

Supplementary Materials: Functional Annotations of Paralogs: A Blessing and a Curse

Rémi Zallot, Katherine J. Harrison, Bryan Kolaczowski and Valérie de Crécy-Lagard

Sequences selected from pubSEED to generate and compare logos

>fig|1007123.3.peg.641 Q6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [SAR406 cluster bacterium SCGC AAA160-I06]

MFQLTRKYEFAARKLTMLDVDHPCSQLHGHTFSVVLELSGEIDSSKGWVVDYDIDKIYKDEIH
ALLDHKHLNDIEELSNTPTTELIKWIWNRIQPNLSGLTGVTVSEGPSYSCTYRGV

>fig|102127.3.peg.996 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Geitlerinema sp. PCC 7105]>fig|102127.3.peg.996 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Geitlerinema sp. PCC 7105]

MQASLTVSTHFSAAHRLARPDLDTNCGIYGKCARPHGHGHHDYHLDVTVRGTTIDPRTGMVVE
LGALHGVLEQIEVIEPLDHRFLNKDIPYFADRVPTAEHIAIYIRDILQEPLRQLGVTLKVKLYESP
NSCEVYGRSSNSATPATTAKPKLVLV

>fig|1075091.3.peg.1875 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I / Folate biosynthesis protein PTPS-III, catalyzes a reaction that bypasses dihydroneopterin aldolase (FolB) [Clostridium sporogenes PA 3679]

MILIKKFKFDAAHNLIHYHGKERCRLHGHTYGVVVKISGEPDKEDMVIDFTELKAIVKENVLDILDH
AYINEIHKQPTAENIAVWIWDKLYTKLRDNCSLYEIEVWETETSGVVYSG

>fig|1075091.3.peg.976 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [Clostridium sporogenes PA 3679]

MYTLKVEHSFDSAHLANYEGKCGNIHGHRWKVEIQIKSESLVQGGQLDGMVIDFGDLKKDVKS
MVDYYDHALLIEKETMREQSLSSLKEDGFRIIEVNFRPTAENFAAFFYKFMKDKGYNVKSVTVYET
PNNSATYEEESGVI

>fig|1079986.3.peg.3739 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [Streptomyces chartreusis NRRL 12338]

MEIFREFTFEAAHRLPRVPEGHKCARLHGHSYKVTVHVHVEAPVEPEAGWVMDFGDIKQAFKPIDA
QLDHYYLNDIEGLDNPTSENLARWIWDRMVTELPGLSAITVRETCTSGCTYRGE

>fig|1121904.3.peg.2753 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Flexithrix dorotheae DSM 6795]>fig|1121904.3.peg.2753 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Flexithrix dorotheae DSM 6795]

MHNPEWSEQKNAEVFGLCNNPNYHGHNYDLIVKVTGEVDPETGYVIDLKILKSIKDEILDKFDH
KNLNLDTPEFKSLNPTAENIAVVIWEKLRKKLEPKFDLKVTLTYETERNFVEYPAS

>fig|1122169.3.peg.1233 Folate biosynthesis protein PTPS-III, catalyzes a reaction that bypasses dihydroneopterin aldolase (FolB) [*Legionella shakespearei* DSM 23087]

MKRYLTTELQKESMKFSAGHTTIFSATEREPLHGHMYCVYLALTTWVEENGMTFDYRYKERI
HVLCHQLNQTFLLMPQFSPFLQYAEDDEYYYFTFNHKKIPFLKEDVTLMPLSNITVEELSRWVFNE
LIKDTEELDRHRIEKVVVKVFSAPGQSANHEWHRVK

>fig|1144275.3.peg.1442 Folate biosynthesis protein PTPS-III, catalyzes a reaction that bypasses dihydroneopterin aldolase (FolB) [*Coralloccoccus coralloides* DSM 2259]

MAPRTTTELHKEEMKFSAGHTTIFSATHRENHGHNFVYVALTGEVSDDGLLSYDGPLKQAI
QRCKAWNETFFLPAHSKHLRLERDEKGNHVAHFNGEELRFLARDVTVPVANVSLEELARVFGE
ELVGDGSAMARDHITGLVVKCASGPGQWASWEWKRDV

>fig|1178537.3.peg.3009 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [*Bacillus* sp. HYC-10]>fig|1178537.3.peg.3009 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [*Bacillus* sp. HYC-10]

