**Дополнительные материалы к статье Ошкина и соавторов «Анализ полной последовательности генома нового представителя рода**

***Methylococcus*, штамма Concept-8»**

**Таблица**. Гены основных метаболических путей *Methylococcus* sp. Concept-8 (представлены в том порядке, в котором они обсуждаются в статье).

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| **Номер** | **Координаты последовательности** | | **Функция** | **Кодируемая аминокислотная последовательность** |
| fig|243233.35.peg.  123 | 136830 | 135586 | Particulate methane monooxygenase B-subunit (EC 1.14.13.25) | MKTIKDRIAKWSAIGLLSAVAATSFYAPSASAHGEKSQAAFMRMRTIHWYDLSWSKE  KVKINETVEIKGKFHVFEGWPETVDEPDVAFLNVGMPGPVFIRKESYIGGQLVPRSVR LEIGKTYDFRVVLKARRPGDWHVHTMMNVQGGGPIIGPGKWITVEGSMSEFRNPITT LTGQTIDLETYNEGNTYFWHAFWYAIGVAWIAYWSRRPIFIPRLLMVDAGRGDELVS GTDRKVAMGFLAATILIVVMAMSSTNSKYPITIPLQAGTMRGMKPLELPAPTVSVKV EDATYRVPGRAMRMKLTITNHGNSPIRLGEFYTASVRFLDSDVYKDTTGYPEDLLAE DGLSVSDNSPIAPGETRTVDVTASDAAWEVYRLSDIIYDPDSRFAGLLFFFDATGNRQI VQVDAPLIPSFM |
| fig|243233.35.peg.  124 | 137671 | 136928 | Particulate methane monooxygenase A-subunit (EC 1.14.13.25) | MSAAQSAVRSHAEAVQVSRTIDWMALFVVFFVIVGSYHIHAMLTMGDWDFWSDWK DRRLWVTVTPIVLVTFPAAVQSYLWERFRLPWGATVCVLGLLLGEWINRYFNFWGW TYFPINFVFPASLVPGAIILDTVLMLSGSYLFTAIVGAMGWGLIFYPGNWPIIAPLHVPV EYNGMLMSVADIQGYNYVRTGTPEYIRMVEKGTLRTFGKDVAPVSAFFSAFMSILIYF MWHFIGRWFSNERFLQST |
| fig|243233.35.peg.  125 | 138602 | 137820 | Particulate methane monooxygenase C-subunit (EC 1.14.13.25) | MAATTLGGAAAAEAPLLDKKWLTFALAIYTVFYIWVRWYEGVYGWSAGLDSFAPEF ETYWMNFLYTEIVLEIVTASILWGYLWKTRDRNLAALTPREELRRNFTHLTWLVAYA WALYWGASYFTEQDGTWHQTIVRDTDFTPSHIIEFYLSYPIYIITGFAAFIYAKTRLPFF AKGISLPYLVLVVGPFMILPNVGLNEWGHTFWFMEELFVAPLHYGFVIFGWLALAVM GTLTQTFYSFAQGGLGQSLCEAVDEGLIAK |
| fig|243233.35.peg.  1332 | 1403648 | 1402404 | Particulate methane monooxygenase B-subunit (EC 1.14.13.25) | MKTIKDRIAKWSAIGLLSAVAATSFYAPSASAHGEKSQAAFMRMRTIHWYDLSWSKE KVKINETVEIKGKFHVFEGWPETVDEPDVAFLNVGMPGPVFIRKESYIGGQLVPRSVR LEIGKTYDFRVVLKARRPGDWHVHTMMNVQGGGPIIGPGKWITVEGSMSEFRNPITT LTGQTIDLETYNEGNTYFWHAFWYAIGVAWIAYWSRRPIFIPRLLMVDAGRGDELVS GTDRKVAMGFLAATILIVVMAMSSTNSKYPITIPLQAGTMRGMKPLELPAPTVSVKV EDATYRVPGRAMRMKLTITNHGNSPIRLGEFYTASVRFLDSDVYKDTTGYPEDLLAE DGLSVSDNSPIAPGETRTVDVTASDAAWEVYRLSDIIYDPDSRFAGLLFFFDATGNRQI VQIDAPLIPSFM |

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| fig|243233.35.peg.  1333 | 1404489 | 1403746 | Particulate methane monooxygenase A-subunit (EC 1.14.13.25) | MSAAQSAVRSHAEAVQVSRTIDWMALFVVFFVIVGSYHIHAMLTMGDWDFWSDWK DRRLWVTVTPIVLVTFPAAVQSYLWERFRLPWGATVCVLGLLLGEWINRYFNFWGW TYFPINFVFPASLVPGAIILDTVLMLSGSYLFTAIVGAMGWGLIFYPGNWPIIAPLHVPV EYNGMLMSVADIQGYNYVRTGTPEYIRMVEKGTLRTFGKDVAPVSAFFSAFMSILIYF MWHFIGRWFSNERFLQST |
| fig|243233.35.peg.  1334 | 1405420 | 1404638 | Particulate methane monooxygenase C-subunit (EC 1.14.13.25) | MAATTLGGAAAAEAPLLDKKWLTFALAIYTVFYMWVRWYEGVYGWSAGLDSFAPE FETYWMNFLYTEIVLEIVTASILWGYLWKTRDRNLAALTPREELRRNFTHLTWLVAY AWALYWGASYFTEQDGTWHQTIVRDTDFTPSHIIEFYLSYPIYIITGFAAFIYAKTRLPF FAKGISLPYLVLVVGPFMILPNVGLNEWGHTFWFMEELFVAPLHYGFVIFGWLALAV MGTLTQTFYSFAQGGLGQSLCEAVDEGLIAK |
| fig|243233.35.peg.  1112 | 1187468 | 1188229 | Particulate methane monooxygenase C-subunit (EC 1.14.13.25) | MATTTAGGLAAVDRPLLDKKWLVFAIGIYTVFYIWVRWYEGVYGWSAGLDSFAPEF ETYWMNFLYTEIVLEIVTASILWGYLWKTRDRNLAALTPREELRRNFTHLTWLVAYA WAIYWGASYFTEQDGTWHQTIVRDTDFTPSHIIEFYLSYPIYIITGFAAFIYAKTRLPFF AKGISLPYLVLVVGPFMILPNVGLNEWGHTFWFMEELFVAPLHYGFVIFGWLALAVM GTLTQTFYSFSHLFERELCPDIR |
| fig|243233.35.peg.  2925 | 2934665 | 2936248 | Methane monooxygenase component A alpha chain (EC 1.14.13.25) | MALSTATKAATDALAANRAPASVNAQEVHRWLQSFNWDFKNNRTKYATKYKMAN  ETKEQFKLIAKEYARMEAVKDERQFGSLQDALTRLNAGHRVHPKWNETMKVVSNFL EVGEYNAIAASGMLWDSAQAAEQKNGYLAQVLDEIRHTHQCAYVNYYFAKNGQDP AGHNDARRTRTIGPLWKGMKRVFSDGFISGDAVECSINLQLVGEACFTNPLIVAVTE WAAANGDEITPTVFLSIETDELRHMANGYQTVVSIANDPAAAKYLNTDLNNAFWTQ QKYFTPALGMLFEYGSKFKVEPWVKTWNRWVYEDWGGIWIGRLGKYGVESPRSLK DAKQDAYWAHHDLYLLAYALWPTGFFRLALPDQEEMEWFEANYPGWYDHYGKIY EEWRARGCEDPSSGFIPLMWFIENNHPIYIDRVSQVPFCPSLAKGASTLRVHEYNGQM HTFSDQWGERMWLAEPERYECQNIFEQYEGMELSEVIAELHGLRSDGKTLIAQPHVR GDKLWTLDDIKRLNCVFKNPVKAFN |
| fig|243233.35.peg.  2926 | 2936327 | 2937496 | Methane monooxygenase component A beta chain (EC 1.14.13.25) | MSMLGERRRGLTDPEMAAVILKALPEAPLDSNNKMGYFVTPRWKRLTEYEALTVYA QPNADWISGGLDWGDWTQKFHGGRPSWGNETTELRTVDWYKHRDPLRRWHAPYV KDKAEEWRYTDRFLQGYSADGQIRSMDPTWRDEFINRYWGAFLFNEYGLFNAHSQA SREALSDVIRVSITFWGFDKIDLAQMIQLERGFLAKIVPGFDESTAVPKAEWTTGGIYK GARLAVEALWQEVFDWNESAFSVHAVYDALFGQFVRREFFQRLAPKFGDNLTPFFIN QSQTYFQITKVGVHDLYYTTLGDDPEFGDYNRTVMRNWTGKWLEPTIAALRDFMGL FAKLPAGATDKEEIIASLYRVVDDWIEDYASRIDFKADRDQIVNAISAGLK |
| fig|243233.35.peg.  2927 | 2937508 | 2937933 | Methane monooxygenase regulatory protein B | MSVSSNAYDAGIMSLKGKEFADQFFAEENQVVHESDTVVLVLKKSDEINTFIEEILLT DYKKNVNPTVNVEDRAGYWWIKANGKIEVDCDELTELLGRPYNVYDFLVDVSSTIG RAYTLGNKFTITSELMGLDRKLEDYHE |

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| fig|243233.35.peg.  2928 | 2937944 | 2938447 | Methane monooxygenase component A gamma chain (EC 1.14.13.25) | MGIHSNDTRDAWVNKIAQLNTLEKAAEMLKQFRMDHTTPFRKSYELDNDYLWIEAR LEEKVAVLKARAFSETDFRHKTAFGEDAKAVLDGTVAKMNAAKDKWEAEKIHIGFR QAYKPPIMPVNYFLDGERQLGTRLMELRNLNYYDTPLEELRKQRGVRVVHLQAPH |
| fig|243233.35.peg.  2929 | 2938505 | 2938912 | Methane monooxygenase  component D (EC  1.14.13.25) | MPFRAGLPARNLWFSRGVPVPAPPSIFRKEITMVESVFQPFSGDADEGFEEPRPQTGFF  PSADWHLLKRDETYAAYAKDLDFMWRWVIVREERIVQEGCSISLESSIRAVTHVLNY FGMTEQRVPPEGGTGGVQH |
| fig|243233.35.peg.  2930 | 2938925 | 2939971 | Methane monooxygenase component C (EC  1.14.13.25) | MQRVHTITAVTEDGESLRFECRPDEDVITAALRQNIFLMSSCREGGCATCKALCSEGD  YDLKGCSVQALPPEEEEEGLVLLCRTYPKTDLEIELPYTHCRISYGEVGSFEAEVVGLN WVSSNTVQFLLQKRPDECGNRGVKFEPGQFMDLTIPGTDVSRSYSPANLPNPDGRLEF LIRVLPEGRFSDYLRNDARVGQVLSVKGPLGVFGLKEHGMAPRYFVAGGTGLAPVVS MVRQMREWTAPNETRLYFGVNTEPELFYLDELKSLEQSMRNLTVKACVWHPGADW DGRQGSPVDLLREDLEASGARPDIYLCGPPGMIDAACELARSRGVPGEQIFFEKFLPSG TA |
| fig|243233.35.peg.  2931 | 2939986 | 2940306 | hypothetical protein | MSAEQFPPQFLREMIEQLDASIQELTRKEKGLAASLGSGRVAELREYWDQVLSPEEE WELKQSMDFRDRELLWIWSRLRRARTSRANAGEAYMRHLSPVARINHKS |
| fig|243233.35.peg.  2932 | 2940327 | 2942006 | Heat shock protein 60 kDa family chaperone GroEL | MAKEVVYNGNARQRMMQGIEILARAVLPTLGASGPSVMIQHRAEGLPPISTRDGVTV ANSIVLKDSLANLGARLLRDVAGTMSREAGDGTTTAIVLARHIAREMFKSLSAGADP LALKRGIDRAVACVSGDIRGRARRGDQESVILGVAAVATKNEPGVGRLLLEALGAVG VHGAVAVELGQRHEDVLDVVDGYRWEKGYLSPYFVTDRTRELAELDDVYVLMTDR EVTDFIDLVPLLEAVTEAGGSLLIAADRVHDKALAGILLNHVRGVFKAVAVTAPGFG DKRPNRLLDLAALTGGRAILEAQGDRLDRVTPADLGRVRRAVVSADDTVLLGTPGT AASRARLEGLRREAEQYRALKPGQGSATGRLHELEEIEARIAGLSGKSAVYRVGGVT DVEMKERMVRIENAYRSVVSALEEGVLPGGGVGFLGSLPALAELEARDVDEARGIGI VRSALTEPLRVIGENSGLSGEAVVAKIMDHPNPGWGYDQESGRFCDLDAQGIWDAA KVLRLALEKAASVAGTFLTTEAVVLEIPDRDAFAGFSGEWAAATREDPRV |
| fig|243233.35.peg.  2933 | 2943874 | 2942039 | GGDEF/response regulator receiver domain protein | MHKPTLCDSLPTPSRTAAAILNLARREDVTAEALAQLIQTDPALTGRILRFANAPAHG TRRPIVSVIDAMSLLGLQAIRQFALSLSLIDAHREGRCEAFDYPVYWQKSLACAVALQ SITTRVPTVAPKEAFTLGLLADVGRLALATAWPLEYSECLRKADGEALIALERERFAT DHDELTRMLLTDWGFPQVFIDALEQNHRDDFRDDDRTGRFARQLALARRIAEYQLA EEPRRMTLSPVMQTEARRCGLDDEDLAQLLRGPQAEWLDWTRVIGLAEDDQTGDAE LSGRRPQVEERLHILLADDDPIMLIRLSRQLEAEGHHIASRRDGEAALAYAIEHEPEMV ITDWHMKPMNGLELCKALRESALGSNVYIIMLTANESEDALVEAFGAGIDDYVVKPP SVRVLKARIRAGQRILTLHKKLARERKEIERYSSELAAANRRLELMANTDQLTGLPNR RYAMDRLEQGWAQARMFGRPLSIIMLDLDWFKSINDSLGHDAGDQALVHAARVMR ESVRTSDVVCRMGGEEFLIITPDTDGPAAIQTAERVRSAIEQRQPQGLELPRPLTASIGV ADSTSAASLKDLLLKADSALYQVKQNGRNGVRYTST |

