Fig. S2

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>PFR_JS14_1□PFR_JS14_1□Chromosomal replication initiator protein DnaA□1:1467 Forward
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SKLRDTIESRLSDVYHREMRLAITVEPSLELDLRPPERDEEAEREVEPVQFIPRQDAPAP
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RDDVDVLLIDDIQFLEGKTQTQEEFFYTFNALHNAQRQIVLTSDRPPKALEQLESRLRSR
FEWGLITDIQPPDPETRIAILQRKAAADNLSVPPGVLEFIASKIQTNIRELEGALIRVTA
FASLNREEVSLAVAEQVLRDLIPDGAEADVTAPTIIHETANYFGVSVDDLIGPSRNQTLV
MARQIAMYLCRELTDLSLPKIGQEFGGKDHTTVMHADRKIRKLMSERRSVYNQVTELTNR
IKQNSARR
>PFR_JS14_2□PFR_JS14_2□Drug resistance transporter, EmrB/QacA subfamily□1442:2911 Reverse
MTTILRQSPGAPEAPESDARRPSGRAGHGLAMVIIAAALPTLMTALDDLVMTFALPVIQK
AMNASVTQLQWFVNAYTIVFAALLLPAAALGDRFGRRRVFLIGITVFTGASAWAAVSGSS
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ATSGARNSA
>PFR_JS14_3□PFR_JS14_3□Transcriptional regulator, MerR family□3153:3770 Forward
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IAQVRHVLDVLDGPQRDPYQAMGEATKNLPLTAPASQTSTPDDDVAMVRALGFTHIIDPQ
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MEPVLLALRRLAHEELAQEMEDDEG
>PFR_JS14_4□PFR_JS14_4□SqdX□3767:4948 Reverse
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RPIYPEIKVGLPTPSIADKMVHFRPDVVHAVNPVALAAFGVEVAVHRRLPLLASYHTDLA
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RPGRASAAMRARLTDGHPDARLLIYVGRLSREKDLADLVEPMRVLGAQGYRLAMVGSGPA
RAELERAFVGTPTVFTGYLAGSELAAAYASADAFVFPSTTETLGLVALESMASGVPVIAA
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AAATRSLVERYREAIERHGIERARGGRSRRGPG
>PFR_JS14_5□PFR_JS14_5□Sulfolipid (UDP-sulfoquinovose) biosynthesis protein□4962:6209 Reverse
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VVFFGEDGAIIARGPHESLLALDAYREVLS
>PFR_JS14_34□PFR_JS14_34□ABC-type multidrug transport system ATPase and permease components-like protein (Precursor)□42267:44234
Forward
MRAHGPVWLPRGPANRWLPLASGRQIAAQVRSHSHGLWRWLVLAVVAMTISALTSLALPV
ATGMVVDQVRTHGPLSGLIAPGVMVVTAVIIGAVASGAGQALTPSYFAAVLARLREDMLA
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FLLPLAAGAVVFTASVRWFLKRAPAIYRNERQASARQSQDILSTLHGLDAVRAFGLAGLR
TGIVARSSWQAVRWELRGRFLSNALVVRLVIGEAVVIIGQLLVSYPLVTGGHVSVGQASA
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QPGAGSPAGARSGVGPSDTGPVESRPVGVGPMDTGAMEAGPIEAARIEAGRIEAGPMETG
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VGARPGTRGPAVVLVSQDIHTFSGSLADDVTMGAPASTVDDQLAALARDALDRVGADWAT
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GRTALVIAHRLSQAAHADRIVVMARDRIAEVGTPDELLARDGEFTRLWRAWQAER
>PFR_JS14_35□PFR_JS14_35□Alanine dehydrogenase□44458:45573 Forward
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FCSARVLDGMGADVTIFDVDAARMEYIEDITHGDIHTEYSTPFAVEEACVLADLVVGSVL
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IDVEPLSTVLG
>PFR_JS14_36□PFR_JS14_36□Amino acid permease□45926:47464 Forward
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DRARELVEQHVTETGGKGASERLKKTGRRTLD
>PFR_JS14_37□PFR_JS14_37□Putative conserved lipoprotein lppS□47681:48880 Reverse
MPRRLHPTSRFSRRGALAAVAVGAGAVGLAACSKARPGSTGASASSKGPATPTLSLTAPH
GLDAVLPQDALTVAVNDGTLKSIVVADSNGNAYSGQLNGSTWTCDRAFWPAANYNVTVEA
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>PFR_JS14_38 PFR_JS14_38 Hypothetical protein 48895:49035 Forward
MLRRRAGLEMDDSAGVIGLAGPTTQARACGSGALLLNAVRRELSPA
>PFR_JS14_39 PFR_JS14_39 Hypothetical protein 49129:49467 Forward
MLGQGSVSGRRRPHNGAMSRGVENLRAVRLVASGRVQGVGFRWQARQQARALGIDGWVKN
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>PFR_JS14_40 PFR_JS14_40 YvyE protein 49500:50183 Reverse
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VRCVVSRPHDQ
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SSTLWVQRSADC
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>PFR_JS14_45 PFR_JS14_45 Conserved domain protein 54241:56331 Reverse
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>PFR_JS14_46 PFR_JS14_46 Glucose-1-phosphate thymidylyltransferase 56387:57256 Reverse
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>PFR_JS14_47 PFR_JS14_47 Dolichyl-phosphate mannose synthase 57420:58166 Forward
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AHGEEAAL
>PFR_JS14_48 PFR_JS14_48 Hypothetical protein 58163:58588 Forward
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>PFR_JS14_52 PFR_JS14_52 Polysaccharide biosynthesis protein 62320:63597 Reverse
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    GDQGR
    >PFR_JS14_53□PFR_JS14_53□Conserved transmembrane protein□63866:65362 Reverse
    MVQRLVPQSVRGDAVLGLVVVLLTLVGAWRVSPWLDEVATAHVVSYSSRDMASMWQGIPT
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involved□65552:67012 Reverse
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    >PFR_JS14_55□PFR_JS14_55□DTDP-glucose 4,6-dehydratase RmlB□67017:68015 Reverse
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    >PFR_JS14_56□PFR_JS14_56□LGFP repeat protein□68104:70938 Reverse
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    >PFR_JS14_62□PFR_JS14_62□Amylovoran biosynthesis glycosyltransferase AmsE□78782:79639 Reverse
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>PFR_JS14_63□PFR_JS14_63□DTDP-rhamnosyl transferase RfbF□79636:80598 Reverse
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>PFR_JS14_64□PFR_JS14_64□Thioredoxin□80822:81238 Reverse
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CAPCVATGRLLSGLTAQRDDVNHVEIDGEERLDLVREFGINRTPTVFLLDPDGAIRYRFV
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>PFR_JS14_65□PFR_JS14_65□Integral membrane protein□81243:81752 Reverse
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VARDPHRLGSAARAVRNKFGVQVHELSADLSDHDDIARVEQVFADRPIDLLVNDAGFAAH
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>PFR_JS14_68□PFR_JS14_68□Acetate kinase□84575:85765 Reverse
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KAPHLISAPESKVKVLVVRTNEELAMAKQTEHLLAS
>PFR_JS14_69□PFR_JS14_69□Phospho acetyltransferase□85927:87459 Reverse
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LDQTTAEAVLDVLFATAQRTGTALVVVTHDDQVAARAQTRRELDGGRFVA
>PFR_JS14_76□PFR_JS14_76□ABC-type antimicrobial peptide transporter, permease component□92635:93783 Forward
MRSFGRELWWDLLGNKTNFWLSCLALFVALFSFIAVVSTGTLAHDSLLAKTLMVDGVPTS
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TVS
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VGG
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activities□118278:119483 Forward
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    VAADPAKAQAIGGLLRAGLATHVVFDTATAAEVLALDQAGQ
    >PFR_JS14_96□PFR_JS14_96□Putative general substrate transporter□121329:122720 Forward
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    VLRLLLGIMEGPTPVGMTSTINAWFPAKEKGTATGIYIASTQFAPIIVPPIAVALAAAAG
    WRSVFHWFAVPGVIMAVVFFFVVRSHPRQSKRVNAAELNHITSSDDGKRDHGGFGTMPLI
    DKIVRVRDADPLDTNAKVLRSWNIWGNTLAYFFMNNVLYGMLTWIPSYLVAARGYSFIKM
    GFVASAPSIGGLVGALIGGVVSDRVFHGRRKPTMLITALMTAVMLVVVLVVPQNTVLVMG
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    >PFR_JS14_97□PFR_JS14_97□Type III effector Hrp-dependent outer protein□122760:124130 Forward
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    KHDLVELRREGTRAFVLDAVTLNDIDQIAQAVVDLRWKVICVDPGPLTDRMAVRSGAITP
    HEGVERTRRLESVPGESGTVLLVAGSATGVTHEQFAALRDVPGTESVAIDVLQLIGDEMT
    ATQERRRVVAEVRRIMQGEQKPRALIVALDTVLTGHRHELSDMEQASGVKGQQVSTLLNT
    RLGEVARGAIDVFAPEDLAGVYLTGGDVMVNCCRAFDARGIALVDYVIPQVDQGTISGGP
    YSGVPLVCKGGLTGTRTTTVESVNRLFDERMRTQNV
    >PFR_JS14_98□PFR_JS14_98□4-hydroxythreonine-4-phosphate dehydrogenase PdxA□124123:125145 Forward
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    FHLITEPEQSLGTYGVIDLMETGVAPDAAIEFGKVQKDAALRAYSYLERSIELGMQGRID
    AVSTAPINKAALKLAGVPYIGHTEIYQELTHSPYALTMFNVHKLRVFFVSRHVSLRQACD
    LANRDRILMFLKNIDHELKQLGFEEPTIGVAALNPHVGEGGMFGTEEIEHIRPAVEDAQK
    LGIRAEGPLSADAIFAFNLDGHNDCILSMYHDQGHIACKTLDFQNAVTLTLGLPFMRSSV
    DHGTAFDIAGKGIAQGESMIESTRVASVYAQMKLDHSDAE
    >PFR_JS14_99□PFR_JS14_99□L-ribulose-5-phosphate 3-epimerase ulaE□125350:126267 Forward
    MTTADGWPIACKINFGGKTEDGTPIADAPASAWRDQLIQVAELGFDYIDPMDDWVPIADL
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    FQQALTPAQEKALWFWLAEGHHDDPKLRPLAIERVRELADHAQKLGLEIALEMYENTFVG
    TPDDAVSFYKDVDHPAVGLNPDIGNLIRLHRPMPTFTEMYEKVLPYSNYWHIKNYIRDED
    PATGSYMSAPMPLKYGVINYRQVIRRALQLGYRGAFMTEHYGSDWLGVGAENADYIRQVL
    RSYLR
    >PFR_JS14_100□PFR_JS14_100□3-hydroxybutyryl-CoA dehydrogenase PaaC□126313:127281 Forward
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    YPKGATAEIKSRLTNGGTIENAVKDADFVEEAVFEQPDVKQEVLKRISAAAPADTVIGTN
    TSTIPVHVLEPAVSHPERFLTVHFSNPAPFIPGVELVASQQTSPEAIATVKEILVRCGRE
    GAQVADTPGMVLNRLQYALLKEAFNVVEQGVATMEDVDTIVRTTFGFRLGFFGPFAIADQ
    AGLDVYADSFKTFEKAYGERLATPEMLVDEVKKGRLGVKNGKGLTGDFDDETKAELIAYR
    NKAYARMQDLLKDLGPAPRGKK
    >PFR_JS14_101□PFR_JS14_101□Permease of the major facilitator□127331:128671 Forward
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    LGAGLFFLGYFLFEVPSNYVMPRFGARKWFTRILVTWGLVTMATALVPNATTFYIVRFLL
    GMAEAGFYPGILYYLTLWYPQRHRTKATGTFVLAAPLAFLIMSPLAGWMLGLDWFSLQGW
    HWMFLLCGGIAVIAAIPTLLLLHDTPEDAPWMSKAEVAWIEAELAKDKATLGQVEHKNPL
    AAMKSKYVWVFALLFFPSTVGVYGLSFWVPTVVHRFSGSDVATGWLSAIPYIFGLVGILI
    TSRWASRFKENWIPLAVIFAGAAVGIGMAGVLSSPLGQMASMSVAAFCLYSIAGVFWPLP
    TRYLVGGSAAVGIAFMNSFGNIGGFVGPYVVGAISDATGAATNGMYFLSGVLFLGAIFTL
    VVRKFWEGRNPEPLVLGSKGPMAGAA
    >PFR_JS14_102□PFR_JS14_102□Transcriptional regulator, GntR family□128785:129534 Reverse
    MPTDTLNAVPSAGRGLSQIAPLRSRALVDEVYDLLLDMLTSGSLAADAPLGIETLARQMK
    ISPTPIREALARLEHTGLIRREANRGYRVAPPLSVEQMTELIDARLVFERGALERAMREP
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PEPSVSPDA
>PFR_JS14_103□PFR_JS14_103□Hypothetical protein□129714:129902 Forward
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ER
>PFR_JS14_104□PFR_JS14_104□DAK1 domain protein□130005:131723 Forward
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>PFR_JS14_107□PFR_JS14_107□Oxidoreductase, short chain dehydrogenase/reductase family protein□133696:134379 Reverse
MTERRSVLITGATRGIGRAIAEELAEGWHILVGGTHADTVNELVASLPSAEPFVVDLTDD
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>PFR_JS14_112□PFR_JS14_112□Arabinose operon protein AraM□139818:141194 Forward
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>PFR_JS14_115□PFR_JS14_115□CHY zinc finger□145494:145805 Reverse
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PDKG
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MWLPSFFSRTFGRAGNNGRMASAPGHVRVRPYMDSDAGITRSIFLQSVTLTAAEDYTKQQ
IDAWASPQDRPLDEWNRDRQESGTLVAVVAGVVMGFTDIRETGYIDMLFVSPKFVRRGIG
SALLREAENRARIAKAPLLYSNVSITARPFFAHHGFVEVAEQHPIIHGVQVKNYRMNKHL
F
>PFR_JS14_130□PFR_JS14_130□Transcriptional regulator□160084:160431 Forward
MIHETREQALARVGHALADPTRCRLLLAIVDGVVYPAQMAEHLELSRANVSNHLACLRDC
GLVSATYEGRRVRYAIADAHLSAALVQLAQVALDVTPTDSCLNEADQPIELEARA
>PFR_JS14_131□PFR_JS14_131□Metal cation transporting P-type ATPase ctpG□160428:162491 Forward
MSSATQCCDHDAPAGADDHDELAWWRDREVIFPIGSGVLLAAGFVSALAQANTASLVLYW
AGLLLGASTFVPGALRALLKGRLGISLLMMISAIGAVILGAVAEAAALAFLYSISEALED
KAMDRARSGLRALLELTPKTATVLVDGKPTDVEASQLQVGDLLLVRPGERVATDGVVRDG
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ASSLDTSAITGESIPVQVGSRDAVSAGCINISGPLQVSATAPGSDNSLTTIVTLVEQAQA
KKGRRARLADRIAAPLVPGVLILAVAVGVLGSLLGSPEVWIGRALVVLVAASPCALAIAV
PVTVVSAIGAASRFGLVIKSGAAFEEFGAVRHVAFDKTGTLTQGSPCVGRVLTASTTDPA
STTSTASTADARPAGVSEQQVVDAAAALERGSNHPLATAIVAAATNAPGATDVTELPGRG
IRGRVQGHEITVGSPRWLAPGALAAGVEQLETDGMTVVLVHRDGQPLGAIGIRDELRPEA
AETIRALGEQRIGVTMLTGDNERTAQALARQAGIDDVRAGLRPEQKASAVSELSRRTPTA
MIGDGINDAPALSAASLGIAMGARGGQGSAGGSDVAIESADVAFTGSDLRLLPGAFAFTR
RGRRIMNQNIALSLLIIATLLPLAITGVLGLATVVLIHEGAEVIVIANGIRAARVARARG
GAPAAQGPVPPSVEGPAAPRMVAHSAR
>PFR_JS14_132	PFR_JS14_132	Hypothetical protein	162540:163031 Forward
MSVSTPGTGLEVFSVVVDTDGSIAQMEDDDQYHTIAPDFAVLFDDLDQQFTQRGVTKIPV
VTGFGDGMAAPRPRPIMVATTGALVSPDDPDAFMDAFVANEAYDGEYHDVTLEQVGTLVN
DLNLAEASHAADQRVQWVPGFILITPDRKLVDLAYALHKGWIK
>PFR_JS14_133	PFR_JS14_133	Hypothetical protein	163150:163755 Forward
MSRSTGPKGPQRGKAPRQVQGYRVSVNPDGTLLTNRPDGELEEVAKDFRELTARLSLRGE
QQGLLILPVVTEFSKLMQRPSLWPVVLGAGGRLRRPTGRQSFINAIQTGSPYEGEFVDTT
LVEVGKDVTEMSASNPMLQWVPVFLILTPDGQLADLGETIMEGRRMLYPQEAANTAPDAP
DEPGAPDASREPGAAEEPSAG
>PFR_JS14_134	PFR_JS14_134	ABC-type Fe3-siderophores transport systems	163811:164620 Forward
MSDELMGGDLLADDLGAPVRISRPVERVVSLVPSLTEALAESARELIYGATDFCVRPENL
DEVAGHPVTRVRGPKNPDRTVIEQLHPDLVVANQEENRAFDVEHLRADGVPVWVTSIDTV
DSAITSLTRLFTEALGRERPDWLTRAEQNWAEPDPTVTASAVVCIWRDPWMVVGPNTYVA
DVLHRSGVDLAPLPVDDWKNARYPKVDLYALQASGADRVLLMDQPYAFSPTDGPEAFEGM
DVRIMPERPMAWYGPGMTDARAEVRKLIF
>PFR_JS14_135	PFR_JS14_135	Hypothetical protein	164693:164917 Reverse
MMHSRRRLVYKWVTITVLMLGLAVAIDVMIGDRRSDIEYLMWSVTAAAIGYAGSFGHDWW
VRAGFSGRHHPLAG
>PFR_JS14_136	PFR_JS14_136	Transcriptional Regulator, TetR family	165063:165671 Reverse
MPEQSRSVRSHQAIIDATADLIRTRGVAGTSIADIITASGTSAGSIYHHFPNKQAIVVEV
AHQTMRWPLTAIEAYLNRPAPPADLFGYALDALRVAPELSDLLVQLGSGSLSDDELGRQL
RAEFSQLRDALDETLAVWATRNGLTDDRVAGLGQMLVGLVLGYAAQRVLIDQFDEEAYVS
HGKAMLDAAVCRPGNDQLPDGR
>PFR_JS14_137	PFR_JS14_137	YghA protein	165851:166540 Forward
MPIGAGTLPIMGEAFLVIDLIGVLANAILGGITAKRLRFDLVGFTVLALATGLGGGILRD
VLLGRGTPVALTNPIYIPLAAVGALVAFVVPIRKVFQERLFPLMDALALGAWAYTGTHKG
LVFGLGPVQAVLLGVVSATGGGMLRDLLSRKMPVIFGDNTLYATSALVSSVLVVIFYKLG
DSAWGAVIAMAVGSLLTIVSAWRGWTLPCSISNPFKGKDFRRYIRIRSR
>PFR_JS14_138	PFR_JS14_138	SAF domain protein	167084:167794 Forward
MGFIYVSHARVPPARAERDLSMVAFPRKSLSELTRRAVPSLRARRSPRLIIIGVLCACLG
GLGCAVAWHQATDARQVVVMARAVPRGATIDGADLGTTSIGSAPGVATIGAEQLSTLIGT
TALVELQQGMLVPASALGEETVRPGRHHVGVHLVAGRVPGDLVAGSAVIISAAPGPTDDA
SFRAEQLSVPATIVGTPSRQSDGSWNFDLDVPAGASLRIATLAAAGRLVVVHGTAA
>PFR_JS14_139	PFR_JS14_139	Hypothetical protein	167794:168831 Forward
MAIVLLTCATGSPGVTTSALALTLCWPRDVLLVDSDRDVSQTVQAGWLGARPLATRGLVE
LAQAHREMRPVAPLLWDRTVSLLDDAPAGSAGVPDQAMGRFDATGQPIADQRPGAPAVAE
SRPVARQFLPGFSHPGSVAVFDPVWPEVAEALAGLAGSGVDVIVDAGRVGHQGLPSALLG
AADVVLMVVRSSLRSLAAARLHLPPLRERTAALAPAAKLGLLVVGPSRPYSDGDVEAQFG
VPVVADMAWQPEEAAVLSEGGDEPRRFRERSFMRSASAAASAVSARVIATPNSSRDLATG
TSRSHDPLTGSIGRAPVQSAGVTPGARDRMAGPVDPPLATGRPRP
>PFR_JS14_140	PFR_JS14_140	Secretion system protein	168828:170603 Forward
MTHRASDLPPLGPGRALPFLRPGQAAPPLHAGDGAPHPDRGDGPSPGGLADALSLLDQVV
TTPANVSASASPLGTQPVDLPQRGVPQESESAPTSAGAAHRVRTPGTVPAGRPVGTPMQA
ADNQRPGAGGVPGPSGHQTTDWSIVAQLRSTISELITAEQARWEQEHHRRMADDDRRLMG
RSLIRRAVHDYADELNRAGRALWPIALEQRYVKAVEDAIFGYGRMQPIFEVSEAENIEIH
GYDCVFAQFGDGRRTRLDPVADSDDELVAAVRFLGENADPPRPFDDAHPTITVALGNKFR
LHAVAFGLADRPSVIIRQHLLTEVSLKQLAHGSMMPTEVADLLRRCVLARKSVVISGDQG
AGKTTLLRAMVGAIPATERFGTLETDYELLTHLQSRRQNMVALQAKIGLGEVVDGRRIGE
YTVADLIPEALRQNLSRLVIGEVRGNEAGAMLQAMQSGAGALTTTHSHSAASTIDRLAAR
VAAGGVLRLDEAYRQIAYNVHLLVHVSLVDDTWRGGVRKRFISEIRALTGSMENGQPTTH
LVYATSRTGEPQVFDPGQGLLDDLAPFAEPTGAPATHRRSAGDPASRERGR
>PFR_JS14_141	PFR_JS14_141	Type II secretion system protein (Precursor)	170600:171493 Forward
MNPVLVALCAAAAIFGVFAVVEGLVRRPRRRGDVSGPGIPVLVRARWHGATRAQQISWSL
AVAGALVGYLLTRSLLVTGGVPALILVLPGLLSAPPNRDVEVLEACDRWVRLLIGSVSTG
KSVPDAIRATRNQVAPVLRAPVDGLIARLDARWSTASALRAMADDLAHPDADAIIAALIV
ATRRGGTGTGDALRALGQHSRRRLQSLREIATERAKPRIVVRQVTLITVVVLVGVAVFNP
DYVAPYLTPTGQLLGAGLLAAYLGSLVMLRRMSTPEQRERILQGDGVELAPAGGDDA
>PFR_JS14_142	PFR_JS14_142	Type II secretion system F domain protein	171486:172391 Forward
MPDPAILVIISGAVAGLGAFLVLAGWARRPVRMGDAFAALDGTVAGRQGPEEDLVRDADS
SLERLGAYAYARLHLPLGRRARGMLQLSDRSIGDFMAEKIVLCLAGLALPTIVTAVSAAM
GSPLRAPTLLVALALGALGWCWPDLSLRAGSKRTRFEADEALLTLFDLVMLERMANRSAT
QALSAAASVSDVAIFRRVRGVLAQAGLEQRPPWDGLRRLAHDLRLPPLEDLADIMQLDEQ
GASLTEALAARVEELRDAHLSAGRMEAQEVSERMTLWMALPVMVFGLSFIAPPLMRLAGV
A
>PFR_JS14_143	PFR_JS14_143	Hypothetical protein	172476:172700 Forward
MASRALETLSRLTALVVGFVAMPTPAVRDDHGARDDERGLSQSTENAVLLAGAVVVAGIV
IAAVRSYVESNMPK
>PFR_JS14_144	PFR_JS14_144	Hypothetical protein	172675:173097 Forward
MSNPICPSEAAGRTRRGSRSVVVRRRRDERGLSESLQWAVLAPVLMLIVLGLIEAGVWLH
GRSIVQQAALTAAETQALSGISSDAAEKVVADMTGQLEAVRTHSLVSDTEISVTVEATVP
LPLDVGLGDVTVTATRAKEQ
>PFR_JS14_145	PFR_JS14_145	Hypothetical protein	173163:173720 Forward
MNTLGRTGRHVGGRAVHEAASPESSGRRRWAGPREWVGRKAGRRESRHGERGAVSIEVVV
IVPGIVLFIALMTAGWRIWSVRAQVHDAAAAGARAASLAATHDKAVQAARSAIAADLDAV
SSHCVDPEVQVDGSAFSLAAGRSGEIGVDVTCRVAFSDLVLAMPGTLEATGHAVSRLDTY
KERRP
>PFR_JS14_146	PFR_JS14_146	Hypothetical protein	173717:177427 Forward
MRRVLSSVTSLLVLLALVPGGAIALVHWGRGDLLFSIEWSGILSRPDDGSLVLLALTVLG
WVAWAMLTGSVVAEALSAVSHGRISVRLPGSRLFGPAAAVLVASIAGLIGVQSAATNSAP
CASVSSTSAAVSAESVAGEGPAAATPLAAADAQEAPSRDSRTDSAATSPRADSQWHQIVS
GDDLWTLAEHYYGAGEQWRDIVGANATLGLSAVDALPVGVMIEIPGATVPDALQDTAVPE
GSHASEGAVANSTVQLLNEEFGAHAPSDEDDPDGVAVLSDGGPDGSAIVTDDDGVDESAE
PSLDAGSPDDPGSPEGAGFSDDAGLSDDAGLSDDAGPATGTGQADEAGQPDAGGNGEAAV
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PGQRLVLPAVAPGQGPATTAGSQPAGPQRADLQLVDGTGTGARAVVPGNAGGDAHAAAPD
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SAREASSDEAGASDIARWTGVAESATGEEPAQQAARDGAVLSSQRDVRNQVLSLVGPIGA
ASAAAVLGVLGLRRRWQLNARPLGRRRHAVGADSARAGAALAAVSASPGSVRGMHGAPGA
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IEAGGPGPDDMGPEDMDPDDPAPDDLGPGGLIPQDAGGGAVQLGVAGDDPVRLDLASLGV
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HAGPPAGADVPLVALPTVPATSLPEESTVLAPPIDAPFLKILGPVELVNTRGRQPSRAVR
QCQEYCAWILHHPGSNAVRMTRDLLIADTTRRSNMSRLRAWLGADEAGEPYLPDAYTGHI
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CTIRDIGATLGERGLAAGNVDLARWAAARALSAAPEDEMLLRLRLRSEHLAGNRFEVERL
VLHITRHARLLGVDLQDETVELLQEVMEGQARARLA
>PFR_JS14_147□PFR_JS14_147□Multiple antibiotic resistance (MarC)-related protein□177438:178028 Reverse
MGHILSSAFTLFLVMDPLGNIPLFLTALRHVPASRRQKVLARELLIALVIMVIFLLAGRG
LLAVLHVTQPALATAGGLILLLIAVRMMFPTPEASLRERTFEEPLIVPLAVPYTAGPSVL
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VATQMLMGGVKEFFGF
>PFR_JS14_148□PFR_JS14_148□Transporter, major facilitator family protein□178028:179455 Reverse
MPRVRRRQRDTIRMLSAPTRANQSFEGEYVEFTQRLRRLWRHRAFRRLTLVRLFSQTGDG
TVQIGMASYLLFSPQSATSAWAVAGVLALTMLPYSLVGPFVSLALDRFPRQRISLLVDTV
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IGALLLAPDGVSPALTIGAGVFYLLAALAFTIGSHSLGNATFNKGTRAVSPVEVP
>PFR_JS14_149□PFR_JS14_149□Conserved domain protein□179791:180756 Reverse
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RGTPTHDGAMILQRAAQPTRPGTRRAARPTEAPLTRISAGTRVSSADPVVDALRTEWQGW
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LAAQASRDRRHEVGDYVSTLWELLHDFPIERRTHAVATNLVLDTRKRLHRAAGREVPCSQ
PPEPPTPPASSSRERAAVIIDLAARRGLITAPSAEVLRSVYLYGLSGREAAGRHEMSEDM
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>PFR_JS14_150□PFR_JS14_150□Response regulator receiver domain protein□181110:181772 Reverse
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PGMDGVEATKQVVALDNGTKVLVLTTFDLDEYVFAALKAGASGFLLKDTRPADLLSAIRA
VAAGDSVVAPSATRRLLDHVAPTLPDHVGEPDERLDVLTDREREVLVEVAKGATNAEIAT
NLFMAEGTVKTHIGRLLAKLHCRDRVGLVLFAYETGLAPA
>PFR_JS14_151□PFR_JS14_151□Histidine kinase□181806:183215 Reverse
MTSTRLPWPTMPGSWDREGPEPVSRWDVMLTAALMVGTSFWGDLMANHQGHYVASVLTSL
AITAPVVLRRRRPLLMLAIVSVASLVQCVTVSGPTASLLAVPVVAYSVAKWVSGHDSRLV
LLSGLIGAVIGPLRWIGSVNFVDGYAGRVRMLVLLFVMCFAAVLVPYLIGRRVRENDITG
QERARAAEQRYQAELATREERARATEARVRNDIARELHDVVAHSLSVIIVQAEGGKALAR
KNPPAAAETLDTIAETGREALTEMRRMVGVLRAGPGGTEYAPQPGLGDIAEMVQRAGDRV
SLQVTGAQPAVPATVGLAAYRVVQEALTNFFKHAGPQATCRVQINYGAADIDIEVADNGM
GSKAPNDGAGNGLKGMQERVGAVGGKLNARARRTGGFQVKALLPIAAKPPKVATSEPASA
PAQADGGEPADGGVPAAQPADPAPEGRVDRGAPHQASPQGPGHHDGPVA
>PFR_JS14_152□PFR_JS14_152□Hypothetical protein□183588:184931 Forward
MSLHDIPTKVPSHRAAEWPGYGMADCDEHYVERLCRDVDQRVDRADHRLLLLLKTWFECR
EQFDDQQRDRVRATILGFRYDVDHPGNDVMCTWTESHQISFAVCEYLAGQEFVDNTFTDG
RRRGEELLGHGATRVVRWLSDRFRYGFSEWLSGDRYAIDVAALTLLIDYARDEKLVIRAS
MVLDLLLADMALHRFDGRFVAASASASAMVRMHPNHSAAQVIVDAAYGPALPLIDTDQLG
AIFVCRHRYKVPLALREIAASEATMRVLTSQGLDVDEVPEVLAADPNFPRTSPAALARFW
WAMQAFTNREVVSATRAVRMSAKQSTNRFLASMTQTGRGAGVLALAIAEGPSSGDRRDGA
AARQCADLPHPRLSAEQRPELSPRQLRRPAGTVAGMPSRRHLRVRKPSRLPHRRRRGFRW
RVQRSGASWLGRRRMGGQRREPRHRPA
>PFR_JS14_153□PFR_JS14_153□Hypothetical protein□185144:185473 Forward
MGCTPDMQWCWATNGSSARSGAFVDQLKQHRVALTGDRLSLRSPYGKAQLTWREGLRVGS
RQVPHEYPRYKSRQVSAERFPQAIPVRGDEHLLLLDWDVGSREDLPITA
>PFR_JS14_154□PFR_JS14_154□Hypothetical protein□185511:185639 Reverse
MRRAALIIAAIAATAAGAVLIHRRNARARDAELWSRAADPIA
>PFR_JS14_155□PFR_JS14_155□Translation regulator□185966:187462 Reverse
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AIPFSAVVKAVSQAQASAEQANLLRTNRAQRRLIGAVGRADAAHELVSATAQIIDGWAAL
TDTSGHVITRAGAVPLERLAELANVHQGAGRASSFETGAMVQNIDGVQGRRIGLLMAGGR
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QVPADPVLLACVAGDPRVLAEIPLADLRVVWGIVEERLWIVLAPAQRQRLVERLRRRALS
FSISGSCGWGDLAEVKHATLAGLLGEGSAGQASLLDLLPPRQASAFATATLGPLATAEFS
DLLATLGVWLDQNGSVERAAEQLGVHRHTVRRRVQRAATLVGPSVETPQGRHELWFACEV
LRRARGDADASGPRPAAG
>PFR_JS14_156□PFR_JS14_156□4-aminobutyrate aminotransferase apoenzyme□187642:188976 Forward
MITYEDYKQYLSPALSKATNLVIDHGEGSYVWDVSGRRYLDWVQGIAVNALGHCHPRVVE
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TGRPGIIAFKGSFHGRTIAATSVTASSAHYRAGYDPLVPGIDLVTYPSADQSPEGYTDDQ
IADWALRQLTDLFAYVRDPHSVAAVLMEPVQGEGGYVVPPTRFVKALRQLCTDNGILLIF
DEIQAGYGRTGRMFASENFDVVPDIMTIGKAMAGGLPASGVVSTPEIMAAWGPGRHGGTF
GGNPVVASAGLAVLDVYAETHLLDNVNAVGSYLAGRLDELKDEFPIVTDARGLGLMRAIE
LNHVDGRPGGDLLEEVRAICLDKGLMTLSCGVRHNGMRFATPLNTTTELIDEGLDILHQA
LTTVSAREAPRHTSGATTKQAVAA
>PFR_JS14_157□PFR_JS14_157□McyI protein□188973:190052 Forward
MSELMDARRPAPARATSSAATAPGVAEPTTGTPRVVYFNIDGDLDYEHALLEQWGMTDRI
DLVDAKPGDNRPDTFVKAVGDAEGVVVEYFEVTNPVLDQLPHLKIAAVQAIGSSNIDPDA
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HTPLMAATHHLIGVRELALMKPSAFLVNTARGAVVDEPALVDALRDRRIAGAAIDVIEDE
DHERSELFGLDNVVITPHAAFISTESLADGKRIALEQLVQRLVAGKRPANLVNTELEIG
>PFR_JS14_158□PFR_JS14_158□Threonine dehydrogenase and related Zn-dependent dehydrogenase□190056:191102 Forward
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FLGQVVDTGSLTDQVRVGDWVVAPFRYSDGQCEYCRAGLTSSCTHGGFWGREVLDAGQGE
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VGLSAVMAARRAGADEVIVLGSAHPDRRQLALTVGADRFISVRGADAVQQVADITHGAMV
SHVVECVGTQGSFDTAFGVVRDGGTVSYVGLPHQVSIDPARLFMHNITLTGGMCPARVYM
PLLMDEVLAGRSHPGRVFTATLPLDRVGRAYELMDRRESIKCLLTVGA
>PFR_JS14_159□PFR_JS14_159□Probable amino-acid ABC transporter permease protein YckJ□191219:191857 Forward
MEGFTAIIAAVPYTALVTLGAFGLGFVLAIPLMFARRARLMVVRGISGFIVDLARGIPPI
VWLLMIYFGLPNLGIMLDPIPAAIIGLGIITAGYLAEIFRGGMLAVRKGQFEAANALGLG
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FFEAALIYLVISVPLGLLARRIEAHKQEASAR
>PFR_JS14_160□PFR_JS14_160□Amino acid ABC transporter, permease protein□191854:192510 Forward
MSDTFSFWWANLPQMLGGLVVSLELTGLALVIGMPFGLLLAIGMGSRLAPLRWLCIGVVE
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VGRGVPALVMLYVVYFGLPAIHWSPTAMVCAVIALAFTTGGYTGEYIRGGLVSVGEGTRE
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SSFRALEIFGLAGIIYAIITIPATWVANRVERRLSLRE
>PFR_JS14_161□PFR_JS14_161□Periplasmic component of amino acid ABC-type transporter/signal transduction system (Precursor)□192577:193437 Forward
MSVSLSRIACVGALATALVLSGCSGSSGSGAKVASDCKPAHTFNTVSSKKLTISAPDFAP
FVSKKDNTQSGIDVDVINQIAAMECLSTNFLQVDYSGAIPAVQSKRADVAIGDYYRTTSR
AEVVGLSKAMYVDGMGLVSKDGLKDIPTVITHNVGTVDGYLWVNDMKKLMGDKLKIYKSN
VEMFADLKAGRIDVGIDSVPAAQFQADQNKDAGLQVATANPDDQVGASVKPAQVGIPYTK
DNADLGKALDDDIATLRGNGKLDQIFTDHNVDTSLTKLDGDYLVQS
>PFR_JS14_162□PFR_JS14_162□Glutamine ABC transporter, ATP-binding protein GlnQ□193507:194310 Forward
MTQHVAAAPAAAPAVRMPGDYAIELGGIRKSYGDHEVLKGVSLRVKQGEVCSIIGPSGAG
KSTLLRCVNLLEEPDHGNMIVDGQYMQGGINHSRKELLELRRRVGMVFQSFNLFPHMTVL
DNIVLPQRRVLKRSPEAARDKGRELLDKVGLADKADSYPAKLSGGQQQRVAIARALALEP
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EEGDPEKVMSHPEKERTAEFLSAVINR
>PFR_JS14_163□PFR_JS14_163□Translation initiation inhibitor involved in amino acid or purine metabolism□194318:194701 Forward
MTPKMISIGESVASYSHGKVVGNLLFTSGATPHDLDTGEVRGSTIEEQTRLSIQTLEKIL
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YVSGDES
>PFR_JS14_164□PFR_JS14_164□D-amino acid dehydrogenase□194698:195951 Forward
MRTVIVGAGVIGLAAAYELMKAGHDVTVLEADGYGKGPSHGNAALVTSVLSFPVPAPGTI
PVAAKAVLTGTGAVSVRPHVQPGYLSFLLRMALATRKSEFVKGTLAQDIMTRMVSDGYGE
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IVGHLPGYVNTFVATGHAMLGLTYAPPTARVLHALIDGVAPADYGAFSMRRFQRAAA
>PFR_JS14_165□PFR_JS14_165□Asp/Glu/Hydantoin racemase superfamily protein□195948:196724 Forward
MNATSPYGYLAPGQPIGKVSMAPGQNIAGYHVGIIYIEDVWYPMVPGNVVNASTWEFPVL
LQPVRGIDIPALFGPEHKDLSKPVLEACRELEQRGVRAISSACGFFGRYQAKIAPKLGVP
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>PFR_JS14_166□PFR_JS14_166□Histidine triad protein□197105:197554 Forward
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MNVAKVIGQACEQAFDSPRAALLIGGFEIEHLHMHVLPAWGEAELSFSNARDDVPGDELD
AATERVRAALRDLGFGAHVPPAMDSAALA
>PFR_JS14_167□PFR_JS14_167□Molybdenum cofactor synthesis domain protein□197558:198142 Forward
MAHHDEPPARGTGGVARGTGTTSSDDVAPTPVPGAVITVSDRCASGEAEDISGPLAVELL
AGFAVQSQSARVVPDGIDSVQDAIARAISEGARVVLTTGGTGISPRDLTPEATEPLLVAR
LDGVADAIRRRGEEHVATALLSRGLVGITGHGMDSAVVVNAPGSTGGVHDAIAVLGPLVA
HLIDQLDGGDHPSR
>PFR_JS14_168□PFR_JS14_168□Molybdenum cofactor biosynthesis protein□198197:198745 Reverse
MSDQHAGNQRPDDRTAGELPHLRADGLPHLRADGTAYMVDVTGKQPTVREATAVARVDCS
PAIMAALQQGTVPKGDVLAVARIAGIQAAKHTPDLLPLAHVIGVHGASVNLELAHDHVDI
SATVRTADRTGVEMEALTAVTVAALAVVDMVKGVDRMVEIRGAKVVHKAGGRSGDWTRPG
DD
>PFR_JS14_169□PFR_JS14_169□Molybdenum cofactor synthesis domain protein□198738:200264 Reverse
MSTSPGSSAPDHGPRAGGESLRANEPLAGHEPLTVEGPPAANEPLTGHEPLTVNEHRTLV
DALAAPLAPLTLPLLGDDPSAQPTEAGSRSSSGAMGTAETHPEKGFSSPGRPARDCFGAV
LARDMDARLAVPPFTNSAMDGFAVRFTDVTPGTPLPVAGDIPAGDTSPHELAAGTAWRIM
TGAPLPAGADTVVKVEHTDHAPGVRRPPTAVTITELPRRGANIRQAGEDVAVGTPVLAAG
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VAQQPGGPQGVGTLGVATGRVPVLCLPGNPVSVFVSFHVYATGLIAVLAGRATTTAPRTV
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APGDRLQFIDTRAGTPLSARRSSEDFHE
>PFR_JS14_170□PFR_JS14_170□Molybdopterin biosynthesis-like protein MoeZ□200261:201136 Reverse
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YLAAAGVGTLGVCDSDVVEVTNLARQLLHGEADVGMAKPESAARRLGALDASVRVEQFGN
VTRDFLDAHGAEWDLVIDCTDNFAAKYLVADWCADSGVPLVWGTVVSMGFQVSVFWSRPP
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LVADAARNRYSVLTFAAAPDGSDSSADRSGRPDRFDGPDSSARHDATGDTP
>PFR_JS14_171□PFR_JS14_171□Molybdopterin converting factor, subunit 2□201136:201555 Reverse
MTDIRTGITSEPLDAAAITQAAADPRCGALVTFAGVVRNHDAGTQVQAIDYSAHPSAERV
LARIAAGIGERDGLGRIEAWHCIGHLEVGDTAMVVVVAAPHRGPAFAAVTDLVDQVKAEL
PVWKNQQLADGTHSWSGIA
>PFR_JS14_172□PFR_JS14_172□ThiS family protein□201657:202772 Reverse
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LGRHVSSVRETLDALLRIGLVTSQRLPASGRGRPALGYSAHVPAGPVGAPQLFDQVCAAF
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TACDDVVARYLPGPGMEAELVLTRTTGQHDSQSPEQSEKPMTHIRYFAAAAEAAGTDSEQ
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VVDVLPPFAGG
>PFR_JS14_173□PFR_JS14_173□Respiratory nitrate reductase, gamma subunit□202901:203620 Reverse
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CVAAGHVVGLAIPESWTGALGVSEQMYHLGATVLGSLAALATLIGLGGLLYRRIVVKSVR
LATTRMDIVTYVLMCIPIILGTIATVSTQVLGDPGYNYRETISVWFRSIPTFNPQPELMA
TVPLAFQLHIVAGMLLFCVWPFTRLVHVLSAPIGYPTRPYVVYRSRKGEVAATPKPRGW
>PFR_JS14_174□PFR_JS14_174□Nitrate reductase molybdenum cofactor assembly chaperone□203626:204435 Reverse
MGEFVGLPSVPVADTVTLDDAPRRIARMACSLLLDYPDEALATTLGAVRAEVGALPAPVR
EEIDAFCAAAEQLGVRALQEHYVEVFDQRRRCALSLTYFTHGDTRGRGQALLAFREAMRR
AGFSQVREELPDYLPIVLELCALDDTGTGEALLAANREGLEVIRTALRSAHSPYAHLLEA
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EPDTHEPGLHASNPHAPNPHAPSPHGRGK
>PFR_JS14_175□PFR_JS14_175□Nitrate reductase, beta subunit□204435:205946 Reverse
MKVMAQIAMIMNLDKCIGCHTCSVTCKQVWTNREGMEYAWFNNVETRPGVGYPRTWEDQD
RWKGGWRRTKSGALVPRQGGRARTLANIFANPTLPDVNDYYEPWTYEYDKLLTAPAGERN
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DVFMDNPPDESIAAAVGMSGEQVQAMYRLLSIAKYDDRFVIPTTHPEMPRGITELEGCPV