MLYLSRKMYFSSLHSYRVKEWSDEYNQQVFGPCSNPNHGHGHDYTLVEMVKGKLNQRSGIVVNI
TDIDKVVKSFAENLDGKFLNMENDYFKHHIPTTENIATYLVESLDGKIDHCQIHKIRLHENNFL
YSEKEDGQLVRLTRKYHFCTAHLRHSEQLSEEENQELFGKCNNPYGHGHNYYLEVTVNGEPPDPV
TGMIANLSDDISVVEKEIMERFDHKHLNLDTEEFKDLNPTSENVAVVIWDLSPQLTNLFKIGLYE
TEKNYFEYCGPQEDMKYGA

>fig|1178537.3.peg.3654 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [*Bacillus* sp. HYC-10]

MLSQIYPQTDHPFSFELNKMHLASAAHFVPREEAGACSRVHGHTYTINITIAGDDLDESGFLVNF
STLKKLIHGQYDHTLLNDHEEFSSNDPYAMPTTEVVAKTVYDKVAAYLTTLANKPVCVQVFVRE
TPTSYCIYRPKRVELK

>fig|1193806.4.peg.1496 Queuosine biosynthesis QueD, PTPS-I / Folate biosynthesis protein PTPS-III, catalyzes a reaction that bypasses dihydroneopterin aldolase (FolB) [*Dehalococcoides mccartyi* BTF08]

MYLSIKKHFEAAHFLRGYKGKCNELHGHRYEVALKIKTGELDECGMGADFSLLKTRLNEVLQS
YDHTCLNDLTPFDNINPSAENIAKDIYDKLKTIVINKKGVELWGVEVWESPSSVLYQPD

>fig|1237500.3.peg.5547 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [*Nocardiosis ganjiahuensis* DSM 45031]

MRHNFETAHRLPHLGKCTNLHGHSWWVEVSAVAPTLDSGTVVEFGTFKSALRSWIDTYLDHG
AMLGFDDPMAKLLADHGSKLFRFGAPDPLPAEPPAGDLPHTVEAVAVLLGRVAEEALSGLAH
VPGARIDTVSVTETHVNNAVWRNGPR

>fig|1297570.3.peg.3873 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [*Mesorhizobium* sp. STM 4661]

MFRITKEFHFSASHQLTSLPPDHQCARLHGHNYIVVVELSGGELDEHGFVRDYQDLASLKHYIDG
TFDHRHLNDVLGHDRVTAELARHFYDWCKVRLPQTSVAVRVSETPKTWAEFRP

>fig|1303518.3.peg.92 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Chthonomonas calidirosea T49]>fig|1303518.3.peg.92 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Chthonomonas calidirosea T49]

MLIMTRRLYFAAAHRDIQGSSELTGHTYTLDDVAVSGHINERTGLLVNIKELDRIVKEHVLNQIDGK
CLNDRLSFFQAHLATPENIATYIAGTVHPFLPSDIHLHSVRLQPTPVLYTEWLSSLKEVSHMLLTKI
YEFSASHRLHSDLSAEENRTLFGKCNNPNNGHGHNYELEVTCGPNPITGRVLPPERLDAVVERE
VLSRYDHRYLNLDVPEFAHVVPSEAEMIVKTIWERLRPCIPAPARLYRLRLYETPRNLFYSEEDDK
EQR

>fig|1308866.3.peg.1216 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Gracilibacillus halophilus YIM-C55.5]>fig|1308866.3.peg.1216 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Gracilibacillus halophilus YIM-C55.5]

MLYLSRRIDFSAMHHYRIDAWTEEQNRRIFGLCSNPNGHGHHDYQLEVMVRGQLNPDYGVVVNT
TDIKASVGEYVREELDGKYLNKEHPYFMKHVPTTEQLVTFWQGIEPKLTNCELYRLRLHENPYI
VAEKGDHEMVRRLTRKYHFSAHRLHSEQLSEQENQYFFGKCNNPYGHGHNYLEVTVCGEPDP
ITGMITDLAELDATVDQVILEKMDHKHLNLDVAEFRDVPNTSEVVAKVIYDMLSPYISNLDKVG
LWETEKNYFEYAGEEVDV

>fig|224911.5.peg.2435 Folate biosynthesis protein PTPS-III, catalyzes a reaction that bypasses dihydroneopterin aldolase (FolB) [Bradyrhizobium japonicum USDA 110]

MWELTKSFRFEAAHSLSGTTFGAASEEIHGHFSFRAEVTVRGTPDPETGMVVDLGLLQRAIEDVRL
TLDHKFLNKIEALGKPTLENLSRFVWERLQHIGKLTRVSIHRDSCNESCTYYGPQG