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| fig|243233.35.peg.  2934 | 2947474 | 2943956 | Two-component system sensor histidine kinase | MSEDLTALPAMRQRFLRSLGSICLIMILTEVIVMAVLEAIRHSRLELMPWQESALDGM LLAILSAPLLWIMALRPLARQIVTESQRNKELLEALDAHALISITDLQGRILYANDNFC AVSRYGREELVGQDHRFVNSGYHNKAYLRDMWRTISRGNIWQGEFCNRRKDGTRY WVDSTIVPLMDNTGRPRQYIAIGRDITAQKEAEAQIARLKQAMDASSDMILLTDRAG RIIYANPALCRFSGLAEQELLGQNPSILDSPLADQETLAAMQAALQAGQTWSGRLLYR RRTGPNPDDAQDYWAEISTTPIHTEGNTPVGYIQIQHDVSAKVERERALAMEQEDTA ARLRIAETLQQSGPLKERCRRVLATLFGLRTLDLQRKGGIFLKAENGHCLNLFVLEGK FSDEFVRREQTIPLGACLCGRSAVSGEILVSDDCFQDPRHEHRFEGMENHGHYIVPIAS GGDIQGVMFLYTDPNPARNEARMAMLRHVGEMLALAILEDRAEASLKAAHDAAVE ATQAKSAFLANMSHEIRTPMNGVLGMLELLKDTDMSREQWDLVETASNSAEALLEII NSILDFSKLEAGKVEIERTEFNLPDLVEEVCALLAGRAHDKGLELNCFLPADMPKLWI GDPTRIRQVLTNLLGNSIKFTENGEVSVKVMQAEASDGRTNLSFEIRDTGIGIAPEVQP RLFQPFTQADGSTARRFGGTGLGLSICRNLVELMGGSIGLESAPGQGSRFWFTLPLEQ VSTASAPPLPDFSHRRVLVVDDNATNRVILTHYLTHWGLKVDEADRGDTALSRLQTA LRESKPYDLVLLDLHMPHMTGYGLARAMNADPELKDIPRLLLSSGGLTGEAELRALG IARSLLKPVRQSLLFNAIADVLAARAQKQPPAVDKVEVALPAYTGRKVLVVEDNRVN QKVIVAMLGKFGIAPDVADNGQAALDLLARSRYDLVLMDCQMPVLGGYEATAELR ARELSAGSGRTPVVALTAHAATGEREKCLAAGMDDYLSKPVSRDRLAEALERWLGA PASMASAEIGQWAADDDGGHEPSGPSWNKEEALARLDYDEGLLGDMIALCIAELPQ HLNTLHAAAAAKDMAALADAAHAIKGMAGHFCAGRVRELAARLEDQARTMGSAP HPTLIRALETAAADLLADMRTGSSPVHPAKGG |
| fig|243233.35.peg.  2935 | 2947915 | 2949612 | sigma-54-dependent transcriptional regulator | MLSEQYLSSVSRPVEFPDWNRFSSVYVDRPDQAWEWMRQTGVLPAALDWVRPEVA EAWCRCFEDCRLPPGTDDWPCKAEPDAPAPSVSVELASVWERVRGVFDFLKGAQAA LIVADAHCRIFRVLDDGLRMAPVVREVLKTGADWREEVLGNNGIGSAAVLGTAVAF EGKEHYSARLHALVTAGCPLRNAAGETAAVVGLVSDQRGSSGALLAFLRMACNGLT APAAEQSRRTGDRPEVPAGFSPGEQGLIRDAAIEGLLDKALRLQERGIPLLVSGESGTG KEYLVRFAHRFGPRRKGPLVAVNCASIPKDLIESELFGYEAGSFTGARSRGKPGKFLL ADGGVLFLDEIGDMSFDLQATLLRVLETGEFVPVGGAKPLRVDVQVVAATNVDLQE AIRQGRFRRDLYYRLNGARLHLPPLRQRPDRCRIFQAVFEQEAAAAGASRIRLGEDV MALFERHPWPGNLRELRNVIRNALFVCSGGVLTVADLPTDFLEEAEQCAACAAPDGR EAAWSADALSLSKMESESIAAAICRCRGNMSQAARVLGIARSTLYKKISRYGLSA |

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| fig|243233.35.peg.  2400 | 2431985 | 2433790 | Methanol dehydrogenase large subunit protein (EC  1.1.2.7) | MHIRNLTSGFGGSVLAMGAMLTGQSAHANPELDRLSKDDRNWVMQTKDYSATHFS RLTEINSHNVKNLKVAWTLSTGTLHGHEGGPLVVDGIMYIHTPFPNNVYAVDLNDTR KILWQYKPKQNPAARAVACCDVVNRGLAYVPAGEHGPAKIFLNQLDGHIVALNAKT GEEIWKMENSDIAMGSTLTGAPFVVKDKVLVGSAGAELGVRGYVTAYNIKDGKQE WRAYATGPDEDLLLDSKFNEHNPHYGQFGLGLQTWEGDAWKIGGGTNWGWYAYD TKLDMIYYGSGNPAPWNETMRPGDNKWTMTIWGRDVDTGRAKFGYQKTPHDEWD YAGVNYMGLSEQEVDGKMTPLLTHPDRNGLVYTLNRETGALVNVFKIDDTVNWVK KVDLKTGLPIRDPEYSTRMDHNAKGICPSAMGYHNQGIESYDPDKKLFFMGVNHICM DWEPFMLPYRAGQFFVGATLNMYPGPKGMLGQVKAMNAVTGKMEWEVPEKFAV WGGTLATAGDLVFYGTLDGFIKARDTRTGELKWQFQLPSGVIGHPITYQHNGKQYIA IYSGVGGWPGVGLVFDLKDPTAGLGAVGAFKELAHYTQMGGSVFVFSL |
| fig|243233.35.peg.  2401 | 2433986 | 2434843 | MxaJ, protein involved in methanol oxidation | MRMNRIAAAGLIASLAVSGGVQAAKRAEPLKICAAENEMPYSNKAGEGFENTLADLI GKALGRPVENVWWSDARYFVRDFLDQGLCEVVIGVDTGDPRMLTSTPYYRSGYVFI YRKDKGERITDWNSDALKTAKRIAFMPDTPAETMIRKIGRYNDMFNYLHALVGFKSR RNQYVRYDPAQLVAEVAKGNAEVAVLWGPAAARYVKDAGLAMTVIPDDNVRSDG EKVPHHYSTSVGVRKGEEALLEQIDQVLAKHANEVKAVLETEGIPLLSMDEKPARMA QRSK |
| fig|243233.35.peg.  2402 | 2434882 | 2435334 | Cytochrome c-L precursor (Cytochrome c551I) (Cytochrome c552) | MAGLCVAGLLSLPALADITLRHAVTGETLDLSYAKAGGDTPAVKQFLQTGKNPYNG NKAVMEQGHSLYLSACSGCHGHEAEGKLGPGLADDYWTYPRAATDVGLFEILFGGA QGMMGPQYVNLNNDDMLKIMAWIRGIYKGDPAKAEWLK |
| fig|243233.35.peg.  2403 | 2435378 | 2435662 | Methanol dehydrogenase, small subunit (EC 1.1.2.7) | MMQKTSLAVAAAAALFALGAQAYDGTHCKAPGNCWEPKPGYPDKVAGSKYDPKH DPNELNKQAESIKAMEARNRKRVENYARTGKFVYKVEDIK |
| fig|243233.35.peg.  2404 | 2435843 | 2436862 | Methanol dehydrogenase regulatory protein MoxR | MNLDNPLADSLERAKCFEAGLRQVVLGQERPIRLLTLAVFARGHALLEGGVGVGKTT LLRAVARGIGGDYERIEGTIDLMPNDLVYYTYLDEQGRPGVAPGPLLKHGEQLSIFFF NEINRARPQVHSLLLRVMAERSVSAFNREFWFPHLQVFADRNRVEKEETFELPAAAR DRFMLEIAIEPPTDAAQMDPILFDPRFYDPDRLVESAPAETLSFRELNGIAEALQGGIH VSARLRAYVQDLWRATRRPEDFGIALHEADSGDMIEAGASPRGMSYLVRLARVQAW LSGRDRVEPEDVQYVFAPAIGHRIFLRPVYEYRRSELIPQLVGKLIRQIAAP |
| fig|243233.35.peg.  2405 | 2436859 | 2437701 | MxaS, protein involved in methanol oxidation | MTRKEFHYRLTWRADSVQPGAHPSRQGGGVHAFQRLVPFLAHPDPRRLHLRASLGD PSGHYWVRLHEQRGRITVHALADLSASMGYRGHASKMAVLADFTEGLALSSNRMG DAMGFVGLSDCSAPDFLLPPTRQVGAALMLAERLRRFRPRGGSARGLRHAVRYLPSR RGLVFLLSDFHFPLGFGKQIMASLAHHDVVPVVLWDPEESAPQASGLAWMQDLENG RERLMWLRPALRSRLSQRFQERRERLVAMLRGFGREPLFLSGGFDPDAVTRYFHAG |

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| fig|243233.35.peg.  2406 | 2437701 | 2438606 | MxaA protein | MLPVLRHSISLLLGLWCCLAPAAELPPGVRAFAFDTPRAFGYVIGDLIHHDVWIETET GQGMDAASLPREGWINRWLMLRRVAVRREGNRQTLQLEYQTFYAPLEVKNLTIPGF ELHVAGSGERLTVPDWTFTTAPIRELSVWRAEGLPPMRPDAVPARLPTEGLAAASAG FGLAAAGALAWWAYLSAWLPFAWRGRHFAAAWRELRRLRRQEDSRGALESGFSCL HQAFNRTLGEPLFIEGLDAFFRGHPAYAPLRNEIRDFFRASYEVFFGEGAPRPPFDLRR MEALARACQLAERRRP |
| fig|243233.35.peg.  2407 | 2438603 | 2439586 | MxaC, protein involved in Ca2+ insertion into methanol dehydrogenase | MTDWALDTPQWLWGLPLTLLPLWRLPLRPAPWSWLALLPADAASRAVDLSLRLAG  AGALLALLLGSAGLHRRAYTVERTGHGAHLVLLLDRSRSMDDSFAGRTPAGGEESKS AAAERLLSGFVSSGRNDLIGVAAFSTSPLFVLPLTDNKAAVLAAVHAMKLPGLAQTH VSKGLAMALSYFGDGPSAGSRIVLLVSDGAAEVDPDSELQLRRWFKEKGIRLYWIFL RTAGSHGIFETPDNPEDDNAQARPERHLHLFFASLGIPYRAYEAEDADALKHAIADID REEQRPLRYVERVPRRDLQAVCYLAAALALAWLIAAKGMEMSR |
| fig|243233.35.peg.  2408 | 2439583 | 2440146 | MxaK protein | MSGDWRVRIAAGLSLMLTLSALFGVREWRKAAAANADIAALLSGHDIALERWAVAS  PAVQLARAVYFVRHERYGDALELLNRLETRGDASFRADVYYNQGNLQLIQALDRVE TAEIDQARVYAELAKEAYRHALLLAPGHWDAKYNLEVAMRLMPEMDRVSSADDEP PRDESKRLWTNLPGFPRGLP |
| fig|243233.35.peg.  2409 | 2440143 | 2441135 | MxaL protein | MNIWRQRLTDPVFAGLVAALILTVAACFPLRLALERPVFRHIVVVDITRSMNVEDYR QGGRAVSRLAFVRQSLIRAAADLPCGSSLGLGVFTEREPALLFEPIETCAGFSAISAAIE QLDWRMAWAADSLIAAGLRNTLERLGRGNANVIFITDGHEAPPLNPRYRPDFSDIRG KVRGLIVGVGGLGLSPIPKYDASGRRSGFYTEDEVPQRSSFGLSELPPEQIEGYHARNA PFGSERAGGTEHLSQLKETYLRQLAEAAGLGYSRLESPEGLARALMVPALAHRQRVA TDVRWIPATLALAVLAAVYLRTLLPRLTFSTATREQGETS |
| fig|243233.35.peg.  2410 | 2441132 | 2441656 | MxaD protein | MKPILTLAALLFASASMAHGPTPQKVVETVEIAAPVDQVWNALKDFGAIAQWNPAL AKSESTGGNATGEKRILHFLNGEQLTEELDAYEPTTHEYTYRLSKENVKALPASSYSA VLKVTATEQGSQVEWKSRLYRGDTGNFPPDELNDEAAVAAMQKFFRIGLDNLKKSF ENGR |
| fig|243233.35.peg.  1107 | 1181164 | 1183023 | XoxF-МДГ | MKKPVKSWLIASSIASLLAVPGVSFANAEVEALTKDPKNFATWGGNYAGTRYSTLDQ  INFKNAKHLQPVWTFSTGMLRGHEGGPLVINDVIYIHTGYPHKVYALDQATQSVIWE YVYAPDKGTDQSQVISVMCCDVVNRGLAYGDGKIFLAQGDATLVALDAKTGKIVW KVKNGDPKTGMTATNAPLVVKDKVLTGISGGEFGVRGFLAAYNIKDGSLVWKKYS MGPDDEVGLDPEHTMTWTDGKMAPVGKDSSLKTWQGDQWKIGGGTTWGWYSYD PDLNLVYYGSGNPSTWNPVQRPGDNKWSMTIWARDVDTGEAKWVYQMTPHDEWD YDGINEMMLIDQEMTAKDGSKHSKLLTHFDRNGFGYTLDRVTGELLVAEKFDKAVN WATHVDMKTGRPQVNPKYSTQHGGVDVDTKGICPSAMGAKNEPPVTYSPRTKLIYIP GNHTCMNYEPFEVEYTAGQPYVGATLNIFPARANVKTGEKESSNHMGSFTAWDPTT GTIAWQFDEPFSLWSGMVSTAGDIVIYGTLEGYLKVRDAKTGEELYRFKTPSGIIGNV STWTYNGKQYIGVLSGIGGWAGVGMAAGLEGDTEGLGAVGAYKGLSSHTKLGGVF TVFTLP |