GYDARAFPGGHTPGGPTLPLEVI
>PFR_JS14_176□PFR_JS14_176□Nitrate reductase, alpha subunit□205946:209761 Reverse
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DAFYRQRWSYDKVVRSTHGVNCTGSCSWKVYVKDGIISWETQETDYPTTGPDLPEYEPRG
CPRGAAFSWYEYSPNRVKHPYVRSALLDPYREARERLGDPVLAWASITDDPAISRSYKSA
RGHGGMVRVSWEEATEIIAASYVHTIKAYGPDRIAGFSVIPAMSMISYAAGSRFHELLGA
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HAQERTMNTPLNESTGKRGGIHNSLTRIMIKPTHLIGGYAQLSYSFNYYGPTGNQRDEVT
LIRRRGQEVQF
>PFR_JS14_177	PFR_JS14_177	Transporter, major facilitator family protein	209795:211153 Reverse
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SAIAPKLNSIGFGLTTGQLYWLAAMPGLSCGLIRLVYMFLPPIMGTRKLVGWSSLLYLIP
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AAVWFWICAAFCALCSVICWIRYARPRAPFPG
>PFR_JS14_178	PFR_JS14_178	Molybdenum cofactor biosynthesis protein A	211297:212472 Reverse
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RLCTLAVTHLGIHKIRFTGGEPLLRKGLESIVAACAGLRTDRGSSPELALTTNALGLAHR
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INAPDLPELFDFCLDNSLQLRVIEQMPIGPEGSWDRASMVSRAEILELLATRHQLAELSS
PPTTGTLPDGALPDGMPPSTVQPEHSAPSTSAPHTAEPTVAEPTTAPLDPHAPAQLWQVD
GRADTTVGIIASVSAPFCQACDRTRLTSDGQVRSCLFSTTETDLRALLRSGATDAQLADA
WRTAMWAKPRAHGLDEPWFAVPSRTMSRIGG
>PFR_JS14_179	PFR_JS14_179	Putative molybdopterin-guanine dinucleotide biosynthesis protein A	212571:213242 Forward
MPGMFGRVMRDDRAMAATPSGARPDAGRRGRVGAVILAGGGGQRLGGVSKADLRLGQRRL
LDIVLSGLVPAVDGDAVVAPRDVEVPPGVRRTLEGPPDGGPVAGLAAGLAALAGSHALVL
VTAVDSPGIVDLAPLLVAALSARPDADGVVARGGEPAPFRQYLQAVYRAGPLRRLLADAG
QVRNRGVARTLRVLNLVELPSPADLCRDIDTPDDLDWWRGRLV
>PFR_JS14_180	PFR_JS14_180	Molybdenum cofactor synthesis domain protein	213615:214121 Reverse
MPHSDYDLAGIRAAIITTNNRVLAGERPDRGGQLAVEQLAAAGLQTSEPVVIPEEHHAVA
EQLRDSLDEGNRLVIVLGGTGFGIRHESPEVVREAIEVEIPGIAEQIRAHGLTNTPLSPL
SREVVGVTARDKTGALVVASPSSKGGVADTLSVLIPLLKDIFGQLDEI
>PFR_JS14_181	PFR_JS14_181	Molybdate ABC transporter, periplasmic molybdate-binding protein	214341:215117 Forward
MRTRPFALVTACLLSLTLAACGSSKGSGGASSSQNATLTVYAAASLTESYDELGKQFEAS
HPGVKVTFSYAGSQTLVDQLDNGAPADVLATANTSTMAKASDKKLVGQPTTFASNVLTLI
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SPAGRQVLDAHGFSTPGQ
>PFR_JS14_182	PFR_JS14_182	Molybdate ABC transporter, permease protein	215114:217234 Forward
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WLSVRTCAAAIVIDLVLGVPAAVALSRRWRGVRVARVLVALPLSLPPVVAGLALLVTFGR
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DDGPVISARITPAAWAELQLAVGQRLWCSVKATQVRLVPAPAPVGP
>PFR_JS14_183	PFR_JS14_183	Putative CoA-substrate-specific enzyme activase	217427:221803 Forward
MSDDALRLGLDVGSTTVKAVVMDGGRIVFSDYRRHNADVRGEMKRLLLDIRNRFPDDVLK
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PSVLGATRGDGNAVNARA
>PFR_JS14_184	PFR_JS14_184	Transposase, ISlxx5	221812:222846 Reverse
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>PFR_JS14_185 PFR_JS14_185 L-aspartate oxidase 2 (LASPO 2) (Quinolinate synthetase B 2) 223088:224677 Reverse
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>PFR_JS14_187 PFR_JS14_187 Methylase involved in ubiquinone/menaquinone biosynthesis 226096:226776 Forward
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R
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GILEGDAVWLEPLLGARTVPAVVPGEDLETPLTDADEQEVGASGTETVAA
>PFR_JS14_197 PFR_JS14_197 Cobalt-zinc-cadmium efflux permease 237907:238947 Reverse
MEAPQHKDGRATRRPGRHKDRHKDRHKDHDHGPGAAELAGRPGDFRKRLWITFAITATIV
VAQAVGSVLTGSLALLTDTAHALTDASGLLVALVAATLMLRPATSKRTWGFRRIEVIAAL
GQATLLLVVGLYAAIEGVRRLVSPPEVPANELLVFGVVGLVANVIAIVVLSSSRDANFNM
RAAFLEVLNDALGSLGVIVAAIVIATTGFQRADALAGLFIAALIVPRAFTLMRETTRVLM
EFAPDDLDLDEVRAHILGLDHVREVHDLHASTVATGLPTITAHVVLDDECLTDGHAADVL
RDVRECVAEHFPVAVHHATIQIEPGGPSACARGICEPLAIGHADRS
>PFR_JS14_198 PFR_JS14_198 Transcriptional regulator, ArsR family 239237:239635 Forward
MDTAPSGDQDPADNDCREPVTTEAMVPAADLFHSLGDPNRLIILHHLQLGEHRVVDLTAH
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LGLSQSTVSKHLIVLRDAGVVAVRPQGRASVYSLAHPETLVELLSAAERFLGLTGGAVTL
CPLHGPGVVADH
>PFR_JS14_199□PFR_JS14_199□ABC-transporter transmembrane component□240000:240830 Reverse
MTTLVENPTVTTSPVATGLHNRADLAQTVRNSLTMAYRGLLKIRHNPEQLVDVLVQPILF
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ALLGVVARTAASVQGFGMIVLFPLTFLSNAYVPVDTLPAALKWFANVNPLSHLITAVREL
INQSTISGEFWLTLLGAAVIVAIFAPLTVRAYMRRA
>PFR_JS14_200□PFR_JS14_200□Daunorubicin resistance ABC transporter ATPase subunit□240827:241897 Reverse
MTETLAVEAHGLVKQFGSNRAVDGVDLAIDQGAIYGVLGPNGAGKTTTISMLATLLRPDA
GSATIFGHDVERQAGIVRQLIGVTGQYASVDETLTATENLMIFGRLLGLSRRQARAKATE
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RSLVAGGSTVLLTTQYLDEADQLADRVAVIDRGRVVAEGTPDDLKRSVGSASLIITLREP
ADAVPTMAVIERVLGVAASRSPESGRLTMPLTDPDHVTDLLNALRADSIGLVELSVQKPT
LDEVFLTLTGHDTHSADPSTGASDSADPTESPRTESPRTDASATSTNSSAREANAA
>PFR_JS14_201□PFR_JS14_201□Transcription regulator□242430:243455 Reverse
MAARNTAGSWNGGSAGRGNAGNGGHNRRHRGRPRNDHGVPRNASRNHRSEGYDPRGNDVR
GNDWWNDDPDRSNASAQPFGTDRADRPDWADRPDRPDRPDRPDRPVRPDRPDRPDRPNRP
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TMRRVWVDNDGWDPEAGPSSGPYQGRGPGFGWPGGRGRRRN
>PFR_JS14_202□PFR_JS14_202□NAD(P)( ) transhydrogenase (AB-specific), alpha subunit□243814:245367 Forward
MRIGIPRESLPGERRVAATPKTVPQLIKLGYEVVVEHGAGQQASLPDEEYEAAGASLGDS
KTVWDSDIVLAVNEPSVEELGAMHRGATLATFLHPRENPGLIEALQKAGVTGMSMDMVPR
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LGAANSMGAEVFATDVRPETAEQVESMGATFLNVKAPEEAEQGVSSDGYAKETSDDYNKR
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DNPAIMIIAALGVLIASINIFGGFSVTRRMLNMFRKD
>PFR_JS14_203□PFR_JS14_203□NAD(P) transhydrogenase subunit beta□245374:246786 Forward
MVLLETDYINNFINSTFIVSGILFILALAGLSKHESSKRGNAFGILGMALALIAAVVSMI
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VVVFKRSMSAGYAGVQNPLFFKDNTSMLFGDAKASVDAINAALPATADAK
>PFR_JS14_204□PFR_JS14_204□Hypothetical protein□247019:247378 Reverse
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RFRDMGRDNANLVDRGLVTLRYGWHDVASRPCSVARQLASLLRRRGWTGTLKPCTRCAH
>PFR_JS14_205□PFR_JS14_205□4-alpha-glucanotransferase malQ□248053:250008 Reverse
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>PFR_JS14_206□PFR_JS14_206□Hypothetical protein□250079:250561 Reverse
MGDNTEDRSVDASASPTNASASTPDAGNYRDLPDDLPPADLVALNDPSGTPSTLAFRMIA
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>PFR_JS14_207□PFR_JS14_207□Hypothetical protein□250619:250978 Reverse
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YGDRFTVSFAPATGGTLVKVEGAGATEFAATSSARMQKEFDRLFSEVYAELRRDKKFIG
>PFR_JS14_208□PFR_JS14_208□Riboflavin biosynthesis protein RibD□251446:252666 Forward
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PRELAALRRAFELSARGPADDPNPRVGCVLLAPDGGVIAEGWHRGAGTAHAEAAALAAAR
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>PFR_JS14_209□PFR_JS14_209□Riboflavin synthase, alpha subunit□252756:253418 Forward
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>PFR_JS14_210□PFR_JS14_210□Riboflavin biosynthesis protein ribA2□253415:254884 Forward
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SPVSERRAS
>PFR_JS14_211□PFR_JS14_211□6,7-dimethyl-8-ribityllumazine synthase RibH□254881:255348 Forward
MSGVGAPALSVDGSGMRIVVVAASWHTTVMEGLLGGALRALAAAGVADPQVVRVPGSFEL
PVAAMKAASAGADAVVALGVVIRGGTPHFDYVCQAATSGLTEVALQTRVPVGFGVLTCDD
EAQALARAGLPGSTEDKGAQAAEAAIATVLALREL
>PFR_JS14_212□PFR_JS14_212□CitT protein□255505:257013 Reverse
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>PFR_JS14_213 PFR_JS14_213 Hypothetical protein 257315:258412 Reverse
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VETNS
>PFR_JS14_214 PFR_JS14_214 DNA protecting protein DprA 259410:260264 Reverse
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>PFR_JS14_215 PFR_JS14_215 Putative type I restriction-modification system, R subunit 260413:263778 Reverse
MGNFDFITADWPQIHNDCARAESYVITDPRSACIYARRSVETLVRHLYFLLDLAEPYRDD
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SVDIDRFRDKVQAYLREHQDNVALQRLRRNRPLTSQDITVLEQLLTASGADRDAIDHAAE
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ESPYTDDAPAGPTVFFPDPEIDTILDIIGRVNDNATPEGVA
>PFR_JS14_216 PFR_JS14_216 Restriction modification system DNA specificity domain-containing protein 263778:264917 Reverse
MIHIGDLLVPFKELPTANHELPVLTLTERHGFMPQAERFNKRLATDDTSKYKVVRRDDIA
FNPYLLWAGAIAQNTIVDAGIISPLYPTFRVRKENDPRYVARLLLTEQLIAAYDKIAYGS
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>PFR_JS14_219 PFR_JS14_219 Putative zinc-binding sorbitol dehydrogenase 267341:268405 Forward
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VQRAFELSLDSRFPTRQILTHILPLSEINEAVELTRSGEAIKVALLPNERSQDV
>PFR_JS14_220 PFR_JS14_220 PTS system, Lactose/Cellobiose specific IIB subunit 268398:268700 Forward
MSELKILIACGSGIATSTVAQEKVKDILANAGIPAKITKGTIGQVESLQDGVDVIMVTTR
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>PFR_JS14_221 PFR_JS14_221 PTS system Galactitol-specific IIC component 268749:269975 Forward
MNLGAVVMLPIVMTILGIIFRMKIGKSLKAGLMVGIGFSGLQLVITLLMTTVQPAVNYYK
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>PFR_JS14_222 PFR_JS14_222 Class II Aldolase and Adducin domain protein 269985:270611 Forward
MQFETERQLICKFVKNMYDRWLTNAAGGNISMRVGEDRYVMTATRLSSHKLWDITPDDVL
VVDGELNVLEGDGVPTREINMHMAIYQKDAKTRAVVHAHARNLMVFAGRGLDMPVQSEAL
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GESLFVAYEMLERMDTNAYIVTQGAGLR
>PFR_JS14_223 PFR_JS14_223 Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2 270625:271140 Forward
MTQMIGASGGDGVKPTGGEELASPDAVWLGLESDSAHALLSDMSQRLLDAGYVRPGYSES
LWRREERYPTGLPVSGGVAIPHTEPELVRRGVVAIASLARPVAFEEMGGSGTVPVSVVFL
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>PFR_JS14_224 PFR_JS14_224 Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2 271266:273179 Forward
MPTLTERQGVLLQLLSEMTDPITNAALADLLGVSPRTVRYDIARVNRLTNAPLIEAARGG
HLLNLPEYRRLVKRLASVDRAGDDRERILLALVNGFDGDLFELAQQQMMSDATVRTLIRE
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>PFR_JS14_225 PFR_JS14_225 Hypothetical protein 273644:273985 Forward
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GLIAPTAGTVAYRGKPLTGANPGVGMVFQSFGLMPWLTVQDNVELGLRARGVAPHQRADQ
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TWAASHREADLMQCAFPAATLVAFDVDGPWSQLTDFDPYDYTDAAHPRVSPVRPADLPTG
>PFR_JS14_297	PFR_JS14_297	Putative DNA modification methylase	359202:360470 Reverse
MTSGHRDKMCDVSAYLMLLAPSANHVYAAETATLAAAELAVTSPDLGAAVERRVAGVDYL
AFEADDLDPRKIAAQSSVLALFERASAPAELPGRASEQAALFGSEPAADVPTTSPSEVLL
RPIELPRSDVLDDDLVTIPKYRGKTNELFTRLLLHVTLSQVTTRRGTAAAGRDAPTGHDQ
TRRQFDVLDPLAGRGTTLLTAWTAGHNAYGVELDTSAFEQFAGFLKTYLRRKRLKHTAEV
TTVRRDGRMMGQRLDATARPGEQTRGHRAVPDAPQLAMTMFTGDTRDAAVLFGKRKFDAI
VTDAPYGVVHGATDARRASRENGKRGSAGHPTGHRPGGDRDRSPATLLADAIPVWAGQLR
AGGALGLSWNTYGLSREDLAAICTDAGLEVRDDGPWLQFAHRVDSSIKRDLMVAVKPARL
VS
>PFR_JS14_298	PFR_JS14_298	Inorganic diphosphatase	360620:361177 Reverse
MTDEFRIATGLPQYDLTFDMTVEIPRGTKNKYEMDHNTGRIRLDRTLFTSTQYPYDYGFI
EGTLGEDGDPLDSMVILTEPTFPGCLVRCRAIAMFRMRDEAGPDDKVLCIPTADVRRDYM
DDIDDVPQMVMLEIEHFFTVYKDLEPGKSVEGASWTGRTDAEAEIRASFERAKGTSYEHL
KVDLQ
>PFR_JS14_299	PFR_JS14_299	D-alanyl-D-alanine carboxypeptidase, serine-type, PBP4 family	361239:362609 Forward
MKSATRRPLTRWIVAFGVVLVLVIAGSVGLHASGALVSGGASTVPAGVFATPATNLNGNG
VIGDAPVPASYAALSADKVAAALNRVGVRNGYSVVARDLSNGQVLDATRGDDAVIPASSM
KLMTTSSVIDKLGPTHTFSTRVMRQPDGSITLVGGGDVLLASTPTSYAYGSPQPATTQDL
AQRTADALKAAGTTSVTLAYDDSLFSGATRHPDWEPGDMAYVNDISALMVDEGGGSTTPA
ATAATTFARQLGANGISVTGTPTAHVSQSGATQLASVDSLPLSQIVQECLRHSDNTIAEV
LFRHLAIAYGQPGSFDGGVQALQQAMTHLGLWSGVDSLHDGSGLSVHDRLTASALTQVIT
LAAGRDDLRNLLAGLPVAAATGSLETRFIDSASSAGGGRVRAKTGTLDTASALVGYTPTA
DGGMVAFALVGNGVGAEVRPYLDQMAGALSGCACAA
>PFR_JS14_300	PFR_JS14_300	Coenzyme F420 biosynthesis-associated protein	362771:363862 Forward
MGVQSTPEEPPQSGAALPWVDWDTTLRVATSSAPIGPPVSLAERRQAVEQLRASAERAPQ
IVADASHLQPPARGEALIVDRAGFARANTDMMRQIWQGIGVEVRPRGPGLIPGIVRGGAV
GKMIGLLSGHVLGQFNPLGSPPRLLLVAPSIMSTERRLGVDPGDFRLWVALHEQTHRAQF
QAAGWLTAWMLGRVRALIEADADHESAVHGALDHFAMLKHHRDSDDDVALTMAEMLTTPS
AAAVLEQVSGVMSLLEGHADVMMDRAGPEVIASLATIRARFDARRGRGGPQMIMLRALGM
GAKLAQYREGAAFCHAVIDAADNDDEGIELLNRVFTSAAEMPSLHEIRQPDAWLARMGVD
VHR
>PFR_JS14_301	PFR_JS14_301	Cell cycle protein MesJ	363862:364851 Forward
MATRALGRAGLALVAAVSDGLQRASEQGSRVRVACSGGPDSLALAAAVAVCARRDPALLA
EALVVDHQLQPGSREVAHAAVDAVRGLGLPARTVAVQVPHSGEGPEAAARRARYEALAAP
DAAGGRRPDLVLLGHTLDDQAETVLLGLVRGSGIRSLAGMPAHFGSAPQFWRPLLGVRRA
DTERACVEWGLAPWHDPQNRDDRFTRSRLRHRVLPVLTAELGEGVIEALARTATLATQDA
DYLDALTSSALTTIMGDGGLDCARLADQPAALQGRLVRRWLATVGIVGLDFERTAAVLAL
VTHWRGQKGVDLPGGHRVVRRAGVLFLDR
>PFR_JS14_302	PFR_JS14_302	Hypoxanthine phosphoribosyltransferase	364957:365508 Forward
MYATDISNDLEHVLIPADKLAARVEELAAQIDADHAGQDLLLVGVLNGAMMVMSDLSRAM
KSLVTVDWMAISSYGAGTQSSGVVRILKDLSTDIHDRDVLIVEDIIDTGLTLSYLVQNLT
SRGPRSLEIAAMFRKPEAVDAPVDVKYVGFDLPNEFVVGYGLDYNGLYRNLRDVATLATH
VYR
>PFR_JS14_303	PFR_JS14_303	PIF1 helicase	365580:368039 Forward
MTTPRVDDGHVGDDGHARDDGLVLTAEFRDALTRLGRGENLFLTGKAGSGKSTLIRLFME
SNERTVVVAAPTGIAALNVDGYTIHRLFSFNTATTPEQVASGDYYPGRFAQTLKSLDTLI
IDEVSMVRADLFDCLVAALERFGPHPGQLLGGVQLVLVGDLYQLPPVVTEGEREYFSTTY
ESPWFFSAHAYRRDDFPTVELTTVFRQIGDARLVHLLNAVRDGRLLAAARAELNQRTDPG
FEPPIDEFWLTLATTNRIAAARNNRQLARLGGRQYSYRATVTGDATGFDAPADEVVTFAV
GAQVMMLTNAQGAHGEGSHGRPRWVNGTIGRIAAVRYDHDEPVVTIALPDGRREEAGPHA
WDITRPVVEGGRLRHEVVGSFTQLPFRLAWAITIHKSQGQTLDHAIVDLSGGTFAEGQLY
VALSRCTSLAGLVLARPVLPKDLKADQRIRRFLASARTSVPRRGLAFLAVTFVGDEGRMW
RPRPLEVAVVTDDGRELVTLVNPDRDMGESARVNALSASDVRFAPMLGEAWPAIERCLDG
YGLIGVDIDQTLDYLDYELKRGGIVSPMPIGGEAESSLSPDEARELDELPTLQRARRLRE
LVLAHRGTGREFPEGTGSRAAAPTADPWADIETFSRAGAADGGPVRHGDGAEQPAVLLVR
DGAQRSFVVDAPDMASEADRAAFLAARLRAAASRTVVDDAALAELEQLERQWGVTIITDA
MRRPADSAEQVLVPGARVCFTGSVIDARGTTISRSDMEQLAAEHELVAVPSVTRTRCDVL
VAADTASRSGKARKALDLGKPVISAAEFLAWANPAGPGR
>PFR_JS14_304	PFR_JS14_304	GTP cyclohydrolase 1	368060:368767 Forward
MGMPSRKGAPLSESTRAGRSDGTRETDATDHAIDNSAYEQPGLELPPGFDGKRIEAAMRE
VLIGIGEDPDREGLVETPARIARAYGEIFSGLGKEPDKVLARTFDISHDEMVLVRDIDVH
SMCEHHLLPFHGRAHVCYIPAKDGRVTGLSKLARLVDLYARRPQVQERLTTQVANALVDQ
LGARGVLVVLECEHQCMTMRGVRKPGSTTVTSAVRGVLRDPATRSEAMSLIVRNR
>PFR_JS14_305	PFR_JS14_305	Transcriptional regulator, GntR family	368778:369245 Forward
MPSAARKPGDAPDHAKGPDGAPRRMAAQDASGGVGGPAGPLVHIDAASPTPVFEQIIEQL
RRGVVQGSLPAGTRLPAVRALASELGVAVNTVAKAYRQLEAEGTVVTGGRNGTTIAALAD
AEPTRVAEAARTLIARARDAGLSRDQTLGLVARLW
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>PFR_JS14_306	PFR_JS14_306	Dihydropteroate synthase 1 FolP1	369385:370218 Forward
MADRADRPGDGHTRVMGIVNVTPDSFSDGGLYLHADAAIAHGVELVRQGAELLDIGGEST
RPGATRVSEDEELSRVIPVVGGLAADPRTRDIPLSVDTMRASVARASVEAGAAIINDVSG
GLADDAMFATVAGLDVDYICQHWRGFGQEMNQRARYHDVVTEVRDELAARLALAEQAGIS
HDHLIADPGLGFAKMGEQDWQLLRHLDVFVALGHRVLVGASRKRFLGVLLNGREARDRDA
ATAAVSAWCAQRGVWGVRTHEVLSQADAIAVTEHLML
>PFR_JS14_307	PFR_JS14_307	Dihydroneopterin aldolase	370365:370739 Forward
MSVEPEMGFVVVSLSGITAMGHHGVLESERREGQPFSVDLRLVAPEPGTDELSEAVNYAE
VAELVSDLIRSQAVNLIETLAARIADAVVELPRVREVDVTVHKPHAPIPVPFNDVTVTVN
RRTP
>PFR_JS14_308	PFR_JS14_308	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	370736:371281 Forward
MNAFIDSDTLGDLKPLNRVVFSLGSNQGDSLDILQGAVDMLAATPQLIMVDVAPVYLTKP
VGNTNQPDFYNTVVLAESTMEPRDLLDRANVIEQAYARHRDPDNPHGPRTLDVDLIVVGK
RTSATQRLELPHPRAHERAFVLVPWLDIDPKATLPQGPIADLVARMDVGGVHKLDAGLLK
P
>PFR_JS14_309	PFR_JS14_309	Hypothetical protein	371837:372193 Forward
MLLILGLRKGFDMARNVKVVLIDDVDGGDADQTINFGLDGVNYEIDLSNANAQKMRDELA
VWVGHGRRVTGRRGAAARKQGPSDAAKIREWAKSTGRQVPLRGRIPNAIRAEYEEATK
>PFR_JS14_310	PFR_JS14_310	Negative regulator of genetic competence ClpC/MecB	372996:375572 Forward
MFERFTDRARRVIVLAQDEAKMLNHNYIGTEHILLGLIHEGEGVAAKALEQMGISLEAVR
EQVIEIIGQGSTPPTGHIPFTPRAKKVLEYSLREALQMNHSYIGTEHILLGLIREGEGVA
AQVLIKLGADLNRVRTTVLQLLSGYQEEGGGQPATAGAPEMGPGTSTNNGALDQFGRNLT
QAARDNKLDPVIGRQKEVERVMTVLSRRTKNNPVLIGEPGVGKTAVVEGLAQAIVRGDVP
ETLRDKQIYTLDLGALVAGSRYRGDFEERFKKVLKEIKTRGDVMLFIDELHTLVGAGAAE
GAIDAASILKPMLARGELQTIGATTLDEYRKHIEKDAALERRFQPIQVDEPSVQLTIEIL
KGLRDRYEAHHRVTITDEALSAGANLADRYIQDRFLPDKAIDLIDEAGARMRIARMTAPP
DLREFDDKIAATRAEKEAAIDHQDFEAAAKLRDDERKLTAARAEKETAWREGESDTPAVV
GEEEIAEVLSSSTGVPVARLTEEESQRLLNMEDEIHKRYIGQDEAVKAISRSIRRTRAGL
KDPNRPSGSFIFAGPSGVGKTELTKALTEFLFGDEDALITLDMSEYSEKHTASRMFGSPP
GYVGYEEGGQLTEKVRRKPFSVILFDEIEKAHPDIFNSLLQILDEGRLTDAQGRVVDFKN
TVIVMTTNLGSRDISRGVNLGFSKTGDTENSYEQMKSKVSEELKQHFRPEFLNRVDEVVV
FHQLSQDDILHIVDLMVGQIENRLGDRDMGIELTPAARELVGKRGFDPVLGARPLRRAIQ
RDIEDPISEKILYGDLKAGSIVLVDVAEGATEKSTEAFTFKGMPKHDEVTDSEFAQLTGA
GSTGGDAGPADPQAPSAS
>PFR_JS14_311	PFR_JS14_311	Hypothetical protein	375723:376409 Reverse
MSIPTPPQGWRSQARLLTMLLWLNMAVQLLAGAMCLLLATRVDTPTDSVDDPGLRMFDAW
QLLTTATGLVFMLTAIVWLVWQRGTARMALRWAPELSQPAWQLFNWVIPLINLWRPLVDL
RALHRVFTIVRKDEMAADGIRGSIELAQVRLDDFRAATTRWWACWITFATAQLVAAWIVA
GASGTTGARAGFIASGIADLLALPAAFLATRVVSELTRRVADAAGLRA
>PFR_JS14_312	PFR_JS14_312	3-dehydroquinate dehydratase 2	376406:377161 Reverse
MAVLELAGLTLGGPHTAIIVPLTGADPGAVQAQAEVASQPAVDLVEWRVDAFAPGADDAL
LADTARHIRTTTGKPLLATVRTGSEGGHFTGSPEDYARLVATLAGLDDVDAVDVEYRHPA
APETIASAHRASTAVIGSFHDFAGTPSLDAMVAHLEAMEQAGAQLCKLAVMPHNPEDTAR
LLLATATRSRDAHTPLLTIAMGRLGLASRLCGRDFGSCASFAALDEHGSAPGQLPLDDLA
QALSIVRHAER
>PFR_JS14_313	PFR_JS14_313	Para-aminobenzoate synthase, subunit I (Precursor)	377307:377888 Reverse
MATDMTLPDDLDRLVDRLVRDARGRRPVMVLDGGSGAGKTRLATRLVGALGERGMHGVQL
VSMDSFYPGWDGLQAASTMLPEVLRVHDPGYWRWDWQAGRRTDRVGLDGDAPILVEGCGA
LTAFSAGVGTTAMWFVMDAARRKQRALGRDGELYAPHWDRWAAQERQHWRRDRPRELADV
ILHDAGQVDAGAV
>PFR_JS14_314	PFR_JS14_314	Cobalt transport protein CbiQ	377899:378726 Reverse
MTALPHAPLTGTDQSGASGADWSGALARLNPVTRLLLTVLVAIPVLISLDWLSATVIFVG
ELVVFLACGVRARMLARRMIPLLIVAPLAAISMALYGKPGGDVYFQWWLVVISQRSLTMA
IAVVLRIFALGLAALVLMGGLDLTATADGLAQICHLPARFVLGTLAGMRMINLFAADWRT
MAQARRARGLGDTGRLRRFATMAFALLVFAIRRGTKLATAMEARGFDASTAAHRTWARPS
RMGRADAVGWLLAVVMVALALAVSIRLGTFTPVTR
>PFR_JS14_315	PFR_JS14_315	ABC transporter	378723:380393 Reverse
MPTPSTDLAPGVVASDWGWRYAGRPRWAARHLDFTIEPGERVLLLGASGAGKSTLLGALT
GVLGGDDEGEEAGSLLVGGKHPTRMRGHVGLVMQDPTSQMILQRIGDDAAFGCENLAVPR
EQIWPRVRAALDAVDLRLPLDRSTTALSGGQQQRLAIAGALAMMGGPGAPGMLCLDEPTA
NLDPEGVTTVHDAIASVVADRHTTLVVVEHRVDIWTDLVDRVIVVSADAGLLADGAPREV
FAAQREVLTRAGVWVPGAPRGVEPRTPPTPGEPLLTTHDLTIGHGRAHPVRTMEPTRVPA
GLSTTIVGPNGAGKTTLALTLAGLLEPLAGSVEAAPSLRPTSARFLTRAMHRRFDPARPI
TWASRDLLTRIGTVFQNPEHQFVTGSVREELAVGLKALGRGARDIDSRVDALLARLHLEA
LADANPFTLSGGEKRRLSVGTVLAAEPRLIVLDEPTFGQDRATWIDLVQLVQDVLEQGRT
VISVTHDRDYLEVLGENELRLDIASPHPASASSPAGGRPAGHAPGERRPKDRQPSADQPS
GERPSADQPSDHRMAP
>PFR_JS14_316	PFR_JS14_316	HMP/thiamine permease protein ykoE	380419:381054 Reverse
MSSSKTTPATSDQTRPLEVGTRHWRVVDIVVAAVLGVACGLIFWIWNSIGYAWYSAMGAL
LPGLGGIAAGIWYLGGTLGAQVIRKPGAAIFVELVAAIVSALIGNAWGIETLTSGLFQGI
GAEIIFLIFRYRAWSLPVTLLAGAFAGFGAWANELFIGSTPNIAKSFGYNAVYLVSNLVS
GAILAGLLAWLLTKALARTGVLSRFSSGREA
>PFR_JS14_317	PFR_JS14_317	Adenine glycosylase	381286:382164 Reverse
MEPGQRRAVVRAVNQWYAHTARDLPWRRVETSPWAIMVSEFMAQQTPVARVVGPWREWLD
RWPTPDALAAEPSSAAVAAWGRLGYPRRALRLHAAATAIRDHFGGEVPHRVEELRQLPGV
GDYTAGAIASFAFGARALVLDTNVRRVLTRLDAARQFPANSTTAAERRLAMDWLPDDAPT
AARWAQASMELGALVCTAANPACDDCPVRADCAWLAAGRPAHDGPPRRTQAYAGTDRQAR
GTLLGALRTTPQGFEVSVLLQHWPADPAQASRALDGLLSDGLAHREGTRVTL
>PFR_JS14_318	PFR_JS14_318	DNA integrity scanning protein DisA	382244:383314 Reverse
MASIGDAKGRVAEQFRQYRSLLAPGTPLREGLERIVNGRTGALVVLGDNAIVQQISTGGF
VINTDFTPTALRELSKMDGGIVLSSGLDRILRAGVHFVPSGSIETIETGTRHRTADRIAQ
QAHVPVATVSASMSTIALFLEGMRFPIEPSHQIMGRADQALATLSRYRDRLTDDTRYLTG
LEIADLVTLRDLVRVCQRVEMARRLAKELEGYVESLGIDGRLLQLQLFELTAGVDETATL
LENDYSIEERPGKPSLEELEELPTGDLLDPESVSSAIGFGATPLDTHLRPKGFRLVHQAA
QLDTALTRRMLDQVDSIQELFDLSVEDLMRVDGMDTKHARALRDGLARLAELGTQS
>PFR_JS14_319	PFR_JS14_319	DNA repair protein radA	383352:384746 Reverse
MAKKQQDSYQCTECGWTGVRWVGRCPQCQAWGSVVERGASVSTSTAVRTSAPTTRALPIA
QVSAQASDRHLTGIGELDRVLGGGLVPGVVVLLAGEPGVGKSTLLLEVAAQWARAGHRTL
YVTGEESASQVRLRATRTDALADELYLAAENDLGTVLGHVEEVEPSLMVLDSIQTVSAGS
GDGVSGGVAQVREVTTALVRVAKARGMAVIIVGHVTKDGGIAGPRTLEHLVDVVLNFEGD
RHSGFRMVRATKNRYGPADEVGCFEMGEGGIVEVPDPSGLFTTRHDEPVPGTCVTVTMEG
RRPLLAEVQGLVAPVPNETPARRVTNGVDFSRVAMILAVLQRKARLPMSRRDVYVSTVGG
ARITDPSADLAVAVAVASASLNRNFPRRVLAMGEVGLAGDLRRVPALERRVAEADRLGFE
LAIVPTNSRDNSRGAPKLHNLKVVEVPSVADALGVLDLRRAERR
>PFR_JS14_320	PFR_JS14_320	Hypothetical protein	384862:385500 Reverse
MHVDHLTFAAGPEGLEVAAKHLGELLGEEFKDGGFHPRFGTRNNILPLLKDRYLEVAEVL
DHPVAEKAVYGQAVRARSEQGGGWLGWVISVDDLAPFEERLDRGAVPGSRHFPDGRELKW
EQIGAKGLMSDPQLPYFVKWESPADVLPSALPGDIALASLEIAGSRQRIEDWMGEALPDV
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FDGVNIEFTSPNAHPGINAAIFSTPEKGLVRI
>PFR_JS14_321□PFR_JS14_321□AP endonuclease, family 2□385719:386588 Forward
MFYRGGVVSKPPPDASGSKRLSVSLSTSSCYPEHTAEAFDIAAEAGYDGVEVMVGLDAAS
ADVPYLARLAAQSGMPVVSVHAPCLLLTQNVWGPDPWDKVRHSCEAALALGSDVVVLHPP
LRWQREYAAGFVAGVRDISEHTGVTIAVENMYPWRTPGRAFQAYLPSWDPTDLDYDALTL
DVSHAATSQLDALELARTWGPRLRHVHLTDGVGLRRDEHLFPGEGTQNVWGLLQYLNDSP
FDGHIVLEVNTRKADNHAERVRELREVADNTRLHLGQLDAARPGTTPTS
>PFR_JS14_322□PFR_JS14_322□CAAX amino terminal protease family protein□386590:387468 Forward
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KSAVYSVLSLVNSLTVGSKLNEQTTTINGAVTPDRPWLDVAYKLADDFFLIVPVVMAIYL
LASVRRPGPSVWRAIGLDGLRVRRDVLVGVGATAAVGIPGLGCYLLGRQLGLNTTINTAG
SGASLAAIAFYVVAAAANAGLEEIVMIGYLLTRWRQAGWNAWAAIVTSALIRGSYHLYQG
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>PFR_JS14_323□PFR_JS14_323□Hypothetical membrane protein, DUF1211 family□387613:388308 Forward
MRAERVQAFSDGVFAILLTILVLEFVVPDYQEGHLFEAILGQWPIMFAYVLTFTYMGVVW
LFHHDLFASVKTTSIWLNILNLVLIFVCSLLNYATSLLSTAIATGNGTDMAAAFGIYDVN
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ALLIGGVIFHALAYAGSAHSYRRSRRKVLRDARRQALKDAPGPGSESGPPA
>PFR_JS14_324□PFR_JS14_324□Aspartate-semialdehyde dehydrogenase asd□388400:389434 Forward
MRVGVFGATGQVGGVMRTLLAERNFPVDEIRYFASSRSAGRHLPWGDKQIAVEDMATADF
SGLDLAIFSAGKTASKEYAPKVAAAGAVVVDNSSGWRMDPDVPLVVSEVNPEDTKNLPKG
IIANPNCTTMAAMPVLKPLHDRWGLKRLVVATYQATSGSGLSGVRALEDQTRTAMADDPH
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>PFR_JS14_325□PFR_JS14_325□ProC protein□389438:390298 Forward
MALRTPAASVDRVHRLAFLGAGTMGGTIVAGLVRAGRDAAGIAVTTHTPAHREKLAAELG
VQAFADNRQAAAWASTIVIGVKPADALALLDEISPELGPDNVVISLCAGLSTDLLSAHLP
PAVHVVRVMPNTPASVGAGMAGVSGGRTATEHDVQAAITLMSAVGRAVAIPEKLQDPLTA
ISGSGPAYVFAFVEALIEAGVTQGLPRGLATELATQTLLGSARLLDEGNDSVTQLREAVT
SPGGTTAAALRELDDHGLRSAVQDAVEACARRSAELAAAAEQADAR
>PFR_JS14_326□PFR_JS14_326□Uroporphyrin-III C-methyltransferase hemD□390787:392403 Forward
MSQRVDVEAPDNAGPDDVAGRLCHGRVVFVGSGLSSADQLTRAGLRALSSATMLVTTPEL
REMLDEAGVEVPDKDATRFVGDLPDVARFVVEAAGDDQSVARFVRGDPLLEGNIADEVSA
YIDADLMLDIVPGVPSLTSVTTLAGVSFPGQSVQLISLPYRAKTAEIPAAGSLAVGCYSS
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KASHRPEGMNWYESKPLFGWQVLVPLTRDRNEELIERLSLHGAHCTEVPTIDVEPPRNAA
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WGLIPDLAPTDVHTVAGLAAEFPAYDDIVDPMNSVLVPRAEIATEPLSEGLAELGWEVDD
VTAYRTVRASPPPAPIREAIKSGDFDAVVFTSSTTVRNLIGIAGKPHAATMVAAIGPATA
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>PFR_JS14_327□PFR_JS14_327□Phosphoglycerate mutase family protein□392458:393117 Forward
MGDQQTIVHVMRHGEVHNPQAVLYERLPGYHLSDNGSRMAQVVAAEFADVPLTHLRTSPL
LRARETMAPVAAEHPGLQVHYDPNLIEAGNKFAGMKFGRYKTALVDPRNWKLLRNPFTPS
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LASVTSFHFLGDECIDITYSEPAAHLLGSDGNAAFSSGN
>PFR_JS14_328□PFR_JS14_328□Mycothione reductase□393233:394753 Forward
MATESSGGTGLSGAGRHSGGGASDHFDLCIIGSGSGNTIVNHEFNDWSVAIVDQGVGEGE
WFGGTCLNVGCIPTKMMVVPADFAASPDRAARLGVELSRGAVDFAGIQQRVFGRTNAIST
DGLAYRESNENVTVFREAAAFIDAKHLQVGDRVITADQFVLAAGSRPRTLDVPGLNDPDL
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ASGASGLPPRACLDAARAMDPQARVELLYMGSVTATTPAAGAGQLANQPVGSVILMGDPG
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DPAGPAAFSSRVVSGLLREQLGYSRVVISDDLGAAVALADYPVAQRGTLFLRAGGDLALD
VDPASVPAMVADTQAAVAADPDFAEQTVAKAARVLQLRADAGLGQCGA
>PFR_JS14_330□PFR_JS14_330□Arsenical pump-driving ATPase□396119:397894 Reverse
MTHLLEEMPRFLFLTGKGGVGKTSVACASAVALASAGRKVLLVSTDPASNVAQVFGQEIG
NHITAISALPGLDALEIDPQAAAEEYRARALAPVRDFLSAKDLASATEQLSGSCTTEIAA
FNEFTDLLTAHGPGAGYDHVVFDTAPTGHTVRLLKLPGEWSQFLSDGLGDPSCLGPMSGL
EKTRDSYAEALGALADPGRTRLALVARAQESSLHEASRTFDELLEAGIAATHLVINGLLP
GAHSDDALARSISHQESEAIGSAPARLRALVTDTLELRHGDMVGVDALRTLLSSTAQTED
SDVDVNQPRRPSVAGPQLSELIAELSQRDHGLVMVMGKGGVGKTTLASALAMGLADRRKD
VLLTTTDPAAHLDWTIAGQAPFDVTSIDPEVATRQYRDHVMATKGASLDEQGRANLAEDL
RSPCTEEVAVFQSFAQAVEQSDHRFVVMDTAPTGHTLLLMDATGSYHREVARNSPELAST
TPLTRLRDPGHTAVIIATLPETTPVLEASGLQDDLERAGIRPWAWVINRSLSATDTEDPF
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>PFR_JS14_331□PFR_JS14_331□Putative arsenic resistance operon repressor ArsD□397891:398358 Reverse
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AFMQVAGADGLPLVVVDGVAVSTNRYPSREELAVFAGLASAAGCCSGDAAGANAPGCCGS
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>PFR_JS14_332□PFR_JS14_332□Toxin-antitoxin system, antitoxin component, ArsR family□398455:398829 Forward
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DLGITQPTLSYHLTRLLKAGLISREMRGKWAHYTATAHGLDVVRAFMDGLGAVGPGTCDA
TDCC
>PFR_JS14_333□PFR_JS14_333□Putative heavy metal reductase□398829:399281 Forward
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>PFR_JS14_334□PFR_JS14_334□Phosphate ABC transport system ATP-binding protein□399262:400041 Reverse
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>PFR_JS14_335□PFR_JS14_335□Phosphate ABC transporter, inner membrane subunit PstA□400046:401206 Reverse
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CVVGVFLVSQLAHSFSVLSWVVISVVAYLVLHYVVSRSVEGRRRAFDRFARDLVTLAFLL
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>PFR_JS14_336□PFR_JS14_336□Phosphate ABC transporter, permease protein PstC□401203:402183 Reverse
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DSIK
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D
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>PFR_JS14_346□PFR_JS14_346□Transcriptional regulatory protein GlnR□412325:412984 Reverse
MSDALFVSPTTDPKPLPGALTLLPHTIDQVQGGDKAILQIPDTDAVIIDGRGDLGATRVT
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>PFR_JS14_369□PFR_JS14_369□Protein kinase family protein with PASTA domain□440250:442040 Reverse
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>PFR_JS14_370□PFR_JS14_370□Penicillin binding protein transpeptidase domain protein□442132:443556 Reverse
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ADSGTSSPKGKR
>PFR_JS14_378□PFR_JS14_378□Mannosyltransferase PIG-V domain protein□450760:451977 Reverse
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ARP
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VALAKATPVYEYLPGWTQDISDVRSFDELPATCKDYVHFLEQRVHCRISGIGVGPSREQT
IIINELV
>PFR_JS14_403□PFR_JS14_403□Amino acid transporter, APC family protein□478008:479663 Forward
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IGPALYGDSFIGHLGMGLLSISILTSSALSTQTTILPTARTALSMATHGAMPKKFATIAP
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DSGVPDRVAVV
>PFR_JS14_404□PFR_JS14_404□Glutamate-1-semialdehyde aminotransferase (Precursor)□479805:481172 Forward
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RWGLAKWRFTNSGSESTMDAIRIARAYTGRDTIMKIFGSYHGHHDAVMVSIGVEYDKIGP
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VLPEPGYLEAVREITRKHGIVLIFDEVKTGLTIAAGGATERFGVKPDLVTLAKALGGGLP
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>PFR_JS14_405□PFR_JS14_405□ATP-dependent chaperone protein ClpB□481531:484131 Forward
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DGAASAAIDKLPSSSGSSVAQPQLSGALARVLADAETRADKLGDQFVSTEHLLIALAEVD
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>PFR_JS14_406□PFR_JS14_406□Oligopeptide transporter, OPT family□484252:486243 Reverse
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TTS
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RTHFE
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EDLGL
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>PFR_JS14_411□PFR_JS14_411□SNARE associated protein□490177:490920 Reverse
MIHAAQRYPCRVLPLSLLPALVPMLPSWMDPATIIHALGNGALWGVCAILFIECAIFPIL