>fig|235909.3.peg.1842 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [Geobacillus kaustophilus HTA426]

MMHQLYPQVAHHYRYELNKDMHIAAAHFIPHEAAGSCANVHGHTYIVNVTVAGDELDESGFL
VNFQTLKQLVHRKLDHTLLNDHSDWFDGHDPNRFPPTSEVVARTIYETIQRYLDTLPHKPKCLQV
FVRETPTSYYVYRPAKAGER

>fig|235909.3.peg.319 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Geobacillus kaustophilus HTA426]>fig|235909.3.peg.319 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Geobacillus kaustophilus HTA426]

MTRRYFSSAHLHSDQLTNEENQRLFGKCNNRYGHGHNYCLEVTVIGKPDPITGMVVNLAEL
DEIVNREVLVKFDHKHLNLDTDEFKQINPTAENIVIVIWELLAPHLSSLYKIGLWETQKNYFEYFG
PHKEK

>fig|272844.1.peg.1490 Folate biosynthesis protein PTPS-III, catalyzes a reaction that bypasses dihydroneopterin aldolase (FolB) [Pyrococcus abyssi GE5]

MRARIIVRTSFDAAHAVKIGDDWESLHGHTFFLEVAVEGEIKRGYIMDFTELKIVDDIVKELNHR
NLNKIFDNPTTENVALWIAEKVEEKLPKVKLKRVLWEGKDNGVELEW

>fig|309798.4.peg.91 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I / Folate biosynthesis protein PTPS-III, catalyzes a reaction that bypasses dihydroneopterin aldolase (FolB) [Coprothermobacter proteolyticus DSM 5265]

MNVCVTKAFTFDAAHNLTNYKKGKCEALHGHTYRLEVTVCCTPNELENGLLMDFGDLKDLV NK
EVLSKLDHSYLNDHFEQPSTELVAMWVFETLKPHEKLGVLTSVKLFETATSWVEIKADASRGD

>fig|313612.3.peg.4950 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [Lyngbya sp. PCC 8106]

MTSNQEEIPKIKRAESNSETWMIGKEFRFEASHQLPNHDGKCARLHGHSWRGVIYVSGNKLIDA
GAKQGMIMDYEDIKKYLKPLDDYLDHYHLNETTGLNNPTSEAIKWYEQLEDKIPGLVAVRID
ETCTSQCVYSKGTSHVFL

>fig|316274.3.peg.132 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Herpetosiphon aurantiacus ATCC 23779]>fig|316274.3.peg.132 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Herpetosiphon aurantiacus ATCC 23779]

MPMDVFATRFRNFSASHRYWREEWSLEQNEAVFGKCTNRYGHGHNYELFVTVAGAVDPITGM
VMNMVELKRLVTMVLDQFDHKHLNEDTPYFREVIPTTENLVRVLWGLIEPQLPKGVRLAKRLRY
ENSDLYAEYFGRQQQATFNRRYEFSAHRLHAQSLTDEANREIYGKCNNPNGHGHNYQLEVT
DGLIDAQTGMVIDLVMDRRVQSVLDNWDHRHLDYQVAEFAEQPSTAENIVVVLWQRLEALF
GSQKHLRLWETANNVFDYPLSQH

>fig|324925.4.peg.1971 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Pelodictyon phaeoclathratiforme BU-1]>fig|324925.4.peg.1971 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Pelodictyon phaeoclathratiforme BU-1]

MNDLLRKPRKVYVSRKIEFNAAHRLFNPLFTEQENLELYGKCSNTFGHGHNYLLDVTISGIANQE
TGFLFDLKELEEEIARFDHKHLNHDVPELQECVPTTEVLAVLIWDILEKRLHNINRELH
EVTIYETGKNAVRYLGE

>fig|326427.3.peg.18 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Chloroflexus aggregans DSM 9485]>fig|326427.3.peg.18 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Chloroflexus aggregans DSM 9485]

MVVATRREFEFSAAHRYWRDDWSAAENERVFGPYTSPYGHGHNYTLDVSITGELDERTGMVMN
MTELKAIVNEVLEEFDHKHLNLDTPYFRDQIPTTENFVRVLWRLIAARIPAHARLAHLRLYEQPD
LWVDYDGVGETQFARLYTFAAAHRLHAPALSDEENLAIYGKCNNPNGHGHNYTLEVTVQGEID
PATGMLVDLAWLDQTVHSVIDLLHLHLDREIPAFERPSTAENIIVYLWNE LAPKLGRLALLR
LWETRKNIFS YAGPASIPA