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| fig|243233.35.peg.  810 | 889169 | 888309 | Methylene tetrahydromethanopterin dehydrogenase (EC  1.5.99.9) | MKKLLFQFDTDLHPSVFDTIVGYDGGADQVIAHGRLTPDNVGPLVEGTIFTRAPKDK KNTAIFVGGSDLVAGQNLLRAVRKKFFADFRVSVMLDSNGSNTTAAAGVAKLASSG TLAGKKAVVLAGTGPVGQRVAVMLAKEGCSEVVITSRQLARAEHACAEMKARFGV DLVPVEAFDDDARAAAITNAQIVFATGAAGVQLLEERHWRDHPNLELLADANATPPL GLGGTDMMDRGTDRYGKIVWGAIGFGTLKLAVHRACIAKLFERNDQVFDAEEIFAL AKTMA |
| fig|243233.35.peg.  1243 | 1325499 | 1326101 | 5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2) | MTTPADIRTRIREWRRAQSPADVHRNSLLIAGHCIGSGWLDSAARIAAYLPNDGEVDT TALFKYLRERGRTAFLPILRQGMLWFGPCAGPAALHPNRYGIPEPPIDGETVTDAKEL DLVFVPLVAFDPRGHRLGMGGGYYDRTFAFRLDKPTPAAPRLIGLAFEGQKVERLEA QPWDVPLDAAVTEAGIYRFPGHPPTSL |
| fig|243233.35.peg.  1610 | 1645474 | 1644569 | Methylene tetrahydromethanopterin dehydrogenase (EC  1.5.99.9) | MEKRAILHMFDPMPHVSPFDINMAVDAGFDVIVPYGNVKAEEVHGLVQDAIFSRGPA GVKRTGIFIGGRDLAVALTMLETAKAAMVPPFEVSVLADPSGGFTTAAALVALVEKQ LKLKHGTELAGQRAVVFGGTGPVGIATGVIASLAGADVTLVDPFNVETALAKADEY NHRCGARLHGTFAGSEADKARLLSNADVVFCTAKAGVEVLNASVLADAKRLKVAG DVNAVPPLGIEGIKLKHNGEPLVHAVNSPGAVGVGALAVGNVKYQLQNHLLALLLQ SESPVFFDFRAAFERAREIV |
| fig|243233.35.peg.  1611 | 1646433 | 1645528 | Methylene tetrahydromethanopterin dehydrogenase (EC  1.5.99.9) | MEKPYILHMFTPEKNLSPFDANMALDAGWLSLVPYTNLELGEITALVQDAIFSRSLAG  VKRTAIFIGGRDVGTAMAMLRTAQKSMVPPFEISAFADPSGAFTTAAAMVAMAEGEL RKHHQTGLEGKSVLALGGTGPVGQIAAVLAARAGAKVKIIGRQLEKAQKVAELCNA EFGEGQTAIEGDADANKGELLKTADVVFATAAAGIQVLSAELLAASPQLKVAADVN AVPPSGIAGLGPHHKGAPIEGSPSGAIGIGALAIGNVKYQAQHRLLLRMRNTDKPVYL AFNEAFEIAREVVRGG |
| fig|243233.35.peg.  1341 | 1412929 | 1413924 | N(5),N(10)- methenyltetrahydromethan opterin cyclohydrolase  (EC 3.5.4.27) | MQNRVSVNAHSQPIVKYLITYADKLRLQIDRLPNGCTIIDAGIKVPGSLEAGRLIGEIC  MGGLGRVTLSHTDTFTKWPLTVNVHTSNPVIACLGSQYAGWSLSHGEGKDGFYALG SGPARAMATKIKDGNEEPVEELYKELNYRDKHTETTIVMEVDKIPPVELTDKIARSCK LDPSHLTVILTPTSSLAGGMQVVARVLEVALHKAHALHFPLENIIDGTGCAPVPPPHP NFIKAMGRTNDAILFGGRVHLFVKGSDEAAETLANELPSSVSRDYGKPFAEVFKEYK YDFFKVDAMLFSPASVIVTTVDSGRSFHAGEVDVELLERSFGG |
| fig|243233.35.peg.  1336 | 1407530 | 1406634 | Formylmethanofuran-- tetrahydromethanopterin N-formyltransferase (EC  2.3.1.101) | MIINGVHIDETFAEAFPMRATRVIITAQNHKWAHHAAQAMTGFATSVIACGCEAGIER  ELDPAETPDGRPGVAVLLFAMGGKGLAKQLETRAGQCVLTSPTSALFAGLDEGEQIP LGKNLRYFGDGFQISKRIAGKRYWRVPVMDGEFLCEETTGMIKAVGGGNFLILAESQ PQALAACEAAIEAMRRIPNVIMPFPGGVVRSGSKVGSKYKTLPASTNDAFCPTLKGQT RTELSPEIESVMEIVIDGLSDADIARAMRAGIEAACGLGAANGIRRISAGNYGGKLGPF LFHLREIMG |

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| fig|243233.35.peg.  1337 | 1409194 | 1407527 | Formylmethanofuran dehydrogenase subunit A (EC 1.2.99.5) | MLIKLTGGTVYDPANGINGQVRNLFIRDGRIVHSLNGATPDQEYDLRGKVVMAGAID MHTHIGGGKVTIARNLLPEDHRADPQPRRGLMRAGCGHAAPSTLTTGYRYAEMGYT AGFEPAVLPINARQAHMEMADVPLLDVGGYVMLGSDDFFLRLLSSGSDQQLINDYV AWTIHSAKAIGIKVVNPGGISAFKFNQRMLDLDEKHAYYGVTPRQILKSLARAVHEL GVPHPLHVHGCNLGVPGNVETTLNTISGIEGLPMHLTHIQFHSYGVEGDRKFSSGAAR IAEAINANKNITIDVGQILFGQTVTASGDSMRQHANAGHAHPDKWVCMDIECDAGCG VVPFKYRDKNFVNALQWCIGLETFLLVDDPWRVFLTTDHPNGAPFTTYPHLIRLLMD KSFRNDMLAAINPDAAALSTLGSIDREYSLYEIAILTRAGAARLLGLTDRGHLGAGAA ADITVYTEQADKEKMFTRPDYVFKDGELVVRNGEVVKVVWGNLHTVQPDFDRGIET RLRDYFDRYHTMKLDNFIINDWEIEGDGRSKILVHPCHQGARS |
| fig|243233.35.peg.  1338 | 1410495 | 1409224 | Formylmethanofuran dehydrogenase subunit B (EC 1.2.99.5) | MTDNTSAKVWESVPSPFCGIASDDLKIEVCGSSVRVLANGDAVTVPGFELAVTDTAP RIAGEPAALEDAVRQAAAILKDARLPVFSGFGTDVNDTRAALALIDKARGVFDQARA GGGVRNLLVLADSGWIATTLAEVKNRLEVLLVFGSDVEAAFPRFFERFVWNQETLFG QDPAKREVIYLGRAPSGDAAVSPDGRRPQVIECAPEYLPELAAVLSALARGASLQAK AVGGVPVGVLQGVVDRLRRSSYSVVTWVAGQLDFPHADLTVQQVCQTVTVLNKET RAAVLPLGGQDGDRTASQVCAWLTGYPTRVSFARGFPEYDPYLNDAARMLSEGEAD ALIWVSSLSAAPPPAAAVPTVVIGRSGMRFDKEPDVFIPVGVPGIDHAGHMYRCDNV VAMPLYPLRDCGLTSAAAVLTAIEQSL |
| fig|243233.35.peg.  1335 | 1406599 | 1405787 | Formylmethanofuran dehydrogenase subunit C (EC 1.2.99.5) | MTALSFTLKSPLRQRLDVSPLVPDLLLGKAPKEIAALDLQYGNRRIAAAELFDIEGDD  AESVRISGSPKLDFAGRGMARGSLIIEGDAGAYAGMHMKGGYLCVSGSTGLYAACEL KGGIVEICGNAGDLLGSALPGNKKGMSEGIVIVRGDAGDRVGDHMRRGSILIEGNAG MYLGARMTAGTIAVRGRVGACAGYAMRRGTLLLYGSPVAIGATFNDCGLHTLGFLP LLLKGYQGLNTCFSDPQARRLRVRRLAGDLSVQGKGEILLVA |
| fig|243233.35.peg.  2339 | 2371924 | 2371637 | hypothetical protein | MTEGKKRKVHSAEFKAKVGLEAARGMKTINEIGQRYEVHPVGGQAVEEGDSGARG DAIRRPARPQAAGARRGRSTVRGDWAAEEGTGRAQKKSGP |
| fig|243233.35.peg.  2340 | 2372863 | 2372285 | Transposase | MFVAIDRATRWLFIAVKPNKTAASAPAFLKALHKACPIKISKRLTDNGKDKVAGSDF  GPPRGSRRDEPLGGDEPCTDRPFGNRVRAPAGQHEFDQLGHALGMEHRLTPPRSPHP FAGSKGGPPSAGPPGEPQGRGGQTQGMVERFNGRIADILKTHPFDSALNLQQTLHRD VTLSTTTCPNPRSAARLRSKA |
| fig|243233.35.peg.  2341 | 2372999 | 2373502 | hypothetical protein | MEKARRIGLEGFGRRLFYGRQQVTATADPVTAQTAVPPGAGHRRGQTRRAAKLKLA GHGEPVIQGQREGFAQIHHKGFLRRGQRGLQALRRGRPVVERRARFPLADGGLRHGV PARQHPDGILTWGYLGSRCRGRAGWFMQSDLHGTDSLTSISHDGAKCAVNSARA |
| fig|243233.35.peg.  17 | 17922 | 18401 | NAD-dependent formate  dehydrogenase gamma subunit | MTQTEWDRDAVTEVIEQKKSMPGALLPILHGIQDRIGFIPEDAVPQIAKALNVSRAEV  HGVISFYHYFRITPPGKRTIHLCRAESCQAMNSDALEAHIKARLGIDYHETTADGAFSL EPVYCLGNCACSPSMMIDHEVHGRVTPQSFDAIIDELKEIAA |