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AAAGADA
>PFR_JS14_412□PFR_JS14_412□TRNA/rRNA methyltransferase (SpoU)□490996:491688 Forward
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>PFR_JS14_413□PFR_JS14_413□Hypothetical protein□491694:492320 Forward
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MPGTIDSGLWAYSGRRLHLDMSRCEQVW
>PFR_JS14_414□PFR_JS14_414□Fructose-bisphosphate aldolase, class II□492549:493571 Forward
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>PFR_JS14_417□PFR_JS14_417□Possible alcohol dehydrogenase□494354:495502 Reverse
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>PFR_JS14_420	PFR_JS14_420	Methylmalonic acid semialdehyde dehydrogenase	499071:500576 Reverse
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SSWWDVVVSETSRLESTQQARVQYEQDRRPQRHYL
>PFR_JS14_422	PFR_JS14_422	Myo-inositol catabolism IolB domain protein	502845:503717 Reverse
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>PFR_JS14_423	PFR_JS14_423	Deoxyribose-phosphate aldolase superfamily protein	503714:504583 Reverse
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>PFR_JS14_424	PFR_JS14_424	Kinase, PfkB family	504586:505575 Reverse
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IEKELFA
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GA
>PFR_JS14_431	PFR_JS14_431	Dihydroxy-acid dehydratase 1	512068:513909 Reverse
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AQSADKGAARRQL
>PFR_JS14_432	PFR_JS14_432	Aspartate--ammonia ligase	514042:515952 Reverse
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>PFR_JS14_466□PFR_JS14_466□Protein of hypothetical function DUF162□555162:555818 Forward
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REAGIPEAVVAGLKATGAEESVVVPAGLDESWVKAIKAAGYTVSNDEPQLSNKELDGTDA
VVTASASAIADTGTIVLDHTEDQGRRALSLVPDRHVCVVRASEVVSDVPESIQALKPSVH
AGHPLTFISGGSATSDIELSRVDGVHGPRKLYVVLVED
>PFR_JS14_467□PFR_JS14_467□Hypothetical protein□556060:556461 Forward
MAEIRKHRPKANLIGDQVRAAMGDAVPRPVVPGSHKVPAAPEASGDDATTSTGGRTRIDF
DAVAEHELVDPFFVEVPTEEPVAPKPDAASEQAGGYTLRAADRGGLISLGADDINAISVV
FREVDRDEDDDTD
>PFR_JS14_468□PFR_JS14_468□Lipopolysaccharide kinase, Kdo/WaaP family□556507:557889 Reverse
MPRFLSAKPDARLIPLPWNVPLAKWPTEHLVALPRGISRHVVRFITVGDEVYAAKEVIEH
LAIHEYRLLHDLTRLGTPAVEAVAVVSGRQDLEGNPLDSILVTKHLEFALPYRSLFTPGV
RHETVMRLLDAMVVLLARLHLQGFMWGDVSLSNILFRRDAGSFAAYLVDAETGELHDRLT
DGQRAHDLDIARTNVFGDFCDLQAGGMLDESLDPMVLVDTIESRYQELWNELTGMEEFSG
SELYRIESRVRRLNALGFDVAELDIRTSADGQTVTLQPKVVDAGHHSRRLLRLTGLDTEE
NQARRLLNDLDTFRARTNQQDVDEAVVAHQWLTEFFEPVVNAVPPELQGKRDPAQIYHEV
LDYRWYMSEREKREVPLSVATQGYIRDILRNLPDEAMVRDAMVQVQEGDNRQLANPYDPS
LGYADDDDLPPVHDPWEDAAQDVDVSQLNHFDINELRARG
>PFR_JS14_469□PFR_JS14_469□Cystathionine gamma-synthase (Cgs) (O-succinylhomoserine (Thiol) lyase)□557974:559161 Reverse
MSDQSGKDPSPELSALTRAVRAGLDTDTQFGSVVPALYPSTNYRFPSIDERPPFDYSRSA
NPTRAMLATTLATMEHGVTATVTGSGLGAITATVEALTGPRGRVVAPTDCYGGTWRLLDH
LATKQRIDVEFVDMWDLDEAARALATPAELVFVETPSNPLMRITDVAAVARLAHAAGAIV
VADNTFCSPLLQNPLTLGADVVVHSTTKFINGHSDVVGGAVISKTAETGELVAHWANALG
LTGGAWDSWLTLRGLRTIDARMRVHQANAAAVVELLSNHPAVQAVYYPGLATHPGHDLAA
RQQSGFGSLLSFELTGGIDAVRRFTDGLQIIDLAESLGGTESLLAHPATMTHAGMSPEAR
AAAGITDSLLRLSLGIEPVDDLLNEIRSALDRAVA
>PFR_JS14_470□PFR_JS14_470□ATP binding protein of ABC transporter for sugars□559431:560540 Reverse
MAESMATVRYKDATRVYPGADHAAVNDLNLEIGDGEFMVLVGPSGCGKSTSLRMLAGLEE
VNSGSVWIGDRDVTNLPPKDRDIAMVFQNYALYPHMTVAENMGFALKMKGVGKEERQKRV
LEAAKLLGLEELLGRKPKNLSGGQRQRVAMGRAIVRDPQVFLMDEPLSNLDAKLRVQTRT
QIAALQTRLGVTTVYVTHDQVEAMTMGDRVAVMNEGVLQQVDRPLALYDTPKNLFVAGFI
GSPAMNLMPGTIVADGVQVTDHVIPVPREVLDKASSKDVVVGIRPESFEVSPSGEGIGMK
INVVEETGADSYLYGTLQDDSATANPSDDQEVVARVTTRTPPARGEIVRLHVGPSKVHVF
DKSTTERIS
>PFR_JS14_471□PFR_JS14_471□L-serine dehydratase 1□560756:562147 Reverse
MFTVGIGPSSSHTVGPMRAGVGFLENLQADGLLDQVHRVRIKLFGSLGATGRGHGTDRAV
LAGLAGEHPDTVDPELPARLMARAAADHTLTLASTSESAARTIVFNPITDLVMEGRRRLR
FHPNALSLTAYRDDDATQELHNEVWYSIGGGFVVRDDGTGEPPMPRDETRVPHPFRNGAE
LLNICAASGMSIPQVVLANEMAHGYSKDEVREKLMGLWTVMDQSITDGCGATGELPGGLG
VRRRAHKLHSDLMNRRQTGYDPLAGLDWVSAWAIAVNEQNAVGGRVVTAPTNGAAGIVPA
VLKHVLTFASPDGLRDDERLVANFLLTAGAIGMVFQQTASISGAEVGCQGEVGVACSMAA
ASLAQVAGGTPQQVCNAAEIGMEHHLGLTCDPVRGLVQVPCIERNAVGAVTAITAARLAL
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AGDGRQLVSLDEVCATMMSTGADMKDKYKETSRGGLAVNLANC
>PFR_JS14_472 PFR_JS14_472 Amidohydrolase 562323:563597 Forward
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SLHEFNTAAFIKARLDELGIAAEPVGETGLLATLPGRGPGPTIMLRADIDALPLRDGCGA
EWANNASEVNHACGHDGHIAALLAAARVLAGHSADFDGTIKFAFQQAEEIGAGGRIFEEA
GALEGLDQVFGLHLFSGLPTGVVSATPGAQWASVDQFTIDVTGVGGHVSTPQLSHDALVA
GASIVTEIQQIVARELSPFDEVVVGIGRFNSGENYNIIASSARLEGTVRAFDEQVREHVL
ASIERIAVSVAAAHQTTAEVRRQVFADVLSNDPGATHFAARVAQQIPGVERVETNTPKAA
MGDDFAVFLHHAPGVYARVGSGGAPQFEQPHHSYAFAINEASLPIAAELHASYALRWLAG
GHQG
>PFR_JS14_473 PFR_JS14_473 Hypothetical membrane protein (DedA family) 563668:564681 Forward
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QPNGPGQPHGPDQPNGSGQPHVADQSATSDEPEWWQDDSMPWKHKPGRSDIACLAWLGGL
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WVWPMIAAVIMSCKFDWIYWWAGKLWGRGMIEVWAGKSERARRRYERLEKWAGKVGWLAF
VLAYLPVPLPLMAVVFVLAGASGMRLRRFVVLDVVVCSCWTVVFGVLGYVVGTPITDVLN
VYSKVANYVTIGLVVLVVAWSIIGSARKARTALHEHA
>PFR_JS14_474 PFR_JS14_474 Putative RNase III regulator YmdB 564706:565215 Reverse
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PAGQAVATTAGKLPATWVIHTVGPVYSRTEDRSALLVSCYRQCLRVADELGVHSIAFPTI
SAGVYGWPMDDATRIAVTTLRQTRTSVERALLVAFSESARVAYDKALQG
>PFR_JS14_475 PFR_JS14_475 Hypothetical protein 565300:565683 Forward
MNLEKVVFGFFVTLAAALNLGFFYGRIDDPALHNGYELAAALVVSFITTVLKFGDRTQLG
AVHLATSLVADLQLVVAAVIWVWATQIVATTMTPGHISLIVSMSGGALLANLVSVILMIS
EIVQIRR
>PFR_JS14_476 PFR_JS14_476 Ktn nad-binding domain involved with k transport 565690:567831 Forward
MPASSTRLKRPGGLTDVFYLIMRRMRFPLILLIVIYTICTVGLGLIPGVDDAGNPTPAMG
LFNAFYVVSYTGATIGFGEIPQPYSAAQRMWMTMTIYMTVVGWSYSLVNILALVQERAFQ
NALRQARFTRRIYGLREPFYIVAGAGETGALVCHGLDRLGLRFVVVERNEERLARMRLEE
FRSDPPLIVADASQPSVMRDAGLVSPHCRGVLALTEDDSTNQAIAVTTRLLAPRVVVLAR
IRNVETETHVGVFGGDLVINPFERFARQLASSIIAPERYRLREILTGLVGEPVPDQRQPP
RGHWIMCGYGRFGHAMVEELRSTGIEVTVIDEAHFDQGGVDVRGTGTDSESLIAAGVKTA
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FLARITTPLLGQYLKRIDQYSEKECAVLSDRLTRFGRGRIPELWDVVIRRGQATAVSQRL
ASGHRVTLADVLTDPDKRTQRSEAAALMVRRGNKSMERPELTMELRPDDRILFAGSTQGH
GNVSLVLQNANALGYVQTGQEGNGGVVWRWITGQRRQSEELHDHDAVPPQEGARALAAKQ
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AGNGVPAAPAQDTPGAPPKDDPARQPEADAGHGTASTGDDKGTGPEPSASEHH
>PFR_JS14_477 PFR_JS14_477 Conserved transmembrane transport protein MmpL13 567952:570282 Reverse
MAAAHWETQLFTRIGRAVSRHPLAFVLIWAVVLGITGSLALTGWGGQNLFSRLTSSETNV
PDTDSQHVADTVAEARGSSTTVTIVVTGVDVRTHRAQAGELVATLRDKLDVEHVASVTDA
FSVLARVPGTDPALAQADPAAARAAAEATARAQASAQAMLAADGNGFTEVITLDAGLDAK
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LVLLVIVFGGLLAAGLPLVGALTSIGVGMGGLWLLTHVMGIDSFILNVISIIGLALSIDY
GLLVVSRYREELAERLDADAAVAADRHRTHQLVRQCVARSIETAGRTVSFSALTIAFSIG
GLLVMRSSILKTIALGGIIVTVIAVLSAVTLIPAIITLLGSHMVRPSVLARVPGLRGLVR
AVGDASSDTGAFHKLAHRVIAHPWIIMVVVSAILALMASPIGTLRLRTAFTDYMPANSMI
RTGYDTLQSQYPAMATPSITLIAEAPPERTGALVSQIEDLAHVTRVSPGALADKPGLTRI
DVRVDASDQVGPEVSDMVRTLRGEDPGYRIWVGGAAASQIDFNHSLAQGAPWSALIIVVS
VLVLLFLMTGSLIVPLKALLINSLSLVASLGVTAWLFEGGHLGLPQVNGLETFIVACMLA
FGFGLAMDYEVFLLARIKEYWEAGHDNNEAVARGLQRSGRIITSAAAIIIAVFLGFVSGE
MLAIKELGVALAIMVATDATLVRLLLVPSTMTVLGHWNWWAPRPLRKVYERFQLHH
>PFR_JS14_478 PFR_JS14_478 Mannose-6-phosphate isomerase, class I 570770:571969 Reverse
MRSLTGIVKNYAWGSPTAIPAILGTVPDETPQAEYWLGAHDSAPAKVDGTTLDRLLADEP
QLLGGPVNERFGGKLPFLMKILAAAQPLSLQAHPSAEQAEAGFAAEEARGVPVDDPKRTF
KDTWPKPEVLVALSPFEALAGFRDPKRTVALFDELQPREPLESLIGPLRHRGAEAGLAEV
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>PFR_JS14_479 PFR_JS14_479 Hypothetical protein 572188:572469 Forward
MPQVAHDAQSGPELSPRDIAILDFEKTWWKSRVSKEQEIRERFDLSTPRYYLILNSLIDR
PEALAHDPLLVKRLRRLREQRQRERSAHRLHKA
>PFR_JS14_480 PFR_JS14_480 60 kDa chaperonin 1 572813:574435 Forward
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LADPYHKIGAELVKEVAKKTDDVAGDGTTTATVLAQAMVREGLRNVTAGANPIELKRGIE
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AKAATLEGLTADEQIGAEIVFTSAEAPLKQIATNAGLEGGVVAEKVKGLKPGEGLNAATG
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>PFR_JS14_481 PFR_JS14_481 Hypothetical protein 577006:578001 Reverse
MPRLPRRFCFINPLSLSDLTAVQSKRFPQPRTCNTCRLSHTYGLASSAFARHYSRNHGCF
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KPRERIHRSVADLRLLATPTSWGRVADPNPN
>PFR_JS14_482 PFR_JS14_482 NUDIX hydrolase 581219:581779 Forward
MALEDEHPRSFVTVPAEQRPIRHRTASRVLVIADDKVLLEEDSDPGKPGVVWWVTPGGGV
GPGETYEQAAVRELQEETGLVITEKDLEGPIGDRTVRHGYSDQVLIQHEQFYIVRTEPFR
TSSSGYTEEEKITLQATRWFTREELATVTVWPKQLVQLWKYRPGIYFDMGVVEESTVPLT
DAQRSQ
>PFR_JS14_483 PFR_JS14_483 Surface layer protein A (S-layer protein A) 582329:584008 Forward
MATGAAAAMFVTTFAGMAPANAKEVASTHEGYCTSADAPGSKSVVVDFTSVDKAKGIQTK
CAVNLSGKDDVTRDVSQLLTDAGFSADTTAFPATTVQGLPAKAVDGEGWLAFTGEPGTKE
WSQLKAAPASVTASVLGLVYGDNTGSGPAKGPAVDLSTWKTAAPVVVAGSLDKSVPRGST
AVGLDFSVTAQSSATSTDQPTKVEYKLDNGDEEGTWTAVPKAGVWDGTSAWTYKWSQANA
ASGIYTATYRVTNADGLVTTSKPTEQAVVAGPVAIAQQPTDVTAAPGGNAVFTVKTTGTG
VDGAAVAYQWQSQDKVTGEWADVTGATKSSYTVRQVTEDQDGTLYRVVVTGADSQGKEAS
LYSSSAKLTVAEVPVATATFVDVPKGNEFFKEIEWLAGEGISTGWVLPDGTKEYRPLDSI
HRDAMAAFMYRLAGSPAYTAPATSPFSDVATSNQFYKEISWLASTGITTGYGDGTFRPLD
NVNRDAMAAFMYRFKGNPAYTAPATSPFNDVATSQQFYKEMAWLSDEGISTGWEDGTYRP
VTPVARDAMAAFIYRLQGN
>PFR_JS14_484 PFR_JS14_484 Surface layer protein A (S-layer protein A) 584657:586048 Forward
MGQGALQVLYRAGFNPSSTGGTDAPTSINGFPHGAQTGYTWLHYTGIAGANWTQSDISNS
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THAPVEGWSYVKTGEQKAPGIGPTFSDVTPPAVTDVTVADVKAGSTSTTASFKTDDPQSR
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KEMAWMQSQGLSTGWPDGTYRPVTAIARDAMAAFLYRMENPTK
>PFR_JS14_485□PFR_JS14_485□DEAD/DEAH box helicase□586211:587890 Reverse
MTHDGPLIVQSDRTLLLEVDHPQADECRAAIAPFAELERAPEHVHTYRLTPLGLWNARAA
GHDAEQVVHALLSYSRYPVPSGLLMDIAETMERYGILRIDKDPAHGLVLTSTDAAVMTQV
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WQLRPYQELAAESFWEGGSGVVVLPCGSGKTIVGAAAMAKAHATTLILVTNTVAARQWRD
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DQLEEVARELDCPIITGSTPNRQREKIFADFRSGDLDLLVVSKVANFSVDLPVAQVAIEI
SGTFGSRQEEAQRLGRLLRPKQRLSGHDADGDNTAHFYSVVARDTVDADFAQHRQRFLAE
QGYSYRIIDGAEVGTDAAR
>PFR_JS14_486□PFR_JS14_486□Conserved protein, putative helicase of DeaD/DeaH box family□587963:590284 Reverse
MSASSRSLADAIRAFDAQQLAVLLRARPDLTQPRPLDLSELIERLSARASTLRALDRLDA
WHLLVAQAVAAWEGGGDPVDDKQLAAAMGLPDDVAAVDRALDGLRQLGLAWGSPVHLTQA
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PAPARPVAPPPVDADALAAALLRRESTGLSPEQIVQALTRAYRDDLWVGVDWADDNGATH
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>PFR_JS14_489□PFR_JS14_489□PF11228 family protein□591926:592705 Forward
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GWHWAVTLTRPPRARTATVDEVVLLPGEGALPTPQWVPWSQRVRPGDVTPGSLLPTPDND
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PSTEHAPAYCLTCGYFQRLSGSLGVEFGVCTNSFAPRDGKVVSVDHGCGGHSDVVADERG
IELPEPVYDTISIEQSLFD
>PFR_JS14_490□PFR_JS14_490□Hypothetical protein□592783:593124 Reverse
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>PFR_JS14_491□PFR_JS14_491□Guanine/hypoxanthine permease PbuG□593170:594732 Forward
MVSQSPGETPVASADDSAKLSSFNRWFSITARGSSASREVRGGLVTFFTMAYILALNPLI
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>PFR_JS14_492□PFR_JS14_492□Hypothetical protein□594848:595234 Forward
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TSPVTVGTTATARPLATASATAGATSSGKGPGRTKTFMALIATGVLAALAAVFVFIRSRR
ENAPEQAE
>PFR_JS14_493□PFR_JS14_493□Phosphoserine transaminase□595277:596398 Reverse
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LLACIDWVLERIL
>PFR_JS14_494□PFR_JS14_494□Iron-dependent repressor and activator IdeR□596575:597252 Forward
MSELIDTTQMYLRTIYELLESGVEPRRARIVERLHQAGPTVSQTVARMERDGLLGLSHGR
TIELSDTGYNEGRAVMRRHRLAECFIVNGLGMDYASAHDEACRWEHVMSEEVANRLCEML
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DAAGIHPGATVDLSRDGEDYVVASEGGKALHVPEKYAPSLRVSAL
>PFR_JS14_495□PFR_JS14_495□Thioredoxin□597368:597703 Forward
MATVELTTDNFEQTALQKGIVLVDFWADWCGPCQRFSPIFDAASDANDDITFGKVDTEAQ
QQLAASLEIQAIPTLMAFKDGKLIYRNAGLLNRQALDALISQVRDFEPANA
>PFR_JS14_496□PFR_JS14_496□Hypothetical protein□597867:598226 Reverse
MLDVEDSLRRVATTVDHHYQHIANRHEFMRAWAVQFELAYTDFRVIQLALQLDGKEHELL
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>PFR_JS14_497□PFR_JS14_497□Carboxylic ester hydrolase□598378:599187 Forward
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YLVVVPEYHDVPDGYYPAPLEDMDHVWQWLQASDLTFDRHRIGAVGSSAGGNMSVELAIK
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ERTDRLTEGTPVHRVSPKTGPVYLANSLNEFVPTSGVLTFTEAMVRNDVPVVAQFLSGSR
HAKGYLDDVYDQTVQFLNHYLLDEGRPES
>PFR_JS14_498□PFR_JS14_498□Isochorismatase family protein□599184:599804 Forward
MTSATRRDPVSDELLTPENSAFVLIDYQPTQVDSINSMDRAKLIDNIAVTTKIIQTYKVP
VVLSTVNVANGRNKDTIPQLKELLPGVPSYDRTAINAWEDADFKKAVEATGRKKLIIAAL
WTEACLTFPTLDAIREGYEVYPVVDAVGGTSVEAHQTALRRVEQAGAQLISIAQLACELQ
RDWNRTDTAGGFVEDLIEAGIFLKLE
>PFR_JS14_499□PFR_JS14_499□Hypothetical protein□599949:600281 Reverse
MNREDKAIGWHLNLAIRVNPPLADDNELLDLIERLARQHTAASISPDHKTITIASTVYSP
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DVMTAIVGAVPAVLVVLEQGGYDGRVVHVDAMDEQAFMAKQSELTDPSAS
>PFR_JS14_500	PFR_JS14_500	UDP-glucose pyrophosphorylase 2	600856:602229 Forward
MSEQGLQQARDKMASAGVGRTAIEVFSDYYKQLETGATGIIPESSIRPIENPPSLADVVV
TDQQARDALSKTVFIKLNGGLGTSMGLAHAKSLLQVRDGKSFLDIVVQQVRATRQQWGVK
LPLLLMDSFSTHDDTMAALADYPDLAVDGLPLDFLQSKEPKLRADDLSPVDWPADPELEW
CPPGHGDIYAALYDSGLLSTLIDKGYRYAAVSNSDNLGAAPDARIAGWFASTGGDWCSEV
CVRTVNDKKGGHLAIRKSDGRVILRDTAQTAPEDMKYFTDEHVHRYFHANNLWWDLVALK
QKLDERHGVMGLPLIRNEKTVDPTDPSSPAVIQVESAMGAAVEVFDDARVLLVGRDRFVP
VKKTNELLLLRSDVYSIGDDGRLHARVERIPGVDLGADYKFVDDFDERIPAPLGMVEATS
LTVEGDWHFGTGVRVRGTVDLGPDGGTVPDGELLQGD
>PFR_JS14_501	PFR_JS14_501	Hypothetical protein	602222:602632 Forward
MTSPAPSDDPTVDDSAPDLAQCASFALTGHYLGGARPEVSEPGQLLTVLRDHGWTPQRLA
ALRDQRHHDGQSWPMALPIGVPVPGGFARFHAWVSEVVVALNLDSRDAGVRDASQPLDAE
TRRLMADLPPHYGSAG
>PFR_JS14_502	PFR_JS14_502	Large conductance mechanosensitive channel protein	602686:603129 Reverse
MKGFKNFIMRGSLIDTAVAFIIGAAFGAVVTSFTQIVLDLLGKLGGTPNFSSWAPGGVHV
GTFLTALISFLILAAVVYFAIVVPINKMRELRHPDAEKTQTEAEILTEIRDLLARNEAQG
IERVNDLAASNSPSLEGRTQARRSSDG
>PFR_JS14_503	PFR_JS14_503	Hypothetical protein	603222:603770 Reverse
MVAVLTALDPSASSSHTVVIASRPLAAGVAVGADDVTTLQVPAEVATSATLADPGAAIGQ
VVAVPRPAGTVLTSSDFVGKGLVADSDGLTLVPFRIEDKGVAGVLGVGNQISVVGANPGA
DTRVIASRVRIAALPSPGSSGALDDSSSSSGALVIVAADSRTARELAAAASEYTLSVVLE
SD
>PFR_JS14_504	PFR_JS14_504	Type I antifreeze protein	603963:604358 Reverse
MPTYEYTCTDCGHDLEVFQKFSDDPLTVCPDCNGHLRKVFSPVGVVFKGSGFYATDNRTS
GASTAPGSSLHDTETAHGADSSQASESATHTSGDASTASSTASGATTSGSTSTSGSTTPA
AAGSSTQAKVA
>PFR_JS14_505	PFR_JS14_505	Hypothetical protein	604515:605198 Reverse
MSGPNTAGRTAPDAGGQSTPPAKGGQSTKAQLRRLARRRRADRTADERREATRELTRRVL
DLARGRIPNDAVIASYLSLPDEPDTHPLVDSFLEAGYRVMVPYMTGGPAADDIDWAWYTT
GSELSPGVLGIDRPRGEPLGAPALSRASVVILPGLAGGRDGSRLGMGAGWYDRALAHTRP
GTLLWLLLFDDEVTDTLPQEPHDHAVGVIITPHHTIVTADNGNRPAV
>PFR_JS14_506	PFR_JS14_506	Molybdopterin molybdenumtransferase	605217:606503 Forward
MALFGRKRAPVAAEPEPEPDPTLPGAPAPQANGLRSVSAHRDFLLSKVQPLMPFGMRLLD
AWGLSLCEDLVADGDLPPLPEAESDGYAVIALDVRDAAVGTRVQLSVRGDVQKVGSAVPV
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EPGGLQGFGIIGQHEVPVVMLPADPLAAYVAFELFAHPLIRTLMGARDMALSSVDCRLTM
DVSGEAGLMQVVAGVITRDAQQWSVTPLDFAQGSLTTLVDADALIVLPAELGTIAAGAVV
TCWLLDRD
>PFR_JS14_507	PFR_JS14_507	Acetytransferase	606507:607217 Forward
MVDLDLPRAHRWPLTLRFGPLALRPIERRDAAELRQLRARNREWTGPWDTTVPPQGVPRS
LTFGRMVAEQRARGRAATQLSWLLTLDPGAAGGGEARRRRRAPIVGQLTVADIVYGAGRF
ASIGYWIDEGHAGRGLVPLAAAIATDYCFEVLELHRLEICIRPENQRSLRVVDKLGYRRE
GLRPRYLHIDGDWRDHLVFVMTSEECPAGGLVRALVEQRVQDAATNPAKAAGDAVD
>PFR_JS14_508	PFR_JS14_508	Hypothetical protein	607292:608095 Forward
MTGLIWLAIVAGWLAYLVPRFLLHKEVSISPTLSAARDALASPMHLVRRGGQDDFAEPTD
PSLQISTPLQRDSVLFQTRRAAQIAMRRRRTGFLGSLLVMVAGVVVSVITPAPWWLALVG
VGVLAVFVVLSRISVHTVNAMIADQLEAADQDWAEDTVTVCEVDLTHVHDENTEISIPLN
LPVDSTIGDLWEPIAVTPPTYVSKPLVPRSVRTIDLTMTADPPAQPKMPVTAERPEDVDD
TTDIRAAQDGRHDHGGDEGDLPRAVGE
>PFR_JS14_509	PFR_JS14_509	Hypothetical protein	608348:608911 Reverse
MTVQNAPATDEYTAYEYATVRVPHTFEPLFRDTYPGFGWTVENPRATTSVASVPLGRTQR
SETVTLQLKRDRNLKNRDMVRALQEEADTALTTIISLERSKTSRAMVVAVTIGIVGSAFL
AGSVFAMNAGLAVLSVALGALGLFGWVGGGISYRQVKRRRARHVDPLIENALDTLHEASR
RAAHLLR
>PFR_JS14_510	PFR_JS14_510	Hypothetical protein	609062:609481 Forward
MTSTARPAIATTGPRWRALPRVAQITVQVILMVAVGVEVVTVAVSRAPVIQYVPAVAMTA
GILLGRFGRSWGYVGLGLVALAPMIAVLVDRQATGIWSMACLAAFWFVLRGLSAWVVGVV
IGVANFVAVGWEAGTIDVR
>PFR_JS14_511	PFR_JS14_511	Histidine kinase	609584:610249 Forward
MREAEQGRQAAVERGVAQERLRIARDLHDGVGHQIAVVNMHLGAAEVHLSDPRALRGDLV
AARAAVQAVLRETQQILAVLRVDNAGERPQATPSPAAVGDLVESYRQAGMVVNANIGSFG
IALSGQSSVAVYRVVQEALTNAHKHGVGPVSLEISQNGEGLVSIEVANMRRSTSSPGPGG
GNGLIGMRERVESVGGSLRTRADDRLFWIVATIPADGREAR
>PFR_JS14_512	PFR_JS14_512	Two-component system response regulator	610246:610905 Forward
MTTVMLVDDQEMIRKGLRVIIDAYPGLDVVAEAGDGFTAVRRLDSVQVDVILMDLNMPGM
DGVEAVRRIREARGPEGPRILVLTTFDQDENVLAAMRAGANGFLGKGAGPDELAEGIRRV
AAGAHALSDNAIGALVSHVSDPHAVPPDPDKAKLFEGLTPRELEVVRLVVEGLDNAEIGR
RVFISPFTAKTHVNRAMAKVGARDRAQLVSLAVQAGIRP
>PFR_JS14_513	PFR_JS14_513	Hypothetical protein	611068:611802 Forward
MQSEDPPSNLPVRDGLAKIRRGMGDANLRYLYFSVLAVPGHLAMAGAKGVVLFTGFSAFM
AANVLFTLGLAAMKVVVIRAAWGAGSASACVLPRAYQVIGVLVIVFSAAFAVSCLPLALG
SSSSGNYSRVQAIAIATITFTELAMAVHGLLSSGRRRNPLMEAIKLSNLAASLVLLVITQ
TALLSFAGEGGDPSRYNGWFGIGMGLSAVSVGVYMVVRHARLSKGDLLGPDSQPANFAPN
APGV
>PFR_JS14_514	PFR_JS14_514	Hypothetical protein	611896:612105 Forward
MDRDKQTDQDKRGPIGPDLGMMPGMNSSPTGSSFRDGGSRQPGSSGLVVSVTIAFLLLVV
VVLCLVAIG
>PFR_JS14_515	PFR_JS14_515	Secreted peptidase	612152:612805 Forward
MDRSPGDVAPLVLGWPLRGFVMARNSPARRVPSHGTHLMGTIYSIDLIPVDARGRAAPWT
WRTALATEAPEEFVGFGAPVMAPCPGRVVIVHDGEPDHRARRSQLALIPYALGQPRRLRA
GAAGVAGNHIVIRIGGDGPFVLIAHLQQGWLTVSAGDMVHRGEPIASCGNSGNSSQPHVH
VQATDTVQWDRAVGLPIAFDAAGNPVLPGESQIIRAG
>PFR_JS14_516	PFR_JS14_516	Lactoylglutathione lyase and lyase	612855:613223 Reverse
MTVTGPDFIALQVRDLDRSARFYETQLGLHRAPVSPPGAVVFATSPIPFALREPLPGVDL
NQPSRPGLGVALWLLGDDVQALHDALADAGVKILQPPTAGPFGLTFTFADPDGYAVTVHD
KH
>PFR_JS14_517	PFR_JS14_517	Putative HTH-type transcriptional regulator MarR	613302:613721 Forward
MGIGRQIGCQLKEVQAVLRARMDEVLRPLGLTTPQYACLTALEQTRGASNSELARRAFVT
RQTMNVLLRGLEARGLVARAEEAPHGRARPVSLTGEGSALLIQAAEAVGVVVMRMVGSLD
DAQRTDLHDALNSCIEALR
>PFR_JS14_518	PFR_JS14_518	Transcriptional regulator	613837:614109 Forward
MEDEARVKVFKALSDPIRLQIIRYLNQVHRGVTCGEIGGVVDISKSAGSYHFKVLREARL
TITRKESREKYVSLNYETLDKYLTRFFDTL
>PFR_JS14_519	PFR_JS14_519	Drug resistance transporter, EmrB/QacA subfamily	614149:615615 Forward
MPLYSSKEVEQLNWKGVVRGDDRTTTGRVPPTSGQRWVLALTSLGFFMAMMDSMIVTTAS
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RHRPLPTS
>PFR_JS14_520□PFR_JS14_520□Proline/glycine betaine transporter□615754:617193 Forward
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LICQWLIQLTGNPYMPAFYIMFFAVIAGIALVPMKETAGQPLMGSAPVVEAPEDSPIPA
>PFR_JS14_521□PFR_JS14_521□Regulatory protein TetR□617269:617862 Reverse
MPTRVRDRSREMFRERLAEALSEVFVARGFDDVTVAEAARAVGISRATFFRYFSSKEDAA
LASVEGSNFDFGAVLADLDLRPDDSCWSLLQRTFRHSLAGVGGATSSQLDQLRMIHATPS
LRARLSFRRLQLEPSLTAALVGHGVPADRAHTAAMAGLAALEVAWERWALHESPSLARAL
DEAFADLTAADKPISAG
>PFR_JS14_522□PFR_JS14_522□Probable multidrug resistance transporter, MFS superfamily□617975:619462 Forward
MTELESTRSTVAGHGARHPGVIVAVLASAGLVASFMQTILIPIQSSLPERLATTRDNTAW
VITITLLVSAICTPISGKLGDMFGKRRIALILLSLLVAGSVVAAVSPSVGPLIVGRGLQG
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RVLAQHDGELAGARA
>PFR_JS14_523□PFR_JS14_523□Glutamate dehydrogenase□619617:620981 Forward
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>PFR_JS14_524□PFR_JS14_524□Transcriptional regulatory protein PadR□621101:621574 Reverse
MSTSLSISFTPAPPDSALGHHLLGLYFAELQTSLPGGFDPSGQESYGPDEYYVAALHDGQ
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>PFR_JS14_525□PFR_JS14_525□CrcB-like protein□621634:622020 Reverse
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GLFLGGLW
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>PFR_JS14_527□PFR_JS14_527□UspA domain protein□622430:622963 Reverse
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>PFR_JS14_528□PFR_JS14_528□Galactokinase□623120:624316 Reverse
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>PFR_JS14_529□PFR_JS14_529□Twin-arginine translocation pathway signal and cupin region containing protein□624580:625101 Forward
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>PFR_JS14_530□PFR_JS14_530□Uracyl permease□625132:626685 Reverse
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>PFR_JS14_537	PFR_JS14_537	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase ispE	635222:636199 Forward
MSETEFPASGARGLGAVDLRVRVRVPAKVNLALRVAARGDDGYHQLATVFQAVALFDELT
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LRSLEQVDETLCVTSPAPGAQLVVS
>PFR_JS14_538	PFR_JS14_538	Transcriptional regulator, TetR family	636234:636995 Reverse
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DDSGPVDRADGQD
>PFR_JS14_539	PFR_JS14_539	Aspartate carbomyltransferase	637138:638184 Reverse
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D
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VPGLAILCAFLSVEQVTTLFFREHAWGTWDRLRASAASTADIVTGKVVVRFLIQLAQTAI
VFAVGALIFGYRPNGSVLAIGIVVIVFTAMLVAFGVMLVALFRTMDQADTVGMLVGMLLA
GLGGALAPVASFPGWVQSLAHVSPAFWVLDALRRLTLDSAHLTDVMPAIIGTLAFTAGFA
LIAAVSFRSNAVKVGTT
>PFR_JS14_575PFR_JS14_575Nod factor export ATP-binding protein I (Nodulation ATP-binding protein I)679820:680752 Reverse
MLVAKGIIKSYGNLKVLRGVDLSVERGQILGLMGVNGAGKTTLISILPGLTRPDAGDVHI
GGVDLLRHRRQAARHIGVAPQALGIYPTLTVQENLDCFAGLAGYSGRKARSRTAEIARLM
GLQDLLDRPAGHLSGGQQRRLHTGMALLGHPDVLFLDEPTVGSDVQSREVLLSIVTHMAN
EGTAVIYTTHYPAELEQLDATINVLVNGRITVTGSVQEVTGQWASSSIFLHFRGKTPEVD
GWKEDRGGLVPIRPVSDPGQMLGQTLSTLGAAAGGLDDVRITRPSLEAAYLAITGDHALA
EKEASDVVAA
>PFR_JS14_576PFR_JS14_576Actinorhodin transporter680900:682327 Reverse
MTQTLTAVEPTTSSRLGRRLWAILAVVLIADAIDLMDSTIMNIAAPTIQREIGGGEGLIK
WLGASYALALGILLVVGGRLGDRFGRRRLFLIGIAGFGVASVLCAVAIDPAFLIAARLLQ
GAFGALLIPQGIGILIATFSREQFPTAASMFGPVLGGASIVGPILAGFLVGANIGGLTWR
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AVPVICLGLGVAGFIGFALRQRLATNPLIVPALFHNRGFTSGLLIGLGYFAVVNGFAYVV
SLYFQMHLGLSPVGAALAMMPMMVGIIIASFVARPLIPKLGRNLVVAGLATTLAGIVALI
AISIAAGDATNQWMLAPAILVLGLGMGASFSSIYDVAIGDLTTDLAGSASGSLSAVQQLA
SAIGSAVVTTIYFQTSAAADANRPFIASLVVVGAITAVCLIAAPLLPKRAPQDAH
>PFR_JS14_577PFR_JS14_577Transcriptional regulator682392:683030 Forward
MEELHKRDLYTEAMSQTAERQGRRERKKAATSSALTAAARRLVLARGYEAVTVVDIAEEA
DTAVTTLFKHFPDGKNAVIFGDNVDSADERMQSIITAVESRADGQSVLDALHQFFRDRGA
FSGTQSAFVRRVVEAPPLRAYAKERWERCEPGLTTLLAGIVGRPEDAVIRALARIVLQIP
DLAATDMDASRADLDAIMARLEAGWSEFAQRA
>PFR_JS14_578PFR_JS14_578Phosphopyruvate hydratase683321:684592 Forward
MPRQTITTLDAMEILDSRSRPTLMVRLSLSDGTRARAMVPSGASTGTHEAVELRDHDPHR
FGGLGVLAAVDHVTHEIADAIVGRRFESVGELDESLLALDGTPNKSRLGANAILGVSMAF
TRALAASGGNELFEYLPGIGGQPPRLPVPCFNVLNGGVHAANPLDFQEFMICPTGMDSMT
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GVAIAIDPASSEFRQADGRYLVNGRSFTSAQMIERYQAIVHGYPVWLLEDGLAEDDWDGW
QQLTRELGSRVELVGDDIFCTNPELIRKGIERHVANASLIKLNQIGTVTETLDAMNICAA
AGYRQFMSHRSGETPDAFIADLAVATGCGHIKSGAPARGERVAKYNRLLEIAADHPELAY
GLG
>PFR_JS14_579PFR_JS14_579Cationic amino acid transporter684650:686113 Reverse
MNTSDRTASPHANPPAPSDDGKASPALKQVMGPGLLLLFVVGDILGTGVYALTGQVAGEV
GGAAWLPFLIAFVIAMMTALSYLELVTKYPQAAGAALYVHKAFGVHFITFMVMFTVMCSG
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LFTTAIAAGLILYVSLARGSAVVGLLGGTTSLLLLAVFAVVNLAVVVLKRDRVGHKHFRT
SRIVAIVACLLCLFLVLPVSGRPIGQYQIAGVLIVIGVALWAVTVVINKRVGRTELKHPE
DIPPEVI
>PFR_JS14_580PFR_JS14_580Similar to Nucleoside-diphosphate-sugar epimerases686331:687104 Reverse
MSKRPHTILVVGATGSVGRFVVAEALKQGYATRALVRNLDKAKTLPEGALAVVGDLTDAA
TLDRALAGTDAVVFTHGSNSTEEQAEAVDYGAVRSVLTALGDRSVRVALMTAIGMTKRDS
IYNKENHGRDWKRRGERLLRASGLEYTIVRPAAFDYNAPDAHKLVMRQGEHPSNGGVARE
QIARVLVDALSNDAARHKTFELLDTTGEEQADLTPLFAALQPDEPAAADAPGDSENLPLS
DEPQRVLDDLKRLTDYE
>PFR_JS14_581PFR_JS14_581Methyltransferase type 11687407:688156 Forward
MRPFAELVAEAQSADITGWGFGFLDGRATEERPPWGYARLLAGRLARAHAALDIDTGGGE
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VKPDWRDIARVLEPGGHYFAQHVGPASSFELIEYFLGPLPENRKRRDPHVEAAQAQAAGL
HIESLLTATLRIEYFDIGAIVWILRKCPWWVPDFSPDKYHDQLVCLDAQLRAGRSFVDHS
SRHLIDARR
>PFR_JS14_582PFR_JS14_582Putative CONSERVED TRANSMEMBRANE PROTEIN688293:689105 Forward
MRSSNPVLTRPDAFVPAGQAGQQYVDAAYQEASYPPGGYPGPSRPAARMTMNDVIAKTAT
LFVILVAVAAAAWMFTAVNPAMALPLALGSSVIALVAAILVTVRRSTSVPAIMAYTVFEG
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VAGINLIALLFGVNLGFFNIGAGAGALSWLFAAIGVVLAVASLLMDFEECERGVRMGAPA
KESWRAGFGLMVTMVWLYTNLLRILSFFRN
>PFR_JS14_583PFR_JS14_583Hydrolase, NUDIX family689281:689985 Reverse
MHVIGVQRVDKAPVVRLPVGHGEDPRVLLWHRGWVVSRWLSATGADEELVVTAQVRQRTA
TSRTPRRRGHRQDPDLVVAPGEVPTKRQRVAAYAIVRSHRGLLGTICSDRTAVPGRWQLP
GGGLEASETSSQAVIREVREETDQSVALRRLVDLQSDHWVGRAPNGRLEDFQAIRIIYTA
VCTAPTEPEVLDVGGTTEASHWVSLRGWRSLPWTSSARSALDRHVDELSGLFAR
>PFR_JS14_584PFR_JS14_584Hypothetical protein690034:690999 Reverse
MSHTVRGYLRSLGAPITLVSVALVFAVTACGAPQAGQASSSATTPANAQSTQAPAFDLTV
AGHARQVIDFLVAASGNKPVLRVEVTPTAANITYLEDDQAHTIGYANGHISPVDSTVKYI
NQAQFKPSGFNIDNVGELFEKAGEISGSRQQQDLQINEYNQGVVLMTVTTTPETSTVFFR
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LPSITSNIKDSSDPGTFDPALIDPGLIARLEQTLPATVGRTPSTSVTVTIAQHAGQRVPF
MYFQFSGAEVVTTMAGDVIAK
>PFR_JS14_585PFR_JS14_585Putative 3-methyladenine DNA glycosylase691208:691858 Forward
MIDFNRRADAVAPYLLGAIIRRGKVAIRLTEVEAYLGPKDPASHAVSGPSGRAAVMFGPA
RHVYVYSSYGIHLSGNIVCSPDGTASGVLMRAGEVVEGVDQALTNRGFIVAASPDEDQAD
ARARRPEAELAKGPGNFGAAIGLSLADNGQPLGGPDDLFELHVPDALAPEIWVGPRVGIT
KARDEPLRFWLPDEPSVSSRKIGSPWTPREGPFTLL
>PFR_JS14_586PFR_JS14_586Hypothetical protein691886:691975 Forward
MAGVMMQRSIAALRTRLSLGQAGPFESEK
>PFR_JS14_587PFR_JS14_587Hypothetical protein691988:692392 Forward
MSEQVSTEDPKTSVVVSRVIAQPIAKVWAVLMTKDGSEALLGRGAVLGEKGQTWTAADGR
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TGVVRSVHRGEQIRFWWRKSEELPPSLVDLTLAPTDDDHTLVKVEHSHLRPDLDPAYLQG
WWEASLERIESDAF
>PFR_JS14_588	PFR_JS14_588	Hypothetical protein	692526:692981 Forward
MKYVKGTLMILGGVFFVAAVAIFIKVYFFDLKALWSLAATNTSIAYSDPRPWFIVTSVGL
LLGGLLFGIGLALTRTTFATRYSRTRKEEKREEADKSGIHGASAAPKPVAAPKRRAGQVA
DKASGGHTGNAPQAGDIVPDEGGTPGPTTTH
>PFR_JS14_589	PFR_JS14_589	PF04978 family protein	693007:693513 Reverse
MNAIDLMQDCFVRVSDTLPHLLDGLSGDDLLWRPGPKANPMAWLVWHISRCEDSELDALT
DIPQAWGQGWQQKFALPYPPEDGGYGQTNEQVAAFNVSDPDLLLGYFYAASARAAKVLEQ
ERAKDLDRIVDTNWNPPVKAGTRLVSVANDITQHLGALGYVRGLVETR
>PFR_JS14_590	PFR_JS14_590	HAD-superfamily hydrolase, subfamily IA, variant3	693510:694124 Reverse
MTVKALLTDMFGVIAQIQPESARTRLVRIAGAEPDAFWAAYWAHRPDYDQGISTPLDYWS
RVACDLRMDFGTEQLMELHAADIDSWSLRHQDMIDALPRVRAAGYRLALLSNIPTSLAEH
VYAVDEFMDEFEVVAMSCHIDAVKPSPAAYQWCIDRLDLPADEILFIDDSQRNVDAAAAV
GLQARLYRGVDDLFATLSIEKSRI
>PFR_JS14_591	PFR_JS14_591	FMN-binding split barrel	694302:694949 Forward
MDNQIHRHPERAVTDRARLDQLLDEIGLATLSTVSPDGEPWAIPINVARAGDRVVMHGST
GAGALRHAAAGAPIVLTIATVDALVVGATAFSTSVNYRSASLRGVATRVTGDEQVALLGA
LTEAFLPGRMGEVPGLTHKQLAATMVLALPITADNWIMKVRAMGPDEMVVDADGGGAGGW
GGIVPVRTVLDEARPAPWAQGAVPESVRLAQERRR
>PFR_JS14_592	PFR_JS14_592	Hypothetical protein	695054:695584 Reverse
MRHFSAPRPRTLRWTAAVLAFATVLTVLAWTSGSNPMLLTLAILLALLTVVALGVAQATA
HPTSHPDLDDAEAGDTELIHLDRSTVPGETEDDRRLDVDPHQVHDLGGLIDWIGSNNYLT
TAAPEGGSWLVRLGQQKAATINADGSVTHVLPASTPLAAGNHVTVQWRAARGLPGR
>PFR_JS14_593	PFR_JS14_593	Peptide methionine sulfoxide reductase MsrA	695704:696339 Reverse
MFRFDEPVTLTAENALPGRDQPVLGMPFFHRVFGDPLDRAFPGAQTAYLAAGCFWGVEKL
FWQQPGVLSTAAGYMGGFTRNPTYEETCSGLTGHAETVRVVFDPTQTSYEQLVRVFFENH
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YFAEDYHQQYLDANPHGYCPVHATGIPCTAA