>fig|411474.6.peg.495 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [Coproccoccus eutactus ATCC 27759]

MYKLKTKASFDSAHLKDYEGKCSNIHGHRTVEIEVGAETLEHDTQNRGMVVDNKKDLR
ELADHFDHSLIMETGSLKQATEDALLAENLRIVKVDFRPTAENFAKYIYDEMTSRGYNVIEASVYE
TPNNVASYCE

>fig|415426.7.peg.182 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [Hyperthermus butylicus DSM 5456]

MRAPMRHRPGSGRPGVMFLVKACTMFSAAHRIEGHPRCGKIHGHNYRVCIVVREERPLQVDL
DALEEWLERNVFQRFDHQYLNKVLAAPDKDEKLVTSEELAVLIADMLEQAFFGRVEYVEVCET
ENLCIEYRPPRRGGFR

>fig|420247.6.peg.1034 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [Methanobrevibacter smithii ATCC 35061]

MKIMINGIQSNLRFSSAHVIPGHESCGYIHGHSYFVDVEIEGERAGDFEFVVDVKAYTKAICN
ELDHRLIPVYNLDLIKDFNKKSDSIFDLKEEKTVHFVKIAGKGYSIPGEDCVFLPLPYSSAEELSKFF
AETLTKKLAEKYDNLEYVAVGVNEGIGQGAITYKKVLDD

>fig|452637.4.peg.1627 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Opitutus terrae PB90-1]>fig|452637.4.peg.1627 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Opitutus terrae PB90-1]

MLRGTVFITRQVHFNAAHRLYNPTKSQAWNTNQYGLCTSPNWHGHNYVLEVTVRGEPDPETG
YIVDLSELKRVLHETVVDRCDDRNLNDDVDFLRNVIPTTENLVIAFWQIEPALPAGKLHCVRLY
ETPRNFAEYFGPDAPARA

>fig|460265.11.peg.7288 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [Methylobacterium nodulans ORS 2060]

MKITQAFTFEAAHWLPNPETHRCRRMHGHSYRVELTLDGPVDPHTGWVVDYDVEHAFAPLL
AELDHHCLNDLPGLENPTAEHIAIWIWNRRARPALPALSSVKVFETPLSWAEYTG

>fig|467200.3.peg.1884 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [Streptomyces griseoflavus Tu4000]

MEIFREFTFEAAHRLPRVPEGHKCARLHGHSYKVTVHVEAPVDPEAGWVMDFGDIKQAFKPIDA
QLDHFYLN DIEGLENPTSENLARWIWDRMTAELPALSITVRETCTSGCTYRGE

>fig|484018.6.peg.2512 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I / Folate biosynthesis protein PTPS-III, catalyzes a reaction that bypasses dihydroneopterin aldolase (FolB) [Bacteroides plebeius DSM 17135]

MYTVIKRMEISASHKLKLSYESKCENLHGHNWIITVYCQAEQLNEDGMVVDFTHIKEVVKGQLD
HKNLNDVLPNPTAENIARWICERVPHCVKVEVCESEGNRVIYEK

>fig|485918.5.peg.3920 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Chitinophaga pinensis DSM 2588]>fig|485918.5.peg.3920 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Chitinophaga pinensis DSM 2588]

MIYLTRVENFNAAHKLSNPAWSKEKNEEVFGKCANENWHGHNYELHVTVKGTPDPETGFVFN
AKTLGVLIKDFIVEKIDHRNLNMDVDFMVGKFTSAENLAIGIWDQLTPHLPEGVELHCKLYETP
RIYVEYFGAK

>fig|536232.3.peg.1673 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [Clostridium botulinum A2 str. Kyoto]

MYTLKVEHNFD SAHFLAGYEGKCGNIHGHRWKVEIQVQAESLVQGGQLDGMIDFGDLKKDKVK
SMVDYYDHALIEKGTMRGQSLSSLKEDGFRIIEVNFRPTAENFAAFFYKIMKDRGYNVKSTTVYE
TPNNSATYEESGVI

>fig|536232.3.peg.879 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I / Folate biosynthesis protein PTPS-III, catalyzes a reaction that bypasses dihydroneopterin aldolase (FolB) [Clostridium botulinum A2 str. Kyoto]

MILIKKFKFDAAHNLIHYHGK CERLHGHTYGLVIKISGERDKEDMVIDFTELKAIVKENVLDILDH
AYINEIHKQPTAENIAVWIWNKLYTKLKRDNCSLYEIEVWETETSGVVYNG

>fig|579932.3.peg.4404 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [Streptomyces sp. FXJ7.023]