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| fig|243233.35.peg.  18 | 18398 | 19948 | NAD-dependent formate dehydrogenase beta subunit | MTTVYVPRDSSALGLGAERVANAIQLEAARRGAAIKLVRNGSRGLYWLEPMVEVAT  PGGRVAYGPVQPDDVAGLFDAGFLEGKAHPLWQGATEEIPYLKNQERLTFARVGITD PVSLDEYLAHEGYRGLRNALAMEPAAIVEEVTASGLRGRGGAAFPTGIKWKTVLNTP AGQKYIVCNADEGDSGTFSDRMIMEGDPFVLIEGMTIAGLAVGATQGYIYLRVEYPH AEVALNQAIEAALQAGYLGDDILGSGKRFHLEVRLGAGAYVCGEETALLESLEGKRG MVRFKPPLPAIEGLFGQPTVINNVISLASVPIILDKGGSYYADYGMGRSRGTLPLQLAG NIKRPGLIEKAFGMTLRELLYDYGGGSASGRPIRAVQVGGPLGSYLPESQFDTPLDYE AFSAIWAVLGHGGVVVFDDTVDMAKMARYAMEFCAVESCGKCTPCRIGSTRGMEVI DRIIGDRDRAKNLALLRDLGDTMLAGSLCALGGMTPYPVLSALNHFPEDFGEKNVAQ VA |
| fig|243233.35.peg.  19 | 20006 | 22849 | NAD-dependent formate dehydrogenase alpha subunit | MALLQDKDFGTPPSASDKMVTLEIDGFTATVPEGTSVMRAAASIGIDIPKLCATDSLEP FGSCRLCVVQVEGGRGLPASCTTPVFEGMKVVTQNDRLAQVRRGIMELYISDHPLDC LTCSANGNCELQDMAGVVGLREVRYGYEGANHFDAKKDLSNPYFQFEPSKCIVCSR CVRACEQTQGTFALTIDGRGFESKISPGQNQAFMDSECVSCGACVQACPTATLIEKSV VEKGQADHSIITTCAYCGVGCSFKAEMKGSEVVRMVPDKNGQANHGHSCVKGRFAF GYATHPDRITSPMIRKSIHDPWQKVSWDEAINYAASEFKRIQAKYGKDSVGGLTSSRC TNEEAYLVQKLVRAAFGNNNVDTCARVCHSPTGYGLKQTLGESAGTQTFDSVMKSD VIMVIGANPTDGHPVFGSLMKKRVRQGAKLIVVDPRDIDLVRSPHIKADYHLKLKPG TNVAVVNALAHVIVTEGLVDEDFVNTRCEVESFNKWKDFVAQERNSPEAMESITGVP AQTLREAARLYASGGNAAIYYGLGVTEHSQGSTTVIGIANLAMATGNIGREGVGVNP LRGQNNVQGSCDMGSFPHELPGYRHVSDSTVRAQFEAAWNARLDPEPGLRIPNMFA AALEGSFKGLYCEGEDIAQSDPDTQHVFAALEAMECVVVQDLFLNETAKFAHVFLPG ASFLEKSGTFTNAERRISPVRRVMPPLAGYEDWQVTQMLANALGYPMNYSHASEILD EIASLVPTFSKVSFKRLDEVGSLQWPCNEEAPNGTPTMHVDHFVRGKGRFMLTEYVP TEERTSGKFPLILTTGRILSQYNVGAQTRRTANTAWHSEDRLEIHPHDAENRGIEDGD WVGIKSRQGETVLRAVVSERMQPGVVYTTFHFPESGANVITTDNSDWATNCPEYKV TAVQVTKVNAPSEWQRRFRRFTEEQLSYLEKATAG |
| fig|243233.35.peg.  20 | 22856 | 23746 | Sulfur carrier protein  FdhD | MAGPAGTVFDPVLRPGSAEGAPAAWTLEDGSRPSHSRVTVQRLRDGVVSVETDEVA EEVPVALVYNGVPHVVMLATPLDLEDFAIGFSLTEGIVRSPSEILAVRPHNRSEGIEVR LRITEDRFAGLPGKERNLTGRTGCGLCGSATLQQAVRHPPWVGVDTAVSMADLRRA QDELRARQDINSLTGAVHAAAWIVPGRGLVHLREDVGRHNALDKLIGVLAKTHTPR NEGFVLVTSRASYEMVQKCAEAGVGFLAAISAPTGLAIRLALETGLTLVGFVRGETC VVYSHAHRLLEH |
| fig|243233.35.peg.  21 | 23797 | 24030 | NAD-dependent formate  dehydrogenase delta subunit | MHSENLVKMANNISAFFQADPDHAAAVKGVVDHLHKFWEPRMRRQIIAHLQAGGE GLSPLAREAVTVLMNEQQKNAA |

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| fig|243233.35.peg.  1745 | 1787636 | 1786158 | Glucose-6-phosphate 1- dehydrogenase (EC  1.1.1.49) | MSQLPFPESFNMVFFGGAGDLVTRKLLPAMYQCHKNGLLVEAGRILCVDRQDLSEEA FLELAHEKARQFIPAAEWDAAVWAGFRQRLAYLRIDATQPEQYTPLKERLKKAPAA VTVFYLSTAPSLFATICAHLTRQGLNGPNSRVVLEKPLGHDLASANAITADVDRYFHE NQVYRIDHYLGKESVQNLMALRFGNALFEPLWRRMWIRDVQITIAEDVGIGSRAGFY DKTGALRDMVQNHLLQLLCFVAMEPPASLDSNAIRNEKLKVLESLVPFTEEDVHQKT VRGQYRAGVCGGKAVPGYLEEEGIAPGSHTETFVAIKAEIANWRWAGVPFYLFTGKR LPERLAEIVIHFHDVPHPIFPLPKSGACAPAKLVIRLQPDEFIRLYLYAKQPGDSMELQP VSLDLNFAEQFKVRRAEGGYERLLLDAIRGNQALFVRYDEQEQAWRWVEPILNTWA NDPKGPLPYAAGTWGPAASRDLLKRDGICWHEGK |
| fig|243233.35.peg.  1388 | 1456262 | 1454778 | Glucose-6-phosphate 1- dehydrogenase (EC  1.1.1.49) | MTLPQPPQALPCHFVIFGATGDLSALKLLPALYHLEAGGHLPAGMSIIALGRRPWSEA DWLRHLEGSIRQRMGEQFSARVYRRFAARFTYVAGDLHDPALYQTLSDRLCADQHC ADTVFYLSIKPSDFGAVIQRLDQAGLNRPRGLHRIVVEKPFGEDVDSARQLNRLLHDS FDEEQIYRIDHYLGKETVQNLLVFRFANTLIEPLWNRNYIDHVQISVAEQAGISTRADY YDKAGALRDMLQNHLLQLLTLVAMEPPPALEADALRDEKVKVLRSIRPIPEQAIHAH AFRAQYGPGSIDGAPVPGYQDEPGVAPHSVAETFVAAKFYVDNWRWRGVPFYLRTG KRLARQLSLIAIRFRHPPQQLFRETPLEFIEPNWVLLSLQPSESMHIELHSKQPGLGMDT RIIRLDASYRRGREKTLEAYETLLLDIMEGDRSLFLRFDEVEWAWRVVDPILRHWTRQ RDFIRAYPAGSWGPPEADRLFDKPEQSWRNQL |
| fig|243233.35.peg.  1965 | 2003610 | 2005091 | Glucose-6-phosphate 1- dehydrogenase (EC  1.1.1.49) | MSQLQLPKSFNLAFFGGTGDLVTRKLLPAMYQCDRNDLLVRDGRIYCLGRQDLTQS  AYLAKIEEKAREFVPKADWDDGLWSAFRSRLQYVRVDAGEPAEYVVLKEILEGNPA EVNVFFLSVAPSLFTTVCDNLARQGLNRPDCRVVLEKPLGHDLASSNAITDAVGKHF RENQIYRIDHYLGKESVQNLMALRFGNALFEPLWRREWISNVQITIAEEVGIGSRGGF YEGTGALRDMVQNHLLQLLCFIAMEPPVSLDSNAIRDEKLKVLESLVPFKDEDVLKK TVRGQYRAGKVRGDPVVAYTEEAGIPPDSKTETFVAIKAEIANWRWAGVPFYLFTGK RLPKRLAEIVINFRDVPHQIFPLAPGAAAVPAKLVIRLQPDEYIRLYLYGKQPGDTMEL RQVYLDLNFAGAFNDKTRRAEGYERLLMDIIRGNQSLFVRQDELEQAWRWVEPILK VWAADPAGLRLYAAGTWGPAASAELLSRDGFCWHDEE |
| fig|243233.35.peg.  2738 | 2757330 | 2758844 | Glucose-6-phosphate 1- dehydrogenase (EC  1.1.1.49) | MSVEIAPVHTGDSCIMVIFGATGDLTRRKLVPALYNLAKAGLLAKKFAVVGAAFDD  MDTEGFRRHLSEAIHEFAAVELDDALWSGLEERIFFSQGDFRDADYYRRLKELCERV RGELGIEDNYFYYLATAPMFFGEIVQQVGRAGLAQESAGHWRRVIIEKPFGHDLDSA RALNALIRQVLHEHQIYRIDHYLGKETVQNIMVFRFANSIFEPIWNRRYIDHVQITAAE TVGVERRGGYYDNAGCMRDMVPNHLFQLLSLTAMEPPISFEADAVRDEQTKVLRAI QAPTPEEVLSRMARGQYREGSVDGEPVPAYRSEPNVAPDSHTETFVALKLNLDNWR WAGVPFYLRTGKRMPKRVTEIAIQFRRAPLVLFRNTQIEQLQTNRLVIHLQPNEGISLQ FGAKEPGPVMKLGAVKMDFDYEDYFGASSSTGYERLLHDCMTGDATLFQRADMVE AGWSVIQPILDVWKALVPRSFPNYAAGTWGPKEADELMEEDGRHWANAV |

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| fig|243233.35.peg.  384 | 417870 | 416350 | 6-phosphogluconate dehydrogenase, decarboxylating (EC  1.1.1.44) | MMKNGNADVGLIGLAVMGQNMALNIADHGYTIAVYNRNYERTREFMAHCERAEPS  RGRILPSAELAEFVQAIARPRRIILLVKAGAGTDAVIGQLLPLLDRGDLIVDGGNAHWL DTIRRERELDAAGFRFIGSGVSGGEIGARFGPSLMPGGSAESWRLLEPVWQAIAAKVD PATGRPLEGAAPGRPVTGGEPCTALIGPNGAGHYVKMVHNGIEYIDMQLISESYWLL KHLGGLEAGAIASVFRDWNEGELSSYLIEITSDILQQKDPSGDGFLVDKVLDAAGQKG TGQWTAASALEQGVPANAIAEAVFARALSAMKEERVAASAILQGPEVQREANATHL VDAVRNALYCAKICAYAQGFQLMASAQKTYGWQLDFATIARIWRGGCIIRARFLQKI TDAYTRDAALSNLMLDPYFRDALHRGQDHWREIVMLAVRNGLPVPALSSALAYFDG YRSARLPANLLQAQRDYFGAHTYERTDRPRGRFFHLDWPAPDRPETETGT |
| fig|243233.35.peg.  2737 | 2756323 | 2757333 | 6-phosphogluconate dehydrogenase, decarboxylating (EC  1.1.1.44) | MRLGMIGVGRMGANMVRRLLRAGHECVVFDLDRAAVDVLAAEGAVGASTLEELA AALAPPRPVWLMLPAAVVDRVAEQLVGVLEAGDILIDGGNSYYVDDIRRAESLASRG LHYLDVGTSGGVWGLERGYCLMIGGEAGPVAHVEPVFQALAPGKGEIAETASRKDR RSTAEYGYLHCGPAGAGHFVKMVHNGIEYGLMAAYSEGFNILSRANVGKAGKAQD AETAPLRHPEHYRYDLPIADIAELWRRGSVVSSWLLDLTAEALGRDSELAKFGGRVS DSGEGRWTVATAIDQGTPAPVLSAALYQRFSSQGEDEFARKILSALRFVFGGHEEKA |
| fig|243233.35.peg.  1212 | 1292915 | 1291746 | D-arabino-3-hexulose 6- phosphate formaldehyde- lyase (EC 4.1.2.43)/6- phospho-3- hexuloisomerase (EC  5.3.1.27) | MARPLIQLALDSLDRNQTLELARLTAPYVDIFEIGTPCIKYNGIEIVRELKRRHPDRLIL  VDLKTMDAGEYEATPFYAAGADICTVLGVSGPATIAGVVKAAQAHNAEVQVDLINV PDKAACAREAARLGAQIIGVHTGLDAQAQGQTPFADLESIARLKLPVRISVAGGINQN TATRVAKAGADIVVVGAAIYGAPCPVTAARTIRELLEGAHHKFIVSKIGGVLAATDKS YEARLTGLLERARRIFVAGAGRSGLVGRFFAMRLMHGGYQAYIVGEVVTPSIRKGDL LIVISGSGETETMIAYTKKAKEQGASIALITTRDKSTIGDMADVVFRIGTPEQYGKVVG MPMGTTFELSTLVLLEATISHIIHAKKIPEEQMRTRHANLE |
| fig|243233.35.peg.  1646 | 1679821 | 1680810 | Transaldolase (EC 2.2.1.2) | MSKNLLDQLREVTIVVADTGDIEAIEKFKPRDATTNPSLITAAAQMPQYQDIVDDTLK  GARQTLGPGASAAQVANLAFDRLAVSFGLKILQIIEGRVSTEVDARLSYDTEGTIEKA REIIKQYEAAGVSKERVLIKIAATWEGIEAAAVLEKEGIHCNLTLLFGLHQAIACAENG ITLISPFVGRILDWYKKDTGRESYAPHEDPGVLSVTQIYNYYKKFGYKTEVMGASFRN IGEITELAGCDLLTIAPSLLAELQATEGELPRKLDPAKAKDYPIEKIHVNKYTFDKMHA ENRMATEKLEEGIQGFTKALEQLEKLLADRLVHLEAA |
| fig|243233.35.peg.  1645 | 1679024 | 1679557 | 6-phospho-3- hexuloisomerase (EC  5.3.1.27) | MHQKLIIDKISGILAATDAGYDAKLTAMLDQASRIFVAGAGRSGLVAKFFAMRLMHG GYDVFVVGEIVTPSIRKGDLLIVISGSGETETMLAFTKKAKEQGATIALISTRDSSSLGD LADTIFRIGSPELFGKVVGMPMGTVFELSTLLFLEATISHIIHEKGIPEEEMRTRHANLE |
| fig|243233.35.peg.  1651 | 1685672 | 1686205 | 6-phospho-3-  hexuloisomerase (EC  5.3.1.27) | MHQKLIIDKISGILAATDAGYDAKLTAMLDQASRIFVAGAGRSGLVAKFFAMRLMHG  GYDVFVVGEIVTPSIRKGDLLIVISGSGETETMLAFTKKAKEQGATIALISTRDSSSLGD LADTIFRIGSPELFGKVVGMPMGTVFELSTLLFLEATISHIIHEKGIPEEEMRTRHANLE |
| fig|243233.35.peg.  1650 | 1685011 | 1685658 | D-arabino-3-hexulose 6- phosphate formaldehyde- lyase (EC 4.1.2.43) | MARPLIQLALDTLDIPQTLKLASLTAPYIDIFEIGTPSIKYNGIALVKEFKKRFPNKLLLV DLKTMDAGEYEATPFFAAGADITTVLGVAGLATIKGVINAANKHNAEVQVDLINVPD KAACARESAKAGAQIVGIHTGLDAQAAGQTPFADLQAIAKLGLPVRISVAGGIKASTA QQVVKTGANIIVVGAAIYGAASPADAAREIYEQVVAAAA |