>PFR_JS14_594	PFR_JS14_594	Uracil-DNA glycosylase 2	696451:697140 Reverse
MNAQPIAQLMAPDWAAALAPQEPQIHAMGKFLRGEIAAGRGYLPDGDKVLRAFSRPMADV
RVLIVGQDPYPTPGHPIGLSFAVNRDVRPLPRSLVNIYQELSSDLGIPPAPHGDLTGWFD
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AGGVPIIASPHPSPLSARSGFFGSRPFSRANAALVGAGAQPIDWDLNER
>PFR_JS14_595	PFR_JS14_595	Integral membrane protein	697321:698751 Forward
MPAFSLGRRMIRRPTRPQHPDEAPHPSSGPEPLTGEQLRELEDLRAASVESLVPRPLRTA
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QGVDGGAGPTADPLATARGASSSGTTSPAASGMDAPPTVAGTDPPSTAGEGGVAQP
>PFR_JS14_596	PFR_JS14_596	Hypothetical protein	698837:699799 Forward
MSESTELDAILTDLVTGAIGTAEAARRIKALAPAPSPSQPPEEAAYDHTEAVDGTPDAGS
HQEAHAEQAGNRSEPAQGPREPSGSHGVTAVQVRVTGRRVRVLGDQTIATVAVEGPHSLR
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LNTAGVPYLDTVRVTGGLTELRDVTRVSDMLVQAGGASIHGDFRGGRSRVKVETGNLNVA
LTPTANVTITASARLGGVSWPDDGAGLDEFVAGNGAGRLDLNAFVGRISVRRDDGSATSP
DAGATRDSGAGKQWWEVWKD
>PFR_JS14_597	PFR_JS14_597	DoxX protein	699915:700349 Reverse
MGIAHFAARSLFATVFVRRGYAVFQNADQMAGVTDDLLDKVPAPVRDILPDVSAVTLTKL
QGGTMTAAGVALALGIAPRLASLVLAAQMVPTTYMGHPFWKYEGGDKVNQQIHFEKNLSL
TGGLLVTALGGAKKAKKAKKAKKA
>PFR_JS14_598	PFR_JS14_598	Transcription elongation factor GreA	700436:700939 Reverse
MSDKQTIWMTQDAYTKLQEELDYLKGEGRSLIAKKIGAAKAEGDLSENGGYHAAREEQGQ
QELRIRQLEQMLQHAEVGEPQGAPDEVTAGSTVTVAYDGDPDDTDVFLLGSREMMGVDKS
VDTQVFSPQSPLGAAVLGRSAGDTVEYQAPNGREVSVKIMKVESFAK
>PFR_JS14_599	PFR_JS14_599	Mycothiol conjugate amidase Mca	701034:701960 Forward
MSVPTSDPSNAGLRLLHVHAHPDDESSKGAATTLKYVHEGVRVMVATCTGGERGSVLNPA
MDRPEVWDHMPEIRRSEMAHAREILGVEQRSLGYIDSGLPEGDPPDPLPPGSFATLDPEV
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SKLYYQMSFHRLRYAALDAAMHERGMDSPYSERLAEWENRDYEQRITTRVPCGDFFARRD
DALRAHESQIDPHGFWFAVPLDIQRKVWPTEDFQLVYSRVPTFVPENDLFDGLRPGTKAP
DPSDTWII
>PFR_JS14_600	PFR_JS14_600	Conserved protein containing thioredoxin domain	702133:704817 Forward
MANRLVAESSPYLRGHADDLIDWWPWGPRALAEARRRQLPVLLSVGYASCHWCHVMAQES
FRDPQVAQFVNDNFVAIAVDREERPDVDQVFMNATQALTGQGGWPMTVFCTPDGEPFFAG
TYFPSQARDGQPSFLQVCQTLARAWAERRDEVVESGAHIASQLADQASVADPAGDQTGEP
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IVGWLSREMAITTDAGTAFASGQDADSLDADGQRVEGAFYLWTPHQVEAVFNRRDALFAQ
AVFHLTPKGTMPDHSSTLRLHGDPDPDRLKRILGELREVRAERPAPARDDKVVAGWNGLL
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SATSIMVTALQVVAGLTGNRDWADRARRAEPGLWQVLEQTPLASGWGLTQLAIDAQATAG
MGRAQVAIVDPESRPMGLLARAVWRLAPEGTVAALGTPDAPGFGELFAQRHDIDGAPTAY
ICRDETCFDPVTDFTRLRDPLWRRVVRASLPADGRRKGTRPAHDHGPGDRAHGAPGHDHG
PATDGMRVMSHVATDKPRFEWRTLRTAEFGFPGDQRDALVAAVLDGTKTATSEPLDGYRR
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DAHLALWTSRVFLDLLGEPPIMLDGDTAVVLTRFRAYRPGDIVAGHVIDFDA
>PFR_JS14_602	PFR_JS14_602	Isoprenyl transferase 2	705386:706195 Reverse
MVHHEGASETWDRLSPTRLIYSTYETRLRAGLDPREMPRHVAVLADGNRRWARTNAPGQP
LEVGYKAGADKLREFVGWCDEVGIGVVTLWVLSTENLQRSGPDELLPLMGVIDRLTRDLA
AVPDYRVQPMGDLDLLPESLATTLREAALETIDNTGIHINIAVAYGGRHELRDAVRSLLA
AEAAKGTTLEELSRTLDPNQIADHLYTKGQPDPDLLIRTSGEQRLSGFLPWQSAHSELYF
CEALWPDFRKIDFYRALRSYQQRERRFGK
>PFR_JS14_603	PFR_JS14_603	Channel protein, hemolysin III family protein	706394:707131 Forward
MGSQRQGSATRRRTARPSTDGAGHPAGAERSDTAAATPAKPKMRGWLHAGMTPLIFLAIL
ALIVHTASWSGRLAEAIYLVTALMLFGNSAIYHRGHWSPRISGMLRRFDHSNIAIFIAGT
YTPLAVLMLHGASRVTLLCIVWACAAVEVACRNLWMGAPRILYTGLYIAMGWAAVFWIPQ
FWRAGGPGVVIWLIAGGLCYTVGAVVYAFKWPNPSPRWFGFHEIFHAGTVVGAACHLVSI
WLAAG
>PFR_JS14_604	PFR_JS14_604	Exodeoxyribonuclease 7 small subunit	707176:707418 Reverse
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DKARQADQAASDAGEIADDE
>PFR_JS14_605□PFR_JS14_605□Exodeoxyribonuclease VII, large subunit□707465:708616 Reverse
MIELRRRAGAYMHFLTLRDTSSEVSAQVTATTAVLDQAGPLTEGTTVLANVRPRVWNKTA
RLSFECFELRIAGEGQLLAELEKLKRKLQAEGLFSPARKKPLPMIPRLIGLITGADSAAE
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GSPATPASAASHGVAGPALTQLGRQGEAQ
>PFR_JS14_608□PFR_JS14_608□M18 family aminopeptidase□711302:712573 Forward
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MGA
>PFR_JS14_609□PFR_JS14_609□GTP-dependent nucleic acid-binding protein EngD□712668:713741 Forward
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>PFR_JS14_610□PFR_JS14_610□Hypothetical protein□714089:714220 Reverse
MARTPGAKNRTPRELRAEAKRLNERANYLEKLAKLKKSKEKKS
>PFR_JS14_611□PFR_JS14_611□Hypothetical protein□716007:716315 Forward
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FLTLVFGLFSNSTWTSLATSFCALLVSWMSLGAKTFKFDETSAAHRDIASKLWDVRESYI
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YTVKWKVLNRGPEAERRNNIRGQIVDPTASGVRTEHSDFRGEHIVECYIVKGGIVVARDR
IDVPISTTSAHAASS
>PFR_JS14_614□PFR_JS14_614□Abi family protein□718707:719636 Forward
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VARRGDAHAKWLRRYNESLRRSREDFVAHHKKKYGGQVPVWAPVELLDWGSISRLFEFAP
LGVQEAVADACSLRAPQLGSWLKVLNVVRNTCAHHGRFFNRVHAITPKLPAAGLHPDLDA
VNADYNRTFGLLTLIQFLLDRLDAGPGDLLPDVVAAYPDVPAIPITHMGAPGEWRGSSRL
WNGGQSPEA
>PFR_JS14_615□PFR_JS14_615□Transposase, ISlxx5□720687:721721 Forward
MARVGLSFSDRSEISTASKAGWSVRRIARHLGRCPSVILRELHRNSTKTRGYQAVTADVR
AQRRRARPQQRKVAGDPVLQARVEADLAASWTPNEIAGRLRLEATDPTVERMANSADARG
RTVSGEAIYQYIYAIPKGELARKGIFLQSKRTKRRPRTTGRTRGGPIVGMVPIAERGEDA
AQRRVPGHWEGDLIIGKNGTSCAATLVERMSGFTGLLALSSKHAEPTADAVIEFFNDLPE
MMKASLAWDQGSEMAQHAKVSLATAMPVYFADPHSPWQRPSNENTNRLYREYLPKGTVIP
DHQPYLTTIAEEINNRPRRRLGYLTPTEAFARLLAGEPHVASTP
>PFR_JS14_616□PFR_JS14_616□Hypothetical protein□722348:722572 Forward
MPPTSPTPPGNQPLWQPAQGYGAEAPAVVTAPGSAPQATAGSAAVTPWAVVLLVVGAVLL
FSVSFFAGYLWGWV
>PFR_JS14_617□PFR_JS14_617□Hypothetical protein□722572:723681 Forward
MKRVLIVVLALLLIIAGGLAGNAFRNARMLAEGASYRFSTTVNPAASASATPAGGSSPSA
STGAGNSATIDVSYEAVIAHVDKSTVAQVTNQTTGQGWQAHIARSSGSGYTLTAPDMPSF
TIKQSANPFGSASLSTSADEIAAKDKSLQAQHPATSAPSAPASPSQGPTAAPSPSSVART
QILSASPLLANGQLDPGVTVRSGDPSAASALECTTSGSILESFDCSPALVTGAEACWLEP
STGAGSVNILCVDAQPRTFIRYKNVAVATGGSASGSEPIWIETDDGSQYRAKADGALDIS
SDNYSPIFLCAAGPCRQSGDNVLWSPTDASPHIDTSQGTWRVLVGTVTSEAPAVKRSEAV
TKAWVTSGA
>PFR_JS14_618□PFR_JS14_618□Hypothetical protein□723775:724545 Forward
MKKLLAGLLIVLIAVAGFAGGNLLRQHTMLADGASYRFSLVVPAADQSVAAATATPAADS
VAGPPAGSSLTYEAVIHTREGSSSADIVNQVTQQSWRAEVVRSVGRGYKLIAPDRPTFTL
EQSLNPLARPTLTTTPQEVTSHPEAAPSAPVSTPTPACRVYSGAELGQIVGRQPIAERGP
AHQEIMYDKGGWTMLKLPDRYYGSGSWHIFHTVDCVPRPVLMYGSDASDNFSVARMTAAG
IPADLQAFVRGLGIFP
>PFR_JS14_619□PFR_JS14_619□Transcriptional regulator□724509:725474 Reverse
MDEPLDTTTLREVLADLPFLVAVADEGGITAAAEVMGVPQPSVSRAMARLSDRIGAPLLR
RDRRGVALTDAGTTLLDYARSTRTAALAGVTAVHRELERAGASVTIAFQHTFGRRVVPAL
LRALLADRPDAHVDLRQGARESCIDLFEKGVADAILVSPPLPPTKHAHTLRLYAEPLVLT
VAPEHRLAGRDRVQLSELADERLLAMTPGYGLRTIVDELLRDAGISRTFAFEGEDIQTLR
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GLASAGLGVAILPPAIQPSDDVVEVPIDHPAARREIGVSWHGDAAPAGSAAAALQDLLAR
DHRWVVTPGGHGKIPSPRTKA
>PFR_JS14_620	PFR_JS14_620	Putative MFS-type transporter yybF	725632:726783 Forward
MVVALTCAGLATFAQLYSPQGILPLISARLHVTAAHSALLISAATIGLAAGALPWAWLGD
RIGRLTAMKSAMAAATLCGALGLLMPGFGAVLVLRVAEGFALGGVPVLAIAYLGDQVSPA
FTARAAAVYVSGTSIGGLAGRLVAAPIAEWFGWRIGMASVLGFAAVATAVFMVIAPAVRT
PGRPEGKGHGTRRAALRALLEPGLLALYAVGFLLMGGFVAVYNYLAFRLRAAPFGLPTTV
TSLLFLAYLAGTVSSQRAGRLAGRRGRLGVLLGAIAVFILGVGLTLVPALPVIVVGLVVL
TAGFFAAHAIASGWAGVRAPAGGAQAPALYNVAYYAGSSVMGWFGGIVFVGMGWVGLVGL
VAVLAAAAAGLAVSTLRGAETVG
>PFR_JS14_621	PFR_JS14_621	FrnE protein	727190:727885 Forward
MTTQLFDHADDRIAVDVWSDVMCPFCYLGDGLLGKALEDFPQADQVDIRYHSFLLMPDLP
EGVTRDLSDVLENERGYPREQTEAMNARITEQGAGIGLDYHFDDALATNMRRAHELSHFA
KDAGKQHAMVQRLFRAYFTEGLDLGDVDVLADLAGDVGLDRDAAVAALQAGTYADDVETD
IAQAQQLGISGVPFFVFNGKYAVSGAQPAEAFSQVLNTVWKESTEAAPAGE
>PFR_JS14_622	PFR_JS14_622	Hypothetical protein	728458:729330 Forward
MSGISRLNRLWHAVKGILPVILTLVMIVASIIVVLAIMSTFSQLWGWATFMAVVMAAIGA
VSAWLNTKRGSARQHHDSLAQREMAAVALLANSDERSQAVAVIELSQLIIDWSLAREASW
KTVEGKQGQRDIVDYPEWDRIRELTRLAFFDIDTTWQHRDNVIIRVSPGDGGSELVRHVR
AERLQLVVKRFQATPVKAGWSHRGARSLLPYLDFSCIDLRGQFLGDINLSGVKLAGAKLE
ESDLSNATLTGADLTGVTYSGKRSRSGRTLPETRFPEGFDPESVGMIRVE
>PFR_JS14_623	PFR_JS14_623	Hypothetical protein	729409:729675 Forward
MSDSLKERFGANLRAERQRRRLTQESLAEFLGVTPRYLGGLERGERNLTLDSIEALAEQL
DIDPLQLLVGPAAARRIQARRVQLRSRS
>PFR_JS14_624	PFR_JS14_624	GlpP family transcriptional regulator	729654:730313 Reverse
MSDREAPHDERSATLPNALIHRLMAVPAGRSLMTRLTHSPVIPAVSGVDALEGFLDSPTE
SCLLGGLSVIALQRALTQLIAADIHPLVNLDSLSGLSRDRAGLDWLQAMGVTGLVTTRLS
LLQSAPHYGFLAIQTLVLGGASLVDSALSALESAHAGLALVAPAPVLGRLDPAALPKLQP
FLASGFVRNVDDVDDALAHGAIGVTSSARGLWGYERERS
>PFR_JS14_625	PFR_JS14_625	Alkylglycerone-phosphate synthase	730402:731934 Reverse
MISKQFQVTGYSEGYYKVGEFTPPRWVDDGLAKPITGATPRYGDGRVVAVPEGIVEQLRG
IGDAVYTGTDETAERTRDWWPGTMLAHTDGDPATPDAVIVEASGVKQVQAVLRLAAANGI
PVTVAAGRSNVTGSTLPLEGGIVLDIHTMNSILGFNPTDLTAECEPGVFGDVLEERLQTA
WGVTTGHWPQSLGLSTVGGWVACRGAGQLSTRYGKVEDMVTELDVVLPSGELVTLGGRQR
AAVGPDLKQLFIGSEGMLGVITRVVLRTHALPDYARYAAYEYDTFEAGLDACRRIMQRGV
TPAALRLWDNMEGDYYFGNGGNTLLLILDEGDPRLVDVTVDIASDEAATTGTAVDAEPIF
QKWLATRFEVPAQNAFEDDGAWMADTLEMTAGWSQLPRIYQRVQSEVGALEGTFVVSAHQ
SHAYTDAACVYFTIQGTLPIKDRAAWYRAVWDVADKVIIEEHGQLSHHHGVGVVRTPYVA
ESLGGGMEVLRAVKQALDPGRMLNPGKYGL
>PFR_JS14_626	PFR_JS14_626	Glycerol-3-phosphate dehydrogenase glpD2	731931:733616 Reverse
MIRVARSDVKAALRQQASAGPLRLERSEALARLGSERFDILIIGGGITGAYAAFDAALRG
HKVALVEKGDFASGTSSKSSKMIHGGLRYLQQANVRLVAHSLLERQRLRNNASFLVQRLP
FIFPVMMRHGVFDRRLSLGFSAALSAYDVLGGYREGVLHRKLSRDELLVHAPTLKPEQLI
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RASVVVMATGSWLRDWDGTAPGTDAPTIRPAKGVHIALPWLKIRNTSSLTFQVPGQKTPA
TITRWGDSVLVGTTDTEYTGDLDHVGCTADDADVLLHAVTSSFDTDVSATDIQGSIAGTR
PLVARSNAKNTAEIPRSSEVRTDPDGLVSILGGKLTIGRHMGMQGIDAAEKVLGVQRRCR
TADTPILGAAGYDEASFTASGGWEDHLAERYGTESRFVSQIMADDPAMREPIVAGQPYLA
AEVVYAARHEMAHTVDDVLARRTRLRLFARDASDGAARRVAGLMAPELGWTPQQVDHQVA
AYHEAIQTERQLLTTNTEAQA
>PFR_JS14_627	PFR_JS14_627	Bile acid:sodium symporter	733756:734859 Forward
MAALSARAPDEQTGYMVTTRPPRHRPDSSGSGGGAAWLERWQVPLYLASLALGAAVGYLW
PAGALGFGTAINPVLMVLLYATFLGVPFARIRAAFADVRFMACVVVLNFVVVPLVVFALS
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FAGGAVVAAIHWAPFARAFLLLIVVPLVLSVLTQQLARRQGAARVVMRAMESAMVPLMMG
TLMVVVASQFGHVAAQFGLLVRVVPLFVGFLVVMPVLANLIGRLGGQPVVIRRTLAFTGS
TRNSLVVLPLALALPPEMALAASVVVTQTLVELLGMVTFVRVIPRLIRQRPGPGRGAPGQ
DVRAIGG
>PFR_JS14_628	PFR_JS14_628	UPF0324 membrane protein	734955:736118 Reverse
MSRVEPDVGAIELPARDAALLGPSDDESVVGRLGWAIGGFAIVIALGVLVGVLSEGVPTW
TKGTGFGKVAGSIEFPVYAIIVGLAGNGLLSALHVRERPSGGFRTEFLIKTGLVLLGASI
NFSVIVRAAGPAVAQAVLLISSVFFATWWIGGKFGLDDRLRALLSTAASICGVSAAIAAA
GAVKAKKEHLAYTASLVILFALPSIFLLPWLAGVLGLSPAVTGAWIGGNIDTTAAVTAAG
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GFLAASVAATIYAGAVPAEVSKAAIGVANNLRTWFLIFAFVSIGLEFNISSIKQAGWRPV
AVFGSAFTVNLVVGLVLALLLWSGFTI
>PFR_JS14_629	PFR_JS14_629	Hypothetical protein	736115:736288 Reverse
MSFSPTPAQPAETTHRSPDDPDGAGKFSVSEDWLAVVVGLVLLALALTGVIPAGLIP
>PFR_JS14_630	PFR_JS14_630	Thiamine-phosphate diphosphorylase	736803:737450 Reverse
MTSRNRQWRLGRLGRSRLYLCTDSRGSLDDFAAFVEAAYAGGVDIIQLRDKHIDALSELR
FLSVLRDAALRHDALFAVNDRADIAAVSDADIVHVGQDDLPVAETRQVVGREVLIGRSTH
SVDQAREARLADTDYYCIGPVWATPTKQGRPGVGVDAVRAVAQQADDKPWFGIGGVNAQN
LAQVTDAGATRIVVVRALTGADDPAAAARELLARL
>PFR_JS14_631	PFR_JS14_631	Glycine oxidase ThiO	737626:738879 Forward
MAKHVIVIGAGVVGLACAWRLRRRGHRVTLLDPSPASGASHAAAGMLAAVSEYYFEEESL
LALSLPASRLYPQIIAELARRTGGPTGFRDIPTIVATADSADRERLEHLGDQQRSIGLTV
TALTPSKAREMESFFSPRISGAFLAEDDRQVNPRVLAGAYLSDLEADEGCDVRPLAATEL
LWRDGAVVGVRAAAVPGAEVFTHRFDERAVDTDEMTGDAPSWSSEDLPAGDSIDIAADLV
VVANGLLSPTLAGLPEGLEWPIRPVYGDVIRLRTPEHLRPLLTRTVRGLVHGRSVYIVPR
EDGTIVIGATEREDGRDAVLGGGVLQLLRDAQDLVPAVAELELVEATARPRPGTPDNAPI
LGPIAPGLIADTGTYRHGILLSAQTAVVVADFVDGTAGQDEWAAFDPWRWSKQEARA
>PFR_JS14_632	PFR_JS14_632	Thiamine biosynthesis protein	738876:739109 Forward
MRVTINGEATQVDADTVAALVTQRTGRALSPDGTPADGGRLGLAVAVNDEVVPRRNWQAT
ALTEGATIEIVTATQGG
>PFR_JS14_633	PFR_JS14_633	Thiazole synthase	739112:739942 Forward
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TTVAMRRHKPTAGPNIFDTITGHGIAVLPNTAGCQTVREAVMVAQLAREALDTTLVKLEI
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MGILNPYNIRTICESLSVPVILDAGIGTASDAALAMELGCDGVLLASAVTRADHPAVMAR
SFRLAVEAGRLAHLGGRIPRREEALASSPMEGRPDL
>PFR_JS14_634	PFR_JS14_634	Molybdenum cofactor biosynthesis protein moeB2	739951:741195 Forward
MTLPVEPTERELTREELDRYSRQMILPGFGMTAQRRLANARVAVVGAGGLGSPLLIYLAA
AGVGELTLIDNDTVDVSNLHRQVIHSTASVGRPKVESAAEAIARLNPHVRVEARAERLDI
DNVLELLDGHDLVIDGVDNFETRYLIADACEILGLPEVWGSVLRYEGQVAVFWSGHGPAL
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AWRELRIAPDPDRVPVSELSLEAVSCLMPIAVAGAAHDDPSLAVSALQLQEMLQARARGE
LDFDLVDIRQPEEYSVGHIEGSRLVPLGTISVDPAPLGTILAGPAHSVDPVPTDPGVPDQ
VALPRDRDIVITCRSGARSGRLLDRLVAAGYGRVKQLDGGVIAWQREVDPSMGV
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>PFR_JS14_635	PFR_JS14_635	UPF0324 membrane protein	741263:742345 Reverse
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PMLVAILAGIVLRNVVPIHAALEPGIALAAKRVLRWGVVLLGLQVSIPTIIGLGPGVLVI
VTCAVAITFCSTLAMGRLLRMDRDMYTLIAAGFSICGAAAVAGMQGTIRASEEKVAAAVA
LVVLYGTLMIPATAGLAALLGFGPGDAGTLIGASTHEVAQVVAAAGIAGGGPLLAVAVTV
KLARVSLMAPVVAGVSLLRNHCATRVPGQKRPALMPLFVVGFIVMILVASIGIVPAPVLG
GVKLVQQFLLATAMFALGLGVHVKSLMKLGARPVLLGLFATVVIMAVVFAGIFLGLGANI
>PFR_JS14_636	PFR_JS14_636	Transcriptional regulator	742382:743335 Forward
MDPRIRSYTFCMTTDGATHPLDRSLTPAVLRLLVLVEDLGGVGAAARACGVSQPSASRAL
AGVEGRLGCLLLRRTALGSSLTPEGLALAAQARLVLKAYDQLESLAHDLSRGTPGHVRLA
ASRTVGEQLVPGWLGALAGQRGDLQVSFHVGNSDAVIQQVRAGEVPLGFVEVPTPPVGLA
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FDSNTAIVRAVAAGLGPAVLSELTIGENARTGDVVVVPWAHDPPKRPLCAIWQSALTSSR
LVRDILTVVRADIAAAD
>PFR_JS14_637	PFR_JS14_637	Hypothetical protein	743339:743554 Reverse
MSIDTAHRLRRLADTLAGWRELWRDFTGESAYDHYVERHEREHPDHAPMSAREFWRWRAD
FDEQNVSTGCC
>PFR_JS14_638	PFR_JS14_638	Carbon starvation protein	743544:745940 Reverse
MSAAVKEGLPSYTPEEEKLIIRNKAGVPIGVKPHNKWTVRKVIVWVVITALGVLGWTMLA
IVRGEEVNTIWFVVTAVCTYAIAYRFYGLYIQRKIMRPDDTNATPAERINNGKDFDPTNR
VVLYGHHFAAIAGAGPLVGPVLAAQMGYLPGTLWIILGVCVAGAVQDMLVLFFSMRRGGR
SLGQMATDEIGRIGGTVATIAVLVMLMIVLAVLAMVCVNALAASPWGVFSVGCTIPIAVG
MGLWLRYISAGKITQVSIVGCALLIGVIIAGRWVSTSAFGKYLHLSPTALVWAMIVYGFF
AAVLPVWVLLTPRDYLSTFMKVGTIVVLALGIIIVRPIVEMPAVTEFASNTAGPVFAGKL
FPFLFITIACGALSGMHAMVSSGTTPKMIQKESQTRMIGYGGMLMESFVAIMALAAAVSL
NQGVYFGMNTSEATVDKLAGPAVVQAADGNREQITAEAVGNLGVTDAHGNKIQATWDSWD
ENGNDKVYYGADALKQVANDAGEPSVVSRTGGAPTLATGMAHILHQIGGGKTMMGFWYHF
AIMFEALFILSAVDAVTRVARFQVSDALGNAFKKFKDPSWRVGAWSSTALVVAAWGSLLL
MGVTDPRGGIQTLYPLFGIANQLIAAVALLLCTVMVIRKGYKKYVWIPLVPFLFDAAVTF
TASWEKIFSTDPLVGYWQQWRNARQLLTTLTDPAKIEIQKAIIRNTFIQGTLSIAFLAAV
VFVLICAIIRVVKVLRTGDTTTSEDPHQESNFFAPGGLFASKLDKKLVAEYHEVGDPALI
PGLKKTERIAEEKARHEH
>PFR_JS14_639	PFR_JS14_639	Glycerate kinase (Fragment)	746305:746904 Forward
MKMSRIIISPDSFKGTISGEDSAAALGAGWARVRPDDEVMALPQADGGEGTCAVIADAVP
GARWMSTPEPVTGPDGRPAPGRWVVLPSGEAIVELAIPSGLTLMAAKDPRGAHTRGLGQV
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AMVAPPAGGVRLLCDVRSP
>PFR_JS14_640	PFR_JS14_640	Hypothetical protein	746883:747422 Forward
MRCAQPLTGPEGSAAVFGPQKGATPADIAYLDAALAHLAEVSGGDADFPGTGAAGGTAFG
LMSLWGASIVSGAEEVARLTGLVDALARADLALTGEGSFDVSSLAGKAVAAIIDAAAASG
TPCVVVAGGFTDEGRAALTQRGIGFLSLTELAGSSGEAMAHPARYLGEAGARMAQQFSH
>PFR_JS14_641	PFR_JS14_641	MFS transporter	747486:749255 Reverse
MRAERGIAATGDDLTAGERASRALERPAADSHRDVPGGSPTAPPWKALWVLAAGLAIIVL
DGTIVSVAMPTIIDSIGISLTDAQWVTSLYNIVLAALLLPLGKLGDEKGRKALFLIGIVV
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RRRGRGPLSFLDVPGTVLASLGAALFVFGLIEGNTYGWWSPTAPFSVAGIEWPTGWAVSV
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ISVTIMKPSMSPLWFAGTLIIYGVGLGLASAQLTSLVLGRVPVAQSGEGSATQSTVRQLG
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QLGELGPRVAEVMAQGFSRAAQWSMGIAAAMLVLGLIGSLMVRRAAQRG
>PFR_JS14_642	PFR_JS14_642	Glyoxalase/bleomycin resistance protein/dioxygenase superfamily protein	749457:750350 Reverse
MSQVIIPSLWFDHVARGAVDFYLDVFPDARQTHIAHYPAEGLPDFQQEFAGEVLEIGFSI
DGFEFSAINAGPEFAINPSISFMLNFDPSTMPDARDRLDALWARLIDGGSALMDLDSYDW
SARYGWLQDRFGVNWQLMLTDPAGEPRPFVIPQFMFPYRSARAHEALQYWTSVFPDARQG
TVVGYQPDQGQPDGTILFSDFQLAGQWFSAMDSGAQLPEGFDFNEAVSLTVQCADQAEID
HFWQALSAVPEAEQCGWCKDRFGVSWQVVPAAMEELMARPGAYQKMLAMKKLVIADF
>PFR_JS14_643	PFR_JS14_643	Peptidyl-tRNA hydrolase PTH2	750451:751164 Forward
MSVDSFHVPHPEPGGVMPWAMQLVVYRDRHEPARQVDVCEATARAVVALLDDARSAEGGP
WHDAVQHWVGGHIRKLVRRADGKRWDDVQLLEGVSVEQAGPADFGVAAARAFVPGPEEPQ
PKAIDKLQIAGTNFPDEGVSLSVDALAVVEVSPLVEMTSGKMAAQCAHAAQRLYESAGTD
GDPESTRASWRADGFRLQVDFPSVEQWHRTPRPVSIIDAGFTELGGLTETTRAYWRH
>PFR_JS14_644	PFR_JS14_644	ABC transporter, quaternary amine uptake transporter family, substrate-binding protein	751202:752101
Forward
MRLPRRAVLGAIGLATLAACSRNDPIGASSSASRTGLVVGSQQYYSNEIIAECYAQVLEA
SGIAVTRQFEIGQREVYIDEMTSGKIDLIPEYSGNLLQYFNKDTQVTDRDAVREAVVKAL
PASLHVLDQADAGDQDSYTVTRASAQEHSMSSIGDLAALGTTITVAANSEFATRPYGPTG
LKRLYGVDATVLGVEDSGGPLTVKALLDGKVQAADIYSADPSIASNDLVVLSDPKHLILA
QNVTPLASARVDAAAAAAINKVSAQLGQSELQSLNAQSVTKQLKAADIAREWLRAKSLV
>PFR_JS14_645	PFR_JS14_645	Cyanate permease	752249:753526 Forward
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GPGVAALLSAMPPFCFAIIGAFAARIGGRFGTTRTLAVAALVITGGLLGRVLVHGEMSFL
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NWQLNLGVWGATAAVALVVWVVVAAIAPHAGHMRDMAEGAVQRKGPTMWEIARTRKGLAL
GLFFGLQSMQAYVSFGWLPQIFRDAGLSVAQASLLLSLFNVIAIPGGLVMPIVAQKLTRP
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SGFSQALGYLIAGVGTWLVGAVHGITNGWTVPLVALIISAVLFVTFGIIASARGDVDDEL
PAFAR
>PFR_JS14_646	PFR_JS14_646	Hypothetical protein	753629:753853 Reverse
MSERKTLLLRLDPAVHDALQQWANDELRSTNAQMEMVLRDALRRAGRLPKDVKPIRKPGR
PPARKNKGDDQPTT
>PFR_JS14_647	PFR_JS14_647	Band 7 protein	753866:754834 Reverse
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GAWLFLAEDMPEFSAPLGVVLAVIGLLLFSGLAVISPGQTRVVQFFGAYIGTVRRTGLVM
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AYAPEIAQAMLQRQQASAVIAAREKIVEGAVTMVQNALNQLEEQDIVALDDERKAAMVSN
LLVVLCSDSRATPVVNAGTLYN
>PFR_JS14_648	PFR_JS14_648	Cysteine synthase	755054:756022 Reverse
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KRGVLKPGGTIIEPSSGNTGIGLAAVGTARGYKVKVVLPASLSVERRALIQAYGGEVILT
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DRYLSTALGQFPELTVHEDVEL
>PFR_JS14_649	PFR_JS14_649	Diacylglycerol kinase catalytic region	756467:757522 Forward
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VCREVGARLLVRHTSRAEPGRAQVLQFLDAGADTVVVAGGDGTVRLAAGVLAGAGANQCT
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LQRAQGARVTIEPDQPLPVQADGDIICARARQLSAEVGGHVAVHIGDGRLD
>PFR_JS14_650	PFR_JS14_650	Hypothetical protein	757613:758776 Reverse
MEQPASGQGHDEALTRLAPTTPGRAILLESGRQALTLIARWCRTQHIELAVLPSYHCDTM
ALPFWLEGMRVHFVEVGANLQFDPPALGTALDDADEPALVVWSRVGAIAPDTALTTVLRR
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LTRELGDAPLEVLNAGRACFPLIGSAAAPAIEDALARHGIFSPQSWPRPAYLPDSLGWPT
DVVSIDCGPTTSTEKVKQIAAIITAAL
>PFR_JS14_651	PFR_JS14_651	Peptidase M20D, amidohydrolase	758937:760106 Forward
MGAELEAGLSGLRRELHQIPELEFDLTRTQARLLQALDGLPLEIHTREGSSSIIAVLRGG
RPGPTVLLRGDMDALPVAEQTDEPFKSTNGRMHACAHDLHMSGMVGAAELLSRVRDDLAG
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SPLARYDDAVLGDQAALLAALAWSGALPE
>PFR_JS14_652	PFR_JS14_652	Phosphoribosyl transferase domain protein	760202:760708 Reverse
MTAYHADAVDQHDKEILTWDGLGEASRELAQTIVDSDFDPEIIIAVARGGMIPAGALTYA
LGTKLTDAINVEFYTGVAQTLPDPVLLAPMLDTESITGKRLLVVDDVVDSGRTMQLVIKL
LRGFGADVRSAVLYAKPTTVVLPDFVWHHTAQWIVFPWSAQPPVEASK
>PFR_JS14_653	PFR_JS14_653	N-acetyltransferase yncA	760768:761280 Reverse
MPIPFIVRDAVNDDAAALTAIHNAQGVATTASYALTPGTVPDRRAWLARQHAARHPVLVA
ADGQGRIVGFADYDRFRSLPGYDLTVEHSVYTAPGHERLGIGAALMDQLIDRARSAGMHA
MVGVIDADNAASIDFHRRLGFRLCGTLPQVGRKFDRWLDACLLVKLLDER
>PFR_JS14_654	PFR_JS14_654	Regulatory protein, MarR	761421:761966 Forward
MSRQDNEKPDTHARRCGTSHSGVAGPHDGGTAHPAPAGADEELANLATDVRIACQRIARG
IRHASDELPGPLMSVLMQLHRTDPQTPTALAAHAGVSTPAITRVINALVAEGLVARTPDP
DDHRQVLIGLTERGRGQLQRTLAARDTWMLRRLDGLDADQRALLRDAARLLTELTEGVVA
R
>PFR_JS14_655	PFR_JS14_655	Putative major facilitator superfamily transporter	761963:763033 Forward
MNPTQSRSAAFWHSVGRTFVSLAQRNYRFYFTGALLSNIGTWMQRTSQDWLVLTQLTDRS
SSALGIVSALQFLAIPFLAPFSGAVADRYPKRTILLITQTLLGLNCALLWLLVVTNNVEL
WHVYVFAFAQGVVASFDMPARQAFVSEMVADSLIPNAVGLNSMSFNAARLIGPGAAGLLI
AAVGVAPGMLINALSFLAMIGALLAMNPAQLHPAPQRKGRGSVREGLSYIRHRPDIMLVL
FMVFMLGTFGMNFQITNATMATKVFGRGAAEYGALGTIMAIGTFGAAIIAARRRAPRVSV
LLLGLGGFALANTFLALAPSYWFYAILLIPTGLCALTVMTSANSTVQISGSSRSRV
>PFR_JS14_656	PFR_JS14_656	Uma4 protein	763016:764323 Reverse
MLHATFTAPSLTTFCRLDELGLEAVGQIVEPDRAVIECRVAEPDRWCRKCGCEGVARDTV
ARRLAHEPFGHRPTTLLIRVRRYKCSGCGRVWRQDTSKAAPERAKISRGGLAWGLAGLVL
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VTVIIDLTPNRNKTGPARLLDMVEGRSKAVFKDWLAGRPKEWSKQIEVVAMDGFTGFKTA
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LTDKQRDRLTALFAAEQHVEVEATWGIYQRVIAAYREPDKDKGKQMMQAVIDAVTTGVPA
ALVEIHKLGRTLKQRAADILAFFDRPGTSNGPTEAINGRLEHLRGTALGFRNLTNYIARS
LLEAGGFRPHLHPRS
>PFR_JS14_657	PFR_JS14_657	Hypothetical protein	764469:764732 Forward
MAVYAAINMGGTPLGAPIVGWVGDVAGPRWSLLAGSIATGAACVMVGLYFFVHKGVRVRI
ERGRPLRLQVWTTDEAIAAQSAAEPEK
>PFR_JS14_658	PFR_JS14_658	Putative insertion element ISCmi2 transposase	764829:765872 Reverse
MWVTTLTLLTTEVFVTHANAPLTPEGRRRLAVLVVEQGWSLRRAAERFQCSPATVKRWAD
RYRAGLPLIDRSSRPTSSPNRLSRKTEHRIVALRFTRRWGPHRIAYHLRLHRSTVGRVLA
RYKMPKLINIDQATGLPVRRPKPTRYEVAAPGQLVHVDIKKQGRIPDGGGWRAHGRGSMQ
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AKPYASEAERAAAYETWLHHYNHHRPHTGIGGQTPSARVHNVTGKYI
>PFR_JS14_659	PFR_JS14_659	Transporter, anaerobic C4-dicarboxylate uptake family protein	765928:767223 Reverse
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SAVAAMQTAGGMDLLVKVSERLLRRHPRRITFYAPIITYVMTFLCGTGNVAFATLPVIAE
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VSVGAMVASFPAVSGLFVLPTYPTVVAAIEMDDTGTTRIGKFVLNHPFLLPGIITIAAAV
ALGFALAPLML
>PFR_JS14_660	PFR_JS14_660	Aspartate ammonia-lyase (Aspartase)	767228:768700 Reverse
MSTRTEEDLLGKREVPNDKYYGIHTVRALENFQMSGRSMNDVPEFIRGMVQVKKAAALAN
KELRVLPADIADAIVAACDAILDEGRCMDQFPTDAFQGGAGTSINMNTNEVIANLALELI
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NGDLVGKEAARTGKSVREVVIEMGLLTGEQVDAILTDQNFLKPHYTGRFYSADEHGLPED
VAPELVSHEA
>PFR_JS14_661	PFR_JS14_661	Aspartate ammonia-lyase (Aspartase)	769027:770496 Reverse
MSTRIEVDLLGKREVPEDKYYGIHTVRALENFQLSGDTMNDVPEFIRGMVQVKKAAALAN
KELHALPGDVADAIVAACDAILDEGRCMDQFPTDAFQGGAGTSINMNTNEVIANLALELV
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NGDLVGKEAARTGKSVREVVIEMGLLTGEQVDAILTPENFLKPRYTGKVYGPDDHRLPSD
ARLRALDER
>PFR_JS14_662	PFR_JS14_662	Hypothetical protein	770708:771070 Reverse
MVDHDEIRRQQESLWQTQLKHPDIDIMGKMGGWLAGPPSPDPPAGPVWQWGPEDMHKRFL
IIYPDGTDSTGSIHEYVSLLARLPPFGPDRRFSYDESIELCRLMHTMGAWSWDEPRHCLV
>PFR_JS14_663	PFR_JS14_663	Fumarate hydratase class II	771234:772658 Reverse
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AKEYDDVVMVGRTHLQDATPIRLGQVISGWVAQIDFALKCIKFSDEQARELAIGGTAVGT
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HIGYDKASKIAKNAHHKGIGLRDSALELGFLTPEEFDKWVVPADMTHPSAADDD
>PFR_JS14_664PFR_JS14_664Putative glyoxylate reductase772822:773790 Reverse
MARICITDGVPAEGIEALRTAGNEVITWDGQEPPTREQLLAHVKGADAVLTVLSDGVDEE
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LTS
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DASPDGS
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READE
>PFR_JS14_682	PFR_JS14_682	Citrate lyase beta chain citrase beta chain family protein	790232:791095 Forward
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IH
>PFR_JS14_689	PFR_JS14_689	Hypothetical protein	796989:797936 Reverse
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>PFR_JS14_690	PFR_JS14_690	Hypothetical protein	798021:798902 Reverse
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RTTVRTNTAQSNSTLRSGNLQVDRISGWGYDSTFYLDWVSDIHSVADTVYPGWMSDIAVG
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PNVPQARGDRVDIYVVDLGRQDQLGLFIGSSNLGDATRNGKVDEAIRTLKVTG
>PFR_JS14_691	PFR_JS14_691	Glutamine synthetase, type I	799109:800443 Forward
MDRQTEFVLRAVEERNVKFIRLWFTDVQGFLKSVAMAPAELEGAFAEGTGFDGSAIEGYA
RVFESDMIARPDPTTFQLLPWRTEASTARMFCDIALPDGSPAMADPRHVLKSALNKAADM
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ELPLPDEAEDDVWALSERERRALGITALPRSLDEAIDAMESSELVAETLGEHVFDYFLRN
KRAEFEEYRAQVTPFELRTHLPHM
>PFR_JS14_692	PFR_JS14_692	Hypothetical protein	800499:801236 Reverse
MADRQLRQTKRAAAVLAAQLPTLLEPAATAGRQSLAHLIAIAEAITSALAVPTRTAPQSI
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QLGAFGEGPTHHRGTPPNVVETDPDTFWALCTGSLSWQQARDEHRLRVSGVHADQVSRML
PVIKH
>PFR_JS14_693	PFR_JS14_693	Glutamate-ammonia-ligase adenylyltransferase glnE	801478:804444 Forward
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>PFR_JS14_697□PFR_JS14_697□Glutamate--ammonia ligase□806783:808222 Reverse
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SSVAGFQKINESDMALVPDPTSAWLDPFREHKTLIVNFFVHDPITHEPYSRDPRNIARKA
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QTE
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GEAY
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NKHEKPVVVIARTNHTYEIGQRSVGIEAVHAIGDDADVTSACGGFARSWIW
>PFR_JS14_707□PFR_JS14_707□Iron-sulfur cluster assembly accessory protein□817886:818236 Forward
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    VLVMDTAHGHQERMIGALGRVRPVRDAYADRTGIRIPIVAGNVVTAQGTLDLLDAGADVV
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    GSVMIGSWFAGTYESTGALLVDPEGRSYKESFGMASARAVRNRTRQQSSYERARAALFEE
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    PLPVSWA
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    RDGAVHQTTLDPAALGLAPARPSDLVGGDPAHNAQVARDVFAGQTGPVRDIVGLNAAAAM
    LAFDGPNFTEPLVDQMRPRLEEAFTTISQGRATELLERWVAISHEVAGV
    >PFR_JS14_711□PFR_JS14_711□Hypothetical protein□821665:822090 Reverse
    MAWARHFWLKVVSAVWVLVAMGSTAVAALTITVNDDLPVRVMAVIATVLLVPGLIMALVA
    HDHPAGRCFLAGRFLTYAGAAAILVRCLFQAGSDLVNIGGWIGVLLEVVLLIVPALLVAT
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    >PFR_JS14_714□PFR_JS14_714□Acetyltransferase, GNAT family□823681:824778 Reverse
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    >PFR_JS14_720□PFR_JS14_720□1-acyl-sn-glycerol-3-phosphate acyltransferase (Precursor)□829670:830611 Forward
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class II)□830760:832106 Forward
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SKLPKGATVKIFII
>PFR_JS14_725□PFR_JS14_725□Polyprenyl synthetase□836186:837256 Reverse
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>PFR_JS14_726□PFR_JS14_726□Methylenetetrahydrofolate reductase (NAD(P)H)□837302:838243 Forward
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REILAILLARRPW
>PFR_JS14_727□PFR_JS14_727□DNA or RNA helicase, Superfamily I family protein□838197:840407 Reverse
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SCEGEWSLIAAVD
>PFR_JS14_729□PFR_JS14_729□DNA polymerase III, alpha subunit□841034:844654 Forward
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N-acetylglucosamine transferase MurG857874:858974 Forward
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APQRTQWAAAFQLRP
>PFR_JS14_756□PFR_JS14_756□Succinate-semialdehyde dehydrogenase [NADP( )] GabD□874185:875651 Forward
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VALPNPWR
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LSGN
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A
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>PFR_JS14_788	PFR_JS14_788	ABC-type multidrug transport system, ATPase component	911051:911749 Reverse
MTTALSVHALTKVYGRVRALDGLDLDLEPGHIVGLMGDNGAGKTTLLKVLAGVTADWQGE
VSLHGQPPGAATKQFVSFLPDQSFLPDWQQPADAIGRYADFFADFDADRAHDLIDFYRLP
TDRRLKEMSKGMREKVQIALAMARRAKVYLLDEPVGGVDPAARSILMEGILKHFEPDQLL
VISTHLIHDLEPVIDTIVFLHQGRLRLQGDADELRAANKTDLEGLFRKVYLP
>PFR_JS14_789	PFR_JS14_789	Transcriptional regulator, GntR family	911746:912120 Reverse
MGFDTTSPLWIQLVDRLQTRVVAGQWAPGQKIPSVRELAVEFGVNPNTVQRALSELDRLG
LTATERTSGRFVTADRQQVAQQRFRLATGAVDGAIDVLAGLGLDRDTAIELFGSRWDDIQ
KEEK
>PFR_JS14_790	PFR_JS14_790	Transcriptional regulator, ArsR family	912388:913152 Forward