MEIFREFTFEAAHRLPNVPEGHKCARLHGHSYKVIVHVEAPVDPESGWVMDFGDLKKAFKPLEA
QLDHYYLNDIEGLENPTSEVLARWIWERLKPTLPDLSALT VRETCTSGCTYRGE

>fig|662475.4.peg.1371 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [Haloarcula californiae ATCC 33799]

MSQRLSKADNTLADAGERELVVGDRPLRISAGHRLHHDGKCSRPHGHNYEVTVRVTGELTD
EGWVVVDKGEITDVIDEWDHRFLLEAGDPLVEAFDASGDGDAVVVLDHPPTAEVMAAILEQRLA
DRLPETVSDVAVSVRETSELCVR

>fig|665937.3.peg.3439 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [Anaerostipes sp. 3_2_56FAA]

MYQLNTHASFDSAHLAGYEGKCRNLHGHRWKL SVTIQKEKVEEQGQTRGMVVDFGELKDKV
KEIADEFDHALIMEKAH

>fig|70601.1.peg.620 Folate biosynthesis protein PTPS-III, catalyzes a reaction that bypasses dihydroneopterin aldolase (FolB) [Pyrococcus horikoshii OT3]

MKSRIIVRTSFDAAHAVKVG DHWEDVHGHTFFLEVAIEGEIKNGYVMDFLELRKIVEEITKELDH
RNLNNIFENPTTENIALWIGERIRDKLPPYVKLKRVLWEGKDNGVELEW

>fig|746697.3.peg.2173 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Aequorivita sublithicola DSM 14238]>fig|746697.3.peg.2173 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Aequorivita sublithicola DSM 14238]

MNKIAIVRCEHFNAAHRLQNKNWSDEKNKAIFGKCNNPNYHGHNYELEVKVIGPCDPETGYVI
DTKILSDLIKQEILDRFDHKNLNLDTLEFKDLNPTAENIAITIYNLLRPAIEAKLELKIKLYETPRNY
VEYPH

>fig|755731.4.peg.3342 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [Clostridium sp. BNL1100]

MEQITITKEFTWDMAHMLAGHLGLCKNLHGHTYKMQVEICNKKDSVCERQDMVMDFKDLKDI
IKEKIIDSFDHSFAYWKGSDDPVEIQIADALTKNGRRVVPLDFRPTAEKMAIYFHELIKEDFESKGF
EIKKIKLWETPTSFAEYTSEKDD

>fig|857392.3.peg.196 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Marinilabilia sp. AK2]>fig|857392.3.peg.196 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Marinilabilia sp. AK2]

MKVSVYRKEHFNAAHRLHNPKWSFEKNQTVFGKCNNPNYHGHNYDLIVKLDGPIDPETGYVY
DMKVLSDLIKVHVLNKFHDHKNLNIDTDEFKNLNPTAENIAVVIWNILRKEIDLKFDLTIRLYETER
NFVEYSGD

>fig|945713.3.peg.1337 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Ignavibacterium album JCM 16511]>fig|945713.3.peg.1337 6-pyruvoyl tetrahydrobiopterin synthase (EC 4.2.3.12) [Ignavibacterium album JCM 16511]

MVYITRRETFAAAHRLFIPELSDEENLKIFGKCSHPNWHGHNYTLEVVIAGEINPETGFVLDIKKL
KEIIHKFVIDKVDHKNLNLDTFMKGLIPTSENICIAIWNQLKDKIPSGKLYSVKLYETENNYFEYR
GE

>fig|945713.3.peg.354 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [Ignavibacterium album JCM 16511]

MKIAKAFRWEMGHRLPEHFGLCKNIHGHSYKMIVEFEGELNKDQMVIDYYDVEKIINPIINQLD
HAFMVNTNDKIVLDFLEKMNSKKVVVDFDATAENICKFLLSEISKSNLPENINSVKVRVYETQFD
YAEDTLQLK

>fig|946235.3.peg.2633 6-carboxytetrahydropterin synthase (EC 4.1.2.50) @ Queuosine biosynthesis QueD, PTPS-I [Oceanobacillus sp. Ndiop]

MYGFTIVENLQKFDKDIKRHELKYHRERVLISKEFTFDDAAHHLHCYQGKCKNLHGHTYRAVFGI
SGYTDEIGILIDFSEIKSIWKEQIEIHLDHRYLNETLPKMNTTAENMVVWIYEKMNQVLINRPDDC
RLEFVKLYETPTSYAEVRREWMIHE



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