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| fig|243233.35.peg.  1644 | 1678363 | 1679010 | D-arabino-3-hexulose 6- phosphate formaldehyde- lyase (EC 4.1.2.43) | MARPLIQLALDTLDIPQTLKLASLTAPYIDIFEIGTPSIKYNGIALVKEFKKRFPNKLLLV  DLKTMDAGEYEATPFFAAGADITTVLGVAGLATIKGVINAANKHNAEVQVDLINVPD KAACARESAKAGAQIVGIHTGLDAQAAGQTPFADLQAIAKLGLPVRISVAGGIKASTA QQVVKTGANIIVVGAAIYGAASPADAAREIYEQVVAAAA |
| fig|243233.35.peg.  1648 | 1682992 | 1684056 | Fructose-bisphosphate aldolase class II (EC  4.1.2.13) | MALISLRQLLDHAAEHGYGLPAFNVNNMEQIKAIMEAAAAVDAPVILQGSAGARTY  AGEPFLRHLVLAAIEMYPHLPVCMHQDHGASPAVCIRSIQSGFSSVMMDGSLLEDMK TPASYAYNVETTRKVVEMAHACGVSVEGELGCLGSLETGRAGKEDGHGAEGELDPS LLLTDPDEAADFVRQTQVDALAIAIGTSHGAYKFTRKPTGQVLRIDRVKAIHQRIPTIH LVMHGSSSVPEDWAQMINDYGGDIGQTYGVPVEEIVEGIRHGVRKVNIDTDLRIASY GAMRKFMVEDRKNFDPRKLYKAAQTAMTAICRARYEAFGAAGQAAKIKPLRLEDM SLAYAQGKLDPIVR |
| fig|243233.35.peg.  1641 | 1676345 | 1677409 | Fructose-bisphosphate aldolase class II (EC  4.1.2.13) | MALISLRQLLDHAAEHGYGLPAFNVNNMEQIKAIMEAAAAVDAPVILQGSAGARTY AGEPFLRHLVLAAIEMYPHLPVCMHQDHGASPAVCIRSIQSGFSSVMMDGSLLEDMK TPASYAYNVETTRKVVEMAHACGVSVEGELGCLGSLETGRAGKEDGHGAEGELDPS LLLTDPDEAADFVRQTQVDALAIAIGTSHGAYKFTRKPTGQVLRIDRVKAIHQRIPTIH LVMHGSSSVPEDWAQMINDYGGDIGQTYGVPVEEIVEGIRHGVRKVNIDTDLRIASY GAMRKFMVEDRKNFDPRKLYKAAQTAMTAICRARYEAFGAAGQAAKIKPLRLEDM SLAYAQGKLDPIVR |
| fig|243233.35.peg.  1640 | 1674312 | 1676324 | Transketolase (EC 2.2.1.1) | MRTRRELANAIRALSMDAVQKANSGHPGAPMGMADIAEVLWNDYLRHNPANPKWP  DRDRFVLSNGHGSMLIYSLLHLTGYDLPIEELQNFRQLHSKTPGHPEYGYTPGVETTT GPLGQGITNAVGMALAERTLAGQFNRPGHAIVDHYTYVFLGDGCLMEGISHEACSLA GSMKLGKLIAFYDDNNISIDGEVRGHGGVPGWFMDDTPKRFEAYGWHVIPKVDGHD  PDAVKAAIEEARAVTDKPSLICCQTIIGWGSPNKQGKEDCHGAALGTDEVALTRENIG WPYPPFEIPADIYEAWDARETGAKAESQWNDRFENYRREFPELAAEFERRMAGELPR DWAEKSAAFVAQVNAKAETIASRKASQNALNGFGPLLPELMGGSADLAGSNLTLWS  GCKNVNAPPCDGNYVYYGVREFGMSAIMNGIALHGGFRPYGGTFLMFSEYARNALR  MSALMQIPVIYVYTHDSIGLGEDGPTHQPVEQTATLRLIPRMQVWRPCDAVESAVAW KCAIERKDGPSSLIFSRQNLPHMPRTPEQIAAIPRGGYVLVDCAGTPDLILLATGSEVEL AVKAAEALTAKGKQVRVVSMASTNVFDAQEQAYRDSVLPPAVTRRLAIEAGVSDG WWKYVGSHGKVIGLDRFGESAPAGLLFKTFGFTVDNVVAQAEALF |

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| fig|243233.35.peg.  1647 | 1680959 | 1682971 | Transketolase (EC 2.2.1.1) | MPSRRELANAIRALSMDAVQKANSGHPGAPMGMADIAEVLWNDYLRHNPANPKWP DRDRFVLSNGHGSMLIYSLLHLTGYDLPIEELQNFRQLHSKTPGHPEYGYTPGVETTT GPLGQGITNAVGMALAERTLAGQFNRPGHAIVDHYTYVFLGDGCLMEGISHEACSLA GSMKLGKLIAFYDDNNISIDGEVRGHGGVPGWFMDDTPKRFEAYGWHVIPKVDGHD PDAVKAAIEEARAVTDKPSLICCQTIIGWGSPNKQGKEDCHGAALGTDEVALTRENIG WPYPPFEIPADIYEAWDARETGAKAESQWNDRFENYRREFPELAAEFERRMAGELPR DWAEKSAAFVAQVNAKAETIASRKASQNALNGFGPLLPELMGGSADLAGSNLTLWS GCKNVNAPPCDGNYVYYGVREFGMSAIMNGIALHGGFRPYGGTFLMFSEYARNALR MSALMQIPVIYVYTHDSIGLGEDGPTHQPVEQTATLRLIPRMQVWRPCDAVESAVAW KCAIERKDGPSSLIFSRQNLPHMPRTPEQIAAIPRGGYVLVDCAGTPDLILLATGSEVEL AVKAAEALTAKGKQVRVVSMASTNVFDAQEQAYRDSVLPPAVTRRLAIEAGVSDG WWKYVGSHGKVIGLDRFGESAPAGLLFKTFGFTVDNVVAQAEALF |
| fig|243233.35.peg.  3 | 1965 | 1003 | D-glycerate 3-kinase (EC  2.7.1.31), plant type | MVADPSMLWPAWILPEDVFRSIWERVRPVFLASMGQQRIPFTLAEPLARVYLPLAAW VVAHKKDGPFVLGVNGAQGSGKSTLCEFLALILREGYGCKVAGFSLDDIYKTRSERE RLAREVHPLLVTRGVPGTHDVGLGLQTLDRLTTAGPEIAVALPAFDKSIDDRCPMSA WPQTSAPVDIVIFEGWCVGCLPQSGEHLVRPINALEAGEDADGSWRTYVNEQLGGPY AELFGRLDRLIMLKVPDMECVYQWRSLQERKLAAAIGNGSSGHRLMDETALRRFIM HYERLTRHMLAEMPARADVTLFLDENHGFARVHINE |
| fig|243233.35.peg.  4 | 2946 | 1975 | Glyoxylate reductase (EC  1.1.1.26) @ Hydroxypyruvate reductase (EC 1.1.1.81) | MSKPKILVTRRWPESCESRLRESFDVVFNTDDHPMSRDELKAALRDYDAVLPTVTDT  LDADVLGVEPLRCKILGNFGVGFNHIDIEAARRRGITVTNTPDVLTDCTADIAMLLML EVARRGGEGEREVRSGRWAGWRPTHMLGTKVTGKTLGLVGFGRIARAMAKKAHFG FDMPVIFYDPFPPPQDLIDALGAEQCGTLEEVLERADFVALHCPGSKENRHLINTERLA RMKPHAYLINTARGDVVDSEALIDALRNRRIRGAGLDVYEGEPRLNPGFLEFDNVVL FPHLGSATEETRVAMGMRVIDNIAAFFEGRPPRDKVA |
| fig|243233.35.peg.  5 | 4230 | 3043 | Serine--glyoxylate aminotransferase (EC  2.6.1.45) | MPGRNHLYVPGPTNIPDAVLSAMHVPMEDHRRPDFPSLVTPLLENLKKIFRTEAGQCF  IFPATGTAGWEIALSNTLSPGDKVLSYRFGQFSHLWIDLARRLGLEVEYEEVPWGQGV PLDRLEARLKADTAHEIKAVLICHNETATGVTNDLPAVRKAIDAAGHPALFYVDGVS SIGSLDFRMDEWGIDIGVAGSQKGFMLPAGLALVGFSQKALKARESAQCRRAFLDIN DHIIHNAGGFFPYTPSIPLLYGLRKSLELLLEEGLENVYARHARLAEGVRRAVAAWGL KLCAQDSKWYSNTVSAVVVPPEFDARDVIHTAYYRYNLSLGAGLSEVSGKVFRIGHL GDLNELSLASAIVGSEMAMRDVGIPVMPGSGIAAASTYWRETAPAIQPRI |
| fig|243233.35.peg.  194 | 206120 | 207082 | Malyl-CoA lyase (EC  4.1.3.24) | MAVKNRLHRSELAVPGSNPRMLEKAPEAGADLVFLDLEDAVAPDDKEQARRNIIFAL  NTYDWSKCAVSIRINGLDTHYAYRDLVEIVESCGDKLDTILIPKVGSASDVLFVATLLS QIEAYKGFKPINIHVLIETAMGMANVEEIARTCPERMEAMVFGVADYAASVRARTTNI GGANPDYGMLTDPDETGTRAYHWGDQWHFGISRMVAACRAYGLRPIDGPFGDFSDP AGFRAAARRAAALGCEGKWAIHPSQIPLCNEIFTPTEKEVTRAYRILEAMEQAAKEGK GAVSLDGRLIDAASIRMAENVVRQMKQIESRR |