MTELGAERPNGDLSTRHQVLHLLLSEGAMTAPDLACRLSITPTAVRRHLTGLIKGGQVVE
NQPDQQPSRGRGRPAKTFQLTDLGRSAFNQAYDDLAMQALRVLVETMGADAVTKLGEKRY
VDVEQRYRGYRAAHPLADPVEALASALNDDGYVTKVDEAPAGAQLCQHHCPVAHVAAEFP
QLCEAETQMFSRLLGTRVQRLATIAHGDGVCTTNIPLDIVVIDHEMVIEHTPRERKRAVE
NHRATDNNREATSA
>PFR_JS14_791	PFR_JS14_791	FeS assembly protein SufB	913149:914606 Forward
MTQLDTGPVGTGPGSSQSTADQLAEDLNTYKYGWHDSDAYSAAAKRGLSEDVVRGISALK
HEPEWMLAKRLKGLKDFERKPMPTWGADLSHLNFDQIKYFVRSVDKQATSWEDLPDDIRK
TYDRLGIPEAEKERLVAGVAAQYESEVVYQKINDELTRQGVIFTDTDTALREHPELFEEY
FGTVVPSADNKFAALNTAVWSGGSFIYVPKGVNVNIPLQAYFRMNTENLGQFERTLIIVD
EDAYVHYVEGCTAPIYKTDSLHAAIVEIIVKKNARCRYTTIQNWSGNVYNLVTQRATVAE
GGQMEWVDGNIGSKINMKYPACYLLGEHAKGEALSMAFAGEGQHQDTGAKMVHAAPYTSS
TIVSKSISRNGGRTGYRGLIAVEPNAHHSASSVKCDALLVDDVSRSDTYPYVDVQTDDVS
MEHEATISKISEDQLFYLMQRGLNEDEARAMIVRGFVEPIARELPMEYALELNRLVELQM
EGSVG
>PFR_JS14_792	PFR_JS14_792	FeS assembly protein SufD	914606:915811 Forward
MTHENENGAIAVAEPVNSGADAVESLASHLHPKVSWDLGDHPMPTGREEVWRFTPVRKLK
ALLEARGEKGDVDLVERTPAGVTSVVIDPVRARELSVEPPADRSSAIAVAQSDEARLIRV
PADVELDEPLELDVRGTGVGRLAYQQLIIEVGTNARAQIVFRFEGSAALAEKIDIRIGDG
ARVDVIMVQDWAPDTLHAAQVSLLVGRDAHVRTVQASLGGAVTRVLERASYAAPGGELEQ
YGLYFVDGGRHVEHRMFIDHNQPRTRSNVDYRGAIQGEGSHSVWVGDVLIRKIAHEIETY
EANKNLLLSRGARADSIPNLEIETGNIVGAGHSSTTGRFDDEQLFYLESRGIPNDEARRL
VVHGFFVDIVRHIGVPEVEERLMKAVERELDSIAPDWGTDQ
>PFR_JS14_793	PFR_JS14_793	Putative ferredoxin subunit of phenylpropionate dioxygenase	915808:916155 Forward
MSFTAVATLSDLDDGPLGIEVDHPTEGALPVVLVKSPDGDVHAMFDECSHAHVKLSEGDF
DEATCSLECYLHGSHFDVRTGAALNPPAIQPVPVYPVRVEDDQILVDVENPLKEN
>PFR_JS14_794	PFR_JS14_794	FeS assembly ATPase SufC	916160:916909 Forward
MATLVIKDLHVDVDTENGPKEILKGVDLTVNDGEVHAIMGPNGSGKSTLAYAVAGHPKYH
ITQGTVTLDGTELQDLPVDERAKAGLFLGMQYPVEVPGVSMANFLRTAKTALDGHAPKVR
TWPKQVNTALAEMDLDSEFSSRSVNEGFSGGEKKRGEIAQLELLDPSFAILDEIDSGLDI
DALKVVAGGIDAFSKKPGKAVLLITHYTRILRYVHPDRVHVFVDGRVSVTGGSELADNLE
ERGYEQYVK
>PFR_JS14_795	PFR_JS14_795	Cysteine desulfurase, SufS family protein	916899:918155 Forward
MSSDFDVETVRRDFPILSRQINGHPLVYLDSSNSSQKPRTVIDTVAEHYAKHNANVARAM
HTLGAEATAAFEGARARIADFIAAAEPEEVVFTKNASESLNLAANTLGSRLGPGDEVVIS
VLEHHSNLVPWQMVCERTGATLRWFDVTEEGRLDLDKAEQEHLINEHTKVVSIAWVSNVL
GTINPVARIAEMAHAVDAVMVIDGSQGVPHLPTDVTALGGDLLAFTGHKMLGPTGIGVLW
GRRELLDELPPFLGGGEMIGVVTMEKSTWAEVPHKFEAGTPPIAQAVGLGAAVDYLDTLG
MDAIAAHDHEITSYALGLLGDLDFVRILGPKQAVDRGSAISFTVDGVHPHDLMQLLDSRG
VAVRGGHHCAAPLHQRFCVQSSTRASSYLYTTREEIDALRDGLVWAHDFFTGKVKARQ
>PFR_JS14_796	PFR_JS14_796	SUF system FeS assembly protein, NifU family	918152:918604 Forward
MNVEEMYQDIILDHYREKHHTGLRDPYEAEVHHVNPSCGDELTLRVDLDGDTIADVSYAG
EGCSISQASTSVMTDLVIGHSVAHAMELFDEFRTMMESQGRIEPNEDHLEDGIAFAGVSE
FPARVKCAMLSWSALRDALARAGASIEEEK
>PFR_JS14_797	PFR_JS14_797	Metal-sulfur cluster biosynthetic protein	918601:919071 Forward
MSVPDSDQMSPTPAQTETGQAQPEQSTAAAARPSDLVRDELPEVSTTPTDPNLKPPTEEQ
VLEALREVVDPELMVNIVDLGLVYGVDIDEHANVLLDMTLTSPTCPLTDQLEWGAQAALD
GIANEVTINWVWLPPWSLDRITDDGREQLRYIGFNV
>PFR_JS14_798	PFR_JS14_798	ABC transporter related protein	919345:920943 Forward
MIQAKELEVRAGARLLLNPVSFQVIPGDKIGVVGRNGAGKTTTMRILAGEGLPAAGAVKR
AGQVGYLPQDPRESDLSITASKRILSARGLDRIMERLTKFTEEMSTASGAAREKAMAGYD
RAEAQLTAAGGYGAEAEAARIAANLGLPDRVLAQPLHELSGGQRRRVELSRILFSNADTL
LLDEPTNHLDADSIMWLREFLKTYPGGVMMISHATELLEETVNKVFYLDANRATLDIYSM
GWKLYLEQRQADEKRRRRERLNAERKAAQLMAQSDKLHAKATKAVAAQNMARRAERLLAS
VEPERVSDKVAKITFPEPAPCGKTPLMAKDLSKSYGSLEVFTGVDLAIDRGSRVVVLGLN
GAGKTTLLKILDGIEKPDTGEVLDGYGLKLGYFAQEHDMLDMSATVLENMQAAAPELNDT
DARKVLGAFLFTGDDDQKPAHVLSGGEKTRLALATLVVSAANVLLLDEPTNNLDPASREQ
VLGAIRSYKGAIVLVTHDEGAVEALEPDRVLLLPDGDEDLWDHEYTELVSLA
>PFR_JS14_799	PFR_JS14_799	Mycinamicin-resistance protein MyrA	921094:921927 Reverse
MTDFSALDAACPLLECPVCRGRGAAEVPLVRHDRQLACPNGHGFDIARQGYVNLAGGAPP
ANADTAPMIDARQRFLDSGVYEPIRQAVSHASDAAHWLVEVGAGTGWYLDGVLTHRRDAV
GLATDVSVAAAKRAARSGLASVVADTWAGLPIRSASVDAVLCVFAPRSAAEFARVLAPGG
RAVVAWPTPRHLAALRERLGLLNVATDKDEQLVTQFGEAGLNPADRELVEFSAECTAQQV
ADLVGMGPNAFHDHAPAQGPTTIDVSVEVGTFLRAGA
>PFR_JS14_800	PFR_JS14_800	Short-chain dehydrogenase/reductase SDR (Precursor)	921935:922681 Reverse
MDLGLASKVFIVTAASGGLGLASARALVAEGARVVLVARRAEALAAAAAELGAQNAVVLP
ADLSAPETADAAAQLALDTWQRLDGAFVSVGGPPKGHVVENTDEQWQAAFSSVFLAALRV
SRAVVGANPAARLGFVLSSSAKSPLADMAISNGLRPGLAMLVKQLANEIAPDGGRAFALL
PGRIATQRMVDLLGHDPTPQDAVDSGIPMRRMGDPDEFGRVAAFMLSDAASYVTGVMLPV
DGGLLQVL
>PFR_JS14_801	PFR_JS14_801	3-oxoacyl-[acyl-carrier protein] reductase fabG1	922790:923485 Forward
MALVTGASRGIGAEIATELLAAGYRVAGTSRSGRAPDGVLGVSADITDPEQVEAAFARVE
EELGGVEVLVANAGITRDMLLMRMSDDDWDGVLATNLTGTFRMVRRATRRMMRARFGRIV
LMSSVSAYVGSPGQVNYSASKAGLIGMARSVARELGGRGITCNVVAPGFISTDMTDELSD
EVKDDYLARIPAKRFGETRDVAHAVRFLCSDAAGYVTGAVLPVDGGLGMGR
>PFR_JS14_802	PFR_JS14_802	Enoyl-(Acyl carrier protein) reductase	923575:924348 Forward
MGILDGKNILVTGVTMNTSIAYKVAEVAEQQGATVIVTAFGRALRLATKVVQKLDPVPQV
IELDASNADELAALPGKLRELGFDHVDGVLHSIAFANPERALGGAFLKTGWDDVAVSLHT
STYSYVSLAMAVRELMSAGSSVVGLTFDASVSWPSYDWMGVAKAGLESANRYLARYLGPD
QISSNLVAAGPIDSIAKTAIPGANSFNDIWTERAPLGWDAKDATPVANAVCALFSDLFTA
TTGEIIHVDGGLASTGA
>PFR_JS14_803	PFR_JS14_803	Hypothetical protein	924423:925172 Reverse
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MSDSLIEGLRLVSVLNAMTGDGLDAARAEDALRVADNGDPNRAHHVFDPAGVLGLEPQVA
TPVRIALGRVANQLPGEHWALLLPQPGRLAGLRGPIATNAAALETGVIVVNHGGGLGWLP
RPVGPAMQWELVPAERPLLPATPGEAAQALNEQILAAGRELGRLDAPAGNRPDDAASIHL
GAAYSHVNQKLLDRALLWREASRAGIEASPQLLHSHGVLVRDKQLRELDDICRDAISAAA
SWPRAPHGL
>PFR_JS14_804□PFR_JS14_804□ABC-type molybdenum transport system, ATPase component/photorepair protein PhrA□925325:926119
Forward
MVEVAKLSGVGVRRGKAKLLDDVNLTINEGDRWVVMGPNGAGKTTLLSLLSAQNHPSEGT
VELLGERMGRVDVFELRPRIGLSSSSLAERIPRNETVENVVVSASYAVVGRWREQYDELD
FQRAHELMRLFAVEGLAQRTFGTLSEGERKRVEIARALMTDPELLLLDEPGAGLDLGGRE
HLVATLSMLCQDPDSPAIVLVAHHVEQVPVGITHALLLDHGHVVAQGPINQVFTDEIMSA
TFGLPLQINQLPDGRWAARARLNY
>PFR_JS14_805□PFR_JS14_805□Sodium Bile acid symporter family protein□926201:927244 Reverse
MSRHEQRGPGKPWFRRIRIDWFVTAICISAIMASIFPVRGGGSVVLDGATKVLIFILFYL
YGVRLEPREAMAGLKHWRLHLLILAFTFAVFPLVVFAIHPILTHVLTPALVAGVLWLSIL
PSTVQSSINFTSIARGNVAGAIVSASASNILGVILTPLLAMFVMSTGGLVIHAQSILDLC
VQLLLPFVLGQLTRRWTAGFVLGHPRLKYVDQLSIITVVYNAFSDGMNEGIWHTVALADI
GRLLPILFAILAFMLWFTWWLPGRLGFNRKDQIAIQFCGTKKSLATGVPMASVLFAPSIV
PLLVLPLMIFHMVQLIACGVIAGRYARKDEAWHEAPGRGVGPEPAED
>PFR_JS14_806□PFR_JS14_806□RNA methyltransferase, TrmH family□927385:928194 Forward
MATLIQIDDAHDERLGDFVRLRDVNLRKSLEAEHGLFIAEGDKIIHRAAQAGYQPRSFLL
APRWIDGLRDVLDATDAPVYVVSEDLAEQITGFHVHRGALASFKRIIAWSMHDLLAMDRL
VVCEDIVDHTNVGAIIRCAAGLGWDGVLLAPRAADPLYRRAIKTSMGSVFSMPWARMDDW
RDGLATLQRAGFTVAALALRDDAVGLDEFAARMRARPGKLAILMGTEGAGLSGHWISQAD
AAVRIPMAHGIDSLNVAAAAAVACYALRP
>PFR_JS14_807□PFR_JS14_807□Peptide deformylase□928228:928848 Reverse
MKSPAEWAVNGKVLRITRWDESIMRSQTRPVTTFDDTLAQLIADMFKTMAAADGVGLAAP
QVDSDLALFVFNCPDIHDKLVYGVMCNPVVTLPEGKDRHLVSAQEGCLSWPGAYQSLARP
DFAVCEGQDETGAPVRVEGTGLLARCLQHETDHLHGTVFGDRLSKRARRRLDQEKEELAP
LYPADWPVHPKIAPSQVPTEPVTPTE
>PFR_JS14_808□PFR_JS14_808□Tyrosine recombinase XerC 1□928997:929923 Forward
MDDAGRMPTGWVRDAGLFADYLRLQRRRSANTERAYLTDLRELALFLQGRGVHDPDHVRL
TDLRRWLASQQASEAPATVARRAGTARVFFGWARETGRLGTDPAAGLRSPKLGRRLPQTL
TQTEVRELMDAAAAAAAEAGGVRGLRDVAILETLYGSGLRVSELCGLDVGDLDEARGLVR
VIGKGDKERIVPLGLPGLRAIDAWRAVRDQWVAPASANALFLGTRGGRINQRVVRRVVHE
SMRAVPEAPDIGPHGLRHAMATHLLEGGADLRSVQEMLGHASLSTTQIYTHVSDERVRAA
YEQAFPRA
>PFR_JS14_809□PFR_JS14_809□Peptidase, M23 family□929967:931151 Reverse
MDHSSADRRSADYRSLDELSTEHHEGRHRPGRHRDPAGRGGPSTRTVEQARALRITGMRR
RACAGHPLGAPRAAVRTLLVCLLTCLALMCPVGAWAQQVDGELRQLLPLDGPVSRDFRAP
DKAWSAGHRGVDLSASEGTPVRAAAAGTISHVGTIAGVRTVSVTHADGLRTTYQPVDPQV
RKGERVAVGQVIGTLLSGHGPTTSLHWGLLRGKEYLDPMEWLSGRAEGRVRLLAGGTTVK
RPVPEGWSGLMEAGVQILSPSGTAVMPADGPLTSPFGSRTNPVLGTTEVHDGLDIGAPCG
APVRAAWAGTVRYSSVMSGFGNRVEIDHGGQPHAAAASSYNHMADAGVGLVRVGDRVQAG
QVIGLVGTTGLSTGCHLHFSTYTAGRAVDPRPFL
>PFR_JS14_810□PFR_JS14_810□30S ribosomal protein S2□931445:932422 Forward
MAVVTTRQLLESGVHFGHQTRRWNPKMKRFIFNERNGIYIIDLRQSLTYIDKAYAFVKDT
VAKGGQVLFVGTKKQAQEAVVEQASRVGMPYVDQRWLGGMLTNFQTISKRIARLKELEAM
DLETVQPGGFTKKELLGFSREKTKLEKSLGGIRDMAKVPQAVWIIDTNKEHLAVDEARKL
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ATPAPEAPKPAEAAPATEEKPAQAN
>PFR_JS14_811□PFR_JS14_811□Translation elongation factor Ts□932461:933273 Forward
MAIKATDVKKLRDATGAGMMDAKKALTEAEGDFEKATELLRVSGAAKAAKRSDREAANGL
VAAAGNALIQLASETDFVAKNAEFIALGDQIAKAVDEAAAASLDEALAITLPDGRTIQQA
VADMAAKIGEKIELAHAAYVPGTIDVYLHRRDPDLPPQVGVIVAVEGDDEDFVHSVALQI
ASMNPSYLSPEDVPADVVERERRIAEETAQEEGKPEKIIPRIVEGRLKSFYKEECLLEQP
EINDEKKTVGQLAKEHGVKILAFERFATGA
>PFR_JS14_812□PFR_JS14_812□UMP kinase□933410:934159 Forward
MHDCAVPNQEDDVAEPFHRVLLKLSGEAFGNGGLGVDPVTVNAIAKQIVKVTEAGTQVAI
VVGGGNYFRGVELQKGGMDRDRADYMGMLGTVMNSLALQDFCEKEGVATRVQTAITMGQV
AEPYIPRRAERHLEKGRVVIFGAGSGMPYFSTDTVAAQRALEIGAEVLLMAKNGVEGVYD
SDPRTNPDAHLYDDLSYDEFLAKDLKVADATAVSLARDNQLNMIFFNMDDPDNIMRAVRG
EKIGTLVHY
>PFR_JS14_813□PFR_JS14_813□Ribosome recycling factor□934232:934789 Forward
MTSDIIKSAEKKMQGAIDFAKEDFSGVRTGRANPAMFEKLEAEYYGVPTPIQQLASFSSP
DPRTMLITPYDKGALGAIEKAVRDSDLGVNPASDGNAIRAVLPELTEERRKEYIKIVRTK
AEDAKIAIRGHRRRGMDAIKAQEKDKEIGEDDARVSEKQLDAVTKKYTELVDELLKAKEA
ELLAV
>PFR_JS14_814□PFR_JS14_814□Phosphatidate cytidylyltransferase□934798:935643 Forward
MSAAKRSPGRNLPAAITTGVILGAVVVATLLWWNWGFALFVALALALGVWEVCNALEKLD
MHPARWPILVGTPIVMIGSYAVGQGSGEPESALGFIVGGLALMVIVALFWRIPRGTQDFV
RDAAASLFVIGYLPLLGSTVALMLAGSSGVARIFCFLLAPIASDTGAYVVGVLFGKHKMA
PRISPAKSWEGFAGGIVTAMVLCALAVHGLLHAPAWVGLLLGLVAGCCGVVGDLVESAIK
RDAGIKDMSHVLPGHGGVMDRLDSLLAAAPAAWLVMYVLIV
>PFR_JS14_815□PFR_JS14_815□Ribosomal RNA large subunit methyltransferase N□935640:936776 Forward
MSTVQSARTIDEIMSTGPGRRPPKHWMDLGVDERIEAVRALGLPAFRAKQISTHWFSRCE
HDPRQWTDLPAAVRDEVADKLFPQLLTPVQALSADHGRTVKVAWQLHDGSLVESVLMRYP
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NVVFMGMGEPMANFKAVLGAVREITRPEPDGLGISARGVTVSTIGMVPRINELSDTGIPA
TLAISLHAPDDELRDELVPLNKHFNIDAVLDAAWAYAENTKRRVSIEYALIKDINDQSWR
ADLLARRLKERGDWGWCHVNLIPLNPTPGSKWTASRREDEEAFVRHLENHHVPVTVRDTR
GREIDGACGQLAAAVKAR
>PFR_JS14_816□PFR_JS14_816□1-deoxy-D-xylulose 5-phosphate reductoisomerase (Precursor)□936847:938040 Forward
MGHNRRVRDVVLLGSTGSIGTQTCEVIDPRRDSFRITGLSAGGAHVALLAQQAVQFEVPV
VGIAEAGHEEEFWHAFEAAGGTRRPKLISGESANQELAAMKTDVVLNAITGAAGLHATLT
TLEAGTTLALANKESLVIGGTLVTQAARPGQLVAVDSEHSAFAQCLRGGGSREVRSLMLT
ASGGPFRGRTRDELRSVTPEQALAHPTWHMGRVITINSATLVNKGLELIEAALLYDVDYD
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HEHHAKPRIGELSVQDVLAADAWARDRARAYCGVNDA
>PFR_JS14_817□PFR_JS14_817□4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase□938113:939279 Forward
MADSGMTNQATDSGEFTRPPTGVLAPRRRTRKIRVGKVFIGGDAPISVQSMTNTLTADVN
ATLQQIAKLTAAGCDIVRVAVPSQDDVDALPAIASRSQIPVVADIHFNPKYVIAAIEAGC
AAVRVNPGNIKAFDNKIAEIARSATEHGTGLRIGINAGSLDKRLHRLYETDPAGALVQSA
LNEARLFEDVGFRDFAISVKHHDPVIMVEAYRRLSQACDYPLHLGVTEAGPAFQGTIKSS
VAFGALLAEGIGDTIRVSLSADPVQEVKVGVKILEALNLRPRQFEIVSCPSCGRAQVDVY
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DAIVETLIEEANKIAADFPEQGTPQVLV
>PFR_JS14_818□PFR_JS14_818□Acetyltransferase, GNAT family□939439:940281 Forward
MSGVVRVLGPQDLPRARALLDRNPLENLFVNARLDMGGLERNRPGTRVWGWESDGELTAL
CHAGANLVSVGADAEALDAFAEQLGPRRISASIMGAADQTRGLYERLAQRWGDAWAHPRE
IRAHQPLMSVDGMSLIVPDERVHPIAPSLLQPYLSAAVSMYTEEVGVSPLDGTRGYENYV
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LCLRAYPVVSLYVNDFNTRARRLYERVGFRTVSELATVLY
>PFR_JS14_819□PFR_JS14_819□Prolyl-tRNA synthetase ProS□940366:942186 Forward
MIGRASSFRKGISFVITRMSKLFVRTLRDDPAAAEIPSHRFLVRAGYIRRVAPGIYSWLP
LGLKVLQRVENIVREEMDAMGGQEVLLPALLPREPYEISNRWAEYGPNLFRLVDRKGADM
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IGVSRAVGMIAESTCDDKGLCWPAEVAPFQVQIVATGKGGEILEAATRIAEQLDAAGVRV
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VLDQLN
>PFR_JS14_820□PFR_JS14_820□Hypothetical protein□942245:943231 Reverse
MPTRRSFLFAALTVALVGCAPSPVVNAPRARGSLKPATDALRTAALDEQALATLTGTIAQ
QGESWRLSTATTAWCSGATTAHREHLTTLVRADPLGGVNADDSPVIDLPATTAVPPQDAA
GALAQLAAGYATAADHCRSTLMAAPTGPGSLLWASLYCFSTAGAATLAAHPDGTSPGTPP
VAGQAVPTGISVGSRDDRLAALLSRIDALRYGLETMIGRSGGARTDMKQRRTAVDNVRNQ
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RSAMAGIDAQCLVPGQHGVGLAWWPGWV
>PFR_JS14_821□PFR_JS14_821□Ribosome maturation factor RimP□943501:943974 Forward
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ISHALDEAEAPSNSPYTLEVSSRGVSAPLTRPAHWRRNATRLVEVTPLEGEKYTGRITSA
DEDGAELEIDGQPRHVDFGQVRRAVVQIEMNRKSRED
>PFR_JS14_822□PFR_JS14_822□Transcription termination factor NusA□943976:945034 Forward
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EVNDEGESVGEYDDTPTDFGRVAASTARQVIFQRLREAEDEQKYGKFSAVEGDVVMGVVQ
QDRGSKTIRVDLGDIEAIMPLAEQVPGEDYKHGTRLRVYVVTVRKEARGPQVVVSRTHPN
LVKKLFELEVPEIEQGVVEVKAIARESGHRTKIAVVSHNPDVSAKGACIGPMGQRVGAVM
RELNDEKIDIIDWSADPAEFVANALSPAKALKVTVVDAGARAARVIVPDYQLSLAIGREG
QNARLAARLTGWRIDIRPDTAPDVPPANPGRPLEVPDGAQQAETGAEGPAQS
>PFR_JS14_823□PFR_JS14_823□Hypothetical protein□945181:945378 Forward
MVPAPELTRFVVRDQQVVADPRAVLPGRGAWLHRNEQCWVGATRGGFARSFRQRVHPPQA
PPPGW
>PFR_JS14_824□PFR_JS14_824□Translation initiation factor IF-2□945574:948495 Forward
MAKVRVYELAKELGLESKQLLAKLNDMGEFVRSASSTIEAPVVRRVTEKITSERGGADTS
SAPKAGAKGATPKTSGAPKSARPAAKPGAGTTPVTPQAPKAAKASSVKPAPRPAAKVKPT
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ERSAGGAAGMPRPSSARGTGGAAGMPRPNPAMMPKRHNNALAPAGQRAAGGGRGRGGRGQ
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APSIGGVRIRKGSGEAVRLRRGSSLTDLAEKIGVDPAQLVQVLFNLGEMITATQSVPDET
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RLLDALRHTHVVEGEAGGITQSIGAYQVEANVDGEERAITLIDTPGHEAFTAMRARGAKS
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EEYGGDTMFVDVSSVTGQGLDQLLEAVILTADASLDLRANPDMPAQGVAIEAHLDKGRGP
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FLVVEDDRMARQIAEKREARMRAAQQAASSKRRTLDELFEQMEKGETNELLLILKGDSAG
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>PFR_JS14_825□PFR_JS14_825□Ribosome-binding factor A□948495:948935 Forward
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VATAAALESAKGLLRSTVGKRLGLRYAPTLDFVPDATSQTAQDMEELIARARKSDEELAS
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>PFR_JS14_826□PFR_JS14_826□TRNA pseudouridine synthase B□948932:949828 Forward
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>PFR_JS14_827□PFR_JS14_827□Putative glycerol uptake facilitator□950073:950864 Forward
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>PFR_JS14_828□PFR_JS14_828□Glycerol kinase□950922:952448 Forward
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>PFR_JS14_831□PFR_JS14_831□Polyribonucleotide nucleotidyltransferase□954443:956653 Forward
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Q
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R
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SKQ
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LTARRRERAFDQIKAHALSWSVVCVGPAECDRLGMQEADLQGLRRALLRLDPSPGFALTD
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LHQERLEALGPSAIHRRSYANVRRAARLNES
>PFR_JS14_862□PFR_JS14_862□Protein often found in Actinomycetes clustered with signal peptidase and/or RNaseHII□984983:985297 Forward
MSSADDLDAYESKLELDLYREYKDVVNIFKYAVETERRFYLCNAVDLKVRTEGGDVYYEV
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>PFR_JS14_863□PFR_JS14_863□UPF0102 protein□985451:985813 Forward
MSTLVTGRYGEDLAAEYLRGLGWTIVDRNWRCGSGELDIVAYEPVERTHTTVFVEVKYRT
GRGFGDPLEAITATKRRHLRASCAQWLAEHGPTGVVRIDAIGIVGMRGSAPVLRHLRGLA
>PFR_JS14_864□PFR_JS14_864□Mg-chelatase subunit D/I family protein, ComM subfamily protein□985810:987348 Forward
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GVLFLDEAPEFGTSVLEALRTPLESGVVSIARSGATVSYPARFQLVLAANPCPCGHYGVP
DSHCTCAPMMVRRYSQRLSGPILDRVDIHVAMTSSGASRLRRTAGPAPESSSVVRARVLE
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>PFR_JS14_865□PFR_JS14_865□DNA protecting protein DprA□987345:988505 Forward
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GLVQQTGPQHWRIRRPRHPAGAPAGG
>PFR_JS14_866□PFR_JS14_866□Tryptophan synthase beta chain 2□988668:989990 Forward
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LKAVLAGLLATAVFLAYPRLMPRPRNSAK
>PFR_JS14_899 PFR_JS14_899 Biotin ABC transport system ATP-binding protein 1027379:1028107 Forward
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PR
>PFR_JS14_900 PFR_JS14_900 Cobalt transport protein 1028104:1028712 Forward
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DGIAACARPFRIIGANPEKFALAVSVMWSSIPYLLVSVRNVRDAARARGLRFSWRFVAPV
LVTAVGHALQVGEALQARGLGD
>PFR_JS14_901 PFR_JS14_901 Hypothetical protein 1028785:1029024 Forward
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AILNGSRDAGIPMPDPPAR
>PFR_JS14_902 PFR_JS14_902 Probable inorganic polyphosphate/ATP-NAD kinase 1029089:1030012 Forward
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RPTPEPC
>PFR_JS14_903 PFR_JS14_903 DNA repair protein RecN 1030006:1031697 Forward
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>PFR_JS14_907□PFR_JS14_907□Sporulation initiation inhibitor protein Soj□1035302:1036198 Forward
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MEEL
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>PFR_JS14_913□PFR_JS14_913□Peptidylprolyl isomerase□1039673:1040731 Forward
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>PFR_JS14_918□PFR_JS14_918□Twin arginine-targeting protein translocase TatC□1044245:1045117 Forward
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LAVLAVALCCFIFYNQLTAVAFHPIQQAIEVYRAKNPGAEVEITTTNVTGGFTLFMKVPF
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>PFR_JS14_922	PFR_JS14_922	Antibiotic biosynthesis monooxygenase	1049981:1050358 Forward
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NMPGQ
>PFR_JS14_923	PFR_JS14_923	Potassium channel beta chain	1050473:1051489 Reverse
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>PFR_JS14_924	PFR_JS14_924	Imidazole glycerol phosphate synthase subunit HisF	1051574:1052338 Forward
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VKQALDQAGFPVRL
>PFR_JS14_925	PFR_JS14_925	Hypothetical protein	1052442:1053548 Forward
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SSPRLPWRVATLAWAAWTCLLPIDLVQGKLAWITPMWGWGSAVGAGILVLLMTIECGRTL
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>PFR_JS14_926	PFR_JS14_926	Acetolactate synthase	1053847:1055607 Forward
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>PFR_JS14_927	PFR_JS14_927	Acetolactate synthase, small subunit	1055604:1056131 Forward
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>PFR_JS14_931	PFR_JS14_931	Hypothetical protein	1058877:1059050 Reverse
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>PFR_JS14_932	PFR_JS14_932	Tartrate dehydrogenase	1059084:1060148 Reverse
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>PFR_JS14_933	PFR_JS14_933	Branched-chain-amino-acid transaminase	1060313:1061398 Forward
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V
>PFR_JS14_934	PFR_JS14_934	Putative alpha-isopropylmalate/homocitrate synthase family transferase	1061430:1063028 Forward
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>PFR_JS14_936	PFR_JS14_936	CAAX amino terminal protease family protein	1063941:1065035 Forward
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DTPS
>PFR_JS14_937□PFR_JS14_937□Transcriptional regulator, IclR family protein□1065437:1066165 Reverse
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EG
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KAYEDKRPSFKPVTTEVA
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QLIALALSRPATVLR
>PFR_JS14_942□PFR_JS14_942□Putative insertion element ISCmi2 transposase□1070360:1071403 Reverse
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>PFR_JS14_943□PFR_JS14_943□Conserved hypothetical membrane spanning protein□1071501:1072496 Reverse
MEDRDVFLFASIPWYSWVAWFVVLGALIGLNELTRRFRWAGLAIFVALPIILTIFVWPTS
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FQVGGMHANGMVDGVYMLSGPWNWMNGVAGLLNLLTICGWFGIFISRDKSKDMIWPDMLW
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PRAG
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GCS
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AR
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>PFR_JS14_970□PFR_JS14_970□Sugar-binding family transcriptional regulator□1108466:1109434 Reverse
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ELEAVTVDVDPDATARLVKQWDDDDLSVPLKVIDSPYRQITGPFIDYVRALVSENPRDIV
CIYIPEYVVGHWWEHVLHNQTALVIRARLHFMRGVMVTSVPYQLESSARLATRYRRRELR
RPRR
>PFR_JS14_996□PFR_JS14_996□Putative 23S rRNA (Uracil-5-)-methyltransferase RumA□1141523:1142701 Forward
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>PFR_JS14_998□PFR_JS14_998□Glutathione S-transferase domain protein□1142993:1144066 Reverse
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>PFR_JS14_1001□PFR_JS14_1001□Hypothetical protein□1145565:1145684 Reverse
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>PFR_JS14_1002□PFR_JS14_1002□Glutathione S-transferase domain protein□1146176:1147204 Forward
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A
>PFR_JS14_1009□PFR_JS14_1009□Outer membrane receptor protein□1156214:1156813 Reverse
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ANTSVTSNLAVAGQLTAGLNLNLNKDNLAMAGTTLTNALDRAGDTATQVDHGLDQLNGAL
DTSDKGVKQLNSAMGQATSSGHTLLSAGAGAVSGLNQLSDGLGRLDTAMPQLSNGAATLA
SGLQKGTDQLPTLSEDQRNTMAEVMASPATVTQTVDNPAGAYGRGLAPMFFSIALWIAGV
SIFLVVRTISGRALTGRASPLRITMLGFGPVATVALAASLLMGLTVWVTLGLNPVHPWKF
LLLLVVTALAFMAPAYLLRLVFGSPQTAVYLILLILQLPACGGTFPALLLPPIYQKLAVI
SPMKYSVDAFRVVISGGLNSTYWGALAILVAITVVCLGCIVLMVSRRRRFRITDLHPPMV
TSTSTADYAFSVRPR
>PFR_JS14_1032□PFR_JS14_1032□ABC transporter related protein□1180468:1181280 Reverse
MSDERVVLHARELESSGRQGRIFGPIDLDVHARQLCMVHGPLGSGKSALLLALTGRFRPL
SGLLTIDGVDAIHDPLEAMQMTSVAQLGDYVRPEDRLTLAESITERCFLDGFPRRLAADR
VAAMEETVGFRIEKHVELESLTPIEKAISSVALAMIRPSRVVVIDDADMTVPHSQQSLLF
ALLERLTTLDDSVIVASVVDDDLIPATAISLSLRSDRPQVVEPLGSEPVPISLAQAALAP
LTARGRPAGAAMGDDQVAAPSPTQTPNPDK
>PFR_JS14_1033□PFR_JS14_1033□Transcriptional regulator, TetR family□1181277:1181891 Reverse
MPLHVAHRPTRQQVRRKVIDAASRAFRTHGYARASMTQIAESAGFTKGAVYSNFESKPEL
FSTICIENINRLSPPVIAELDAMFANGARDASAIDRIADSFAQIVIESGPWQVALGEFRQ
LAVHDPQVAESYATLLRERTEQAMRLLDGHPLARRLGPQRTREAIWTVFELISLLALEHA
AAPHMVTPAAIRSVLASVLGGLSA
>PFR_JS14_1034□PFR_JS14_1034□Adenosylcobinamide-GDP ribazoletransferase□1181985:1182806 Reverse
MAPARTPNRRTRSDVATRNGLLAAWGLFTVLPAPVVAEVDERLAVRAIASMPWVGLGLGL
IAGLGCAIVTVAGGGQPLAIAAGLAILALCTGFLHLDGLADTADGLGSRKPAHEALTIMR
QSDIGPMGVTAIILVLALEIAAGGSGHLDGWRGVWLLVTMPMVARVSALSATGRWIPSAH
KKGFGALFAGKTHPATIVVASVIAAVIAAGSGWLLFGWRAALVAVCACLASWVFGVAWRR
HILARLGGLTGDTFGSLVEMSGLAYLLTLALFA
>PFR_JS14_1035□PFR_JS14_1035□Bifunctional cobalamin biosynthesis protein cobU□1182766:1183437 Reverse
MTRIVVDVPDSPESRRLLDQLSGLGARQRPARTLVTGGARSGKSSYAEALLGSFDHVDYI
ATSQRNPDDPEWMARIAAHVARRPKSWNTVETLDVAQVLSDDGSPALVDCLGVWLTRELD
VTDAWQHPEQARPELQHRIDELATAVAGSPRRVVLVTNEVGSGVVPATQAGRTFRDWLGI
LNASVADACDEVLLCVAGRALSLPPRPGGPHGAGTDPQPKDAI
>PFR_JS14_1036□PFR_JS14_1036□Cobyrinic acid a,c-diamide synthase□1183434:1186019 Reverse
MVTATALPRVLIAAPASSQGKTTVAIGLMAALRASGRSVAGFKVGPDYIDPGYHALACGR
PGRNLDPYLCGPERIAPLFAHGALHPEPADISVVEGVMGMFDGKLGAWPDGTDDPAGFGS
SAHIARLLDAPVLLVVDGSHSARTAAALCHGLASYDPRIHVAGVILNRVMGARVVDEITR
GCARVGLPVLGALPKSTRVAVGSRHLGLVTADEQGDAIGIVQQAGELVAAHLDLDAIATI
AGGAPDLAVDPWDPAAEVEPVPGRPVIAMASGPAFTFRYTETAELLEAAGCRVTAFDPLT
ARGLPADVSGLYLGGGFPEEHAEALAGNTSLGAEIASRVSEGLPTVAECAGLLYLCRSLD
GLAMAGVVDADSSMTPRLTIGYHHARAANDSFLMRAGERYRAHEFHRTTLDTPPYDRDPG
PQRLGDQRLAWDVETPTGGNRPEGVLVAPTPGSAPSVHASYQHLHWAGSPVLAQRFARAA
SEYGHTGHHSPRPAATTPGDALSAAPDLTHHGDRDVLPGLVDLAVNVRDVRPPAWLVERI
VASSDQWAHYPDQREATRAVALRHGVNPDQVLLTAGSSEAFSLIAHGFSPRWAVVVHPQF
TEPEVALRNAGRPVGRLVLHASDGFQLDHELLDPRADMVVIGNPTNPTGVLHSAASLRAL
CRPGRVVVVDEAFMDAVPGEPESLIGARMDGLLVTRSFTKTWSVPGLRIGYVVGDPALIR
VLAHEQPCWPISTPALVTARECSTPRAVEQATSDARQAAQDRRHLVARLAGIGIQTVGEA
RAPFVLVDLRAHPPGGLRAGLRTLGFTVRSGESFPGLGAGWLRLAVRHPDISDAFVAALA
RTIDALDTAQHPMRPPQGDIR
>PFR_JS14_1037□PFR_JS14_1037□Cob(I)yrinic acid a,c-diamide adenosyltransferase□1186013:1186615 Reverse
MSGSAPQRTEPTTAELRHRPRLIVNTGNGKGKSTAAFGMGLRAWAQGWSIGVFQFIKSGR
WHTGEQQAYAQLDQAHRTTGVGGPVEWQSLGSGWSWLRATEGTDQAAMAAAGWAHVRTLL
AAQTHRLYILDEFAHVLNKGWLDVDEVADDLAHRPGTQHVVITGRNCPAGIIGIADIVTS
MDNVKHPFGKGERGQAGIEW
>PFR_JS14_1038□PFR_JS14_1038□Adenosylcobyric acid synthase (glutamine-hydrolyzing)□1186612:1188057 Reverse
MTGILLTGTSSDAGKSALVTGLCGALRQRGIDVAPFKSQNMSNNSMVCPDGAEIGRAQYL
QATAAGVTPEAAMNPVLLKPGTDRRSFIVLMGRPDGELDAGEYATGRKHLAEAAYDAYSD
LASRHELIVCEGAGSPAEINLRAGDYVNMGLARHFGLPTVIIGDIDRGGVLASLYGTWAL
LEAEDRALLKGYIINKFRGDGALLEPGLQEITTRTGLANLGVMPWLEDVWFDGEDALQVD
RWPAQSGAGDRLVVAAVRLPRISNSTDIDALATEPGVEVQVTADPATCARADLVVLPGSR
ATVDDLDWLRKRGIAQAIVQRRREDKPILGICGGFEMMANTIDDDIESSAGSVPGLGVLP
ARFRFDAEKVVRTAQYHFDELAVDGYEIHHGRFEVDGGEAFLDGVRSGNSFGTMLHGSLE
NDGFRRRFLHMVARNTGSTWEPDDARPGYQQLRATMIRTLSTAMAEYVDVDAMLAMTGLA
R
>PFR_JS14_1039□PFR_JS14_1039□Cobalamin biosynthesis protein CobD□1188054:1189085 Reverse
MSLAADDHGWGSRAVGLISAVTADRLIPDPANPWHPVAWFGTWAGWLEKKMWRDSVGQGA
AYLVVALLPVATLGVAVEAATRRHPLAHATATAAAGWLVIGSQSLATEGEQMADELEGDD
LSAARDRLPHLCGRIPDTMPEQELARGTIESLAENTADSGVASLWWGSVAGIPGMLIHRA
SNTLDAMVGHHNEHFEHFGKCAARLDDGLDWIPARLTGILGAICAPSVGGRVVTTARIVA
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RDARNHPSPNGGWCESAWAGALGVQLGGRNVYPGGRVEHRGLLGDGHRPRAGQVRDGARL
VRVVTAAATALAAGACLGIGQLIRAHSSARKAPTHSPSRKASR
>PFR_JS14_1040	PFR_JS14_1040	Phosphoglycerate mutase family protein	1189089:1189667 Forward
MLDRGIDFALVRHGESTGNIGGRVLGHELGPELTTLGRTQARGAAHGLTRWHADMLWSSD
MVRARSTAQEIARTTRLPLNCTALLREQDHGAMDGLPVGDLVAQPTPAGREITEVRWGGG
ESIADVYARLRLFVMMVAARGARRVVVVGHGDMACAFTSMLAGLGHRDVAWDRLAHGQVR
YLGWDGRALLPS
>PFR_JS14_1041	PFR_JS14_1041	Alpha, alpha-trehalose-phosphate synthase otsA	1189926:1191407 Reverse
MSEDQLSIPSAPANDGRTEDPVPRDAPAAGTSQFVVVANRLPVDRVQNDDNSSGWALSPG
GLVTALIPVMKDHGGTWVGWVGSADEHIQPFTFDGYGIMPVDLSAQEFNEYYEGMSNATF
WPLYHDCVEHPEYHREWWDSYMEVNQRFATAAAEVAAPGATVWVQDYQLQNVPALLRQMR
PDLKIGFFLHIPFPPSELFMQLPWRYQVISGLLGSDQIGFQDPGSARNFAHLVRRLAGMR
TQGDRIFSPDGRVILARAYPISIDAQEILDLSRTPQARAEAEQLREDLGNPDKIFLGVDR
LDYTKGLRHRVRAFGELFTSGQLDPMRNVYLQIATPTREGVARYQVLRSIIDEMVGRINS
SVGRIGRSPIEYRHASYPKMALAAMYRAADVMVVTPLRDGMNLVAKEYVASHDSDAGALV
LSEFAGASLELKQAYMVNPYDLNGMKNQLLRAAGDTHANHVRRMRSMRKQVFRHDIDAWA
NSFLTDLGTERPV
>PFR_JS14_1042	PFR_JS14_1042	Trehalose-phosphatase OtsB	1191569:1192426 Forward
MTSGSDLVSFPTDEGRATTEAIIDDPSNALICLDFDGTLAPIVADPQDARPDPEAMAALE
RLLTRVGQVAIVTGRPVDVALQLGGFAMLPDTSRLRVFGQYGAETWNGATGHIHVPAQPP
AIGEAKLQIERMLADLSAQNPALRGTAIEDKGLAIGVHTRRAADPAEALVELTPRLDTLA
DRLGLITEPGRNVVELRAGHSDKGDVVAKLLDDPSIGAAAFCGDDLGDISAFAVLIKWRR
RTGQRAACVVSASDEVPSLRERADVLCEGPSGIAAWLTSLTSTGS
>PFR_JS14_1043	PFR_JS14_1043	Hypothetical protein	1192738:1193397 Reverse
MSTNPPVPPTPPQQGAPQYGAPQPPKKTGLSTAGLVLGIIGVVFAFIPMIGMPVAIIAGV
LALLFGIIGIVKKHGGKAIASTILGIAAIVVAIIATTTIYGAAKSISDAASSLPAATSST
TAGSTAAGQKTVTMKATATGNGTVVWGLDTGTNTEQFSGTWTKEIQAAPGKMITVSVTGD
YADGDSQKMTCEIDVDGVSKKTGEGSGAAGSASCSVFGV
>PFR_JS14_1044	PFR_JS14_1044	Hypothetical protein	1193505:1193915 Reverse
MLTTDDLATPPPGWTIIVRRLPTGFGWCLWSSRQIALDDRLTAAEARCTRAHEILHARRG
RPPAWMRDREETLIEQTVASILIPLEALTRALQWTASLSEAADELRVDDRTLATRLQHLH
PSGQAALNTRLADVTR
>PFR_JS14_1045	PFR_JS14_1045	Hypothetical protein	1193973:1194614 Reverse
MSDKEAEQPDTSETDVAAQEKHVHSRHDHAKHGGRLPPGNSSGDDAGPESRLPAGRNGSQ
EPEAPGINEDPLPLDYSGVEADEDRLTAEIRKELQLQVTAGWSAPLPQPRVLAEFEKVLP
GAAERIMRAFESSTTDAAARDDKIVESRTWVAKTGAGWAFFFLLVMIAAAIVFFARGNNQ
AGMTMIGTPFIVSLVSIITSAISKRGERKGNDS
>PFR_JS14_1046	PFR_JS14_1046	Hypothetical protein	1194614:1194706 Reverse
MPIDEAARDGDLSDRLGDEDYSQDPGDEEE
>PFR_JS14_1047	PFR_JS14_1047	Hypothetical protein	1194774:1195316 Reverse
MKRTRLILALAAIAPLLFAGCGGGGSTSTASSSAAPVSSTASPAPTPSVVAPALDIAKTV
GGSDVSTTYALTEDNDANNLLGRSNGYSSAAVGVIASLDASQCDAAKPGVDCGFTIEVWP
NDAAAIQRGQHIQSMKTGGALGTEYDYAKGGVLLRVSGEVKPSQATQLNGRFGGQQVSKG
