

>SAEMRSA120150_putative_ATP_synthase_subunit_b
VTETANLFLVLAAGGVWGTIVVQVLTFIVLLALLKKFAWGPLKDVMDKRERDINRDIDDAEQAKLNAQK
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LSVLIASKVLRKEISEQDQKALVDKYLKEAGDK

>SAEMRSA120170_ATP_synthase_subunit_a
MDHKSPLVSWNLFGFDIVFNSSILMILVTAFLVFLAIICTRNLKKRPTGKQNFVEWIFDFVRGIIEGN
MAWKKGQGFHFLAVTLILYFIANMLGLPFSIVTKDHTLWWKSPTADATVTLTSTIILLTHFYGIKMR
GTKQYLKGYVQPFWPLAIIINVFEFTSTLTGLRLYGNIFAGEILLTLAGLFFNEPAWGWIIISIPGLIV
WQAFSIFVGTIQAYIFIMLSMVYMSHKVADEH

>SAEMRSA120690_putative_membrane_protein
MDFSFFQNLSTLKIVTSILDLLIVWYVLYLLITVFKGTAKIQLLKILVIVIGQQISMILNLTATSKLF
DIVIQWGVLAIVIFQPEIRRALEQLGRGSFLKRYTSNTYSKDEEKLIQSVKAVQYMAKRRIGALIVFE
KETGLQDYIETGIAMDSNISQELLINVFIPNTPLHDGAMIIQGTKIAAAASYLPLSDSPKISLGLTRHR
AAVGISEVSDAFTVIVSEETGDISVTFDGKLRRDISNEIFEELLAEHWFGRFQKKGVK

>SAEMRSA121190_putative_cobalt_transport_protein
MKNKLIIGRYLPINSFVHHLDPRAKLMFVFLFIILIFFCHSPLTYLWVFALIFFMRLAKIQLWFLIKGL
TPIFFFLIFTLMMHIFLTGGYVVLVEWHGITETNGILEGLYISLRIGIVMIATIMTLSTSPIDLTDAF
ERLLAPLKMFKLPVHQLSMIMSIALRFIPTLMDELDKIILAQKSRGSEISSGNIATRIKSFIPLLVPLFI
SAFQRAEELAVAMEVRGYDANVQRTSYRQLKWQLRDTLSLIMIIPFAIILFVLKYSKV

>SAEMRSA121290_preprotein_translocase_SecY_subunit
MIQTLVNFFRTKEVRNKIFFTLAMLVIFKIGTYIPAPGVNPAAFDNPQGSQGATELLNTFGGGALKRFSI
FAMGIVPYITASIVMQLQMDIVPKFSEWAKQGEVGRRLNNVTRYLAISLAFIQSIGMAFQFNYYLKGA
LIINQSIMSYYLIALVLTAGTAFLIWLGDQITQFGVGNISIIIFAGILSTLPASLIQFGQTAFVGQEDT
SLAWLKVGLLVSLILLTVGAIYVLEAVRKIPQYAKKQTAQRLGSQATYLPKVNAGVIPVIFAMAFF
LLPRTLTLFYPDKQWQAQNIANAANPSSNVGMVVYIVLIIIFTYFYAFVQVNPEKMADNLKKQGSYVPGIR

PGEQTKKYITKVLYRLTFVGSIFLAVISILPILATKFMGLPQSIQIGGTSLLIVIGVAIETMKSLEAQVS
QKEYKGFGGGR

>SAR081prolipoprotein_diacylglyceryl_transferase

MGGIVFNYIDPVAFNLGPLSVRWYGIIVGILLGYFVAQRALVKAGLHKDTLVDIIFYSALFGFIAARI
YFVIFQWPYYAENPGEIkiWHGGIAIHGGLIGGFIAGVIVCKVKNLNPFQIGDIVAPSIILAQGIGRWG
NFMNHEAHGGPVSRAFLEQLHLPNFIIENMYINGQYYHPTFLYESIWDVAGFIILVNIRKHLKLGETFFL
YLTWYSIGRFFIEGLRTDSLMLTSNIRVAQLVSILLILISLIVYRRIKYNPPLYSKVGALPWPTRKVK

>EssA

MLMNSVIALTFLTASSNNGGLNIDVQQEEKRINNDLNQYDTTLFNKDSKAVNDAIAKQKKERQQQIKND
MFQNPQASHSTRNLNETKKVLFKSNLEKTSSEDKSPYIQNKQEKKIFPYILMSVGAFTLGFFVIFSIHKGR
RTKNESARKSNI