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| fig|243233.35.peg.  195 | 207135 | 208304 | Malate--CoA ligase subunit beta (EC 6.2.1.9) | MNIHEYQAKELLKTYGVPVPNGAVAYSDAQAASVAEEIGGSRWVVKAQIHAGGRG KAGGVKVAHSIEEVRQYADAMLGSHLVTHQTGPGGSLVHRLWVEQASHIKKEYYLG FVIDRGSQRITLIASSEGGMEIEEVARETPEKIVKEVVDPAIGLLDFQCRKVATAIGLKG KLMPQAVRLMKAIYRCMRDKDALQAEINPLAIVGESDESLMVLDAKFNFDDNALYR QRVITEMRDLAEEDPKEVEASGHGLNYIALDGNIGCIVNGAGLAMASLDAITLHGGR PANFLDVGGGASPEKVTNACRIVLEDPNVRCILVNIFAGINRCDWIAKGLIQACDSLQI KVPLIVRLAGTNVDEGRKILAESGLSFITAENLDDAAAKAVAIVKG |
| fig|243233.35.peg.  196 | 208310 | 209212 | Malate--CoA ligase subunit alpha (EC 6.2.1.9) | MSVFVNKHSKVIFQGFTGEHATFHAKDAMRMGTQVVGGVTPGKGGTRHPDPELAH  LPVFDTVAEAVAATGADVSAIFVPPPFNADALMEAIDAGIRVAVTIADGIPVHDMIRL QRYRVGKDTIVIGPNTPGIITPGECKVGIMPSHIYKRGNVGIISRSGTLNYEATEQMAA LGLGITTSVGIGGDPINGTDFVTVLRAFEADPETEIVVMIGEIGGPQEVAAARWAKEN MTKPVIGFVAGLAAPTGRRMGHAGAIISSEADTAGAKMDAMEALGLYVARNPAQIG QTVLRAAQEHGIKF |
| fig|243233.35.peg.  1178 | 1249139 | 1250557 | Pyruvate carboxylase subunit A (EC 6.4.1.1) | MIKKILIANRGEIAVRIARACAEMGLRSVAIFSEADRFSLHVKKADEAYCIGSEDLAGY  LNPHRIVNLAIETGCDAIHPGYGFLSENPELARICTLRGVRFIGPDARVIRLMGDKTEA RRAMMQAGVPVTPGSAGNVENLDEALKEAERIGYPIMLKATSGGGGRGIRRCNDKK ELKANYERVISEATKAFGSADVFIEKCIVNPRHIEVQILADRHGNVAHLFERDCSIQRR NQKLIEIAPSPQLTPEQRACIGELAVRAARAVNYENAGTVEFLLTAQGEFYFMEMNTR IQVEHTITEEITGIDIVKEQICIAEGQPLSFTQEEVQPRGYAIQFRINVEDPKNDFLPSFGR LTRYYAPGGPGVRTDTAIYTGYEIPPHYDSMVAKVIVWGRTWAETVARGQRALNDM MIGGVRTTIPFYQEILDHPDFQAGRFDTGFLAAHPELTHYSLKRSPEETTLAIAAAIAA HVGF |
| fig|243233.35.peg.  1179 | 1250577 | 1252382 | Pyruvate carboxylase subunit B (biotin- containing) (EC 6.4.1.1) | MSKVYITDTILRDAHQSLIATRLRTEDMLPVCPQLDRIGFWSLEVWGGATFDACLRFL KEDPWERLCRLREALPNTRLQMLLRGQNLLGYRHYPDDVVREFVRLAAREGIDVFR VFDALNDIRNLKMALTAVKEQGKHAQGTICYTISPVHTTALYVKLASEMVDMGADSI AIKDMAGLLTPHATSELVRHLREHVDVPLFLHSHATAGLAEMCQLKAIEAGCRHIDT ALSAFAGGTSHPPTESMVAALRGTEHDTGLDLDALQEVSAYFAQVRRKYRQFESEFT GVDTRVQVNQVPGGMMSNLAKQLEEQGALNRIHEVFAEIPRVRRDLGYPPLVTPTSQ IVGTQAVLNVITGERYKTITNEVKRYLQGGYGQPPAPVDAELKRKAIGHEAVIEARPA DLLEPELDGLREEIGDLAGRDTDVMSFALFPEIARTFLEERREGRLNPEPLIPPSPIGTAP CGERFAPTEFKVSVHGETYDVHITGANIGDQRHRRFYITLDGVPQEIDLEVLSGYQRE PQAGQRPVPSKPGDVVTTMPGNIVDILVKPGDQVQAGDGVLVTEAMKMETQIQAPIA GTVTRIHVSKGERVNPNEVLLEIEP |
| fig|243233.35.peg.  2032 | 2074800 | 2074117 | Phosphoglycolate phosphatase (EC 3.1.3.18) | MIGFRPELVAFDLDGTLVDSAPDLAWAVDAMLESLGRAPVGLERARGWIGNGADML IKRAMTGEMWPESEPEDFREGMRLFLEFHEAHLCERGGLFPGVLEGLRDLKAADYAT AVITNKLARFAEPLLERLGVTEYLDFIGSGDLFERIKPDPLPLLKTAERFGVRPERCLM VGDSSNDVRAARAAGYAILCVPYGYRGEVATPEQLGADGILNSIGELPALLNRAT |

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| fig|243233.35.peg.  3306 | 3356060 | 3357622 | Glycolate dehydrogenase (EC 1.1.99.14), subunit GlcD | MATGRPGWMEATAHSDPVPLAGEGGQKNAAHCFTSGMERAAFLRELKRVLPAAAV  LSEPEDLRPFECDALSAYTVLPWLAVLPETVEQVRAVLRLCHSQSVPVVTRGAGTGL SGGALPVAEGVLLSLAKFNRILEVDPANRLARVQPGVRNLAISEAAAPFGLYYAPDPS SQVACTIGGNVAENSGGVHCLKYGLTVHNVLQVTLLTIEGELLTLGSLGLDGPGYDL LALINGSEGLLGVIVEVVVKLLPVPETARTVLAAFDSIEAASEAVAGVISAALVPAGLE MMDNLTLRATEAFVHAGYPVEAAAVVLCEMDGMVEQVEAEIARARTVLAGHGAVE VRESRDEAERRKFWAGRKAAFPAIGRIAPDYYCIDGTIPRKRLAEVLGRIGELSERYGL AVGNVFHAGDGNLHPLILYDASHPGELERAEALGEEILVLCVEVGGTVTGEHGVGIE KLNPMCVQFGTAELRRFHALKAAFDAGGLLNPGKAVPTLARCAEFGRVHVHGGRLR HPELERF |
| fig|243233.35.peg.  3307 | 3357631 | 3358692 | Glycolate dehydrogenase (EC 1.1.99.14), FAD- binding subunit GlcE | MRSLDDSENLAGRVAEACARGEPLRIQGGGSKDFYAGPCTGQPLSTRTHSGIVHYEPT  ELVLTARSGTPLTAIEAVLAESGQMLGFEPPHFGSDASWGGTVACGLSGPRRPWAGS LRDAVLGCRIVDGRGKVLSFGGQVMKNVAGFDVSRLMTGALGTLGLLLEISVKVLP KPECEITLSFECSHVESRERMIRWGGSGLPVTGLAWDGRLYLRLAGAEPAVSTAVRRI GGDRAEDAAGFWNGLREHAHDFFSGEADLWRLSLPPAADTGRLSGAWLIDWGGAQ RWLRTDADPDEVFAAAQAAGGHARLFRTLNPQAPRCAPLAPALAALHRRVRAVFDP AGILNRGLYPEAA |
| fig|243233.35.peg.  3308 | 3358693 | 3359901 | Glycolate dehydrogenase (EC 1.1.99.14), iron-sulfur subunit GlcF | MLTRLDEHFKDSREGQEAAAILQSCVHCGFCTAACPTYRLLGDERDGPRGRIYLIKA  MLEGEPATERTQSHLDRCLGCRACESACPSGVRYGRLADLARGIIEEQRSRPAMERLE RKLLRMFLPYPSRFAPWVGLARRLRPLLPAVLRNKLPPASGTPPWPPARHRRTMLAL GGCVQPVLAPSIDATAARVLDRFGISLIRVPASGCCGALSHHLGAHGEGLDFMRRNV DAWWPAIEAGAEAIVITASGCGVVVKEYGELLRDDPAYADKAARVSELARDLSEVV AAEDWTSLAPLATRRIAFQSPCTLQHGQHLDGVVEALLQRLGFELTPVADAALCCGS AGTYSLLQPELSSRLRDDKLRNLEAGEPEVIATANIGCLLQLASGTRRPVRHWVELLD RC |
| fig|243233.35.peg.  1217 | 1296761 | 1298182 | Ribulose bisphosphate carboxylase large chain (EC 4.1.1.39) | MAVKTYNAGVKEYRETYWDPNYTPADTDLLAVFKITPQPGVPREEAAAAVAAESST  GTWTTVWTDLLTDLDYYKGRAYRIEDVPGHDEQFYAFIAYPIDLFEEGSVVNVFTSL VGNVFGFKAVRGLRLEDVRFPIAYVKTCGGPPHGIQVERDIMNKYGRPLLGCTIKPKL GLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRQRFDFVMEAIEKAEAETGE RKGHYLNVTAPTPEEMYKRAEYAKEIGAPIIMHDFITGGFCANTGLANWCRDNGMLL HIHRAMHAVMDRNPNHGIHFRVFTKMLRLSGGDHLHTGTVVGKLEGDRQATLGWI DLLRDKFIKEDRSRGIFFDQDWGSMPGVFAVASGGIHVWHMPALLSIFGDDAVFQFG GGTLGHPWGNAAGAAANRVALEACVAARNEGRQLEKEGKEILTEAAKSSPELQAA METWKEIKFEFDTVDKLDVAHR |
| fig|243233.35.peg.  1218 | 1298208 | 1298564 | Ribulose bisphosphate  carboxylase small chain  (EC 4.1.1.39) | MSDMQDYKSSLSDSGSRKFETFSYLPPMDPAKIRRQVEYIVSRGWNPAIEHTEPENAF  DHYWYMWKLPMFGETDVDAILAEAEACHKAHPNHHVRLVGYDNFKQTQGAAMVI YRGPAV |

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| fig|243233.35.peg.  1220 | 1298806 | 1299612 | Rubisco activation protein  CbbQ | MTAQSADQYLIEEQPYYRPTGDEVALFEAAYAARMPVMLKGPTGCGKTRFVEYMA WKLKRPLITVACNEDMTASDLVGRFLLDATGTRWQDGPLTLAARIGAICYLDEVVEA RQDTTVVIHPLTDHRRTLPLDKKGELVHAHPDFQLVISYNPGYQNLLKDLKQSTKQR FGALDFGYPETAVEVDVVSHESGVDPKIAEKLVQIAHRARNLKGHGLDEGISTRLLV YAGHLIARGIDPRAACMMTLVRPLTDDPDMRDTLDAAVATFF |
| fig|243233.35.peg.  3029 | 3056843 | 3058105 | Pyrophosphate-dependent fructose 6-phosphate-1- kinase (EC 2.7.1.90) | MAARNAFYAQSGGVTAVINASACGVLETARQYPDRIGTVYAGRNGIVGALTEDLIDT  GQESAEAIAALRHTPSGAFGSCRYKLKGLEENRAQYERLIEVFRAHDIGYFFYNGGGD SADTCLKVSQLSEKLGYPLQAVHIPKTVDNDLPITDCCPGFGSVAKYIAVSVREATFD  VRSMAATSTCIFVLEVMGRHAGWIAAAGGLASDERHQLPLVILFPERVFDPERFLRAV DEKVRTRGYCSIVVSEGIKDADGRFVAESGSRDVFGHAQLGGVAPVVAALIKERLGY KYHWAVADYLQRAARHIASRTDVEQAYALGKAGVEMALKGRNAVMPAIVRTSDSP  YRWEIAAANLAEVANVEKKMPLEFISADGFGITEACRRYLQPLIEGEDYPPYVGGLPD  YVTLRNVAVPKKLAASFSV |
| fig|243233.35.peg.  1612 | 1649279 | 1646553 | Pyruvate,phosphate dikinase (EC 2.7.9.1) | MTMKKRVYAFSEGDGKNKRLLGGKGANLCEMTQIGLNVPPGFVITTEACLEYLADK  KLPVGLMDEVREHMARLEQATGKRFGDPGNPLLVSVRSGSALSMPGMMDTILNLGL NHDTLQGLIRQTGNERFGYDAYRRFIQLFGKVALGVPDELFDAEFEAVKHQAGVAA DIGLSAAHLADIGERFLAVVRRHTGKPFPEDVYEQLEIAIRAVFDSWMGKRAVDYRR EFHITPDQANGTAVNVVTMVFGNMGDDSATGVGFTRNPGTGENEMFGEYLVNAQG EDVVAGIRTPKPVHEMATEMPELYAQLVELRDKLEAHYHEVQDFEYTIEKGVLYCLQ TRNGKMNAQAMVRTSVEMCQEGLITRERALLRVNPAHLEQLLHPCLDTSHNPVPLA QGLPASPGAASGRCVFDADQAELLGRAGEKVILVREETKPEDIHGFFAAQGILTSRGG KTSHAAVVARGMGKACVAGAEGIRVDSRARLATVGDVTLHEGDIITIDGSTGNVYLG AIPTIAPTFSEHLRTLLSWADEAAHLKVKANADTPEAAKEAREFGAVGIGLCRTERMF NASDRLPVVVEMILAPDVEERKAALDKLLPMQRGDFQAIFALMAPYPVTVRLLDPPI HEFLPDEHFLADEIDALRQFRRVAKGRAAALSALGQAAEADGVGEDAVAAVIARKE RLLAKVRELHEINPMLGHRGVRLGITFPEIYEMQIRAVLEAAAECAKAGVATAPEIMV PQVVDGAELECVRAMVDRLRQEIEASHGVHLDFKFGSMVETVRACVTADGLARTAE FFSFGTNDLTQATWSFSREDAENKFLPQYIGSGILKDNPFEVLDVAGVGAMMRMAVE KGRSVRPDLEIGICGEHGGHPGSIRFCDGIGLSYVSCSAPRVPVARLAAAHAALMNGD |
| fig|243233.35.peg.  3024 | 3052984 | 3051299 | Glucose-6-phosphate isomerase (EC 5.3.1.9) | MSGSHQPARHYDKETMPQSTDLPAWRTLSEHYKTIAPRHMRDMFADDPGRFDAFSV RLGDLLFDYSKNRITRETVATLIRLAEEAGLREKIDAMFNGERINVTENRAVLHVALR NRSNRPILVDGKDVMPEVNRVLDRMRRFSQSVRTGEWRGATGKAITDVVNIGIGGSD LGPKMVVKALLPYADPRLRAHFVSNVDESDLVEILRPLNPETTLFVVASKTFTTQETM TNGRSARAWLLERIQDETAIARHFVAISTNRSKVVEFGIDPLNMFEFWDWVGGRYSL WSAIGLPIALSIGMDHFEELLEGAHFVDEHFRTAPFARNIPVLMGLLGIWYINFFGAQS HAVLPYDQYLEDLPTYLQQADMESNGKTIDIEGRPVTYSTGPVIFGQPGTNGQHAFY QLLHQGSVLVPCDFLAAAESHYPLAEHHDILISNFLAQTEALMRGRTTDEARQEIAAE NLPPDRLEALAAAKTFPGNKPTNSFLYRRLDPHTLGMLIALYEHKIFTQGVVWHINSF DQMGVELGKKLAKTILAELPGDAPVTSHDASTNGLICYLKSLR |