>PFR_JS14_1048	PFR_JS14_1048	ADP-ribosylation/Crystallin J1	1195631:1196443 Reverse
MEFSPQVMDRAAGVLVGQAVGDALGVPYEFAAPIRAGDARMVGGGLGPYEPGEWSDDTQM
AVCVARVAASGTRLTRSDALDAVAAAFIDWKHNAASDIGNQTATVLEMASRHDGVGLGEA
MTAIARDVGRRGQAGNGGLMRTSVVGLAAVGSAEETASAAARVCALTHGEPRCIESSVLW
SLAVRNAVLTGNLDVRSGLPQLAPERRSWWQRQIASAVETARLAGVSESTIIRIEQGKRD
LPVALLFELARVLDFEPGVFMDAAQARYQR
>PFR_JS14_1049	PFR_JS14_1049	Hypothetical protein	1196548:1197981 Reverse
MDAHTLEDEFEELLAAAYRSSFGKDPTDLWLAAIASRAGTRGAVATLNQAGDLLGVSRER
IRQVMARITPALQGMLRAQLWMIALTIAQYSPAAEPVGRYLAPLGLSRPTLTGEGFLNLL
KLTGTSAGELIGDDLVVVDGWLVRGTQMQVTKSLPMANRQTSSFGMTTITTICHALMTPS
ESPDPAAVQRILRAEPTVRWFGDWLWVHKDDQGPHANRLVNTARSILSVNSPQTITSIHE
GAQRLWKFRRLELLPPVEAMRAFFGNHSGFEVDGDQVRALEPLDYHEVLGGVTATMIDIL
KSSPYQVMDRQSLREACREAGIAPGTSTVWTTYAEWMQKFAQNVWGLRGSEPDMQAVERI
RRAARARSEAEPHRKSSSLIPGGAIQTMDVTTSCLATGVLSFAPEVHRLVAGSALDIVRA
SESLGRAKFGASHFFSWGWLPMLRSLDAKPGDVLRISIDPAAARAEVQLGGPELWGP
>PFR_JS14_1050	PFR_JS14_1050	Hypothetical protein	1198251:1198583 Reverse
MVGRCARAHNGAMSEGNVIRVLARIYVDDLAGSLPLYEQLTGQSSPHTFTFGATRLARVG
DFLLIEGADARVRSHAATIAVRDVAEVVAAVTKAGGQLLEGPAEGPNGPR
>PFR_JS14_1051	PFR_JS14_1051	Transcriptional activator, TenA family	1198621:1199316 Reverse
MRMQTDPPTSGPAAVGRQITDGWWGRIGDIRRQIDELEFIRGLGDGSLPREAFLWYLRQD
ALYLHDYARILAAAGEVSPTPAEQEFWTHGAQSSVAMELELHKSWIPADAMAHLAPSPVT
QAYLDQLADVAAGRDYGQIVAAVLPCYWIYADVGARLARLNRPGHRYGSWLDTYSDEEFA
EQTRQAIGFAGAAAARSTEPGRHRMWQAFNEASWHELRFFAAPLELGVREG
>PFR_JS14_1052	PFR_JS14_1052	DNA primase	1199486:1201354 Forward
MAGRINDEDIALVRERARIDNIVGAYVTLRNAGGGSLKGLCPFHDEKTPSFQVTPARGLF
YCFGCGVGGDVITFMQKIDNLTFTEAVQTLADKVGVQLRIVDDGKPSLPAGLRVRIMEAN
KLAAEFYSKALAAPEALEARRMLDGRGFDRPAAEHFGVGYAPRDGRALHRHLNHAGFRDD
ELVSAGLIREHGGWDYFQGRVMWPIKDSGASVLGFGARHLYDDDRLPAKYINTPETPVYK
KSHVLYGLDLARQNIGKKLQAVVMEGYTDVMSAHLAGVDTAVAVCGTAFGPDHARLLQRL
MGNNDSTQGEIVFTFDGDKAGQAAALKVYKLDRSFTTQTYVAVEPNGLDPCDLRMAKGDA
AVRELVGRREPLYRYVMAHTVAGYDLDRADGRVAAVRAAAGMLASIRDANLVGEYVRDLS
RLVGMDVDEVRRILKQARNQGAGGRREPPVPVVSEDADPVEPGDSPGWPDRNDRNLDVER
GTLKLMLQHPTLFDTAWNGVSTSDFTHPAFRALFGAILSTPYVPTGWTDSLQQATGDELV
RQLEIALLVEPILRSPDEGYASAYTSRLKLLTTARAIDDLKSRLQRTNPLQDKDAYDAMF
MKLLDLETSRKKLSQASLGLTE
>PFR_JS14_1053	PFR_JS14_1053	RNA polymerase sigma factor	1201427:1202281 Forward
MVAPTTRRQTAAMDATQIASISPRLDAADERELARLIEAGVFAGHALEQDQSPCGASAEE
LRQVVAHGELAWQKFFEGNISLVRCVVARWVPVTHPDSEDLVHEGCMGLVEAIMRFDHAL
GWRFSTLAWYLVSQQVAIAAVGNRSCGSGTVAHARRVARIERARSRASASRGAPVSDREV
ADLVGRSVEAVRRDLGQARRVEADQDILEQTIPDERPVHDVSFLSELADQERRVLELNFG
IRNGRAQTLVQIAEHMGMSVSAVSRLKQRALRRGRALVHAELAA
>PFR_JS14_1054	PFR_JS14_1054	Hypothetical protein	1202361:1202927 Forward
MGHNWVMASSRDTHAGPGREQLKALSTVLGHRPSVLATASGPTGTCLATPEAFCVLTTEV
PTSDAGQSGRGTWQVIGWENIQNGDWDNATKTLSWLLLDGTVGQIAVTTTDRLPGVFRER
VRASILVEDTSEVSEGKGSVLIAGRRNPVADGPITWTAQPLKRTNMADPEVREHIVRRTA
ELRDEYEL
>PFR_JS14_1055	PFR_JS14_1055	Phosphofructokinase (Precursor)	1203258:1204472 Reverse
MVKKVALLTAGGFAPCLSSAIAELIKRYTEVSPETTLIGYRYGYEGLLKGDSLEFSPAVR
AHYDRLFSFGGSPIGNSRVKLTNVKDLVARGLVASGDDPLKVAADQLIADGVDVLHTIGG
DDTNTTAADLAAYLAQHDYPLTVVGLPKTIDNDIVPIRQSLGAWTAADEGARFAANVIAE
HNAAPRELIIHEIMGRNCGYLAAETSRRYVAWLDAQQWLPEAGLDRRGWDIHALYVPEAT
IDLDAEAERLRTVMDEVGSVNIFISEGAGVPDIVAQMQATGQEVPTDAFGHVQLDKINPG
AWFAKQFAERIGAGKTMVQKSGYFSRSAKSNAQDLELIAATATMAVDAALAGTPGVVGQD
EEAGDKLSVIDFKRIAGHKPFDITLDWYTQLLARIGQPAPIAAT
>PFR_JS14_1056	PFR_JS14_1056	Hypothetical protein	1204696:1205118 Forward
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MNHPRREVRPRPDDERGASVSVLIAACIPAFILICGLAVDGAHQVSAQRAATVTAAQAAR
VGSDSAATGRLNGLDARQEAMRAAREHVGTQPGMACTVGIDANDRVHVEVSTRADTAFLS
IVGINHLNARGAATAELRPV
>PFR_JS14_1057□PFR_JS14_1057□Translation factor SUA5□1205187:1205804 Forward
MARYYPVHPENPQARSIHQVADLLREGAVIAYPTDSGFALGTLFGNKEGIDTMRRIRDLD
ERHHLSVVVSEFAQLGRYVDMDNREFRAIKASTPGPFTFILRATREVPRSMQHPNKTVGV
RVPDHVTALALLDELDEPLVSSTLILPGQEEPMSEGWQIKEALDNDIAAVLDSGDVGHVP
TTVVDLTGEEPVVVRRGGGKTELFD
>PFR_JS14_1058□PFR_JS14_1058□Hypothetical protein□1205854:1206753 Reverse
MNDDSGSGDAPPERPDFEPPRSQSPGSGQVPGAGSFGPPPRYGGWNPPSGSATPPPRQPP
PRQSSYPTPPRAHARSQHWFNQPAQGGWARTHSSMPVTYTIIAICVVVWLCQLVVPGFNR
DVILTTWSWQSQPWRLITSAFAHSVSGFMHIAGNMLMLWLLGRAIEPAIGRRDYVLSYLL
SALGGSALFILFAALSGTHSAVVGASAAVFGLFGLLVGLYKLAGIRNTGIWVLLGINLVF
DFIVPGIAWQGHLGGFLIGLGAGFLIAHARRRGRTTTPTLWLLLVPIVAALGASLALTG
>PFR_JS14_1059□PFR_JS14_1059□LmbE family protein□1206919:1207719 Forward
MATWVFLHAHPDDESTQTSGTMAMAHERGDRVVLVVATDGEQGTTPPDLKPGESVSDRRH
AELTAAAAVIGIDRVVWLGYADSGMTGWAQNKAPEAFCNADLDVASQRVADILREEKADA
FVHYDPHGSYGHPDHIMVHRVGAAAAAKVTGPMRVLEETIDRDARGDDPDKIEALGLADN
DFATGAALGDDGKPIGSPRSEIRWAVDLPQRIIDIKHEALACHASQSDAEFFLSLPRPAF
DFVFKTEWYREPGNPGPYTHAWPLDG
>PFR_JS14_1060□PFR_JS14_1060□Proteasome assembly chaperones 2□1207858:1208895 Reverse
MIDPTTLFSYEPTIDQRTIHDRVMVVTLGSFGDVGASQAQVDEHLLNTLTHRKIGTFDVD
QIMDYRGHRPPIDFDQDHYDNYVPPSMTLHEVVDKSGNPFLLLTGPEPALQWERVSATIE
WLMDQMDVQLVVTAQGVPMPVPHTRPINLLKVATRPELIPGNRGSGSFRMSSSFLAMMTQ
RLGEKGRDVIGLVARVPQYLADTEYPDGAIAMVNGLNELAGLNIPVASLEQASHLARAQI
DAQVEQSEELQQMIGQMEEQYDRYMQDHSLPMNEEDIPDADEIGQEMEDYLASLDPGTPD
SDKGPQVGPVDHDEDEHHSDHHGDNGPRDGHDGPQPPADPDIPND
>PFR_JS14_1061□PFR_JS14_1061□ABC-type uncharacterized transport system, ATPase component□1209061:1209852 Reverse
MLEVSSVSKAFFPNTVNEKVALRGIDLTLDKGDFVTVIGSNGAGKSTLLNIIAGRYRPDS
GSVTIDGKDVTKMPDYRVARYVGRVFQDPMAGTAAHMTIEENLSIALSRGHFRGLVRGVS
RARRARFRKELTVLQQGLEDRLTAKVGLLSGGQRQALSLVMATSSNPRVLLLDEHTAALD
PQRAELITKLTGELVEAHALTTLMVTHNMEQALRLGNRLIMMHEGQIILELSGQAKKDAT
VADLLAQFEHIKGAQLSDRSLLT
>PFR_JS14_1062□PFR_JS14_1062□ABC transporter, permease protein□1209854:1210807 Reverse
MLGAIDLGLIYGLMALGVYLTFRILDFPDLTVDGSFTTGAALTATHLAAGGNPVVATLLG
FCGGLAAGAITGLLSTKGRIHPLLAGILTQIALYSINLRIMGKANVPLLRSKTLMTPLRS
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LSLSNGLVGLAGSLIAQYQGFADIGMGIGLIVAGLASVIIGTAILNSSLVVVATIAVVLG
SLLYRVIIQVALMVGLDPNDMKLVSAVIVVLALLLPRWGVVSRMRARRRARGLPAEPDII
GPLEDRDQASGLVGPGA
>PFR_JS14_1063□PFR_JS14_1063□ABC transporter permease protein□1210814:1211815 Reverse
MNPKAIIMKRRTLLGTLGIMGLSVPLAACSSKSSGSGSSGTGKKVKIGITQIVTHSSLDA
AREGFKKAITDAGFNASFDEQNAQGDQGTAASIATKLASENLDLVLAIATPAAQAAAQAI
TNVPIVFTAVTEPKSADLVASNDAPGGNVTGTSDMNPVADQIGLIKQIKPDATSVGILYS
SGEVNSQVQVNLAKEAAAKDGLSVQEKTITTTGELQQAAQALNVDSIYIPTDNNVVSGLS
TVIQVCEDRKIPLISAEGDSVRNGAVITYGIDYTELGRQTGEMAVKILNGDAKPATMPVE
TQKNLKLYVNEKAASLMGVTIPDDLASKAEKVG
>PFR_JS14_1064□PFR_JS14_1064□Phosphoglycerate mutase family protein□1211983:1212606 Forward
MTTPRFVLMRHGETDWNTKNQYQGSSDIPLNAVGRAQAGAVAGWIAHLNPVAIWASPLER
ALDTARAVASFTGQQVNVDPRLAELDYGDFEGWTWEQIEKVEPGLAAWRDGESDGRWSAS
GETGAEVMARMGETLTHLDRVTEPGPILVCSHGTAIRLGVAALVGWDYPEIWKLASMGNC
CYTEVIREFDAWRVERFNVPPQWNFSG
>PFR_JS14_1065□PFR_JS14_1065□Glutamine--tRNA ligase (Precursor)□1212628:1214340 Forward
MAKPADNIAASDFIADAITKDNEVGTYAQRVQTRFPPEPNGYLHIGHAKAITVDFGTAEE
FGGLCNVRLDDTNPVAENPEYVESILADIAWLGYQPHTVVHASDYFEQLYQWAEYLVEQG
LAYVDDQDTETISAQRGGFGKPGIESPCRDRTVEENLDLLHRMRAGEFDDGACVLRAKID
MQSDNMVMRDPVMYRIRHATHHQTGNDWPIFPTYDWAHGQSDAIEGVTHSLCTLEFDSHR
PLYNWFLEHLPLPGDQPRQIEFARLELTYTVTSKRRLAKLVADGVVSGWDDPRMPTLRGL
RRRGYPAAAVRDFCRDIGTTRTNSRHNIEELESFVRRELNKTAQRRMVVTRPLRLVIDNW
PTDEHGAPEVDWFDVTNNPENPADGTRRVPFSGELFIERDDFAEVPPPKFFRLSIGREVR
LRGAYFVTATSVVTNEAGEVTEVHATYDPATRGGDAPDGRKVKSTMHWVSAAHAVDVKVA
LYNRLFTTPAPGERTGEPLDDLNPDSVELLTDAKGEGVINEVEPGQVVQFERLGYFCADL
DEPRLFHRTVGLRDEWAAQQRRAAKQAKKG
>PFR_JS14_1066□PFR_JS14_1066□TIGR03085 family protein□1214385:1215131 Reverse
MSTPDGGRWTSRPAYSDYVAIHPRYDAAHVFRLALADALTQAGPDARTLCTGWTTADLAA
HLYVRENDPLSLPGIAGLPGPAGPAAQRMTIRSMERALTRHGYQGVVDLFRAGPRPWSVW
RAPQLDRIGNALEYFVHLHDVTDAVPHDGNDPLGSDRGLSQRLRDELWHRMPPLATMLLR
GSPAGVQLERLDAPHPSRIIARRGLPIVTARGSAPQLALWMFGRHARVELVGDVEPLAAV
STLVASGV
>PFR_JS14_1067□PFR_JS14_1067□Phosphoribosyl-AMP cyclohydrolase (Precursor)□1215147:1215599 Forward
MGNNGGMSTNSARSTRLDASAPTQADTGVPTLDPSIAQRLKRNEAGLVPAIAQEATSRRV
LMMAWMNDDALARTLATRKATYWSRSRQELWVKGETSGHTQAVRDVWLDCDGDTVLLSVD
QVGAACHTGADTCFDAGGPLPLAGESVIAS
>PFR_JS14_1068□PFR_JS14_1068□Anthranilate synthase component I□1215596:1217128 Forward
MSRQLRIEPSLEGFREQAVDRRVVGVRTRLRADDLTPIALYEQLTGEAEGSFIFESVEQG
TWSRWSFIGVRCPSMLVGRGNTSEWLGRPLEGIPRHGPCLDVLAATLRALHTPADPELPP
FSSGLVGYLGWDVKRQVEPSLGEPNPDDIGVPDSVMMLATDMAVLDHHRGEVWLIANAIN
FNDTAEGVDEAYRDAVARVHRMATKLTSPRPALLASIEPDARPQVTEQRAPGEFEAMVEK
AKEYVMAGDIFQVVPGQRFDVDVTASGFDIYRELRVANPSPYLFLLKLPGFDLIGSSPEA
LVTVKDGVATTHPIAGTHPRGDTEAEDRRLEDEMLADEKERAEHLMLVDLGRNDLGRVCI
PGTVTVTQFMHVGRYSYVMHLEAAVTGSVEPGLSALDVVMACFPAGTLSGAPKLRAMQII
DELESTARGPYGGVVGYFDFAGNADTAICIRTALVKDGVAHVSAGAGIVADSVPANENAE
SHNKAAAVLVALARANASHRITPQTLLEQS
>PFR_JS14_1069□PFR_JS14_1069□Indole-3-glycerol phosphate synthase 1□1217125:1217985 Forward
MTTVLDDIITGVRADMAARMAVVAPSQLKERIRWMGPTLDPRPGFGGDTISVISEVKRSS
PSKGALATIEDPATIASAYEAGGAAAISVLTERHRFNGTLDDLRAVREAVGIPVLRKDFV
IDPYQVLEARAFGADLVLLIVAALDDKQLAGLYDLALSLGLLPLIEVHTAEEMRRAALLK
PELVGVNNRNLKTLDVDLAQFERLAPLAPHDAIVVAESGIRDAADVQRVRAAGADVVLVG
EALVTSGNPREAVQTMIEATRPGRGPAGSPGKATVMNDDRQGESNE
>PFR_JS14_1070□PFR_JS14_1070□Tryptophan synthase beta chain□1217978:1219231 Forward
MSSSARALPDELGHFDFFGGQFVPEALKAALEELTAAFRDAQDDPSFAEELKDLQVNYAG
RPSPITEARNFGDKYCGGARILLKREDLNHTGSHKINNVLGQGLLTRRMGKKRVIAETGA
GQHGVATATIAALMGFQCRIYMGKVDTDRQALNVARMQLLGAEVVAVEAGSATLKDAMNE
ALRDWVTNVATTHYLIGTASGPHPFPMMVREFQRIISTESRAQMLQRFSQLPDAICACVG
GGSNAIGSFADYIPDENVALYGFEAGGEGVETGRHAASINGGSLGVLHGTRTFVLQDDDG
QTIESHSISAGLDYPGVGPEHAYLSRTGRAHYEPVNDDEAMEALDHLTRCEGIMPAIESA
HAVAGAERVAKRMLAENPDHRPTLLVTISGRGDKDVDTAMKYFGVRGTVDATTGSMS
>PFR_JS14_1071□PFR_JS14_1071□Tryptophan synthase alpha chain□1219228:1220124 Forward
```

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MSTTDLTKPFPDKNRLGISGKMVAACREQGRPALVGYLPVGYPDVPGSIEAMQALTSGSQ
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NLVEHYGSHGRTTHPEESVRGFARDLANAGGAGLITPDLTPDDAAMWAAASDEFGLDRVY
LVAPSSTERRLKMTTDACRGWVYATSVMGVTGARASTSSAAPQLVERVRRAAPDLPVGIG
LGVSNGEQAAEIGSFADLVIVGSALVKRLLDAEDAGTRDLGPLRATVDDLAAGVRKAR
>PFR_JS14_1072PFR_JS14_1072Prolipoprotein diacylglyceryl transferase1220121:1221092 Forward
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VVIGIIGARAYHVITDHELYFGPGRHPIDALKIWNGGLGIWGGVAAGALTAWVWCRRNGM
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INNYTSAIVFVLATILFIWQLRFRPGNAPDVWRASPDMAVPTGDHPAGPAPIADDAPTQV
SPGPDASGSGTHVPNVPRGESFN
>PFR_JS14_1073PFR_JS14_1073Class II glutamine amidotransferase1221236:1225744 Forward
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GAGILVQMPDAFFRGAVDFMLPPTGQYAAGMAFLPTDEEEREMAMISIEKIAIEERLKVL
GWRTVPVATSTLSPISLGVMPHMAQLFVSARDGSAGIDLDRKVYMVRRRAEHETNTYFAS
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GEFNTVKGNRNWMRAREALLHCDVIPGDLERAFPICTPGGSDSASFDEVLELLHLAGRSL
PHAVMMMIPEAWQHNDAMPPSHRDFYSYHASLMEPWDGPACVAFTDGTLIGATLDRNGLR
PARYWITDDRVIFASEAGVLPVEPGDIRQKGRLQPGRMLLIDLAKHQVIDDQQVKDELAR
QEPYGSWLRDGLVSINDLPERTHIVHSHSSVTRRQEVFGYTHELLRRIVAPMANLGRDVI
GSMGNDAPLAVLSDRPKSLFDFFTQQFAQVTNPPLDAIREQMVTSLESRIGPEDNLLDPT
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TGEGGEDPERLHDIERCSAIKQVASGRFGVTSEYLSYASDLQIKMAQGAKPGEGGHLPGE
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LHRVDVPEGTSLYRTTMQDHELAGTVDEQLVELARPALERGEHVHAELAVRNVNRTVGTV
LGHEVTMATDGKGLPDDTIDLDFHGTAGQSFGAFLPRGITMTLVGDANDYLAKGLSGGRI
IVRAPAESTFDQSTQIIAGNVIAYGATSGEIFLRGLVGERFCVRNSGATAVVEGVGDHGC
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RG
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RRGNIVRDEDFQTTVPGVFACGDAGRGQSLVVWAIAEGRSCAHGVDAFLNGHPSPLPRPI
GPQVRQLML
>PFR_JS14_1075PFR_JS14_1075Hypothetical protein1227226:1227897 Reverse
MNLSDALTESLRTLGLLPLISGILAVVFAAVALFWPGGTVTSIVVILSLYLLLSGAGTVV
TSLRLRSLPGSGLMTAVGVLGVVLSLVMLWHPGMSTRILVSFMGACLVMFGIFVVAISLA
VRRATGRWAWSLPAGAVAGVLGLVFLARPGFGADALGMLLGIGVLVFGLALIAAGVQLRR
FAAGVRRAARDAGFGGPTVVEGSVVPDEGPDAGGPANPPITRA
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MASKNFAHLHVHTEYSMLDGAASNDKLFAEVARQGMPAVAMTDHGNMFGAYEFYQTAKKY
DGEQNPLVKPIIGIEAYVAPSTRLSRSQEFWGNRRDTGSPDTEGGKDVSGGGRYTHMTML
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PERVNPPDIDLDFDDRQRDKVIDYVTHKYGEEYTSQVNTFNKIKAKAAVKDANRILGYPF
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FDDIIAVLALYRPGPMGANAHIEYADRKNGRRPIVPIHPELKDDLDEILAPTYHLIVYQE
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>PFR_JS14_1077PFR_JS14_1077Hypothetical protein1231768:1232493 Forward
MSESVGTAPEAPGPAARDAGGPPPGAGPSRGRAWLASRRRELRFLALFVVICAVAGAVCA
VIWKLTAPVPTITVSNDGSAAVSNQALSEFFGADADFMIIGMFGGVALGTLAWHWFKGWG
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GATVPVLLYSALGRDEEKDEHQAADHDQDAVGAREAPGPKPATGLTRSGHRLIRFPAFGR
H
>PFR_JS14_1078PFR_JS14_1078Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase ybaK1232530:1233048 Reverse
MSKSANKSTGTPATVALARTGLPHTLHPYVHDPRSRYFGEEAAAALHVDPARVFKTLVVE
LTSGPEPLVTAVIPADNHLDLKQIAALSKAKRAALADPAVAQRVTGFVRGGISPLGQKRQ
TPVIIDQSAAAAPTIFVSGGRRGLSVEMAPDDLVRATHGRLGTISRPGLHWS
>PFR_JS14_1079PFR_JS14_1079Uncharacterized membrane protein, possible Na channel or pump (Precursor)1233094:1233894 Reverse
MAPGCHWWWNTCVIPAQLFLGAGTVINALCIVVGAAVGTLFGEHLPSRVRDAVTPVLGLV
VVTIGGLSIPSLLDASVPRAVGQAGVVIVLLALVIGTMLGAWWRLEQRIEQLGEWARSTF
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LSASFGFAVAGGAAVVLVYQGLLTVLGWWLGGLLPPAELNVLDATGGIILMALGLRLAGI
ARLAVAEMVPALVLAPVGVVIVGLVT
>PFR_JS14_1080PFR_JS14_1080Histidinol dehydrogenase1233972:1235285 Forward
MLRMIDVTGQRLDDYTAVLPRGHFDVEHAVAAVEPICRAVAEEGETALRRFAEQFDHVVP
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MSAAPRDPRTTQLQASAVPGPEISLAELPLRPELVGEEPYGAPQLDVPVALNTNENPYSP
SVLVRAQMAAAIERVARTLNRYPDREALELRADLAKYLGFGLHARNIWVANGSNEVMTHV
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LITTPNNPTGTLTPVKVVEEILERTDALVVVDEAYQEFTEFPEDSALALLPRFGRLIVSR
TMSKAFALAGGRVGYLAAAPAVVDACRIVRLPYHLSAQTQAIARVALANKSELLAQVDEL
RQACQDLQDWLRRTGLDVVPSQANFCLFGRFVDRHAVWQALLDEGVLVRETGPEGFLRVS
AGTPEEMAAFRAALGPIIIHQGVLAPGLMARVKPEGPAKLPKGMKK
>PFR_JS14_1082 PFR_JS14_1082 Imidazoleglycerol-phosphate dehydratase (Precursor) 1236502:1237110 Forward
MSRSAAIHRVTSESDVSVELDLDGTGSSQISTGVGFYDHMLTSFSKHSLIDLTVRTTGDI
QIDGHHSIEDTAIAIGQALGEALGDKRGIRRFGDAIVPLDEALAQAVVDVAGRPYVVCSG
EPDSQITVRIGGTEPLYPGSMTYHVIESLASNAGLCVHLKLLAGREPHHIVEAEFKALAR
ALRMAVEPDPRVSGVPSTKGLL
>PFR_JS14_1083 PFR_JS14_1083 Imidazole glycerol phosphate synthase subunit HisH 1237107:1237784 Forward
MTGPTLAPGALREPGALAASPSVGVLDYGSGNLHSAVRALAAAGARVTLSSSRAELEACE
RLVVPGVGAFAACMEQLRSVGGVELVRDWAASGRPLLGICVGHQVFFRHGVEKGISSEGI
GIYHGTVEMLDAVRLPHMGWNTVEPPADSRLFAGVGDKRFYFVHSYASHAVEQPGAMVTW
CEHGGDRFVAGVEWRNVCSTQFHPEKSGAAGARLLANWLAMSPAA
>PFR_JS14_1084 PFR_JS14_1084 Phosphoribosyl isomerase A 1237853:1238578 Forward
MTTALTILPAVDVQNGQAVQLVQGVAGTEKVFGDPHQAAKRWAEQGASWLHLVDLDAAFG
RGSNAELLAEVIAGVDLNVELSGGIRDDASLERALSTGCKRVNIGTAALENPQWCRKVIA
AYGERIAIGLDVKGTKLAARGWTREGGDLFETISAMDEAGCQRYVVTDVASDGMLTGPNV
TLLRQVCEHTDAAVVASGGVGSLDDVKTLRTLVPEGVEGVIIGTALYLGKVKLPEALAAA
R
>PFR_JS14_1085 PFR_JS14_1085 Acetyltransferase, GNAT family 1238575:1239612 Forward
MTPEWAEAFVDDVLEWSFMGFDDLEEVAELRAAIEYFDDPVQTISYADFVAAWNRPGAHA
SHHAVVGRERSGSIVSYGWNHPGLPTDANPSVWFDIGVHPAWRHQGIRHRLTMWLIGRAQ
QWWEHIRTAQTGALWVGTTVDEKRGGLTRSMIEAGLTPQRWFFDMHRPLEAGDSLPPLPK
LTDVSIVPFDDSLSELVRQAHNEAMATRPGSSPVSAQAWESSINNHPENSQLSWVALVNR
DTPAHEGAAHGRVVGYAMNLAYDDETSEGWTERLGVCPWCRKKGIGRALVIASMRGFADA
GLTSAGVGVDTEDPNTAARFFGVLGFEETERVVVYGRTFRVEQPD
>PFR_JS14_1086 PFR_JS14_1086 Probable transcriptional regulatory protein yebC 1239776:1240576 Forward
MSGHSKWATTKHKKAAIDAKRGKLFAKLVKNVEVSARVGGGDPSGNPTLFDAIQKAKKNS
VPNDNIDRAVKRGSGEGADAVSYEDIMYEAYGPDGVAILIDCLTDNRNRAIADVRTTITR
NGATLADGGSVRRLFERKGVVRVPKTWEVEEGRKSVEKSVDEDQLMEATIDAPVENIEDQ
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LDDVQEVYTNAEYSEAVEKGLEEADD
>PFR_JS14_1087 PFR_JS14_1087 Crossover junction endodeoxyribonuclease RuvC 1240845:1241456 Forward
MGVDPGLTRCGVGIVDGTPGARPQFVAVGVIRTDPHTEHAYRLLAIEEGLGEWFDHYQPQ
AISIERVFAQHNLSTVTGIGQVAGIAMMLGARHGIDVALHTPSEVKSAVTGSGRADKAQV
GVMVAQVLHLAKAPTPADAADALALAVTHLWRGSAQNRYATAALQGRSSAAVARARRSAA
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>PFR_JS14_1088 PFR_JS14_1088 Holliday junction ATP-dependent DNA helicase RuvA 1241453:1242064 Forward
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QKIVIELKDRVDALFVAPTNGSASVAPVTPAWQEQVMAGLESLGWSSRDAEAACETVAPL
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>PFR_JS14_1089 PFR_JS14_1089 Holliday junction ATP-dependent DNA helicase RuvB 1242128:1243153 Forward
MEHSAVDPWPEPEERAAEAALRPSTLEEFEGQPRVSDQLGLVLSAAKHRGTTPDHVLLSG
PPGLGKTTLAMIIASEMGVPLHITSGPAIQHPGDLAAILSGLVEGEVLFLDEIHRMSRPA
EEMLYLAMEDFRVDVVVGKGPGATAIPIEIPAFTLVGATTRVGLLPSPLRDRFGFTGNLD
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MNGPYLIIAFVALIALFYFMTIRPQRKQAEKQREMHNAIEPGTRVMLTSGIYGTVTAIGD
KQFVLELAPGVDITVLKQAIVRVVQPDDEEFEFADPGVEISRGDDEQGDHELEPGASSTD
SVTDAPAAGQAAPSDTSHDDASTADPGNPSSDHEPGTDNKSADAEQK
>PFR_JS14_1091 PFR_JS14_1091 Protein translocase subunit SecD 1243795:1245513 Forward
MAASNRNKHTHPGRRLIVFALVIVFLYGLMGLTKTWTPRLGLDLRGGTTITLTARNNSDG
SAPSKDNLETARSIIQKRVDALGVGESSVTVQGDRQIEVAVPNVSSDELVSLVGTTAQLG
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MSESTSTLDRPADHGTDKARKGKYTGNFAHRLYTGEFEFNFVARRKLWYSISIVLIVISL
AALLFRGLNLGIEFKGGSVFTVPVSSTSSQSVDQVRKAVDESKVPDLTGAQATAVGTGTV
RVQVRSLSTDEVTQMRDALASTVNTTPDKVGYSLIGPSWGGQITMKAFQALIVFLVLVAL
MIWAFFREWRMAISALVGLIHDLIVTVGLYALIGFTVTPSTLIGVLTILGYSLYDNVVVF
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TTVPGGATVSSVEGTADHDVSASAHEGGGPTARQMRDVGDGRAQPARTPRSKRKK
>PFR_JS14_1093 PFR_JS14_1093 Adenine phosphoribosyltransferase 1246763:1247302 Forward
MRPDPRVTRIHSLVRTIADFPKPGVQFRDITPLLADPEGLADTMAVLVDMAPDEVDVVAG
IDSRGFLFGAPVAVAMGTGFVPVRKPGKLPGPVFEEAFDLEYGSSTLAIHQDALRPGQRV
LLVDDLLATGGTLGAAVKLILREKAVLTHVETVIELPDLGGRAKLESLGVTSFSSILQF
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MPSDGVYGPYARSAVPATDPNTPTRAADERISTGPEQPRLRMRERLARLGGVKAPQSAVL
DPLFSVVRATHPKADLSMVERAYRTAEHYHSGQTRISGDPYITHPLAVATILAELGMTEP
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FSTLQPKVYDEIVRLVAEAAPKREQQLREVIDQVKVYLDDAKLTATVYGRPKHYYSIYQK
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HTTVLGPGSRPVEFQIRTHEMHRRAEFGVAAHWKYKEDPNAQGGKIDPEGTDLAWVHQLN
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ARVNGKLASLESQLANGDIVEILTSKAENAGPSRDWLNFVVSPRAKSKIRQYFTRERREE
AIDQGKDELAKQLRKTGLPMQRLLTLEHLSAVADSFRLASVDALYAAIGEGNIGAPGVVQ
RLIGTEGGLDGAADESLEETTVLPKRGTVRHTGQGNPGIVVEGDPDMWVKLAKCCTPMPG
DEILGFVTRENGISVHRRDCTNAANLLTHPERIVEVSWAPNSSSGYLVSIQVETLDRPGV
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IKQ
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>PFR_JS14_1095	PFR_JS14_1095	Conserved alanine and arginine rich protein	1249797:1250936 Reverse
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LLASLDSLNPLLEAQSAERKEERARQHAETKQQKEAMVAQAEKLAAGSDWRGGVDRFRQL
LEKWKALPRIDRTTDDELWHRFSSARTTYTRRRKTQFARNAAQRDEAKKLKQEIIAEAEQ
LADSTEWSETAREFASLMTRWKAAGAAPRNVDEKLWKRFRGLQDTFFEARNAVFAEQDEE
YKANQQAKEALLDEAEKTLLPVTDVAGARTQLREFLAKFNAYGRVPRNAIRPIDSRVRAL
EQAIKGAEEKEWKRTDPEARERAADTVAMFTSQIEKIIGQAEAADARGDAKKAKELRDSV
TTYQSWLEQAQKALDEFSA
>PFR_JS14_1096	PFR_JS14_1096	Putative glyoxalase II (Hydroxyacylglutathione hydrolase)	1251040:1251759 Forward
MPLILPDRLANVFIAYFVTGAWQSNCYVIADEDAGLAVAIDVGMDAARTVEELLAQRDFQ
LAGILLTHGHIDHCAQAAVLADAHQAPVWVHPADRELMTHPAEGLSPQMAGQLHQLIGDA
PLHEPRDLRTFEAGVPVRCAGFEFSVTPAPGHTPGSVLLGLEGDEHMIVFTGDVLFAGSI
GRSDFPGGDDHTMRAVLRDVVSTLPPQARVLPGHGPFTTVADELATNPYLTDAYLEVQS
>PFR_JS14_1097	PFR_JS14_1097	HisS Histidyl-tRNA synthetase	1251759:1253090 Forward
MARPKPLSGFPEFLPRERLIELEVLDTLRETFELHGFSNVETRAVEPLSQLSRKGDITKE
VYTVRRLHADEHDKSELGLHFDLTVPLARWVLEHAGHLEFPFRRYQIQKVWRGERPQEGR
YREFTQADIDIVGRGELAAHHDIEAPLVMLEALEKLHDRIGLPPVLMHVNNRKLSEGFYR
GLGVEDTLSVLQIVDKYDKIGADATVELLGSELGLDTDTARRCVALASIHSLDTGFVDQV
RALGVSDPLLDEGLSELVTLIEEANRRVPGRIIADLSIARGLDYYTGAVYETQLVGHESM
GSISSGGRYDSLASDGKSTYPGVGISLGVTRLIAPLIAAGEFSVTRSVPTCVVVAVDSEE
TRETAMDVAAALRARGVSCEVAPKADKYGKQIRYADRRGIPYVWFGGPIGEVKDIRSGDQ
QPADANIWMPSRDDLRPGVHAAE
>PFR_JS14_1098	PFR_JS14_1098	Alpha-acetolactate decarboxylase AldC	1253204:1254019 Forward
MTTTAKNTATSDPQGHRRPARGAAPRAHRARHSPVVRHEVFQTSLMSALLDGIYDGDMTL
AELLGHGNFGLGTFEALDGEMIILDSVPWQLRVDGSVTRASLDQLTPFATVTNFVPSISE
EIKGPLTRAELSELVDHLGVSANYLYGLRITGDFEWITTRTVRRQKRPFPPMSQTTSDEP
VVRQTQTSGVMAGFRTPLFEQGINVAGCHVHYVNNEHTHGGHVVDFVMNSGLIEVCLGTD
LRVRLPLSEAFQDADLAPDDLDEQVRAAEHH
>PFR_JS14_1099	PFR_JS14_1099	Hypothetical protein	1254228:1255301 Forward
MGIAIKYGAMVDDPIVDDDGKLAIRGGAGALVERLLKIYPGACLVGYEDRQCDGFEMKRD
INLDAEKDLVINLDVMDSVGVFQVMHRHGAEPMIMNLQWLPPRHYHHKVNFAAMGLSYAL
FPTLCSGERTAAEVSELTHRWTIPALANSAQIAWFQPGIRDDLLQPRVDTEVPEVLYPSI
HLDAEKHPQQFMQIVTEVAAKVPLQMVARLAPRDLVSLQAMRMSSAKWTTVGPLSADREG
YWGTLAHTTAFLSTATAEAYGLEELEALVAGVIGVMPKLPWAEVLVPTGYPYLYNSDAEA
AMMLENVLRDPKAARRAIDESAGGSIKDWVFAKHARAAGNEAIENQVKEWFPKALED
>PFR_JS14_1100	PFR_JS14_1100	Aspartyl-tRNA synthetase aspS	1255501:1257348 Forward
MIRTHDAGTLRASNEGETVTLAGWVAHRRDHGGVAFIDLRDASGVAQVVIRDEVLASSGA
HDLRNEYCIAVTGVIEHRPQGNENPEMPTGDIEVNISDLEVLNAAAPLPFPVDEYTNVGE
DTRLRYRYLDLRRPRMHDALVLRSHVTHAIRGVLEGRDFYDIETPTLTRSTPEGARDFLV
PARLSPGSWYALPQSPQLFKQLLMVAGMERYYQIARCYRDEDFRADRQPEFTQLDIEMSF
VDQDDVMALGEEVMAACWKLVGVDLPRPMRRITWHEAMDRYGSDKPDLRFGNEITEVTDF
FADTPFRVFQAPYVGAVVMPGGAAQPRRQFDAWQEWAKQRGARGLAYIVVTDSGELSGPV
AKNISDTEKAGIAEKVGAKPGDAIFFAAGARTAGQELLGAARLEIGARCELYDPKDWAFC
WVVDAPLFKPTSEAVAEGDVAVGAGAWTAVHHAFTSPKPESMDSFDTDPGSALSYGYDFV
CNGNEVGGGSIRIHRRDVQERVFKVMGLSQEEAQQKFGFLLDAFKFGAPPHGGIAFGLDR
LVMLLGGFDTIRDVIAFPKTGNGFDPLTQAPAPISAQQRREAGVDAKPATKKDGASDKDG
VPEEGAGADLDTSAE
>PFR_JS14_1101	PFR_JS14_1101	Recombination factor protein RarA	1257473:1258897 Forward
MSEDLFGNPVADPHGGGTAAGIGGSLGDAVNPSAPLAVRLRPRSLDEIVGQQHLLGPGSP
LRRLAEGHAAMSVFLWGPPGVGKTTIAAVVSRATNRRFVEMSAVTAGVKDVRRELDIARR
ELARGRPTVLFVDEVHRFSKAQQDVLLPAVENRIVTLIAATTENPSFSVISPLLSRSLLL
TLKPLTADDISILLDRALTDERGLRTPEGREYTLDDQARADLLRLAGGDARRALTYLEES
AAGASAADSATITTDSVASAVDRAAVRYDRDGDQHYDVISAFIKSVRGSDVDAALHYLAR
MITAGEDPRFIARRLVILASEDIGMAAPSVLQTAVAAAQAVQLIGMPEAQLNLAQATIAA
ATAPKSNAVYLALTAAMNDVRAGKGTGVPAHLRDAHYATAQDYGHGVGYRYAHDWPHGVA
PQQYLPDDLEGTSYYQPTDHGNEAAIGERLATIREILHEQDEPGSGAASRGPTG
>PFR_JS14_1102	PFR_JS14_1102	Lactate/malate dehydrogenase, NAD binding domain protein	1258952:1259932 Forward
MRSNKLVVTGAGHVGSQVLTEALHMGLFGEIAVIDTNESVAVGEALDSLQATGAPHMAAI
DVHSGGIEDYKNADVVICAAGPSIIPDPDDPTGRPDRSLVTTVNSKVIRQVMGDIASQTR
EAIVILITNPLDTMVYIAENEFGYPPDRVFGTGTMLDSTRLRQIIAAHCMVAPSSVQGYM
MGEHGLTAFPVLSRLTVGGYRFDELPAVFPINPDLSADDIREEVVQAAYDVFNSKGWTNA
GIAQSAVSLARTVMLDERAIHPVCSTLRGEYGHLDDVALSMPCIIGRNGIERRLPVELNA
WESAHLETTIVQIRATMVEAGTPRVR
>PFR_JS14_1103	PFR_JS14_1103	Alanyl-tRNA synthetase AlaS	1260097:1262784 Forward
MKAAEIGRRFVDFFVSKGHTEVPSASLLYNDPTLLFVNAGMVPFKPYLMGELPAPWKRAT
SIQKCVRTLDIEEVGKTTRHGTFFQMLGNFSFGDYFKKEAIEFAWELVTGPLAEGRLGFD
PNMVWVTVLGPGFHPDYPEGDTEARDTWLSLGVPPEHIQGRGLKDNYWHMGVPGPGGPCS
EIYIDRGPKYGAEGGPEADEDRFLEIWNLVFETEELSTVRSKEDFDIAGPMKTRNIDTGA
GLERIALLMQGVDNMYETDEVFPVIERAAAMAGKRYGADHTDDVRLRVVGDHVRSSLMLM
TDGVTPGNEARGYVLRRLMRRMIRSMRLLGVEKVSLTELLDVSRQCMHATYPEIDDQWER
IKDIADNESESFERTLNSGTQLFDMAVAEARAAGSNELGGDKAFQLHDTYGFPIDLTLEM
ASEQGLHVDETAFRTLMDQQKARAKADAKAKKGNLQDAESYRELRDRGETPFVGYSELTV
PTRVRGLVADGHVVDHLRAGQLGEVVLEETPFYAEMGGQDADAGVLRSDAGEFEVIDVQR
PVPGLVVHTVRAGGELRPGDEVQAMVDAVHRQGACQAHSATHIIHAALRELVGPTATQAG
SYNKPGYLRFDFNSSHGLSAALKAEIEARCNAAIRDDLEVSATQMPLAQAKGMGAMAMFG
EKYPDIVRVVEMGGPWSRELCAGTHVLHASQIGMLNLLGEQSVGAGTRRVEALVSTDAFE
HMAAERALVNQLTGTLKVQPDQLTDRVGALIEELKVAQKQIAELKAAQLLAGAPQLVSDA
KDMWGVSFASKRYHDVDAGALRTLAGQVRDQFGDRSAVVALVGGSATKPALVVATTRAAR
DRGLNAGALVREGAGVLGGNGGGKPDLAQGGGTDAGKADEALRTVEYAIGHVVQG
>PFR_JS14_1104	PFR_JS14_1104	Putative crossover junction endodeoxyribonuclease	1262768:1263313 Forward
MSSRAEEPIDPDPGPEHTWRPGVRLCLDWGKARIGVAACDRDGLLAYPVETVANGSGTMK
RLKALVDEYEPFEIIMGMPTDLRGRQGIAASAMIDNARRVTRALHRDVRLVDERLTTAAA
TRRLAAAGRDSRHRRSVIDQAAAVAILEQAIEMEKRSGHAPGELVSHETEESQGGGTQAG
G
>PFR_JS14_1105	PFR_JS14_1105	Aminodeoxychorismate lyase	1263288:1264520 Forward
MAGPKRAADEDAEDLYLPASRGEEPEPIRSGAATEGPHGPAASGGEQPPLITMTRDYHRT
PGSWLKSVIAVLVSLAVIGGGGFLIYHKVTEYQGADYTGAGQSDVTVTVKSGESVSQMGD
LLVAEDVVASRNAFMRAAKKEKRTNNIQAGTYKMKTRMPAADVVAVLVDPSNIVNNRFTV
PEGLRNTHVLAQVSSATGIALGQLTAASKDPSLPVPSYAQGSSEGFLFPDTYTFEPDFTA
SQVLTRMVDRFNQVAADENLEKRAAAAGRSPHDVLVVASIIERETSDHKYAPLVAEVIYN
RLAQGMRLQSDATVAYANNLEGKVTTTDEERGLNSPYNTYMVDGLPPTPISNPGKAAIDA
ALAPASGDYLYFVTVNLDTGETKFASDSAGHDQNVKEFQTWCQANSDHCK
>PFR_JS14_1106	PFR_JS14_1106	Chorismate synthase	1264658:1265860 Forward
MLRYLTAGESHGRALVSTMDGLPAHVRISTADLQTALARRRLGAGRGARMKFEADEVTML
AGVRHGETLGSPIAVMIGNTEWPKWEQVMSPDQVDPEVLASLARNAKLTRPRPGHVDLAG
MQKYDWDEARPVLERASARETAARVVLGEFAKQFLAQGFGITVLSHVVQIGQVRAHVAEP
PRMADLAHIDDDPVRCLDREASAAMQAEIEQCRKDGDTLGGVVEVLAWGCPPGLGSMREG
DTRLDARLASALMGIQAIKGVEIGDGFDLASVRGSQAHDEIEPGPHGIRRISGRAGGTEG
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GISTGEVLRARAAMKPIATVPRALRTLDVTTGEATTAHNQRSDVCAVPAAGVVAEAMMAL
VVAQACLEKFGGDSLSETRRNYLAYLKRLRDRGLGVAESL
>PFR_JS14_1107□PFR_JS14_1107□Bifunctional shikimate kinase/3-dehydroquinate synthase□1265857:1267506 Forward
MSHPTPRPRKQPGVIRQVILVGLPGVGKTTVGHLLARRHGLDFVDVDDFLERQQGMTVAE
IFAQQGEQAFRDLEAQATAELLDDAGVIALGGGAVVNPVVRGALAGRCVVWLTASVAQGV
ERIGQTTHRPLMRGDVSSTLERLRHEREHFYAQVARHRVDTDARPAGEVADQVAALVGLD
GEEAPMTVAHFATDRPYDARIRPGALDDLTTHLGGATKVAIFFPEVLGGAAARASDVVRA
AGAEPIMIELPEGEQAKTPVVLADCWGRLADAGLTRTDLVIGIGGGATTDLAGFVAATWL
RGIRWISVPTTVLAMVDAGIGGKTGADLPQGKNLIGAFWEPSVVLEDPDLLVGLPARQVR
SGLAEVIKHGFIADERTLELVSGDPGQAQDVTSERLAELIARSVQVKARVVSSDLRESTS
VGDDVGREQLNYGHTLGHAIEAAEHFTRPHGECVALGMVFAAELAHRVIGLDEATVARHR
RVLGSVGLPTSYHGVAWPALHELMMRDKKTRGSVLRFVGLRAQGEPTIIVDPDPQALRGA
WQALTATTD
>PFR_JS14_1108□PFR_JS14_1108□Translation elongation factor P□1267665:1268246 Forward
MTKGCYVATTNDIKNGTVLNLDGQLWQVLWFQHHKPGKGNTVVRTKIKNVLNGKVVDRTF
PADTKIEMAQVDRRDMQYLYDDPSGYVFMDTDNYEQLTIPADVIGDDKDYLLEGMIVTVA
TNEGTPLYIDLPASVELEVTYTEPGLQGDRSTGGNKPATVETGKTVQVPLFITTGEKIKV
STDDGGYLGRVQS
>PFR_JS14_1109□PFR_JS14_1109□N utilization substance protein B homolog□1268246:1268872 Forward
MSQPDDEIIPLAHGEHPPVPDAVKIASTDFAEAHHSTRTKARKQALDVLFQADLRNEAVH
RTMARRTEQGEPALRDFTRQILDGYSEHGHEINEHIDRALTGDWALERMSRVDRNLARIA
VWELDFTTIDLKVAISEAMELANELSNDESVTFLNGLLARIAEERPAIPTAPGAEAPDEG
PVEPAGDASAEPADNGAVAEQDSENIGQ
>PFR_JS14_1110□PFR_JS14_1110□Carbamoyl-phosphate synthase small chain□1269051:1270235 Forward
MSANDNSAILVLEDGRSFTGRAFGAIGETFGEAVFSTGMSGYQETLTDPSYYRQVVVATA
PHIGNTGWNDEDDESSRIWVSGYVVRDPSRMPSNWRSARPLDEELEAQGIVGICDIDTRA
LTRHLRERGAMRVGISSVDTDVATLLARVQGSPQMAGADLVGYVTTDKPYVVPAVGEKKF
TVAAIDLGIKRMTPRRMTQRGMEVHMLPATATWADVVATGADGLFFSNGPGDPSTLTSPV
ELCRTALAEQMPLFGICLGNQIFGRALGFGTYKLKYGHRGINQPVLDRATNRIDITAHNH
GFAVDAPLGEDTTTPFGEVAVSHVCLNDDVVEGLSLTRDGCTRAFSVQYHPEAAAGPHDA
SYLFDRFADMMAAHRGDDPAINTHVNQSNAGEQN
>PFR_JS14_1111□PFR_JS14_1111□Carbamoyl-phosphate synthase large chain□1270235:1273576 Forward
MPKRTDISSILVIGSGPIVIGQAAEFDYSGTQACRVLREEGYRVILVNSNPATIMTDPEF
ADATYVEPITPEFVEKVIAAEKPDALLATLGGQTALNTAISLHENGVLEKYGVELIGANV
DAIQRGENREKFKEIVENLGEFSGSRPEVARSHICHSVDDVMAAAKDLGFPVVLRPSYTM
GGVGSGFANDPDELLQMAQIGLDASPVTEVLVEESILGWKEFELELMRDKSDNVVIVCSI
ENFDPMGVHTGDSITVAPAMTLTDREYQRMRDVGIAIIRAVGVDTGGCNIQFAINPADGR
MIVIEMNPRVSRSSALASKATGFPIAKIAAKVAVGYTLDEIPNDITEQTPASFEPTLDYV
VVKVPRFAFEKFPYADATLTTHMKSVGEAMAIGRDFTEALNKALRSTEKNGGFWTIDDPS
DGDLDRLLADVGRPHDGRVLELEIALRRGVSVERLHELTGIDPWFLDQVSMIHEIGEQVR
NAPELTNQLLRHAKRHGLSDAQIAILRNVPEQEVRRARWDAGIRPVYKTVDTCAAEFAAR
TPYHYSSYDEESEVLPREKPAVLILGSGPNRIGQGIEFDYSCVHATQVVSQHGYESIMVN
CNPETVSTDYDTSDRLYFEPLTMEDVLEIYHAESQAGPIAGVIVQLGGQTPLRLSQQLED
AGVKIVGTSPEAIFLAEDREAFEKVLDDAGLPAPKYGMATSFTEAHAVAAEIGYPVLVRP
SYVLGGRGMEIVYDDDALQDYIERSTLIGPDSPVLVDRFLDDAIEIDVDALYDGHELYLG
GIMEHIEEAGIHSGDSACSLPPATLGDEVIDRIRTSTEAIAAGVGVRGLINIQYALASDT
LYVLEANPRASRTVPFVSKATNTQLAKAAALIMLGSTVAQLRESGMLRDGVDGAERWGGM
PIAVKEAVMPFNRFLTKSGRSVDTLLGPEMRSTGEVMGIDHSFGVAFAKAQDAVYGALPT
SGTVFVSAANRDKRHIILPLKELSDMGFTILATAGTASMLRMHDMNVTTVRKYSEGRGPE
GEPTIVDLIDDEKVDLIFNTPTGETRGGRPRGDGYEIRTAAILHGVPSITTVQGLEAAVQ
GIHAIERGDIGVRSLQSWGADMDRHLRNSQREG