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| fig|243233.35.peg.  1745 | 1787636 | 1786158 | Glucose-6-phosphate 1- dehydrogenase (EC  1.1.1.49) | MSQLPFPESFNMVFFGGAGDLVTRKLLPAMYQCHKNGLLVEAGRILCVDRQDLSEEA  FLELAHEKARQFIPAAEWDAAVWAGFRQRLAYLRIDATQPEQYTPLKERLKKAPAA VTVFYLSTAPSLFATICAHLTRQGLNGPNSRVVLEKPLGHDLASANAITADVDRYFHE NQVYRIDHYLGKESVQNLMALRFGNALFEPLWRRMWIRDVQITIAEDVGIGSRAGFY DKTGALRDMVQNHLLQLLCFVAMEPPASLDSNAIRNEKLKVLESLVPFTEEDVHQKT VRGQYRAGVCGGKAVPGYLEEEGIAPGSHTETFVAIKAEIANWRWAGVPFYLFTGKR LPERLAEIVIHFHDVPHPIFPLPKSGACAPAKLVIRLQPDEFIRLYLYAKQPGDSMELQP VSLDLNFAEQFKVRRAEGGYERLLLDAIRGNQALFVRYDEQEQAWRWVEPILNTWA NDPKGPLPYAAGTWGPAASRDLLKRDGICWHEGK |
| fig|243233.35.peg.  1388 | 1456262 | 1454778 | Glucose-6-phosphate 1- dehydrogenase (EC  1.1.1.49) | MTLPQPPQALPCHFVIFGATGDLSALKLLPALYHLEAGGHLPAGMSIIALGRRPWSEA  DWLRHLEGSIRQRMGEQFSARVYRRFAARFTYVAGDLHDPALYQTLSDRLCADQHC ADTVFYLSIKPSDFGAVIQRLDQAGLNRPRGLHRIVVEKPFGEDVDSARQLNRLLHDS FDEEQIYRIDHYLGKETVQNLLVFRFANTLIEPLWNRNYIDHVQISVAEQAGISTRADY YDKAGALRDMLQNHLLQLLTLVAMEPPPALEADALRDEKVKVLRSIRPIPEQAIHAH AFRAQYGPGSIDGAPVPGYQDEPGVAPHSVAETFVAAKFYVDNWRWRGVPFYLRTG  KRLARQLSLIAIRFRHPPQQLFRETPLEFIEPNWVLLSLQPSESMHIELHSKQPGLGMDT  RIIRLDASYRRGREKTLEAYETLLLDIMEGDRSLFLRFDEVEWAWRVVDPILRHWTRQ RDFIRAYPAGSWGPPEADRLFDKPEQSWRNQL |
| fig|243233.35.peg.  1965 | 2003610 | 2005091 | Glucose-6-phosphate 1- dehydrogenase (EC  1.1.1.49) | MSQLQLPKSFNLAFFGGTGDLVTRKLLPAMYQCDRNDLLVRDGRIYCLGRQDLTQS  AYLAKIEEKAREFVPKADWDDGLWSAFRSRLQYVRVDAGEPAEYVVLKEILEGNPA EVNVFFLSVAPSLFTTVCDNLARQGLNRPDCRVVLEKPLGHDLASSNAITDAVGKHF RENQIYRIDHYLGKESVQNLMALRFGNALFEPLWRREWISNVQITIAEEVGIGSRGGF YEGTGALRDMVQNHLLQLLCFIAMEPPVSLDSNAIRDEKLKVLESLVPFKDEDVLKK TVRGQYRAGKVRGDPVVAYTEEAGIPPDSKTETFVAIKAEIANWRWAGVPFYLFTGK RLPKRLAEIVINFRDVPHQIFPLAPGAAAVPAKLVIRLQPDEYIRLYLYGKQPGDTMEL RQVYLDLNFAGAFNDKTRRAEGYERLLMDIIRGNQSLFVRQDELEQAWRWVEPILK VWAADPAGLRLYAAGTWGPAASAELLSRDGFCWHDEE |
| fig|243233.35.peg.  2738 | 2757330 | 2758844 | Glucose-6-phosphate 1- dehydrogenase (EC  1.1.1.49) | MSVEIAPVHTGDSCIMVIFGATGDLTRRKLVPALYNLAKAGLLAKKFAVVGAAFDD  MDTEGFRRHLSEAIHEFAAVELDDALWSGLEERIFFSQGDFRDADYYRRLKELCERV RGELGIEDNYFYYLATAPMFFGEIVQQVGRAGLAQESAGHWRRVIIEKPFGHDLDSA RALNALIRQVLHEHQIYRIDHYLGKETVQNIMVFRFANSIFEPIWNRRYIDHVQITAAE TVGVERRGGYYDNAGCMRDMVPNHLFQLLSLTAMEPPISFEADAVRDEQTKVLRAI QAPTPEEVLSRMARGQYREGSVDGEPVPAYRSEPNVAPDSHTETFVALKLNLDNWR WAGVPFYLRTGKRMPKRVTEIAIQFRRAPLVLFRNTQIEQLQTNRLVIHLQPNEGISLQ FGAKEPGPVMKLGAVKMDFDYEDYFGASSSTGYERLLHDCMTGDATLFQRADMVE AGWSVIQPILDVWKALVPRSFPNYAAGTWGPKEADELMEEDGRHWANAV |

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| fig|243233.35.peg.  1744 | 1786156 | 1785449 | 6- phosphogluconolactonase (EC 3.1.1.31), eukaryotic type | MTEIRWFDDNASLAPALAAAVAEDLRAALATAPAATLAVSGGRSPVPVFEALREADL DWARVVVTLVDERWVPETDPASNAALVKTHLLQGKASAARFLPLYTGDASAAAGE ASLAEAFAELPRPFAALILGMGDDGHTASLFPASPNLEAGLALGGTVENTPPCLAQVG AVAPTERISLTLPWILDARHIYLQFGGPSKVEVFNAAQAGPNRQYPVSFVLAQTQTPV TVFAARS |
| fig|243233.35.peg.  1387 | 1454766 | 1454059 | 6- phosphogluconolactonase (EC 3.1.1.31), eukaryotic type | MYPRQQKRWHIYPTATDFENRVVRGILRMAWEAIAIRGVFHIVLAGGKTPEPIYRRLA  AAREEAEWRQWHVYWGDEFCLPTDDPGRNSAIARRVWLDHGPIPATQIHPIPAERGP QTGAEAYAEVIAGVEEFDLVLLGLGTDGHTAALFPGRDWGAGPASPDVLAVTDAPG PCAERVSLSAARLSRSREVIFLATGFGKFSAVQRWRCGEPLPAAAITPACGVDICVTLD AFDFA |
| fig|243233.35.peg.  1748 | 1789973 | 1791802 | Phosphogluconate dehydratase (EC 4.2.1.12) | MFLHHTLVDVTDRIRARSHDRRAAYLDLMHRARQKGVERSHIACTNVAHAYAATPA  NDKLVLKAAAVPNLGIVTAYNDMLSAHQPYEHYPEIIKAEARKAGVTAQVAGGVPA MCDGVTQGQTGMELSLFSRDVIALSTAVALSHHVFDANLYLGVCDKIVPGLLIAALR FGHLPGVFVPAGPMVSGISNSEKAKVRQQFAEGKVGRDALLESEMASYHSAGTCTFY GTANSNQMLLEIMGLQLPGSSFVNPGTPLRDALTRAATRVAADLAQDATAPALCHIV DERVIVNAIVGLLATGGSTNHTIHLVAIARAAGIEVNWDDFNDLSAVVPLLARVYPN GKADVNHFHAAGGMGFLVRELLDAGLLHEDVQTILGPGLRRWAEEPWLDNGTLAW RDAPEKSHDPEVLAPASEPFSPDGGLRLVTGNIGRGVIKVSAVAPENRVVRAPAIVFES QDELIAAFKRGELERDFVAVLRFQGPRANGMPELHQLTPALASLQDRGFKVALITDG RMSGASGKVPAAIHISPEAAMGGPLTLLRTGDTILLDAVRGKLEAEVPADRWSLREP VTDDLSGNQFGCGRELFSGFRHLADTPERGAFTFNFDDGVR |
| fig|243233.35.peg.  1749 | 1791834 | 1792457 | 4-hydroxy-2-oxoglutarate  aldolase (EC 4.1.3.16) @  2-dehydro-3- deoxyphosphogluconate aldolase (EC 4.1.2.14) | MNLDQIIEATSVMPVMVVDRPEDAVPLARALVEGGIRVLEITLRTAAGLDAVKAIRQ EVPDAIVGVGTIAAPAQLEASIAAGAQFGVSPGTTPTLLKAIVDSRLPFFPGVATTSEV MQVLEGGLTVMKFFPAVAAGGVKMLESFRGPFPQVRFCPTGGINARNAPDFFKLPNV VCVGGSWLTPKDLVAAGNWAEITRLAREAAALKP |
| fig|243233.35.peg.  3117 | 3147992 | 3145557 | Xylulose-5-phosphate phosphoketolase (EC  4.1.2.9) @ Fructose-6- phosphate phosphoketolase (EC  4.1.2.22) | METQPPFSSEFERLTVYGPTRATVGGTPLDAEEARKIHAFWRACNYLALGMIYLRGN  PLLREPLKPEHIKNRLLGHWGSSPGLAFVYTHMNRAIRKHDLNMIFMAGPGHGAPGV LGPLYLEGSYTEIYPDKDLSEEGLLNFFKQFSFPGGIGSHCTPETPGSIHEGGELGYVLS HACGAAFDNPDLIVAAVVGDGEAETGPLATSWHINKFLNPIRDGAVLPILNLNGYKIN NPTLLARISHDELENLLKGYGYTPYFVEGSEPESMHQAMAATVDRCVEDIHAAQTEA RASGLARRPRWPMIVLRSPKGWTAPRQIDGRHVEGFWRAHQVPVADVAKNPEHLKL LENWMRSYKPEELFDAEGRPIPEIREMAPAGLRRMGLNPHANGGLLKKALRIPNFRN YAIEVAKPGQIEAPNTQPLGVFLRDVMKENMHNFRIFGPDENTSNKLDAVYTAAKKF WIAEYFPEDQDGSELAPDGRVMEMLSEHTLEGMLEGYLLTGRHGFLSTYEAFVHVID SMFNQHAKWLSICNNLSWRQDVASLNLLITSTVWRQDHNGFTHQDPGFLDLVVNKS AEVTRIYLPPDVNSLLSVADHCLRSQNYINVIVSDKQLHLQFMDMDAAIAHCTEGLGI WEWASNDEGQEPDVVMACAGDIPTLEALAATAMLREEFPELKIRFINVVDLFKLQPE SEHPHGLSDKDFDSLFTKDKPIIFNFHGYPWLIHRLAYRRTNHVNMHVRGYKEKGNI |

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|  |  |  |  | NTPLELAINNQIDRFSLAIDVIDRIPEIAVSGAHAKARFRKQQIACRQYAYEHGIDMPE  VAAWRWPG |
| fig|243233.35.peg.  3115 | 3145182 | 3143998 | Acetate kinase (EC  2.7.2.1) | MDGPVAVVNGGSSTVKFSLLNGEQRLLSALLDRLGDKPGNGACAHLRDAAGTVLFQ  GPIPAQTHEEALDWLFAWLQRNDGGFEPAAVGHRVVHGGDRLIRPVRVTDEVIGQIE ALIPLAPLHQPHNLAPIRLLATKFPDLPQVACFDTAFHATQSAIEKRFALPREYEAAGI RRYGFHGLSYEYIASRLAEIDPVAAAGRTIVCHLGNGASLCAMRAGRSVATTMSFTA LDGIPMGTRCGAIDPGVLLHLMDQPGMDTRTLSDLLYKRSGLLGLSGLSGDMRDLLA SARPEAAEAVEYFCYRIAREIGSLSAALGGLDALVFTAGIGEHAASVRARICELSAWL GVAIDPAANRVLHTPESRIHVLVVPTNEEAMIARHVRRTLALPPGSPRPL |
| fig|243233.35.peg.  3288 | 3332667 | 3334775 | BioD-like N-terminal domain / Phosphate acetyltransferase (EC  2.3.1.8) | MSHAFYVTATEADAGKALVVLGATEFALRKTTRVGFFRPVIPEADGPDEDIRLVLDH  FALPQRYEDSYALTYREAQTLLSENRADELLERIIAAYKKLEAGCDVIVCMGTDYLGE MASLEFELNGEIARNLGAPVLMIAGAQGKTLDEAVHPLAIAVDACRERGGRVAGVFL NKADPADLAAYRQALVGHFGDKVGLKAVIPFDARLGSPTVREIADRLGAEILSGGER LDGLVSGYLVAAMQLQHALTWLQEGQLVITPGDRGDIIIGMLQADRSVRYPSLAGLL LSGGQRPEPSILDLIEGSSDSLPILAVATDTYTTATRALQVKSKLRAGDRGKIERSITAF NDHVDAESLESQVRNLRFDGLTPRMFTYNLMQRAKADKRHIVLPEPTDSRVLRASAF LLERDAVRLTLLGSRQEVENALRRHAIVLDPAVLDIVDPATDARRESYAETYFQLRRH KGMTLDAARDCLLDVSYFGTMMVYRGDADGMVSGAIHTTQHTVLPALQIIKTRPGC SIVSSVFFMCLDSGVVVYGDCAVNPNPNAEQLAEIAISSADTAKAFGIEPRVALLSYSS GDSGHGEDVERVREATRIARQRRPDLLLEGPIQYDAAADAGVAAQKMPGSPVAGRA TVFVFPDLNTGNNTYKAVQRETGALAIGPILQGLAKPVNDLSRGCTVADIVNTVVITA IQAQGATAAEER |
| fig|243233.35.peg.  478 | 511822 | 513756 | Acetyl-CoA synthetase  (EC 6.2.1.1) | MKTEHVYPVPADIAASTRITEEVYREMYDRSVKDPEGFWAELAQEFVSWNAPWQRV  GRWNFDTPAIEWFSGARLNVSYNCLDRHLADRGAQTAILWEGDQPGDQRRLTYGEL HDRVCRFANVLKSHGVGKGDRVCIYLPMIPEAAVAMLACARIGAIHSIVFGGFSSEAL KDRILDADCRLVVCADEGRRGGKFVPLKHNVDAALSQCPLVETVLVVRHTARPVDW TEGRDRWFHEAVESASPDCPPEDMEAEDPLFILYTSGSTGKPKGVVHTTGGYLLFAA VTHKYVFDYRDGEVYWCTADIGWITGHSYVVYGPLCNGATTLMFEGVPTYPTPARL WQIIDKYQVSIFYTAPTVIRALMGLGTDWVKQADRHSLRILGSVGEPINPEAWEWYY QEVGEKRCPVLDTWWQTETGGIMITPLPGATPLKPGSATRPFFGVVPVILDAQGNELT GPAEGVLAIAASWPGQARTVFRNHDRFRETYFALYPGKYFTGDGARRDADGYYWIT GRVDDVINVSGHRLGTAEIESALTLHDSVAEAAVVGYPHNIKGQGIYAFVTLVADAT PSEDLKRELIERVREEIGAIATPDIIQWTPALPKTRSGKIMRRILRKIAANDLDQLGDTS TLADPAVVEDIIRGKPA |
| fig|243233.35.peg.  3328 | 3380493 | 3381098 | ADP-ribose pyrophosphatase (EC  3.6.1.13) | MMTREFKVLREEQLHGGFFTLLRLRLRHTLHGGGWSEVLTRELYHRSSCVAVIPYDP VADRVVLIEQFRVGPLKSGENPWLLEIVAGAVEPGEQPDEVAHRETMEEAGSRILELI PVSEFFTTPGGCSESIVLYCGIVDSSGLGGIHGLADEHEDILVSVVDFAEAMVLLGEGR IRSAIPIIGLQWLALNRERLRMRYGPA |

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| fig|243233.35.peg.  3329 | 3382598 | 3381117 | Glycogen synthase, ADP- glucose transglucosylase (EC 2.4.1.21) | MKVLFISSEVFPLMKTGGLADVSGSLPAALSALGHDVRILMPAYPEAIAAAETPKQLS LRQAGSQLTLLSTRLPGTAVPLWLLDAPASFGRFGNPYLAPNGAPWPDNAERFALLA RVAVDLTQDRLGLGWKPDVVHCNDWQTGLIPPLLSDEPSRPAVLFTVHNLAYQGLFP YETFQRLALPPRLWKMEALEFYGQLSFIKGGLVFADRINTVSPSYAEEIQTPEFGCGLD GLLRSRRSCLSGILNGIDDVAWNPATDPHLPATYGPDTLERKKINRAALRQRFGLPDD QEVAVLGMVGRMVEQKGVDLLIDILDDLLQLPVQLVILGSGDKEFERSFERAAAACP ERIAVTIGYDEPLAHLIEAGADIFLMPSRFEPCGLNQLYSQRYGTVPIVRKVGGLADTV EDATPERIAAGQASGIVFETAKPAFLLEAIYRALALYREPEVWRAICKCGMTKDFSWR KSASQYVELYREALAGLNAGRSIADPRYAA |
| fig|243233.35.peg.  3330 | 3384817 | 3382595 | 1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC  2.4.1.18) | MTDSSTLTELSPDFQRLIEARHHDPFAVLGRHRREGRDIIRAFLPHAEEVRVGPDGRV  MARLAGTAIFECEVEAGAADLHYRLYWTDQTGQTHSFIDPYTFPPRLSEFDLYLFGEG RHWNIYRILGAHPHSVDGIDGILFATWAPNAERISVVGEFNGWDGRRHPMRVRGASG VWELFIPELQPGLLYKFEIRNRPHGTIHLKSDPYGRQFELRPNTASIITRESGYAWNDA GWLAQRKDWPWLHRPLSVYEVHAGSWKRDLEGGYLNYRDLAHDLVDYVKSAGFS HIELMPVTEHPLDASWGYQTTGYFAPTSRFGTPDDFRYFVDHCHQNGIGVILDWVPA HFPKDAHGLARFDGTALYEHEDPRLGEHRDWGTLIYNYGRNEVKNFLLGSALFWLE EFHLDGLRVDAVASMLYLDYSRQPGDWIPNKYGGNENLEAIAFLRDLNTVVHQQFP GVLVIAEESTAWPQVTRPTWTGGLGFSMKWNMGWMHDILVYMSKDPVHRHYHHD QLTFGLLYAFTENFVLPFSHDEVVHGKGSMLAKMPGDEWRRFANLRVLYTMMFTYP GKKLLFMGCEFAQTGEWNHTTALDWPLLESNLHKGVLHLVSDLNRLYQSTSALYTY DFESQGFEWIDSHDAAQSVISYVRRDDDSHVIVVLNFTPVPRHNYRIGVPEPVRYREV FNSDAECYGGANLGNWNIETENVEWMGRAQSAVLTLPPLAGIVLAPVAPPAKPDTRT PADE |
| fig|243233.35.peg.  3331 | 3384966 | 3386240 | Glucose-1-phosphate adenylyltransferase (EC  2.7.7.27) | MPESMHASSRFVSRLTRRTLALILAGGRGSRLQKLTEWRAKPAVPFGGKFRIIDFPLSN CVNSGIRQIGVLTQYKADSLIRHIQQGWGFLRGELGEFVDIMPAQQRLQESWYAGTA DAVYQNLDIIRQRHPEFILILAGDHVYKMDYGLMLAYHVEKNADLTIGCLEVPLADA RAFGVMQMDAEQRIQKFVEKPSDPPAIPHRPDYAAASMGIYIFNTGFLFEQLIKDADT PGSNHDFGMDIIPQVIQKYRVFAYRFRNAQSGVQSYWRDVGTVDSYWAANMELIGV DPELNLYDQEWPIWTYQAQTPPAKFVFDDDDRRGMAVDSMVSGGCIISGAEVRHSLL FSNVRVNSFSHVLDSVILPEVNIGRHCRIRRTVIDKGCNIPPNTVIGEDLEEDRKRYYVS PDGIVLVTPDCLGQQLHFHR |

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| fig|243233.35.peg.  3332 | 3386312 | 3387796 | 4-alpha-glucanotransferase  (amylomaltase) (EC  2.4.1.25) | MDAHGIFDRRRAGILLHISSLPGGPGNGDLGADAFRFVDFLAAAGVSVWQTLPINPTH EDGSPYQCTSVHAGNPLLIGLGWLIERGLLEADAIPAAEDAKTVRQQALERAFEAFRR RGTADTLCSAFGDFVSANDWWLADYALYAALKEVNGGLPWQAWPKALRDRKPDA LASAGTLYADIIARVRFEQFVFFEQWQGLHEYARRLGVLLFGDMPIFVASDSAEVWA GREYFELDDDGEPRVVAGVPPDYFSTTGQRWGNPHYNWENMERSGFSWWLNRLRT QLNLYDLIRIDHFRGFEAYWEIPASSPTAMEGRWVKAPGEALLSRCIETFGETLPLVAE DLGIITAEVDALRRRFRIPGMRILQFAFEGGPRNPYLPHNHALDSVVYTGTHDNDTTL SWFEGLSPDQQRYVYDYLGRSGLPMPAALVQAAMASVARLAIVPMQDVLELGRGH RMNTPGTVGDNWSWRFDWAQLHEEHADRLAHQVRMYGRAA |
| fig|243233.35.peg.  2009 | 2047030 | 2048763 | Glycogen synthase, ADP- glucose transglucosylase (EC 2.4.1.21) | MEETVPEPVDLPEAAGTTADSRVESGTAAVEAEMPPPPSQAEVPGENLPESPHAPEWS  PPVAAEMPESRPEVGPQPAQQPHIQHRPALFVVHITPELAPVAKVGGLADVVFGLGRE LEIRGNHVEIILPKYDCMRYDQIWGLQRTFDDLWVPWYGGAIHCSVYFGFVHGRKCF FIEPHSQDNFFNRGAVYGFHDDILRFAFFSRAAMEFLWKSGKHPDVIHCHDWQTALV PVYLYEIYQPMGMRHPRVCFTIHNFKHQGVTGAQVLHASGLNRPEYYFHYDRLRDN HNPHAINLMKGGIVYANFVTTVSPRYAMEAKDQGQAFGLEPTLHIHHMKYGGVVNG IDYDVWNPETDPHIPVHFNVDTIEGKYADKKALRDRLLLADNEKPIVSFVGRLDPQK  GIELIRHALFYTLGQSGQFVLLGSSPDGAINGYFWGLKRQFNDNPDCHLEIGYNEELA  HLVYAGSDMIVVPSRFEPCGLTQLIAMRYGTIPVVREIGGLADTVIDKDFSHRPLHER NGYVFRDYDERGLESALGRAIACYYQYPDHFRELMKNAMRYDYSWNHPGQDYLNI YDYIREK |
| fig|243233.35.peg.  2010 | 2048770 | 2050032 | Alpha amylase, catalytic region | MRIYNLFPRLAGRFRQWTPHLERAAAMGFDWIFVNPIQQTGRSGSLYSIKDYFGIHPV FLDARPSAEEQVRAMIRAANRLGMRVMVDLVINHCAYDSPLPGAHPEWFVRENGQI AHPSCDQDGQRVVWEDLAQFDFHQRAERESLVRYCLEIVRFLCRLGFSGFRCDAAYQ LPPEVWERLIREIKREWPETVFVAETLGCSPAQTRRTALAGFDAIFNSSKWWDFSSPW LLEQYQLTREVAPSIGFPESHDTPRLMEEAHGNVDALKQRYLFAALFSGGVMMPVGY EFGFRRPLHVVETRPEDWEPPACDLTGFIRTVNEVKARCPVFQEDSITQLLPHPNPAIL MMWKAGRKPGEEALLVFNKDPWNRQYFRVDDIYQYVQGRAPLRDLSPEWRLDYIP APFEFELAAGMGRIMVTETE |