>PFR_JS14_1112□PFR_JS14_1112□Dihydroorotate dehydrogenase (quinone)□1273658:1274758 Forward
MTIDELYVRAVRAGYEGLVRPLLFTMHGGDPEKIHGQLISTMGHLPDSLVGLIERFIGQG
RQPVDVAGVHFPGRIGVAAGLDKDGVAAGIWSPLGFGFAELGTVTAHAQPGNPRPRLFRL
IRSGAIINRMGFNNNGAEAMAARMANLGVARGNNALGCPMGISIGKTKATPLADAVDDYL
FSLTTLAPYADYVALNVSSPNTPGLRSLQGRHELEELTGALVARARELDADDPVPVFVKV
APDLTTGQLDGILSSCEQAGIAGIIATNTTIERDGIKGSDARYASQAGGLSGSPLTAMAL
DRVRWITAHTDLPVMGCGGIMTPADAQAMFDAGARLVQLYTGFIFEGPALVMGINRLTRP
GKGARA
>PFR_JS14_1113□PFR_JS14_1113□Orotidine 5'-phosphate decarboxylase□1274755:1275564 Forward
MSGGFGARLQALADERGRLCVGLDPHEPLVRAWGLDYDAAGIERLARDTVAALADEVMVF
KPQSAFFEVFGSRGVAALGRVLDDIRAAGALSILDVKRGDIGSTMSAYARAYLSDDAELR
ADAITLSPYLGFEALRPAIDLAHATGRGLFVLCHTSNPEGEEVQFATHGGHTIAQGVVDH
AQAENTEHGLDDMGLVIGATHDNAGVDLSGFTGWTLAPGIGAQGGTVEGLSAIFGASAHH
VLPSSSRGVLRAGPDRQALQEAARALILH
>PFR_JS14_1114□PFR_JS14_1114□Integration host factor family protein□1275727:1276038 Forward
MAIPTLSPEQLHSARCAATLARRARADFKMRVRQGNLTLSEALDLASCDDVLAHVRVIDL
LKALPRVGDKRAAGIMERLDIASNRRVRGLGRHQLAGLKTEFH
>PFR_JS14_1115□PFR_JS14_1115□Guanylate kinase□1276042:1276662 Forward
MNDTAPSAREHQPEAVPRANGAERLSPRVYVISGPTAVGKGTIVERLRRIHPEIFVSCSA
TTRKPRPGEVDGVSYYFLDDAQFDELVTSGGLLEWAGVHGDRYGTPREPVERALREGRPV
ILEIDLQGARQVRHSYPQAVEIFLAPPSWEELVHRLRGRGTENQDQQSRRLRTARHELDA
EDEFDHVVVNREIGTTVREMVDLMRL
>PFR_JS14_1116□PFR_JS14_1116□DNA-directed RNA polymerase, omega subunit□1276722:1277090 Forward
MRFNLTSTASIRPSSEGIINPPVDELLEHVDSKYRLVLFAAKRARQINAYYSQLGEGLLE
NVGPLVETSVQEKPLSIALREIQSGVLEYKKIDPVAEANARAEAAKDPDFKFDDPFSGID
PA
>PFR_JS14_1117□PFR_JS14_1117□S-adenosylmethionine synthase MetK□1277156:1278346 Forward
MPRLFTSESVTEGHPDKVADAISDAVLDEMLSKDPSSHTAVEVLISNGVAVVAGEATTES
YVDIADVARARMLEIGYDSFDKGLDGATCGVMVALNNQSPDIAHSVEHSWEERNNKATDD
ADRQGAGDQGLMFGYACRETPELMPLPIHMAHRLAQRLAEVRRTGVLGDLGPDGKTQVTI
EYDGLKPVRVVNVVISTQHLEGVDLQERLTPEIRQEVIAPVMEGYDIDSREMTTLINPSG
TFVIGGPMGDAGLTGRKIIVDTYGGMARHGGGAFSGKDPSKVDRSGAYASRWVAKNIVAA
GLAQRCEVQVSYAIGRANPTSFYVNTFGTGAAPDDRICDAAKQVFDLRPRTIIDQLDLKR
PIFSQFTNYGHFGREVPDARWELTDRADALLAAMKG
>PFR_JS14_1118□PFR_JS14_1118□Primosomal protein N' PriA□1278457:1280478 Forward
MMTIQQPDGGAGTHPGIARLALDVYLPHLDRFFDYSIPDRLAQQVQLGCRVRARFAGRMA
NGFVVGLPARAEVDKLSPLDRVISPEPVLLAQQVSLLRAVADHYAGTFADVMRLAVPPRH
AATEAAEQNPWPAPDARDVPGGGLTEVDDGRRFLDAVGQSRPVRAHWCALPRWRSDESGL
DDWTRGFVQAVGAAVGAGHGALVIVPDVDRVRRMRDVLRAVLGPGCVAELHSELGPAARY
RNYLAVSRGQARVLVGTRGASYAPVHDLGVICLWDDGDDLLSEPRAPYPHARDVAALRAT
QESCALLFGSYARTAEMQAWVSTGWLVPLGLTPARTRRLAPPVRAAIDSDIDLQRDPMAA
AARVPKEAFETIRTGLLSGPVLVQVPRAGYLVALSCQRCRTPVRCPTCGGPVGADRLGAG
QRRLTCRWCGRSLNNWSCPVCGSRELRAPVVGSQRTAEELGRAFPSFRLVSSSAQKVVDQ
VGATPALVVATPGAEPRPEAGYSAAVLLDAGLMLTRADLRAAEESYRRWLTVVSLVRSGD
QGGTVSVVGPAEERTVQALVRLDPAGFAERELSDRQAAGFPPAVRMVAVEADEKTLADFR
SVVEWPSDAQELGPVPIADSTPGSTEQLWRLMVRIDRTMGGELIVAARRALSIRSARKRP
GAVRVRVDPIELF
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>PFR_JS14_1119	PFR_JS14_1119	Methionyl-tRNA formyltransferase Fmt	1280556:1281503 Forward
MRIVFAGTPDLAVPSLRALSRAGHEIAAVVTRPNARSGRGKQLVSSPVARAAEEMGIAVL
KPEHPRDPGFADQLARLSPRACAVVAYGGLLPQSLLDLVPDGWINLHFSLLPAWRGAAPV
QRALMAGDTQTGVTTFRIVKKLDAGPLYRSVRVPIGPDETAGELLDRLSVIGADVLVETF
ADITAGLEPVEQDDDGVSIAAKVSVDDARIDWRQPAARIVNLVRGTNPAPGAWSVLAGRH
FKVLRVVPAGDTGAGTALLSGELRATNKHLWVGCGDGAVELIQVRDFGKKSMSGADWARG
ARPTPGIRFEAADHE
>PFR_JS14_1120	PFR_JS14_1120	Putative ribosomal RNA small subunit methyltransferase B	1281496:1282965 Forward
MSEQRHSDHRTAGRDSGRARDRSAGDRRRPSTDRPGARREFNRDGTPRRPMDRPRRTAFE
ILREVDRRGAYANLATRQAINDQELTGRDAAFVTELAYGTCRMLGTYDAILAQASGRDLN
DLQPDIVDALRLGAHQLLGMRIPDRAAVDTTVDLAAIVVGERVAGLANAIMRKVAAHDLE
AWCRQLAYDEQDFRCLVSGHPDWIVDAYQDLLPTEEVDAALAADNIAPVPTLVVRPGLYK
RKDLLRDGGDPTRWSPWGVIRPGNPGDLGAVRDGRAGVQDEGSQLICLAATRADIPRDLP
WLDMCAGPGGKSALLRGMAPEHGAFLTASEVQPHRAHLVAQSLRRYPAEGHETICADGTA
PAWQRDSFGLVMADVPCSGLGALRRRPDARWRKDVDDLVELGDLQRSLLSSALDACRPGG
VVAYVTCSPHRMESADIVLADTSRFEILDAPALIPEVPGAAASTDARFIQLWPHRHGTDA
MFMALLRKR
>PFR_JS14_1121	PFR_JS14_1121	Ribulose-phosphate 3-epimerase Rpe	1283000:1283662 Forward
MRITPSVLNADLADLAGEVARIPSADAVHIDVMDNHFVPNLTLGLPVVSSLQRHTKLPFD
IHLMIEDADSWAPQYAEAGCESVTFHAEATSAPVRLAREIRRLGSAASLALRPATPIEPF
ADLIAEFDQVLIMTVEPGFGGQKFLDIMLPKIRRTRAIAAASGVELAIQVDGGVSVDTIG
RCAEAGADVFVAGTAVFRATDPDEMVTTLRQTAMQAAHSH
>PFR_JS14_1122	PFR_JS14_1122	Aminopeptidase C	1283722:1285053 Forward
MTSPNSEFSLDRYADLTARFTADPTARVAQNAVSTTNADKLSLDRQVLTSIDTSVSDKVD
TWKVSNQKQSGRCWLFSGLNLLRSHLINDLKLTPDFELSQNYLHFFDKLEKANWFLASMA
EMSDRDIDDRTVHQMLSDPISDGGQWDMFVSLVNKYGVVPKYAMPETDSSSSTRVMNRRL
EEILRRGALIVRGAADRGQADAARESILTQVHRVLSIHLGTPPASFLWQYRDKDNAFTRV
GQLTPREFADTVVPINLDDFVCLVNDPRTSSGFNTMLTVDHLGNVVGGRPIRYLNVEIDV
IKKITIDQILAGHPVWFGCDVLPQFDRDIGYWDLHLHDYEGLYGIDMDTTKANRMVSGAS
AMTHAMMFTGVDLLDDAPRRWRVENSWGDDHADKGFFTMNDSWFDQYVFEVAVPKASLDQ
SLRDTLATEPKVLPLWDPMGALA
>PFR_JS14_1123	PFR_JS14_1123	Proteasome assembly chaperones 2	1285154:1285963 Reverse
MRDPVVIAAFEGWNDAADAASEVVNHLTDTYPTDLIWELDSEDYYDFQTTRPKVEMVNGR
STLRWPTIRMSVVHMPHRDLVAISGPEPNLRWRSFCRILVSTFRACNPTMVIILGAMLTD
SPHSRPLPVNASSSDNRIIAGLGIEPSQYEGPTGIVSALADECRKQRLECVSLWASVPHY
VSGSPNPKATLALLGRVEDLLDEAIDLGDLPELTRAWQRGVDELADEDPDVAEYIQGLEE
QQDAEQLPGSTGDALAADFQRYLRHRRTR
>PFR_JS14_1124	PFR_JS14_1124	5-methyltetrahydrofolate-homocysteine methyltransferase metH	1286136:1289603 Forward
MLGHEVILGDGAMGTMLQAAVLGPDDFEGHDGCNEILNVTRPDVILDIHRAYLAAGSDVI
ETNTFGANAAALGEYGITDRLAELAGAGARLARRAADEAGPGHWVFGSVGPGTKLPTLGH
IDFVTLRDAYYTQVSAMIDGGVDAVQIETCQDLLQAKAAVIGARRAARDAHVDLPIIVDI
TVETTGTMLLGSETGAALTSLAPLGVDVIGLNCATGPTEMSEHLRYLSAHADCAVMAMPN
AGLPELTADGAVYPLGPDEFARAQLDYVERYGLAIVAGCCGTTPEHIARLRAALGAHRPV
EHRDPELVNTVSSLYSEVELRQETSYLAVGERTNANGSKAFREAMLAGDLETCIDLAKAQ
SREGAHCLDLCVDYVGRDGVDDMAELSQRFSTAVTLPVMLDSTEPEVIRSGLEHLAGRCI
INSVNFEDGDQPGSRFARLMPIIAEHGAAVVALTIDEEGQARTAERKVAIAERLVDQLVG
TWGMDEGDILVDCLTFPIATGQEETRRDGLETLNAISEFKRRHPRAGTTLGVSNISFGLN
AAARVVLNSVFLHEAVEAGLDSAIVRAAKIMPMERIDPEQRQVALDLIYDRRTPDYDPLT
RMLDMFAGVSSADVRAEHAAELAALPLNERLRQRIIDGDTNGLTDDLDEALRTRGALDIL
NSDLLEGMKTVGELFGSGQMQLPFVLQSAETMKRAVAHLEPHMDSTDEAGKGILVLATVK
GDVHDIGKNLVDIIVSNNGYTVVNLGIKQPISAIVEAAKQNHADAIGMSGLLVKSTMVMK
DNLAELDRLGVGKDFPVMLGGAALTRTFVEDDLQRDFSGQVRYAKDAFEGLSLMDSVMAI
KHGDPDAALPEPRKHRVVAMPRATVEPADGGPVRSDVARPVPGSLDVPRAPWFGNRMAKG
IGLAEITEWLDERALFTGRWGLRGPRKTDGTRDLIEQEGRPRLRGWLDRIAAEGLAVPGV
VYGYFPCYSQGNTLILLDPTTPEALDSEASRFDFPRQAAGRRLCVADFFRDRREAEEFGP
DTVALQLVTMGERFSQVTAELFAANAYRDYLELHGLSVQLAEALAELWHHRIRTELGIAG
EDGEMTAMLQKQAYRGGRYSFGYGACPDLDQRSLIEDLLQPDRIGVHLSEEFQLHPEQST
DAIVVTHPEAKYFNT
>PFR_JS14_1125	PFR_JS14_1125	Signal peptide peptidase SppA	1289756:1291012 Reverse
MSIPQPPDDAATRGAQPPPDRPPEGAAEQPPPPFQPAPPFFPHVVGGYPPAAPPAGLKRG
FGQGMGVALGIGAVLCALSLISAIAMVALVGVARIGRANTSAETSVTKTLWGSSSAKNTL
RAISVSGTIQASGGSSSGMFSSATYGYDVAKLIDSLTADSAAGLVLLMDTPGGSINGSRA
IADAVDRYEQRTGKKSFAFVEGMSASGGMYAMAGVNRIYADQGTMVGSIGVIMGPFARYR
DVTAVDGGLLGNGVTASGGIDQFYLTQGEAKDFGNAFRDMTQKERDVYTAGLSREYDAFV
NWVSTSRGIAPETIRNDLGAYMFDAQTAKDKHLVDDVLGREEAFRQIARDAGVDPDQTKL
VTDAEPGFLSSLMGSRKQAFGHGEALQAGEGVKASSSLCTGAPAVLAWTGDMNAMCGR
>PFR_JS14_1126	PFR_JS14_1126	HAD-superfamily hydrolase, subfamily IA, variant 3	1291196:1291921 Forward
MTSVSPRLPAAVLWDFDGTILDTEPAWMASEIAYVASHSAVWTLDDARGYIGASWRTLGN
ALGQRIAEETGTTGLDPWDIYQSVSAGVVDQVRAGQAPLRPGALELLDALGAAAVPCALV
SSSPESLLRAGVAALGIPDPFEALIAGPMVEHGKPAPDCYLLAAATLQVPIGQCVVLEDS
PTGCEAGQRSGALVIGIPSVAPLPSVAGQLRRDSLVGLTVADLAAMVRAHGAHSAHKEDS
Q
>PFR_JS14_1127	PFR_JS14_1127	TRNA (Adenine-58-N(1)-) methyltransferase	1291918:1292988 Forward
MSQLDPAALSGVHTGPLRAGERVTLTDIKGRRHTLVLEVGKDFHTTKGAVNHDEMIGRPE
GGVVTTAGGAQFTVFRPLLYEYTVGMPREAAVIYPKDAAQILMWTDIFPGARVLEAGVGS
GALSLSLLRAIGPTGTLHSYERRQEFADVAELNVTSFLGGTHPGWTITVGDLVDEIADEP
IDRAVLDMLSPWDCIDAVAERLVPGGLLCCYVATTTQLGRVADQLRYHGGFTEPSLTETD
VREWHAEGLAIRPGHGGHGHTGFLVISRRMAPGVDAPMKKRRPAPAAYGADYAGPVPRNV
LPEQLAANRQRSLDDSDQIAPAVKRALRRHVDAQRSIHPADGAQRAQPAPGDGHDE
>PFR_JS14_1128	PFR_JS14_1128	Proteasome subunit beta	1292981:1293847 Forward
MSSLDRMNETQWSRPHARPGLDDALMSASTSSFVDLLHAVHPELLATAGVGTDGVQPTRA
TTIVAVKYRDGVVMAGDRRATRGHEIAQRDIEKVFAADEATLIGVAGAAGMAIDLARLYR
LELSHYEKLEGASLSFEGKANRLATMIREQLTMALQGFVVVPLLAGWDPHRREGRVVSYD
ATGGHYEESEFASIGSGSAFARGSLKKLHHPDLERDEAALVCIQALFDAADDDSATGGPD
LIRAIYPVVMSASEQGVHGFSDDAVAGLTNTMMSGRHGRPNGPGAASS
>PFR_JS14_1129	PFR_JS14_1129	Proteasome subunit alpha	1293844:1294569 Forward
MSMPFYISPDQMMKDRAEFARKGIARGRSAITARYHDGIVFLAGNPSHTLHKVSEIHDRI
GFAAVGRYHEFENLRVAGIRYADLRGYAYDRADVSARALANSYAQLLGTAFSAGAEKPYE
VELVVAEVGDADPDTAVAQGGDHADRLYRINFDGSVSDEGPFAVIGGHPGAVQDVLRTRL
DPTAPLAMVVSTAMDALRRGGSPELGPADVEVAVLDRTRIPSRKFVRLDVAQVAGLLGKE
S
>PFR_JS14_1130	PFR_JS14_1130	Prephenate dehydrogenase	1294571:1295665 Forward
MARSTSTADDEESQPLSPVVIMGTGLVGASIGCALTAVGEDVRLRDRYRSHAVVAAGLGA
GSVEHPIPTSVHLVVVAVPPQAVPEVVDWALSHYRNAVVTDVASVKAPVLADLRARGRDL
SRYVGSHPMAGSQYSGPLTATATLFVDRTWVVARGTGNEASQRMVERLAVMCGAHVVHLD
ADEHDRAVAEISHMPQLMSSLTAARLRDVPASDLLLAGQGVRDVTRIAGSDPALWRQIIT
ANSTEIGTQLRAIRGDLDRLIDQLDDPDAIADLVERGREGVAALPGKHGRKIGDMSAVVV
EIPDTPGALARLFTDIQAQGINIEDLSIEHGLSREVGYLSVAVDAERAPDLRAAMVRAGW
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DLRS
>PFR_JS14_1131□PFR_JS14_1131□Putative cytidylate kinase□1295705:1296376 Forward
MADKPALVIAIDGPSGAGKSSTARGVACRLSMAYLDTGAMYRAISWACLTDGVDPTSHSA
LFARAETADLQMGLDPRHPTIIVDGHDVTREIRDPRISDAVSAVATTPEIRTLLTSHMRQ
IINRNPRIVAEGRDVTTQVWPQARVRVLLVADAETRIARREAQLLGKVDRHRVSSSIVDR
DRKDSTMSEFDKPAPGVTLIDSTYLDLGQVIDQVVGLVPTELR
>PFR_JS14_1132□PFR_JS14_1132□GTPase Der□1296491:1297840 Forward
MTIAETAQAQSTRPVVAVVGRPNVGKSTLVNRILGRREAVVQDTPGVTRDRVSYDANWAG
REFVLVDTGGWIAKAEGMSAHIAEQAEMAIQLADAVLFVVDAKVGLTDEDEAVVKVLRRS
GKPVVLAANKVDDERVEAEASSLWQLGLGEPYPVSALHGRGSGDLLDALVKVLPKTSAVE
PDEVGGPHRVAIVGKPNVGKSSLLNRLARAQRSVVSDVSGTTVDPVDELVTIAGEPFRLI
DTAGIRKRVKEASGSEYYAWLRTQAAIERSEVCVVVIDASEPISDQDLKILSSVEEAGRA
MVVAFNKWDLTDEERHRYLGREIEQDLQTWKWAPTVNISALTGRNVDKIAKAVNKSLAGW
ETRVSTGKLNAFLGRIVAANPHPVRGGKQPRILFGTQAQNRPPTFILFTSGLMDAGYVRF
VERKLREEFGFEGSPVHIQVRARAKRKDR
>PFR_JS14_1133□PFR_JS14_1133□Protein of hypothetical function DUF1706□1297875:1298384 Reverse
MAVPRTKDELLVAIADNYAKLSIDLGRVPASRAREASMPGHVAGTVMSPADLVSYLVGWN
EQVLEWFTERQRGVEPDFPARGLGWNQLGELAQRFYADHGELTWPQLLDRLARAEQGLIE
LVSAHDDTELYGRPWYRTHTAGRMIQFNSSSPYANARRRIRAWLRDQGL
>PFR_JS14_1134□PFR_JS14_1134□Major facilitator superfamily protein 35□1298508:1300010 Forward
MSLTKRQRWTLLATVSIGLLLITLDNSILYTALPLLTEELGANGSQTLWIINAYPVVIVG
LLLGAGTLGDRVGHRRMFLIGLVIFGVASAAAAFSPSPAWLIASRAVIAVGAAAMMPATL
ALIRLSFDVERERNFAIAVWGTVSVVGSAIGPIVGGLLLEHFWWGSVFLIGIPFVVIALI
ATVVVAPPNDPDPSKHWDAISSLQAMVGLVGAVFLLKELANVPPNWTVVVLGAVAAGLGL
TSFVRRQQRSNDPLLDFAIFRNRAFSAGVLAAAISMFAVSGAQLMTTQRFQLVEGFTPLE
AGLLVTVVAIGSLPTSLLGGLYLDRVGLLPLIAGGLAVSAIGTAVMIFGIEDHLFWLMVA
GLLISGIGLGAVMSVASTAIVGNVSARRAGMASSVEEVSYEFGSLIAVAVLGSMLNFIYS
ATVRLPPGTPAVARSSLTEAIGVAQGDQAIVGAANAAFDNGFLVTMIVLTVVLALGAAAT
ARLLRHYGPGSRSQEFSDNH
>PFR_JS14_1135□PFR_JS14_1135□TetR-family transcription regulator□1300036:1300614 Forward
MRPSKRDAILGAALGVVERGGVSAVTFESVATAAGVTKAGVVYHFPTREALLLALQEYLA
HQWQLDLEAQLGTPVESASQGDKLAAYARDSSHSSSRAELLLMLETVDDPQAYAPWHAVM
SRWTPALDTDQPMGDAELDHAVARLAADGLWLYESLSTHALSPGVRQQIVSRLSALAHRP
DGPAAPGGPGRH
>PFR_JS14_1136□PFR_JS14_1136□Zinc-binding dehydrogenase family oxidoreductase□1300660:1301586 Reverse
MRAAVVEEFGSPPRWTEVPDPVVDVVAVGLHPRVRSQAAGSHYTSTDELPLIPGIDGVGR
DAEGRLRYFVLRDTVHGSMAQRAVIDVRHSVLLPPGADPAQVAAVMNPAMSSWIALRQRV
GLRAGQSVLVLGATGNAGAMAVRVARRLGAGRVIAVGRGAQRMAAADPDAIVALDDAPDR
VAEQLGRAASDVDVVLDYLWGRPTADALRAIVPARHDDDQKLTWVQIGSVAGTESPIPSA
ALRATRLDIVGSGQGSVPATRIVAELGELLDEVAAGHFTSDVLTMPLSQVGQAWLTGTHG
TQRVVLVA
>PFR_JS14_1137□PFR_JS14_1137□Putative membrane protein□1301695:1302570 Reverse
MSPALPARSTLFGPSLVVTGLFCQETGASIAVMLFPAVGPAGIVALRLVFSAIILCAVAR
PSLRGRRPIAWYTAIAFGLVLTGMNLFFYLALDRLPLGTTVTIELLGPLTLSVVAGRRWM
NLVWAGLALVGVVLLGGSATHLDPLGVAFTLVAAAFWAGYILLSKATGRHFAGIQGLAVA
MVAGSVVTVPIALATTGSRLFGPHVLIAGLGIALLSSVAPYALEMTALRRTPAATFAILL
ALAPAVAAAAGFFILGQTMTIHDVFGIVAVICASIGAVCTPPGKPGGRQKA
>PFR_JS14_1138□PFR_JS14_1138□Hypothetical protein□1302741:1303262 Forward
MESESGGAGNFHGAKGPHAEGSAGDGHRDEAAATLDALSADRHRLADRLAVPWALMAAFG
ALAAWWVGSAVTTTPGSGYEPPLAGWMTLPVALVIAHLVRRGTGIRFRALGARANGAMLA
VLVACLLLFSVSLGAVSLGMAWLVGVMSLVAFGVTTWLSGVAYRSAVERVRRG
>PFR_JS14_1139□PFR_JS14_1139□Transcriptional regulator□1303255:1303560 Forward
MVEARFDAVIHAPLRLRICGLLRPVDGLDFALLRDSLEVSDATLSKHVKTLTAAGYVTSR
KAASTERSDGRRIMWLSLTGPGRLAFDGHVRALREIVGTGS
>PFR_JS14_1140□PFR_JS14_1140□S-ribosylhomocysteinase LuxS□1303957:1304421 Forward
MTQHMNVESFNLDHTKVKAPFIRVADVKHLPQGDTLTKYDVRFCQPNVNHLDMKAVHSVE
HSFAECVRNHSDSVIDFGPMGCQTGFYLIMVGEPDVPRIADLVEQTFRDILALDAVPAAN
VVQCGWGANHSLQGAKDAVSTMLRHRAEWEQVMA
>PFR_JS14_1141□PFR_JS14_1141□Antiseptic resistance protein□1304613:1306193 Forward
MPLNPTQHTGINPDRRRWIALIVLSLALFMASMDNTILNVALPTLGRELGATTDELQWTV
DAYQVTYAGFLLVAGGLVDRWGRTRTFVAGVAVFGLCSLAAGLSTNTTMLILARGLTGIG
AALLTPSTLALISVLFRRPGERTTAFAIWSGANSAGAAVGPLLSGGLLAHFSWGSIFLIN
VPVAALCLVGAVFLLPRVRAERDEDHIDWPGTGLSIAGLCAVCWAVISAPGLGLFSAPII
FAFLGGIALLVGFVWWQHHASAPLLRLSLFRSRPFAVSVAVSGLVTAGGAGALFVLTQFL
QFVLQFTPWQSGLSIMPVAAMMLVGAILAPISLKRIGIKRAVIAGLICVALGFTLLSLTH
VGMTYLQMLPGAMFFGLGAGLLMPAATQAVMDSLPSESEGAGSATNSALMQVGSAMGVAI
TGSLLAWRYREVMSADAAVRGLGEPLHSDILASVGRAFDLSSGGAHPDILAALKRGFVSG
MQVGLGASAAVVVLATIAVAIFFPRHPVAPDEAEIEGSEPKASPAP
>PFR_JS14_1142□PFR_JS14_1142□Nitrate/sulfonate/bicarbonate ABC transporter, permease protein□1306500:1307390 Forward
MASSRFTRHPAPTGVRIGAPLVVGALLLLAWHAVVSTHTVPLTLLPTPGSVWSRLVHDIV
HGELLARTATTIWEAVLGCIVATVFALPVGYLVARVRLAEAAISPYLAASQAIPAVALAP
LLVIWVGYGLTPIVLLCSLIVFFPLLLSTVLGLRSIDHEVVEAAELDGASGWRMIRYIEA
PLSRAALLSGVRNGFTLSVTGAVVGEFVMGGTGLGLVVSMQSASADTTGLFSTLIVLCVL
AMVIYLGLIAVERFTDPYRVPRAAHPVPLETAPDLRLVAATQAHQSHTSAQKELVA
>PFR_JS14_1143□PFR_JS14_1143□ABC-type nitrate/sulfonate/bicarbonate transport system, periplasmic component (Precursor)□1307387:1308394 Forward
MTRHSRLTRFLLVLLALTLGTAMSACGNQSGSSSASSSAGIPLTVGLTYTPDIQFSPFYV
AVQKGYFADEGLNVTLRHHGASESLMGALQSGTEDVVYAGGDEMLLSRSQGVDVVNFATM
YQSHPAELIVPQGSSISSFADLRGHSIGIPGPFGENWYALLAMLRQAGLTQGDVNIQSIG
YTQQAALMGNKVDAVVGFSNNDAVKFGQAGFPIREIRLDAATPLVALGLGASKATVTDKQ
DQLKAMMRALDKAVAYCTSDLDGTVALTEKYVPALSDDAQRAAARATLEATNKLYGSQLG
KQDAQRWSDMATFMAESGIISKPVDAKESFVSLVG
>PFR_JS14_1144□PFR_JS14_1144□Homoserine O-acetyltransferase (Precursor)□1308576:1309829 Forward
MGHPGDGDDAASASRGIPGMTSSRHQYLPPTPEDIVETKFMDLFDTPGEPMHLVRGGTLP
GITVAYETYGTLNERRDNAIYICHALTGDAHAAGYHEGDDRPGWWDALIGPGKAIDTDRW
FVVASNILGGCSGTTGPSSVNPETGKPYGLDFPLLDMHDFVVVHRALLTKLGVPHLHAAV
GGSLGGMQVLDWALTHPEDMNQAVVIASSSRLTAQNIAFSAVGREAIMSDENFMNGAFAE
NDTNPDVGLAVARMMAHITYTSEEGFEEKFGRRPQFDAQQPGFGVDFAVESYLDHQASSF
IGRFDALSYLYLTRVMDYFNPFADAHALDRLVATPVRFLVMSFDSDWRFGTAHSRRIVRR
LQDAALPVSFREIHAPWGHDSFLLHIPPYLDSVRAFVEQPAVPRPTIRRRRLRKWGR
>PFR_JS14_1145□PFR_JS14_1145□Methionine biosynthesis protein MetW□1309826:1310512 Forward
MSQSSARDSVIGGANRLGEGLLRQDLQSVARLIRPGERVLDLGCGTGDLLAYLIGAMGCS
GTGVERDPDAVLQVIGRGVPLIELDLDTQLEEFGDDSFDVVVLSRTLQAVLKPKEVLLQM
RRIGQRMIVTMPNFGYWRHRLRLLTGRMPQSKDLPYTWYDTPNLHHTTLVTLEELFDDCG
LDIERRIPLDGDGRRPRLPLELTQHTANVLAGSAIYVLTRRDAADAPA
>PFR_JS14_1146□PFR_JS14_1146□Transcriptional regulator, AsnC family□1310648:1311061 Forward
MSFTEIGRETGLSTSAAQQRVRRLEQRGIITGYHARIDGAALGHTLAAFIEIRPLGQVDE
SLVDVLASMPEIVSCYSVAGDASHLCLAEVTSTQELDDLLTRIRTAVNVSTSTTVVLRTL

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FRDRPPIDDPDVPAAKR
>PFR_JS14_1147	PFR_JS14_1147	Hypothetical protein	1311155:1312789 Forward
MNTTSDIVAAGSPVALRGWSRLLRGDHAPVRLHWALASLLSLVAGALLALGFQPFGLWPT
TVVGIALLSWLSDQARARRVAWCGLLAGLALYSMTVSFQAVVAWWLPVLMVPVLACWVLL
TALGQHYVQFLRAWPLWSASIWTLVEALSARFPFGGFAWDRLAFTLPDQPLGGYLWLVGA
AGAGWLLALSGCLVVVVVRAVVARGGRWLPRMAAGIAAMGLLAAGGAVLSAVPATTGAGR
GVTVGVVQGNVDGSAGPHTMGYARSVTDNHLSETIMAMARARTGLDAMPDFLAWPENSTD
MDPNQDEETHQLIADAQAIAARPILVGAVTLGPGDDGRQTAGLWWDASGETARYAKRNAV
PFGEFTPLKDLVFAIAPMAREVGRQTIPGTAPGVITGTLPDGSSVRVGDIICYELAFDST
VYDTVRHGAEVVVVQSNNATYAGTMQPRQQFAITRVRAMEMRREVVVSTTSSLSGLIDAR
GRVVEHSQEDTAWARTFTVPTRQGVSAGVSTGPAFEAIACAVAAVAVVAGLVAPRRARRG
GSLH
>PFR_JS14_1148	PFR_JS14_1148	ApolipoproteiN n-acyltransferase Lnt/dolichol-phosphate-mannosyl transferase Dpm1	1312876:1313682
Forward
MVDHSESLDKVLVIIPTYNEAENIESIVERLRQAVPQADALIADDNSPDGTGDIADRLAA
DDDHIHVLHRAGKQGLAAAYVAGFRWGLERGYDVLVEMDADGSHQPQFLPSMLNALRDAD
MVKGSRWMPGGEVVDYDKKREWLSRLANIWVQASMNIPVRDTTGGFNAFRASALRKMNLD
TIASKGYTFQIDLTRRVLDDGGIVREVPISFPDREKGESKMSGSIIGEALLRTTQWGAQR
RGAQVAQFAREAADRVEPLVDRVKDKLD
>PFR_JS14_1149	PFR_JS14_1149	PF13397 domain protein	1313778:1314116 Reverse
MADRALRGMGLGAKSFEDEEGVEFATRKVLGFTCPKGHHFEVTFSTEADLPTEWECPRCG
AVATRSDGTKAEDKQVKPPRTHWDMLLERRSVSELEDLLAERLEVVRKSPHY
>PFR_JS14_1150	PFR_JS14_1150	Glycerophosphodiester phosphodiesterase family protein	1314223:1315020 Reverse
MVSRRRTADDYEFFDAPFAAMAHRGGWDALVPARFENSLLAFEHAVNDLGYRYVETDVHA
TADGVLVALHDTRLDRVTDMHGAVAGLPWRVVRRARIGGSEPVPTMDEVFEALPNTRINI
DIKESGAIAPLAAAIRAHRAEDRVCVASFSPRRLAGFRALMGDRVATSVSVGAVAWSAYV
PWLPRVLNSGAQVFQIPTSQAFGAVGIPVLTRNLARVAASRAMRIHVWTIDQSDEMVQLM
DSGVDGIVSNRIDVLRRVARERALW
>PFR_JS14_1151	PFR_JS14_1151	Hypothetical protein	1315065:1315589 Reverse
MEYVSLTSTDRSLRCAHLTRLRQRASVMATHGISPALPRRDIPRRERFAWRARIRANPPA
LLAYRVVVAIIGFAFIIAAGLTGWLPGPGGIPLFLAGMAILASEFRWAHSLTIRAMGVLR
AFGRQSRRRKTLLVCGFLAAVLLLGYVALIIVGSPGWLPGWLHAALAMLPGVRG
>PFR_JS14_1152	PFR_JS14_1152	Pyridoxal kinase	1315727:1316596 Forward
MTRILSVQSEVSYGFVGNSAVVFALRRIGVDVWPVNTVQFSNHTGYPSWRGPRLTPIDEA
EIVRGLDELGILGQLDGVLTGYLSGPSMGRQIMAAVQLVKRRRPTALYCCDPVLGDDETG
FYAAPGTLELFREQALPLAQVITPNRFELAALTNLPTSSLEEILIAADTLLDAGPSTVVV
TSVPSLRPSQGAGHDDRIAMVAVQRDGAWQVSTPRLPGEFSGAGDLTSALFFAHSLAGES
PGQALSHTASSIHGVLGATVAAGSRELELVAAQRELVHPSAVFEAERVR
>PFR_JS14_1153	PFR_JS14_1153	UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA	1316687:1318156 Reverse
MTQNQLAEELSTSQSAIHRIESGHQNLSLETINRIAGALESPLIVPGNSSTLNFRIGGET
HLSGSIETRSSKNAAVALLCACLLNQGRTVLKGIAHIEEVNRLLEVLTSIGVDASWSPDG
KDLTLQRPETLDLENMDVAAARRTRSILMFMGPLSRFFSEFRLPYAGGCDLGVRTVEPHM
QSLRHFGVNVLATEGFYRASVTRTGPDTRHIVLTERGDTVTENTLMAAAVSPGVSVIRNA
SSNYMVQDLCAFLMLLGVEIDGVGTTTLTVRGLSAAPSMDVSYEISEDPIEAMSLITAAV
VTKSELTITRVPIEFTEIELSILGEEMGLHYGLSSEYKSGNGLTRLVDLTIYPSELKAPP
DKIHPMPFPGLNIDNLPFFAVLAATAHGQTMIHDWVFENRAIHLLQLNQLGAHVQLLDPH
RLIVQGPTRWRGREMVSPPALRPAVTIMLAMLAATGTSVLHDVYVINRGYEDLPARLNAL
GADIETFYD
>PFR_JS14_1154	PFR_JS14_1154	Dihydrolipoyl dehydrogenase	1318369:1319769 Forward
MSAHYDVVVLGAGPGGYVAAIRAAQLGLKTAIIEKKWWGGVCLNVGCIPTKALLRNAELA
HLVQKEADTFGISGQVSFDYGKAFTRSRQVSERMVKGVHYLMKKNKITEYNGWATFSDAR
TLQLAGNDGTTDTITFDNVILDTGATVKMLPGTSKSANVLSYEELIMSDSLPESIIIGGS
GAIGTEFAYVLNSYGVDVTIVEFLDRMVPNEDADISKELTRQYKKLGIKVLTSTAVQSVV
DTGSGVDVTIAPAAGGEAQVLHADKMLQAMGFAPRTEGYGLENTGVALTDRGAVAIDDFC
RTNVPGVYAIGDVTAKMMLAHTAEAQGVVAAETIAGAETMAVDYRMIPRATYCQPQIASF
GLTEQQARDEGYDVKVAKFPFSANGKAVGMGAPDGFVKIVADGRYNEILGAHMIGEGVTE
LLPELTLAQKFDLTTEEISRNIHSHPTLGEAVKEAAEGIEGHMTNL
>PFR_JS14_1155	PFR_JS14_1155	Extracellular ligand-binding receptor (Precursor)	1319965:1321128 Forward
MRRAVSAVLAAVVGLGMVACGPNKVNSAVGDTIKIGVNYELSGTVASYGSSNVKGIEMAI
DEINAAGGVRGKQLKEVKYDSKSEPAEATTLATKLTSQDKVVTIIGPATSGSFKATIPVA
NKHEVPVVSGSATANDATVLHGKVQPYAFRTCFSDNYQGTGMADYAVKRMKATRAVIIKD
NSSDYSKGLAESFRQKMTEEGGTITNEVTYNTGDQDFNAILTSIKNQKFDVIYLPGYYAE
AGLIIKQARAQGIDTPILGGDGWDSPKLEDLAGDSALNNVFFSNHYSSLDPSAQVQDFIK
AYKARYGAEPDAFNALGYDTAKFVADSINRASSIDGPSIAQAMATTTNFSGVTGTFSMDA
NHNPVKSIVVVGLTNGKQASSESYKAS
>PFR_JS14_1156	PFR_JS14_1156	High-affinity branched-chain amino acid transport system permeaseprotein LivH (LIV-I protein
H)	1321225:1322109 Forward
MDQILQQLVNGASLGSVYALIALGYTMIYGIIQLINFAHGDVYMVGAYVGYACMAHFHLG
FFTSLVVAMAVCTVLGVVIERVAYKPLRKSSRIAVLITAIGVSFLLEYTMMFFVGADVRS
YPPLPHWMQVSWHLGGVIITSLQVLIFAIAVALMIALQLIVRRTRLGKAMRAVSQDADAA
RLMGINVNNTISFTFALGSALAGAAGVLVAVYYNSINPLMGMVPGLKAFIAAVLGGIGLL
PGALIGGYFIGVVETFVSGTGFSTFKDAVVYALLIIILVVKPSGLLGKNEKEKV
>PFR_JS14_1157	PFR_JS14_1157	Branched-chain amino acid ABC transporter, permease protein	1322106:1323125 Forward
MTMSGSQTLGLDTSTTPSRSFVHASWFRKTVLLAAVYLVVLLLVQADVINDYRLITIATI
CINIVLATSLNLITGFTGQFSLGHAGFMAIGAYVTALVTIQIDSVWGFVLGLLAGALLAS
LVGLLIGLPTLRLRGDYLAIVTLGMAEIIRIVLLNLKVTNGAAGLQGIPQFVNWTWLFIL
TAGSVVLISNYLHSRHGRDSIAVREDEIAAESIGVNSTRTKTMSFMVGAFFGGIAGGMYA
SFFYFIKPDTFNFMKSVDILVIVVLGGLGSLSGSVIAAILLAIVSTLLQPFPEIRMILYA
LILILIMIFRPQGLMGSRELSVKLFSRLIPGRARKERTR
>PFR_JS14_1158	PFR_JS14_1158	Branched-chain amino acid ABC superfamily ATP binding cassette transporter, ABC
protein	1323122:1323913 Forward
MSQPILTVEHLTRNFGGLAALSDMSMTLNRGELVGLIGPNGAGKTTVFNMLTGVYAPSSG
SITFDEHGTAVELGGRKPNAICRAGVARTFQNIRLFKELTVLENVVSAMQLQESYGLLAT
FGHTPVWKRSEADIRQRSREMLGILGLADKESELARNLPYGDQRHLEIARALATAPSLLL
LDEPAAGMNPAETAELTTLISWIRENFDLTILLIEHDMSLVMTICERIYVLDHGIVIASG
TPDEVQHDPQVIEAYLGQEASDV
>PFR_JS14_1159	PFR_JS14_1159	Branched-chain amino acid ABC transporter, ATP-binding protein	1323906:1324610 Forward
MFEIHDLQVNFGGIQALKGISLSVEDGQIVTLIGANGAGKTTTLRTASGLERPSGGTITL
AGQDITRASARERVKQGLVQVPEGRRVFPKMSVLENLELGAFLRKDRAGITRDLRDVYER
FPVLADRLKQQAGTLSGGEQQMLAMGRALMSRPKMLLLDEPSMGLAPLFVQEIFDIIKAI
NEAGTTVLLVEQNANMALQIADHAYVMETGRIVLSGTAAELSASDEIKRAYLGG
>PFR_JS14_1160	PFR_JS14_1160	CBS domain protein	1324612:1325262 Forward
MFIRDHMTANPFTVTPEDTVPKAVEVMKLNHVRHLPVLRDGKVVGVIANSDIAKASPSQA
TSFSIGEITYLFSKLKVGKVMSRDVYTIAADALLEQAAVLMRDHKIEMVPVMEGDKLVGV
ITESDILDSFVDIMGMRMRGTRLVLEATDAPGQLSRITGLVADHGMNITHLAVYPGSGTS
QIVLGVNSLNTADLETQLVGLGYRVIARLRNEPGKD
>PFR_JS14_1161	PFR_JS14_1161	Putative fructose-specific phosphotransferase enzyme IIA component	1325294:1325716 Reverse
MIRVVVAAHGNLASALVKSTAMILGSNPDVVAIDFDPEGDVHALYRSVQDATKDAAGVIF
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LVDLLGGIPYNAAVRWCSRHLDSDVVTGVNLPMVIDVSTLAQQETHVPRAVSAAKAAGVS
SVASWRTGPASRHHTVTDDR
>PFR_JS14_1162	PFR_JS14_1162	Dipeptidase pepE	1326189:1327322 Forward
MTTDGLLRTASVDELTARQQMLRARAARSGVDAVVISTGADMRYLLGRSQGSHERLTALV
VPTKGSAFLIVPELERPGWEGSSAESMGLEMSTWPDGDSPYRLLAARLGPIAELAVDDVM
PVRHAHEIRTAVDCRVEPAGELIGGMRVVKTDEEITALTAVAAAIDRVHRRVHEWLRPGR
TERQVGADIAAAIVAEGHQRPDFVIVGSGPNGASPHLEQTDRVIGAGDPVVVDIGGPAPS
GYFSDSTRTYCVGSPGDPEFATVHDIVRTAQQKAFETARAGVSAAAVDQAARTVIEQAGY
GPYFITRTGHGIGLEVHEEPYIVRGDDRLLSPGMAFSIEPGIYLPGRFGVRIEDIVLIGA
DGSPVRLNHSPTRWELP
>PFR_JS14_1163	PFR_JS14_1163	Hypothetical protein	1327352:1327684 Reverse
MSVSGEAYPGFDHAPDVLANVFHGDQGAYDAVKPSTILAKNHYPDTWAFFSYGTDDHYFG
PSLQELAQQAAAAGMTVKVDPLENAGHLMPAVRGGLGAGLEWLYPRTGLS
>PFR_JS14_1164	PFR_JS14_1164	Hypothetical protein	1327650:1328669 Reverse
MTQLSRTWRSFVNWLMARNIVGPKELIPAAVIAALVVAWLVIRRHRGWTRTVAICAGVGA
VVGVIAWFLGEKVLNLTLGPMPMLGRIWVVAFFIGLGLVVANFRWSTWRRKVAAVLAAVV
LLGATVLAVNKAYQINTTLGALLGRVPANPITLPSQPTSSPSHHEDFDGAHWVAPADMPA
KGQAGNQYLPGKVSGFHPRSASIYLPPAALVANAPKLPVVVFMMGQPGTPDAPLFKDQLD
GIAAAHNGLSPIVVFVDQLGNPNVDTLCLDTQKFGNVETYINTDVVNWVRENLNVSTDRQ
DWTVGGYSQGGAVRGEFRGKASGPVGKCDECLGGGVSRI
>PFR_JS14_1165	PFR_JS14_1165	Hypothetical protein	1328666:1331149 Reverse
MVLAVLGVATIAWQLSPAGEWLRHWVRTGGGTAHIGGASNVARGLVMLVDPGSIGATVAL
LVLMVSVFPYIERRLGAWRFVAALVCCHVVATGLTLGFASLIASQWPRWSDALVNGWSNG
AIPALLGVAMAASGGFNHLWRVRTRWIGLAITLTLGFYDASTFAAMTLGSMVAGLVIGAF
WWRGAERFDLWPRFRERRVLVSLVIACASLGPLLAAWSTRAAGPLEEIAGYVRTGQFESP
EAHAICRLASSHACTLAHLHQNLGWPVLLMSVLPAVIMLVLCLGLVRARRSAWFCALLVE
AAMAATTVTATVVRAKAELAWRQTHASTGFIFFVRMVMAFLPAAIPVGVVVLLLLTVRLF
PVRLPRRVAVGQLVRYVALFGVATIVYVVVGMLLAAQWSPQASVVALLHDVVTRVFGLEV
LLSLGSTLSPASTATQSLAYLTGPLVMFVALVLMARNMQVDPRELAGADAKRLRGLITRY
GGGIFAWMTQWTGVRHWYDPALEGVVGYRLAHGVAVTLGEPIGQDPMATALSFARRSDEG
GLTYCFYSVGADFARQARGFGWRALQIAEESRIELGEVAFKGKRFQDLRTAMNRAKREDI
SIVWTRLAQCSPERRREIREVVEGWQRQQTLPPLGFTLGGFAEMEDPEVRCELAVDESGH
VHGVASWLPLYRDEKVIGWLLDVMRRREGATGVFHSTIELLISKAILQFQDEGFEVVSLS
GSPLAMEPRDQPPVTDAVSGTLYQGLGSVSGLLERYYGFTSLHHFKAKFGPEFHPRYLVY
QDPTDLPKIGRALTTAYVTTEPTVRISRIIKYFRGRRGSTDENGSDT
>PFR_JS14_1166	PFR_JS14_1166	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	1331358:1332869 Reverse
MSVQYSDDRLMDYDEVMARFDVVLGLEVHVELNTESKMWCGCSTKFGAEPNTHTCPVCLG
LPGALPVVNGKAVESAIRIGLSLGCSIASWCRFARKHYFYPDMPKNYQISQYDEPIAYEG
EVRLDVEGTQYTVPIERAHMEEDAGKSLHVGGATGRIQGSDYSLMDYNRAGVPLIEIVTK
PVYGTGTRGPEVARAYMSYLRDMVRALDVSEGRMEQGQLRCDANVSLMPKGSTELGTRTE
TKNVNSLRSVEAALRYEICRQGAVLADGGRVKQETRMWNESGGFTTAGRSKEEAEDYRYL
PDPDLVPVEASAQWVDELRKTLPELPAVKAARLQKEWGLTDLEMRDIEGNEGALALIEAT
VVAGADQAAARKWWLGELSRRANETEVELAELPISPVQVAQVGKLVDSGKLTDKMARQVI
EAVLAGEGEPAEIVKARGLEVVSDDDTLSRAVDEAIAANPGVADKIRGGKVQAAGALIGA
VMKQMHGQADAARVRELILKALQ
>PFR_JS14_1167	PFR_JS14_1167	Glutamyl-tRNA(Gln) amidotransferase subunit A	1332866:1334398 Reverse
MTNDILTTPALELGRRIAAREQSSTEVTGAFLDQIDAVEPAVHAFLAVDRDLALRRAGEV
DAQIAAGERLSPLAGVPVAVKDLLCYQGLPTTAASRILEGWMSPYDATVVRRLQAGGLVI
LGKTNLDEFASGSSTESSGYGPTHNPWDLERIPGGSGGGSAAALAACEAPLAIGTDTGGS
IRQPAAMTGTVGVKPTYGGVSRFGIIAMASSLDQCGPCARNAADAAALHQVIAGYDPQDS
TSLDRPVPPVRQAAERADVTGMRIGVVRELGGEGYAPGVEARFGEAVAQLEAAGAEVIEV
SCPRFEQALATYYLIMPSELSSNLARYDAMRYGLRVGDDGHHSVEQVMRLSRGQGFGAEV
KRRIILGTYALSAGYYDAYYGSAQKMRTLIARDFAAAFDRVDALVSPVAPTTAFKLGEKV
DDPLAMYMGDLCTIPSNLAGIAAGSFPCGASPDDGLPVGFQVMAPALGDDQVYRVGAALE
RLVGPGYDAALSDRAAALPGSLVSMGKDAK
>PFR_JS14_1168	PFR_JS14_1168	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C	1334406:1334708 Reverse
MALTPHDVSRLADLARIELTDDELAELAPQLDVILNAVAGVAEVADEDIPPTSHAVPITN
AFRSDAMKLSWPAGEMLRSAPAEQDQRFRVPRILDDSDEQ
>PFR_JS14_1169	PFR_JS14_1169	Amino acid-binding ACT domain protein	1334929:1335555 Forward
MLLLRVELPDRPGALGQVATAMGGVGADISAIEIVERRSDGHVIDDFILAMPPGSLAETI
INACAEMPDVKVLWLSRYPDQWNLESDIEVINRMSKQRARAAEILTEDAPTVFRCEWASL
VDRKGLKVLHATERAPEFTADQLRELGDLAKAGRHAMGEDWMPDWGDVAVAAAPVDEDRT
LLVGRQGGPEFLDSELFRLEHLASVARA
>PFR_JS14_1170	PFR_JS14_1170	Hypothetical membrane anchored protein	1335576:1335779 Reverse
MRRFSSDLDLTGGAPVRARPSIGEWGPDQVPTTAQKKRLRIWVSIALVAATTAIGVLMYV
FYKLLGY
>PFR_JS14_1171	PFR_JS14_1171	Methionine synthase, vitamin-B12 independent	1335848:1336834 Reverse
MIATALGSFAGTDLRATARAVLGELPDRAPIVELPDRGPQASMIARTAAMLPDMPFDRRP
SGWRLAPGPSLVGRRAAALFNDDVTMTAEVIEDWQGTLTLTMAGPWTLLASLDLVRGGRA
VGDAGARRDLAQAWLAGAVDRIAHTRSQLDRPLAVQIDEPALPAVLAGAIPDESGRRRLP
AVEAQEVQESLGACVDATRGAAEDIVVIHCCADRPPLTELAAAVPDALSIDTQRLDAGSW
DALAQWFSAEPGPGMDHALWLGLLSTSTPGFGVDAIRGALDECRRKLEADPGGPADRRLA
ITPACGLASADPVDAFRALADLAAVARG
>PFR_JS14_1172	PFR_JS14_1172	TRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	1336880:1337953 Reverse
MRVAVALSGGVDSAVTAARVVEAGHEAVGVHLLLGAGSVPETRDARGVADAVGIPLVVWD
LRDRFEHRVLDYFTSSYAAGRTPNPCLRCNREVKFRGLLSRGIEEGFDAVATGHYARLQP
ARDGSIGLHRAANVRKDQSYVLGVLSQDDLRHCLFPLGTVTTKDEVREEAERRGLPVAHK
PDSTDICFVTEGGAAEFLAGRLADRQGDIVDARGTVLGTHHGIQHFTVGQRKGLGLRRPA
DDGKPRYVTALDAATNTVHVGQGRELLVGQVDVEDLSDTGMPLGPHWRGLVQFRAHGRAV
PARLEEADGQLRVHFAEPVSGVAPGQFIVFYDADRVRGAAEIVASHAPGPSMVPEHE
>PFR_JS14_1173	PFR_JS14_1173	Glycogen debranching enzyme GlgX	1338210:1340402 Forward
MTEINRSDAAHVLGAHLSADGCHFGLWAPRAERVELALVDGDGSTQRNVDMTLGGGAWSV
FVPDVVAGQRYGFRVHAQWDPDQGLRANPAKLLVDPYARAITAGVDYSGPIFDHVPGSYF
EPDTRDSAGSVPLSVVVADSPAPEPIAERRPLEECVIYETHVKGLTQLHPTVPEHLRGRF
AGVAYPAVTEHLKSLGVNAVEFLPVHHFISEPFVMGRGLSNYWGYNSLGFFAPHAAYCSV
GTEGDQVAEFKEMVTALHRAGIEVILDVVYNHTCEGNHEGPTLSFRGIDHRGYYRLTDDL
RNDYDITGTGNSVNTAHADVLAMVVDSMRYWVQEMGVDGFRFDLATELIRDGEHHVDQNH
DFKKLIAQDPAFKGVKMIAEPWDLGPYGYQVGNWGPGWSEWNDRFRGYMRDYWRGQVDGV
DELATRLSGSADLFDHDDRPPSSSINFFDAHDGFPLRDLVTYNEKHNEANGEDNRDGSDD
NRSWNCGVEGETADEVINALRHRQIRNMVATLMLSDGVPMYCAGDEMGRTQQGNNNAYCQ
DGPINWLRWDQMEEWGDVLDTVRTFTDLRMSTPLLHANDYRYRTEVTDPTGAGLGRYELA
WMNGSSGEMGEADWHDGSRRLLGMYVSDASSVAYLSWFYSGDQPIQVQMPPAPWGESFHI
VASTCEDGEVPDADLAPGDSFTMPPRTVVTMRVAVMTTAPVPDDQPVTDQEIATGDPHIP
DTPQAAAPTS
>PFR_JS14_1174	PFR_JS14_1174	Hypothetical protein	1340620:1341207 Forward
MSSRSMRAGAIALAAVMMSSMVACSGPSASEKASASFHNSVSAARDALFEEAKATNQGFF
DLQESLGLQGGAEELPAQMHRYVMGNAAKYVADLNAQLKESGERTEPDTHAEMVGPVLYE
GEKKSGAEEADSRAEIVIERCVDARKSPRLDSRGEPIPGSTNLVHHILYMDHDSDGELKI
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FEAWSQEVTTCPVNA
>PFR_JS14_1175	PFR_JS14_1175	Hypothetical protein	1341189:1342055 Forward
MPSKRITTWPGISALSALIAGMLLAPLPVAADGDGFAFNDRARTGVSASRSGNSISVEAW
AGGSTATTNTAGTTATEFDSTAWTRWALSPCSTIMKPAANTGALFTPETKKQAATRQGID
CTTPNTTTIATTAHHAIATMTLPDTTIKLDPDPTTNQWHAAAVGQQLWFTLDNPGPQHTT
TNTDITITLTATPGAVTINPGTINPGAHTTPIRCTTGRPRPTTTNGNQPSPVCGTSYQHP
GHYTITATRTWTITWTAQGHTGTETITRPATAPTLDVIELHSLLVPNN
>PFR_JS14_1176	PFR_JS14_1176	Phosphorylase	1342199:1344712 Reverse
MAVLARNLRWSWHQDTQDLFEAIDPVLWEETSHDPQKLLSRASRERLDTLAGDRRYLRHL
ELAAADLSDYVSGDRWYQGFVSRHPEAPKAIGYFSAEFGVSSVLPQYSGGLGVLAGDHLK
SASDLGVPIIGVGLLYTHGYFRQSLNAAGWQQEHYPVLDPNELPVEMLREDGEPVTITLT
INHRPVVAQLWVAQVGRVPLLFMDTNVDANDEAARSITDRLYGGSADHRLAQEILLGVGG
VRALRAFCRVTGRPDPDVYHCNEGHAGFLGLERIREYMTSGDDFDTAWEKTRAGNVFTTH
TPVPAGIDRFGNEQVANEFGDFTPLPIDRVLALGAEDYEGGDPSRFNMAVMGLRLGEHAN
GVSRLHGKVSREMFQGLWPDFDVSEVPIGSVTNGVHAQSWIHPDLLELLQAQTGDSETVV
DGLDLTALDRVDDNTLWSLKRQMRGEMIKMARERLVRSCKSRGMSSEWVSNALNPHVLTI
GFARRGASYKRLTLMIQQPERLKKLLNDPEHPVQIVIAGKAHPADDIGKGFIQQMVQFSD
DPEVRGKLVFLPDYDISLARPLYPGCDVWLNNPLRPQEACGTSGMKAALNGAANLSILDG
WWDEWYDPAYGWAIPSATNAASPEERDRMEAESLYQIIERDVVPKFYARDANGLPTGWIT
MMRETMEGLGPKILATRMVRDYVTDLYTPAAQSASALLDNDVAANLAAWKQRVRQAWDGV
AIDRVESDLPNPVAVGSRNVFSAWVKLGSLEPTDVSVQVVSGDVDADDQIHNVRIFELAP
TDQVDQQGQLFRANLVSAISGSIGYTVRVVPKHPLLHDAAELGLATVATAAVAGQDR
>PFR_JS14_1177	PFR_JS14_1177	Alpha-1,4-glucan:maltose-1-phosphate maltosyltransferase	1344818:1347031 Forward
MDSTHHTPRASNNGHAIRACQPRFESALDSVGGVVSKKKRQRSAQARVRSRVTVQASADP
KPTDAQARPTEVPPEPAALSVPPPIPPGFGRIPVHNVQPVLEGGDYAAKAVENGDLPVTA
NIFREGHDAVAAAVVLTDPAGATQRFEMAQIEPIGLDIWKAWIRVGRPGDYSFHIEAYDD
RWGTWRHNAGIKFSVGQDIALVCLEGLQLLDEARDAARAAGDDAAVTLLEQAASQLDPEQ
PMTVLASLPTREDLHQAMVRWCPRRLATPTREFPLVVHRKAAQFSAWYEFFPRSIGAERH
KDGSWTSGTLASSEEMLEHVAAMGFDVAYIPPIHPIGHSFRKGPNNSLTAGPNDPGSPWA
IGSADGGHDAVHPDLGTLEDFDHFVARARELGLEVALDFALQAAPDHPWATQHPEWFTTR
PDGSIAYAENPPKKYQDIYPLNFDNDPAGIYAEVLRLMEFWIGHGVTIFRVDNPHTKPVS
FWAWLAAELHSRHPEVLLQAEAFTRPEMMHALAKVGFHLSYCYFVWRTTKQELSDYLNEL
AHETESFFRPNFFTNTPDINPKFTRSGNPAAFAIRMILAATMSPAWGVYSGFELFEHAAL
VDGGEEYLDSEKYEYRPRDFTAEPNLNQLMTKLNRVRHDHPALQQLNHTTVLETSSDQLF
AFAKRSGDDRVIVVVNLDPDNTVEGTVYTDLGALGLPADAHLVAHDELTDTVFDWNAAHY
VRLWPAQPAHILTISWA
>PFR_JS14_1178	PFR_JS14_1178	Maltose alpha-D-glucosyltransferase	1347117:1348916 Forward
MTSDQHSETPPIRALLGEDEERTADARAKLEMALSLTQPTGAVDPHDTSWFETAVFYEVM
VRSFADSSGDGIGDLAGLTEHLDYLQWLGVDCLWLPPFFASPMTDGGYDVADYRAISPDL
GTLSEFGDFIDKAHDRGIRIIIDFVMNHTSDHHPWFEESRRHPDGPYGDFYVWRDNPDGY
PDARIIFIDTETSNWTFDPVRGQYFWHRFYSHQPDLNYENPKVLAEMLDALRFWLGFGVD
GFRLDAVPYLVEEEGTNCENLPGTHDILKQVRKMVDEEFPGRILLCEANQWPHDVVEYFG
DNDECQMAFHFPVMPRLYMGVARHTREAITTILASTPPVPQGCQWATFLRNHDELTLEMV
TEDDRQYMWREYAPDPRMRLNLGIRRRLAPLMGNDPDKIRLMNAMLLSLPGSPVLYYGDE
IGMGDDIWLHDRDGVRTPMQWTADPSAGFSTATPDKFFLPLLADPYSPQQVNVTDQMADP
GSLLVWMRSMLTTRRQFPVFGRGEFIDMGGQNDAVLSFLRVLDDDKHGSQRLLCLNNLSP
EEQDVLLYLPDDAGTKPVSLLTSQAMAPIAANGEFHDTLPAWGFAWLDLSKGSDEHESE
>PFR_JS14_1179	PFR_JS14_1179	Maltokinase	1348932:1350269 Forward
MVAPNDDPRWRYASTARWFAGKGRGGVARRIEALDWYRAPEPGHPGVRSEIITIAYPDGA
HDYYHLPISYRTAPLSDALIGPADDPQLGYAHDATRDPEAMELLIASLGRRVNSGDWSAM
LPRGDRLTGPMPARPFTGEQSNSTVFLGSTALVKFFRHLEVGNNVDIQLHEALGRYRVRD
VDELYGWVTAHFRAISGRAVHADLLMITEQLKTLGEGWPMAVESATADTDFSAHAAGIGR
ALAHVHLALVQAFPPVMLKGDDVADGMVARLDRAIEAVPALSDYRSMLVVGFNRLRGHRL
PAQRVHGDFHLGQTLLTPGGWRIIDFEGEPLRPLADRTLPDSVWRDVAGMVRSLGYAAAQ
DGSPDAPARQHWLQRSQAAFIAAYLEITGVHDQVDLLDAYVADKAIYEVVYETRNRPDWV
HIPMAAITSWHEHQFQAPRGRTHHA
>PFR_JS14_1180	PFR_JS14_1180	1,4-alpha-glucan branching enzyme GlgB	1350262:1352166 Forward
MHDKFGNLTGTDLEGFHSGGDTEAWRRLGSHVVTVHDDARGDLSGTRFAVWAPNAQRVQV
IGDFNWWQGDDMEFVPGSGVWGLWKEGVGAGARYKYKIQHRDGSWQEKADPFAFSTEVPP
ANASVVFEREHAWAPSEESWLAHRAQADPYHSQMSIYELHVGSWRKGLDYRQLAQQLPAY
LTWMGYTHVELMPIMAHPLEASWGYQVTGYYAVDPRHGSPDDLRVLIEALHAAGIGVILD
WVPGHFPKDDWALGRFDGTALFEHADPRQGEQLDWGTYVFNFGRNEVKSFLISNALFWVS
EFHIDALRVDAVASMLYLDYSRPPGGWVPNKYGGRENLEAIDLLRYINRHLYRRQPGVMM
IAEESTSFPKVSAPVDVGGLGFGFKWNMGWMNDSLEYIKLDPIYRQYHHNEMTFAMVYAY
SENYILPISHDEVVHGKGSMVNKIPQDDWRKFATLRSFYSFMWAFPGKQLLFMGQEFGQR
SEWNEAVGLEWWVDSLQWHKGLRDMMREINHVQARTPALYELDSEPEGFRWINDNDWMAN
TFSWLRFDRQGGMVACVANFSPEPYPEYGLRVPRAGRWREILNTDEQRWDGSGEAANGTR
IAQPVDGEEGAELVISIPPMAGVWLRFEPEATDS
>PFR_JS14_1181	PFR_JS14_1181	Hydrolase, NUDIX family	1352202:1352987 Forward
MDDFKVNVVVDAGIGTLHWQGTVDQKTLDEAVSLAADDALIGHELHRVEASITADDLMAM
RALHRAGFRREGRRRQAVRADDGSWHDALLYARLIDDQVYGAGGFTAVMDTVMATHRLIG
HVLIRDERGRVLFVETTYKEDWELPGGIVEAGESPRVGAERELREELGVDIRLNQPLVAD
WMPPYLGWRDAMEFIFDGGQLPSSTVQRFERPAQEIRSYHWVAPEEIAEHVTPLSARRLA
LLVAGIAPAYTEAGSPVTPDA
>PFR_JS14_1182	PFR_JS14_1182	Phosphoglucomutase PgmA	1353102:1354733 Reverse
MADPRAGQPAQPSDLIDVDALIAAYYDKRPDPTNPDQQVVFGTSGHRGSAFDTAFNEAHI
AAITAAIVEYRASQGTTGPLYLAKDPHGLSLPAWKTAIEVLVAAGVHVLAEAEDEYTPTP
ALSRAVILHNRGRERDLADGIVVTPSHNPPRDGGFKYNPTNGGPADTDATGWIAGRANEL
LGNLEGIKRIPYERAKGQVEHFDYRSRYCEDLRNVVDIEAIKASGLHIGADPLGGASEQY
WEYIGEHMLPNLSVVNKVIDPTWYFMTLDTDGQIRMDCSSPDAMASLVAKRDQYDIATGN
DADSDRHGIVTPDGGLMNPNHYLAVAIQYLFGNRPRWASNTAVGKTLVSSTMIDNVAGLL
GRSLYETPVGFKWFVPGLISGELGFGGEESAGASFLELGGKTWTTDKDGLIMDLLAAEIT
ARTAKTPSEHYRELEARFGTYYYARIDSEADRAQKARLKALSPSDVTATVLAGDPITHIY
TNAPGNDAPIGGVKVTTEAGWFAARPSGTEDKYKIYAESYRSAQHLGELQDGAREVVSDA
LKG
>PFR_JS14_1183	PFR_JS14_1183	Thioredoxin	1354865:1355857 Forward
MSQPLTPRQPSGPQGPARGQSSAAPQGHAPSAHSDFSRPGAIDLSKIAATSPAAPQPGQA
GASTGSYVVDVTEAELNDVIQQSVNYPVILALLSANDPGSNQLRSMLTRLADESAGRWLL
AVVDIDTQPRIAQALQVTAIPTVLALLAGQAIPLFQGTADEAQVRGVLEQVMASAVANGV
AGHVKPVSHGEAGPDPRFAAADTAMEAEDYDRAADEFGKLLAANPKDSEAAAGQATARLM
SRAANADPEATLAAAKAAPDDVPAAMAASDVDMIAGRPKDAFGRLIGLIRTTAGDERDAV
RTRLLELFETMDQADPELLAARRALGAALY
>PFR_JS14_1184	PFR_JS14_1184	4-hydroxyphenylpyruvate dioxygenase C domain protein	1356089:1356535 Forward
MSNEDLFICIDHVAYACPDADEASKYYQETFGWHELHREENPEQGVVEIMMAPAAKLTEH
MTQVQVMAPLNDESTVAKWLAKHNGRAGLHHMAWRVDDIDAVSATLRERGVQLLYDEPKL
GTGGNRINFMHPKSGKGVLIELTQYPKN
>PFR_JS14_1185	PFR_JS14_1185	Putative phosphate acyltransferase	1356691:1357266 Forward
MMRVRQAIARIGWAISPYQLVGRELTSEPGVVLGAPHTSNWDFIAFLGVSWYYRVPLKVL
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VKKSWMRGPLWALGKALGAVAVDRAHPGQVVDHLVAQAEQGHSFKLVIAPKGTRSPRQYW
KSGFYRIALGAGLPVTLAGIDAGRRQVEVGPTIRLTGDVHADMDRIRAFYDRFDGVHPQL
RSDPRLREEDS
>PFR_JS14_1186	PFR_JS14_1186	Hypothetical protein	1357425:1359218 Forward
MSQYDDSHTGDDQSEETGLNLFDDRASAAGSFPHAMMGYDRSTVDNYVRDLEQRLSAARQ
LNRDRLRDLESLKSEQGTTDFTRLGAHATNLLRAAEAQADDLVTKAGVEAERIKEEGRRV
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QEAEQQAEISAHKADDAAKASEQQNQQKAAQTALEAKNRAQEIEAQAHIQAEQILAGARR
DGEATKAKAQQALTDAHAQADQVLADARREADATRAKAEAALADAHAKADEILADARNEA
QATKANAESTLADAHTKGEEILADTRREADATKASAQSQASELVDKGKQEAADVRAQGQA
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VGPEGQQSGGHEDDQQWLAHSGDNGATNASPDEETTMLKTKDPQGEPRSSRRNKKSR
>PFR_JS14_1187	PFR_JS14_1187	Endonuclease NucS	1359259:1359906 Reverse
MAKRLIIIKSDGSVAVHSDDRAYKPLNWMSPPCTLTVLDAPQDLAATTADLDAEIDQVWM
VKARNGDILQIAIAEIIDDHEYDLGIDPGLQKDGVEAHLQALLAENPQTFGKGYRLVRRE
FPTAIGPVDLLLRSDDGGYVAVEVKRRGEIDGVEQLTRYLELMNADPLLAPVRGVFAAQL
IKPQAKVLASTRHIDCVTVDYDALRGIDNAEERLF
>PFR_JS14_1188	PFR_JS14_1188	Hypothetical protein	1360063:1360341 Forward
MGHHRPSKHLRAARPLNVGAMRTAVQKYDGRWIVQQIVAGRSVKEYRCPECNRMIPAGTA
HVVAWLETPPIGATSPVEFRHHFHTSCWNRRP
>PFR_JS14_1189	PFR_JS14_1189	Abhydrolase domain-containing protein 11	1360338:1361168 Forward
MNQSSGSLHVTTIGSGPATAVFLHGLLGQGKNLAGAAKALDGVATSLLIDAPNHGLSPWT
GEFDYRAMGDAVAAELEQRGAAGKPVVLIGHSMGGKTAMCLTLDHPELVEKLCVVDIAPV
TYSHSKFFTDLISAMRGLDLAALGSRRQADQSLAPQIPDPVIRGFVLQNLHHGPSTPAPG
DRGPETWHWRANLALLARALPQMEAFPDFAGRHWDGPTLWVSGGRSDYVQPAYHAAMRAL
FPRVELVTVPGAAHWVHADEPAEFGQLLRNFVTHGE
>PFR_JS14_1190	PFR_JS14_1190	ATP:cob(I)alamin adenosyltransferase	1361247:1361855 Forward
MVNITRVYTRTGDAGTTRLSNNEVAPKTDPRVQAYGQVDETNCTIGVALTLDPSDDMQKV
LAIVQNELFDVGADLSSPVVADPKFRPVRVDQTSVDRLEKWIDEFGEDLPALRSFILPGG
SPLAAQLHVARSTCRRAERAAWEAVEAFGGEDGSSEPKGGVSLIAVKYLNRLSDLLFNLS
RHANYEAEHDEVLWVPDGEREV
>PFR_JS14_1191	PFR_JS14_1191	Lipoate-protein ligase LplJ	1362028:1363092 Reverse
MAEAALRGEYKVRGGKLVAVDLEIVDGRLARVHVSGDFFLEPDDALDEINAALEGQPANA
SVADLAAAIRARLSPDARLIGFDPEAVGIAVRRAVRGALGWNDLTFEVMGPKVMDPTLHV
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GAMFMEQGNCITYSMVVPGSLVEGLSYEQSYAYLDDWVLGALAEVGVNATYKPLNDIASD
KGKIGGAAQRRLVDGTVLHHVTMSYDIDADKMMEVLRIGREKLSDKGTKSANKRVDPMRS
QTGLPRDEIFTRFLAYFKNRYNCVDSDYTPEEMARAQQLVDTKFNTPEWTYRVP
>PFR_JS14_1192	PFR_JS14_1192	Hypothetical protein	1363116:1363574 Reverse
MIAALEIVAVVLALAVVAGLGVLIARRQWLLSREGIFSCEVRQRLPRNGSRWVPGVARYS
GNSLLWYKMLSASFRPTLVIRRRGARLMDHRAPSPQDGLLAVNSHRIVRLEVHTPGGAEH
VMELGLAPESLMGLMAWLEAGPPGGESYREFD
>PFR_JS14_1193	PFR_JS14_1193	ATP synthase F1, epsilon subunit	1363616:1364083 Reverse
MPNLLQVEVVAAEGKVWEGQAVSLIARTTEGDIGILADHEPFMAALVPSAVQVTTPEGID
EIIAVSDGFISVFRNRVSLLSSFAELAQEISVEQARVTVANLHERIDSSEATTDEAREYN
RALAQLRAAGQYQAKMKGQSYSEITPQPAKIAPGD
>PFR_JS14_1194	PFR_JS14_1194	ATP synthase subunit beta	1364083:1365534 Reverse
MTATQTAPEDAGTAGTGHVVRVIGSVVDVEFPSGRLPEIDNALHVSLDSGDGSTTITMEV
ALQVGDNTVRCISLKPTDGLRRGTEVVDTGAPIKVPVGDVTKGHVWNATGDLLNADPATV
KIDERWSIHREPPAFDALEPESQMLETGIKVLDLLTPYVQGGKIGLFGGAGVGKTVLIQE
MIYRIAHNFGGTSVFAGVGERTREGNDLIHEMEEANVLKDTALVFGQMDEPPGTRLRVAL
SALTMAEYFRDVENQDVLLFIDNIFRFTQAGSEVSTLLGRMPSAVGYQPNLADEMGQLQE
RITSTRGHSITSMQAIYVPADDYTDPAPATTFAHLDATTELSRDIASRGLYPAVDPLSST
SRILAPEYVGKEHYDVATEVKQILQRNKELQDIIAILGIDELSEEDKIVVGRARRIQQFL
SQNTYMATKFTGVEGSTVPVAQTVESFKMIAEGKCDEIPEQAFFNVGDMDDVNKKWDQLK
KEG
>PFR_JS14_1195	PFR_JS14_1195	ATP synthase gamma chain	1365535:1366470 Reverse
MATSLRELKQRRNSVATTMKITKAMELIAASRVTKAQQRARNADEYTRELVRAVSTVAAY
TREDHRLTQIKEHPKRAAVLVINSDRGLAGGYPANVMRASEGLLKHLAEGGLETDIYTVG
RRALDYFNFRHVPIKQSWQGFSEDPHYANAHDIGRVLIDQIMKDTEAGGVDEIHVVYTRF
LSLVSQRTELVRLLPLQVVRDQEETAHAGDDVVSDNAEIAPPYNFEPDAETVLDALLPLY
VIDRIKYMLRESAASELAARQQAMHSATDNAQQLIDTLTRQANTARQAEITQEITEIVGG
ASALSESTQEM
>PFR_JS14_1196	PFR_JS14_1196	ATP synthase subunit alpha	1366473:1368110 Reverse
MAELSISSDEIRDALDTFVHNFTPTQAAPEEVGHVTTSGDGIARVEGLPNVMANELLRFD
NGTMGIALNLDEREIGVVVLGESEGIDEGSIVRGTGEILSVPVGDGYLGRVVDAMGNPID
GKGAIDGIAGRRALELQAPGVMDRQEVTEPLMTGLKAVDSMIPIGRGQRELIIGDRKTGK
TAIATDTIINQLDNWRSGDPKKQVRCIYVAVGQKNTTVAEVHENLRKAGAMEYTVIVNAP
ASDPAGFKYIAPYSGSSIGQHWMYEGKHVLIVFDDLTKQAEAYRAMSLLLRRPPGREAYP
GDVFYLHSRLLERCAKLSDELGAGSMTGLPIVETKANDISAYIPTNVISITDGQIFLLSD
LFNANQRPAVDVGNSVSRVGGAAQTKAMKKVSGTLKIDLAQYRDMQAFAMFASDLDATSR
RQLDRGARLTELLRQQQAQPLRMEEQAVSIWAGVNGKLDDVPVDDVLRFESEFLEFLRES
TDLLTTIASSGALSDETVASLDDRIASFKQTFRTSDGQLLAGARDSEKVGNEDINQAKIV
ATKRS
>PFR_JS14_1197	PFR_JS14_1197	ATP synthase F1, delta subunit	1368185:1368964 Reverse
MTNVNGTRIERLDEAADKIVATSFLSTELFALVDELNAQPDLGRALTDPALEAEGRGKLA
GALLGKRLSGPTVDFVVQALALDWASGREFTSGLGRQAIRIALRSTDADQVRTELNVVRE
TLATHDELRVAMAGHTAGEEARAKLVDQLLGDKVDPVTAMLVGRAVRDGEHVQDALWSCM
ELASQVLGRILARVTVARPLPAYQMAELGEQLRRLYGQPVDMAEHVDPSVLGGVRVELGD
DVIDGTVATKLSEAQRELA
>PFR_JS14_1198	PFR_JS14_1198	ATP synthase subunit b	1368961:1369515 Reverse
MTPNGLVPHIDLGPLLPELPEFLAGLLLLGLMWIIVAKAVAPRFEQLYEKRSSEIEGGIQ
HAEQVQAEAAKAREQYQAQLSEVRESAAKAREDAKTRSAEILRDAKNEAAQEQARMIAEA
RAQIASEREIAAGQLTTQVGGLATTLAGRIVGESLDDDERAKRTVERFLKELENQPARNQ
TIGK
>PFR_JS14_1199	PFR_JS14_1199	ATP synthase C chain (F1F0-ATPase subunit c )	1369526:1369744 Reverse
MTPLEISGSLNVIGYGLATLGPGIGVALIFAAAIQGIARQPEARGYIMTPVYIGFAIVEA
LAILGFVLAFIK
>PFR_JS14_1200	PFR_JS14_1200	ATP synthase subunit a	1369790:1370671 Reverse
MSNEATVVDAPETSKGHPVAIVVTMLVVWIALTFLAERIGGGVSSWHAPSQEDFEFSGWF
GTTWFNKPMLLAIIGFVGVLAYWLIASRRLKVIPSKAQFFAEYVYDFVRNIGRDMIGPGY
RRFTPYLLTLFSFILVSNWFGETFVFMFPTFSRVSYAYAGAILTFLAYVISGFAKHGLGY
LRVALIPSGVPPWLYPVIIPLEFLSSFITRPLTLSVRLFANMFAGHMSIMVFVGGGAALL
GWVHNSFYNVTGVFALLFGVAMLCLELFIGFLQAYIFTILAAQYIGSSVGAAH
>PFR_JS14_1201	PFR_JS14_1201	Hypothetical protein	1370664:1370888 Reverse
MSEPVEHDEHPDQAQPGSGLQSVSYLLAGIALYGGLGWLADKLFNTVWFLPAGLLIGTAA
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AVYLIVKRFGGRHE
>PFR_JS14_1202	PFR_JS14_1202	Hypothetical protein	1370885:1371322 Reverse
MNPSVNSAWLRSMTRRGLLFAMVCAVPAGVVNGIVGGLESVIGWLLAVGLVGLYFIAGVV
GDALAVRRADAFGMTMLLAGFLVRAAAVALVLWLLASHGLLAGANRGNGFVWTVLAMVIG
WTAGLVDAHRRARLPIYASVGRETP
>PFR_JS14_1203	PFR_JS14_1203	Glycosyltransferase, group 4 family	1371400:1372536 Reverse
MREYLLVMLTAFAATYLFAGLCRRVAIRTGALAPVRERDVHATPTPYLGGVAMLVGVGAA
FLLAAHMPFLGRHPTVSRDALGIFLAALVICVIGAIDDAIDLPWMAKIAGQVLAAGVAVL
NGVRMYWVSLPHQIFALDEPTSILITVLYIFVCVNAINLIDGLDGLAAGVVGIGSLAMFV
YTYLLAYQQQFVVATTASLVTATIAGICAGFLPHNFFRAKMFMGDSGAMLLGLLLACSTL
SLTGQIDSSALTPSRGDALPALLPIVLPIAIMALPLIDMTMAYIRRTWNGNWWFVADKKH
LHHRLLQRGHSQIKAVLIMYMWTAIIAFGVIALGLAWYWPVILAVAVAIAIAIVLTVVPM
RQPKSPARRLVEPKPVER
>PFR_JS14_1204	PFR_JS14_1204	TRNA threonylcarbamoyladenosine biosynthesis protein YwlC	1372545:1373423 Reverse
MTHVSGAQTNKTDQMGQGTSAASPQEGGSGEESFRRFDLATQRDQALRTAQAAVGAGQNI
VLPTDTVYGIGADAFSADAVQGLLNAKHRGRDMPPPVLIAEPAMLPALVSSIPLGAERMI
KECWPGALTLILNAATALHMDLGETAGTIAVRVPDNDDARALLLHTGPLAVSSANISGQP
SATDVGAAIAMLGDSVAVYLDGGRTPGPVASTIVDFTVAPAGRILRQGVIGFDQLEGLSP
GLEDLVTEQVQADQAAAATPPASSPDVPSGSGPSGTPDSSADAGAGSGSGQD
>PFR_JS14_1205	PFR_JS14_1205	Release factor glutamine methyltransferase	1373420:1374298 Reverse
MSTHRPAALIKQGINELTSAGAQSPRAEARHLLAAAADLDPAGLATTREVDDAVADRYAD
LIRRRAAGEPVQYLTGRAWFRKIDVQVGPGVFIPRPETEAVVHFALDQLLNLRADTGPSP
VIVDLGTGSGVIAKSILSEYPGTPRMYAVERSPQALEWARRNLADTPATVVAGDMADALP
QLEGKVDLVISNPPYLSAAHADELPADVLDYDPHEALFGGDDGLETIRGIVPVATRLLRP
GGWLIVEHDDMQGHSAAGIISAAGRFEHVEDHPDLTGRPRFVTAIRRNDVGQ
>PFR_JS14_1206	PFR_JS14_1206	Peptide chain release factor 1	1374295:1375374 Reverse
MFESAQGLRQEFADLEKQLADPAVVSDQARSRKVGRRYSELTGVVHALDEHQQLTEDLSA
ARELADDDPAFAAEADQISARLDEVTDKLTALLAPRDPLDSNDAIMEIKSGEGGEESALF
AGDLLNMYQHFAEREGWSTEIIDAEPTDLGGFKSVTLAFRATGHDAQAPYGALKFEGGVH
RVQRVPVTESQGRIHTSAAGVLVMPDVEESEIEINPDDLRIDVYRSTGKGGQGVNTTDSA
VRITHLPTGVVVTSQDQRSQLQNKEQALRVLRARLVAAAEEQAAQQAEQARKSQVRTVDR
SERIRTYNFPENRITDHRIGFKAHNLDAVLGGELEPLIEALQAADLAERLGQATESEKQ
>PFR_JS14_1207	PFR_JS14_1207	50S ribosomal protein L31	1375482:1375706 Reverse
MKNSTHPEYHDVKVVCTCGNEFTTRSTFPGDVMSADVCSNCHPFYTGKQKILDTGGRVAR
FERRYGKAKAAATK
>PFR_JS14_1208	PFR_JS14_1208	Transcription termination factor Rho	1375843:1377813 Reverse
MSETTQAVAENGPADPMSTLSAMRLTELKQVAAQLGIRGVSAMRKGDLINAIDSRRGGSG
AQPVQQQPTRHEEGPAERRTRSASRASREATGEEGPARDVSTADAIAARLEAAEHSSGRS
RRERNTDSESGTATERTTDNDRGGRSERNSTRTNNSRSDGARNEGSRTSNQGIDDEVGAR
LEQLSGRGNRSEKNERKRDERPERHHNQSNRNHSESTRNDSNRNDSNRNDSGRNDSGRRD
DDEYSGGRRSRRRRQRDRQGRRSNRNSPMNEMETPTVQEDDVLVDVSGILDVLDNYAFVR
TSGYLPGPNDAFVAMGMVRKNGLRKGDVITGAVRQPREGERHSKYNPLVRLDTVNGAGPE
AMRERPDFGKLTPLYPQERLRMETVSTNMTGRIIDLVSPIGKGQRGLIVSPPKAGKTMVM
QNIANAITVNNPEVHLMVVLVDERPEEVTDFKRTTTAEVIASTFDRPADDHTTIAELAIA
RAKRLVELGRDVVVLLDGITRLGRAYNLAAPTSGRILSGGVDSAALYPPKRFFGAARNIE
NGGSLTILATALVETGSKMDEVIFEEFKGTGNMELKLSRQLADKRIFPAVDVEASSTRRE
ELLMSRQELDIIWKLRRALSGQKEQQALETLLSRMKKTRNNSEFLVLISSTTPGSD
>PFR_JS14_1209	PFR_JS14_1209	Phosphoserine phosphatase/homoserine phosphotransferase bifunctional protein	1378207:1378830
Reverse
MHIACLDLEGVLVPEVWINVAERTGIDELKLTTRDISDYNELMDHRLAVMAKHGLTLSAI
KKVIADMGPLPGAKEFLDWLRARWQVVILSDTFYDFADPLMEQLGRPTLFCHSLVVRDDM
VVGYQLRQPNGKYEAVRAFQSLNFTTLSTGDSYNDTAMLNQADYGALFNPPANVIAEFPH
LPVAHDYEELKEQFLAASEQLESGLQA
>PFR_JS14_1210	PFR_JS14_1210	Homoserine dehydrogenase	1378839:1380164 Reverse
MNQDARVTAPTRVLRVALLGCGTVGRQVAGTLLDKAEDLAAKAGCHLELIGIAVRNVNKP
REGIPPELLTDDAAGLVANGGADIVIELIGGIDPPRELIVSAINHGASVVTANKALLAAH
GEEIYAAAEKNRVDIYFEAAVAGAIPIVRPLRESLVGDEIRSVMGIVNGTTNYILDKMTN
DHQDFEEALATAQQLGYAEQDPTADVEGYDAAAKAAILAGLAFHSPVSGSDVFREGITSV
STADIEAARASDCVVKLLAIAKIDEHDRISVRVHPAMVPYSHPLAMVNGPYNAIFVEAAN
AGRLMFMGPGAGGSPTASAVTGDLVTVARNRMRGVVGPAHSVYQAHQLAPMGETRTRYYV
RFRVADQSGVLASVASLLAKHHVSVHSIRQTPIEDGREAASARVSMMTHEAQESDMMVCL
EELEKSDYVLGSVRLMRAEGA
>PFR_JS14_1211	PFR_JS14_1211	Diaminopimelate decarboxylase	1380175:1381569 Reverse
MHVAGAIHADVSTPGPQWLTKPADLNELDPALWSRNVSRDEHGRVGVAGIDVVDAIEREG
SPLYLFDEDDFRHRARDFKSAFDGWNVYYAGKAMLTRTIARLVMEEGLGMDVCSGGELQV
ALAGGMDPARIGMHGNNKTSDELALALSNGVGHIVVDSLDEIGRIEQLCRDNDWHARVMV
RVTPGVEAHTHEYIATAHEDQKFGFSIANGQAMVAMVRCHYSPYMDLLGIHSHIGSQIFD
TGGFEVAALRTMKLSSQFTDATGVHLPELNLGGGFGIAYTSADSPSTPDALATGLREIVE
HEARAHSMAVPKMSIEPGRAIVGPTTMAVYTVGTVKVVDLDGGGQRVYVSVDGGMSDNIR
PALYGAEYSAVLANRTSSEPGVLSRVVGKHCEGGDILVRDVFLPSDIEPGDLIAVPDMGA
YSREMASNYNHALRPPVVRVHNGELSAMIRRETMDDLLSLDVGR
>PFR_JS14_1212	PFR_JS14_1212	Transmembrane protein dedA	1381930:1382700 Reverse
MSAPPCHDGNFPANGGHDGNWWLASDGGWVMDLSGFFFGLPAGWAYVLVGLVVGLESLGV
PLPGETILISVVLLTHHPDAGFSAWGIGIAASAGAIIGDSIGYTVGRRLGPRLFGWLGRR
FPVQASAVRLAYAEHLINRFGVTAVFFGRFIALLRMFAGPLAGSLRMSYRRFLIANICGA
VAWAGGTTALMWALGSVASHWMSRVGWILLVAVILVGLVVGHVSGSALSAKARDWARDHP
DEVARATGVRDELPGA
>PFR_JS14_1213	PFR_JS14_1213	LigA	1382805:1384223 Forward
MGPSGADMAELPVTSAGATAATPARFSTRMSRQFTLSFTRERLRSAKFLLFFWFAARFLI
LATWAFITPATQGDVVYYYQKIQVLFSDGPANTLQEYPTPVIWVLLIPYLIGFGNEHGYV
IAFVCMMLALDALFSWSLWHSGGSMGGQAVVFWTLFLAMVGPTAFLRFDLITSVLAGWSI
IFLLRRYSAAAGGLTALGASVKLWPALLWPALLPGPARQKFRATAGFLLTGMAMVGLSLL
YAGWDRLLSPLTWQQGRGLQIESVWATLPMLARTVNSDNYAVTLSRYQAFEIWGPGVNTL
LSASDIFFAGGLAVAVLAYLVWLWRGHGRLIEAVVLVQFVIIVMIVTNKTFSPQYMMWLG
GPQAAAFAVLGTRSHHVEEFYVDRSRLNTLSVWILVATFLTLLVYPISYDFLVNDWNVRD
SLLRFPATLLLAARNIVVVIVLIDVIRWVWSFLRPRAVKAVRQRRRGVEAPQ
>PFR_JS14_1214	PFR_JS14_1214	LigA	1384364:1385659 Forward
MPRVRPNGWWAVVAWIVSRSLMACLFINLGSYLRSDVIYYFTSVQGASPMHLAGVLSEYP
VPIVWLIQLLAAISGPSADVFVFVFAATMGGLDAACCRWLWRHSPRACSLWIAFTFLIGP
LIWFRIDLVPAALVLAALTMTTRRPAWSGAAVALGAATKLWPALLIVPLAGTRRSARRRA
GGFLLVGALIGTAVVVSQGLARSASPLTWQATRGLQIESVWATLPMVQRLVSPDDSWSVA
VSSFHAYEISGPGVAGWLQVSSAATAALLALTALLGWLIALDGMGLPGHRRALPADPDRD
AQRHEAMLWALLAIIVGVIVANKAFSPQYMMWLAGPLAMLWADGTRPGSRRPAGRVTIMA
LAAAGLTQLVFPLNYTALVGDHPGGFVTTVLVARNLVMVSLALYCTRHALRAAWRVGLRS
DPAPDSGRELV
>PFR_JS14_1215	PFR_JS14_1215	Hypothetical protein	1385652:1387058 Forward
MSESNTPSGSNAPGPTAASADNRSTTGVTVTIGPPAIADAGTGSWVARFPLLVAFWALSR
VVMACIFMTDLCSYIRNDVLYYGTAVAGSPLPLLGRMTNVLDEYPTPIVGFLQVINALAS
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GSTSTFVSVFVLVLCLADGFAVAALFFRESPRAGWVWAAAGLLLGPLLWFRLDLLPALAV
LGALHWMDRRPRLAGVMIALGAALKLWPALLIIPMMGRGRRARSRTLGFVVAGLVLGLGS
LLTQGWARSASPLTYQGDRGLQIESVWATVPMVRRVISGDSGLTVFFSQYKAYEVSGPGV
AGWIQVSGLLLVVMIVATVALGWLIGLRGVGLRGHRWAAPGEKDLGAIDWAIQLSLLAII
CGVIVANKTLSPQYLMWLFPSLAIITARARGERQRRVVRRILAFAATSLALTPWVFPLGY
SGLISSTPNAGVTWLLVLRNLGLVTLTAYSWFEAWRAAVRSGVFEPEL
>PFR_JS14_1216	PFR_JS14_1216	Oxoglutarate dehydrogenase (Succinyl-transferring), E1 component	1387128:1390898 Forward
MGTDKFGANDWLIADMRQRYLADPTSVDERWRAYFQALGVTPDPSTPVASPAPVTPAPTQ
APTPQAPTSSAPGPNEPAQPPSSRVQAPVPTLEPREIRRNAPEQPGMGGGLSADVPNPAV
RPAKKAEGQATRTVLRGIPKTTAVNMNESLSVPTATSVRQVPMKLVIDNRALVNSFMART
RGGKVSFTHIIAFAMVQAIRDVPEMNHSFDMTDGKPTLVENPAINLGIAIDTTAKNGTRE
LLVPNIKDAGSLDFAQFWSAYEDLVDRTRSGKLTLEDYAGTTVSITNPGGIGTNMSVPRL
MSGQAMIMGVGSIDYPAAFQGTSTQRTNDAAISKVCTLTSTYDHRIIQGAVSGEFLRRIH
QLLLGADGFYEHIYEALRIPYPPLHWDRDFTANSQSEISKGARVTELIQAYRAEGHLLAD
LDPVEYRMRTHPDLDLATHGLSIWDLDREFPVGRFGGEEGRHIVLRQMLDILRESYCYTL
AIEYMHIDDPEERAWVQERFERPRKPRPREEHLLILDRLSEAEVFETFLQTKYVGQTRFS
MEGAESSIVILSELCAAAADGGMAEVSIGMPHRGRLNVLTNVVGKLYSQVFREFDNKVPT
EEDITGDVKYHLGATGQFTAMSGEKIKVSLAANPSHLEAVDPVLEGIARAKRDRQPVPAD
YPVLPILMHGDASFSAQGIVYEVLQMSQLRPYRVGGTVHLVVNNQLGFTTSPSDGRSSKY
CTDVAKALGAPVIHVNGDDPDACARAAELAFDFRARFHKDVVIDMVCYRLRGHNEGDDPS
FTQPQMYDLVARKGSVRKIYTDALIGRGDISVEDAEQAVNRFRARLEEVFSMVRNPQIPR
DEVDHQVAYRLAPQYPAKERAASAPPTPTREQFERVADVYENLPEGFTPHPKVGPQLKRR
ADSIHNGPVDWATAELLAFGTLLQDRRHVRLVGQDTRRGTFSQRFGAVVDRVTNEAWVPL
KHLSDDQAPFDIYDSNLTEYAGMGFEYGYSTAAPDALVLWEAQYGDFANGAQTIADEFIS
SGFAKWQQRSGVVLLLPHGYEGAGPDHSSCRIERWLQTADEGNIAVTMPSTAASYFHLLR
QHAYVNWHRPLVVATPKSMLRNKAAASPLSDLLDEPWRPALADPTITDPGAVRRVLLCAG
KIRWDLVAERRKLGLDGQIAIVSLEQLFPLPTAELAEILRAFPQVNDFRYVQEEPENQGA
WEFMDRFLTPALSEALNRPFRMRPVTRPRSSAPSVGSHTVHLAQQRSLLAESLGQD
>PFR_JS14_1217	PFR_JS14_1217	Transcription factor WhiB	1391143:1391391 Forward
MDWRHKAACLNEDPELFFPIGNTGPALAQIEEAKKVCQRCEVREECLAWALEAGQDHGVW
GGMSEDERRAMKRRAARSRRSA
>PFR_JS14_1218	PFR_JS14_1218	Sensor histidine kinase	1391496:1393004 Reverse
MVSMNRVLADHTVLDEDDREWLTSLVREWHLLADMRFSDLVLWVPDEDENVFWVAAQQRP
VTGPTALEDDVVGDEIRYEPDSLVTEAFMSREVSETSNNRLRAGIPVDVWAIPILRHGDV
IGVVERHTNRMGVRAPGAMEDYYLEIADILTDMVHHADYPVSPASDPSMSPRVGDGLIYA
GMDGAIKYASPNAVSAYRRLGMVGDLVGEDVHHPAPDSLRVSIFAVSPHGEGTFADHESE
PSQSVFRTDIAGEYDLENDAGCIRARVLQLRKDGRQVGVLMLCRDITELRDRERELVTKD
ATIREIHHRVKNNLQTVAALLRLQARRTHSDEAKNALTDATNRVQSIAVVHEILSQSYDE
EAEFDQVADKLLQMVGDVAAASGTVRAKREGSFGLVPAKVATSLSLILTELCQNAIEHGL
ATHSGNVFVRPQRNAAGDLVLDVVDEGEGLPEGFQMGATNSLGTSIVTTLVADLGGEFTL
FNNADGPGATSRIVVPASTLSV
>PFR_JS14_1219	PFR_JS14_1219	Hypothetical protein	1393506:1393817 Reverse
MSEMGHGDFVSATDEHACEMALGSLQAFLHGELPEANADEIRHHLMICESCMNDFDIEEM
ISSMVKRCTGTPCASPALRTRITALSVEHRRSMSGGDVTTESA
>PFR_JS14_1220	PFR_JS14_1220	RNA polymerase sigma factor	1393810:1394397 Reverse
MRDTETDAERAERFERDAMVYIDQLYGAALRMTRNPSDAEDVVQETYAKAFSSFKQFRPG
TNLKAWLYRILTNTYFNTYRKAQRQPQTGSDDVEDWQLAKAASHDATGLRSAEMEALREM
PDAAVTNALEQLSDEFREAVLLADVEGFSYKEIAEIMGTPIGTVMSRLNRGRAQLRKLLA
DYARENGIGGDRNHE
>PFR_JS14_1221	PFR_JS14_1221	UPF0361 protein yoqW	1394538:1395290 Reverse
MCGRYALSADPDELVEVFDISEIAEDSGESLALTPGQPQADYPQWMRPRFNIAPTQTIPV
VVTRGQDHPVRKVAGMYWGLVPSWSKGPGSTRRMINARVETLDEKPVYRTALARRRCILP
ASGYYEWQHPADKSVPARPFYIEPADGGLLALAGLYDFWRSPQGSWLSSCTIITTEATGE
MAAIHNRRPVLLQPDAWGDWLDPSCTDSREALGLIAPLAAGLLSAHPVSRRVNSPRTDDP
GLTEPIMAGE
>PFR_JS14_1222	PFR_JS14_1222	3-phosphoshikimate 1-carboxyvinyltransferase AroA	1395438:1396790 Forward
MTEHVAGDRQTAADPRVTTSQGWPAPRARVPLHATVHVPGSKSEGNRALVLAALGDGPST
ITGLPDARDIRLMIAALRGLGTTIAPGDAHEVTVHPGPLHAATAPIDCGLAGTVMRFVPP
LAALVAGTTRFVGDDRAAERPIAPLLEGLRQLGAATSSDAIPFDLTAPDELTGHEVSIDA
SASSQFISGLLLAAAAFPQGIDLMHTGATVPSAPHIDMTIAMLARHGVRVAQPERGRRWV
VESGMIRAADERIEPDLTNAAVFLIAGVITGGSVAVADWPRHSTQPGALIGPVLARMGAA
FATGAGRATATHRDDLQGAELDLRPASELTCSVAALAVAARGTTTIRGVGHIRGHETDRI
AAIATELTRVGVDVAELPDGLRIEGMAGRLDQLHPSTGDGLFRCYADHRMAHLGALIGLM
VPGIRLDDVGSTTKTMPDFPGEWDRLVNAR
>PFR_JS14_1223	PFR_JS14_1223	Putative ribosome biogenesis GTPase RsgA	1396787:1397857 Forward
MSPRQTRGVIGRGTDFDSHDFGRPAKRTRPRTKRRPDYSEAPTARVITVDRGRYHLLLDA
PDSPRHLVAAKARQLGRGAVIVGDVVRVVGDTSGEEGTLARIVQVEPRRTELNRTADDTD
PYERPIVANADQLVVVTALADPQPSAGMIDRVLVAGYDAGVKPLICLTKADLADPTELVD
LYEPLDVPIFVSMPDSNLDELRAALAHHVTVFVGHSGVGKSTLINRLVPDADRATGVVND
VTGKGRHTSTSAIALQLPPFAGDPEAGWVIDTPGVRSFGLSHVSAETILEAFPDLMRFTA
DCPRGCNHHAGAPECGLDAALARGDLSAQRLTSFRRILEAVDGARADYSSVQERNH
>PFR_JS14_1224	PFR_JS14_1224	Putative histidinol-phosphate phosphatase, inositol monophosphatase family	1397911:1398726 Forward
MADRIDSTRSDLTADLLLAQRMASEADTITTGRFRASDLRVQTKPDHTPVSEADKGVEGM
VRATLATERPDDAVHGEEMPDTGWGSRRWIVDPIDGTANYVRGVPVWATLIGLMVDGEMT
VGVVSAPALGRRWWASKGHGAFAGPDFSRGTRLAVSAVGTVHDAFLSYSSLGGWSRDHRG
QAFAELLASCGRTRGFGDFFSYMLVAEGAVDLACEPDLELYDMAALVPIVTEAGGRFTNL
EGAPGPVGRGALASNGLLHDEVLNRLQRDDH
>PFR_JS14_1225	PFR_JS14_1225	PF14262 domain protein	1398780:1400513 Reverse
MNLSWQKRLAALAVAATLTGCGATTASSPTTTASAQAAATSVSSSAQSVLADNKDSHYKA
SDLDYEASSVVTVTLSGSSASASGPGVGIDGSTVTITEPGTYKVSGQLTDGRLVVNSTAS
GETRIILDGADITSSSGPAIDIQAADEVNVILADGSQNTLTDGSGYDTSADGAANAALYS
RADLTIAGTGSLSVDGRTNDGIASTDGLVIVSGTIRVQAIDDGIRGKDYVIVEDGTINVT
SGGDGIKSDNSQDSTRGYVDIENGTIAVNATAGDGVDATSDFVQTGASLTITTAGGSSSR
PSDSTDAASTKGIKAGAQLVISDGTDTITSSDDAVHSNDTVQIDGGTLKLSTGDDAIHAD
NALTTNGGTIDVTASYEGLESNAITLNAATINITSSDDGINASDGSGEADDPGAGSASNS
TMVITGGAITVDAGGDGLDSNGAMTISGGTIVVNGPTDSGNGALDTGGPLRISGGTLFAA
GSSGMAESPDTDSSQAWLQSELTASAGQSVTISTTDGTQIASYTVAKATGNIVFSSSAIS
AGSSYLVSVNGGSATTVTANQSTGNTMGGAMGAPGPR
>PFR_JS14_1226	PFR_JS14_1226	VTC domain protein	1400510:1401322 Reverse
MSRTITDLADIGLDELNRTAALQTRVDRKYLATPAEVRTFLGALPADSRVLTIAGIREFR
YVSVYFDTPGQDSYLASARGRRRRWKIRERDYLDSGMRWLEVKTCRGERTVKQRLQIDVA
ERGRWSAGDRHEMHRALSVCGMPSVPLDALAPRLNTSYLRTTLVEPGSGTRVTLDRRLIW
TSADDVRAVRLGELTVVETKSAGMAPGRVDHLLWSIGVRPHRFSKFATGLAILEPGLPHN
RWHSTIGHLRSRLREGRPETAAATMRSESS
>PFR_JS14_1227	PFR_JS14_1227	Conserved domain protein	1401319:1401954 Reverse
MTDLVALGADALMIVILTFAVYLPRHHRRDMVVAYLSVNVGVLAVSTALSVSSVAAGLGL
GLFGVLSIIRLRSEELSQIETAYYFSALALGLLGGVDVPLGYSVPLMALIVAVTCISDSR
WIGRGMQRQVVALDRAYPDAAQLRAALGERLGGRILSVSVQRLDFVNDTTLVEVRFRPGS
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RAGGAPDIAVDGRAPVPCAEREVPGAREAVA
>PFR_JS14_1228 PFR_JS14_1228 Exopolysaccharide biosynthesis protein related to N-acetylglucosamine-1-phosphodiester
alpha-N-acetylglucosaminidase 1402111:1403058 Forward
MTHLPSRFSRRAVLTGAGVAVAGGGAAWAAERFLIPHVENSDVAAAEAAASASNSSSTGQ
MAADRREIGTNYYRNGQTQLTIANHSSGNGSDALAWFVADLRMGDATVLRSAFANNQFGE
NITQDPSTIATAHDAVFAVNGDYYGFRDDGIEVRNGVAWRDKGTRQGLSLYRDGAVRLYD
ETATNAAQLVSEGVWNTLSFGPGVVADSQAVGGIDRVEIDTNVGNHSIQGDQPRTGIGYL
ADGHFALLVVDGRSAGYSRGVTLPEFAQMFVDLGARTAYNLDGGGSSVMYFNGSLVNNPL
GTGRERGVSDILYLA
>PFR_JS14_1229 PFR_JS14_1229 GtrA family protein 1403369:1404232 Forward
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LRGCPAPMLGWLCTVPGERFDYEFRVLLEARRAGWPLVEVPIATVYSQHNESSHFRPIRD
SARIYAPLVGHIARSGPGRLLVFGASSFGAFLVDLVLLLVLHAALGNLLVSVVGARAVSA
AANYLVNDRIVFARGAGRRATRTSLPRYALLAGVLLGANYGLMWLGTVPLHLPLVPTKLV
TELGLFAVSYVVQRTLVFRAARTRTTPSTPGRVKGVAARRTDVRVSG
>PFR_JS14_1230 PFR_JS14_1230 Putative phosphoglycerate dehydrogenase 1404222:1405415 Reverse
MKALLLENIHPEATRILTAAGYDVETRAGALSEEELVSALDGVNLLGIRSRTQVTDNVLR
RIPAGLNAIGAFCIGTNQIALPQCATKGVAVFNAPYSNTRSVVELAMAEIVAMARHLTDR
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STRGDVGYAVTDVTAATSGWEEDLAEVPNTISCRVIR
>PFR_JS14_1231 PFR_JS14_1231 Dipeptide ABC transporter ATP-binding protein 1405476:1406303 Reverse
MSDTPATPEFRVRGLRKGFEQGARSGYRHVQAVDGIDLDVMAGQRLGIVGESGSGKSTLV
RMLDAIIAPSSGEIRFRGQRIDGARERQLGELRSSVQMVFQDPRSSLDPRMKVGQIITEP
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VLIADEAVSALDVSVRAHVLNLFADLVSRHELTLLFVSHDLEVVRHVCDSVVVMKSGRIV
EHGSIEQVYEHPSQEYTRTLLASIPRLRATGPRGS
>PFR_JS14_1232 PFR_JS14_1232 Oligopeptide transport protein of the ABC superfamily, ATP-binding component 1406296:1407153 Reverse
MAGEPLLAVRDLRVDFGRRRAPALRGIDFDLRAGQRLGLIGESGSGKSVTALALMGLLPE
TAHVGGSIRWEGTELVGMSDGEYTKLRGDAMSMIFQEPMTALDPTMRVGRQVAEALRLHG
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>PFR_JS14_1233 PFR_JS14_1233 Putative oligopeptide ABC transport system membrane protein 1407155:1407970 Reverse
MRRASLVVGVGLLTVVVVFALVGLFWLPDDPVKVQAQQALLRAGGDHLLGTDGYGRDILA
RLMVGARSCLLVGVVSVAIGAIVGVPVGIWSGMSRPKVGRRIMQGSDILYAFPAILLAIL
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>PFR_JS14_1234 PFR_JS14_1234 Putative glutathione ABC transporter, permease protein GsiC 1407967:1408920 Reverse
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YRLLDPRLRDPDQERTL
>PFR_JS14_1235 PFR_JS14_1235 ABC transporter, substrate-binding protein, family 5 1408942:1410465 Reverse
MGFRVGRRPLIGAVLAGSMATLVGCSTSGSGSGASSQAHNLVIGTSVAPNALDPSTNSAA
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>PFR_JS14_1236 PFR_JS14_1236 Biotin synthase 1410851:1411996 Reverse
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>PFR_JS14_1237 PFR_JS14_1237 Hypothetical protein 1412159:1412449 Reverse
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>PFR_JS14_1238 PFR_JS14_1238 Prolyl aminopeptidase 1412616:1413830 Reverse
MTRSIRVDVPLDHINVLDGRRLSIFARVVALPGGTGRPYLLFLQGGPGHESPRPSLDPPT
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QEAR
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REHTLRMVICGDAGQLVGPLEADGFRVEPFAPIL
>PFR_JS14_1241 PFR_JS14_1241 UPF0182 protein 1416694:1419633 Reverse
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PALTSALARTFHWGENEES
>PFR_JS14_1243	PFR_JS14_1243	Lon protease proteolytic domain protein	1420348:1421391 Reverse
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>PFR_JS14_1245	PFR_JS14_1245	Similar to metal-dependent hydrolase	1423067:1423696 Reverse
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DRIVVMLPARMNHAEQEHWVAQMVTKVAARTPSRGPLAGHDDLARRADTLSVRYLQGRAR
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>PFR_JS14_1247	PFR_JS14_1247	Hypothetical protein	1424447:1425574 Forward
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AVALGFSRRVPPDPDQLDRLLLSPLTSLDPTALRRVGGALWHEAASGTTSDPMTLVRQFL
MRRAGDHLPSPVVPPATAQDVGALVHRPDTSGAAPTDVTTPPTGPTAQTATSALPTDPDL
EPVRELAALLGDAAARIMRGEGAYDVLWRLWDGTDWPSRLRGEALSGSASSGQANSDLDA
VLALFDVAARHMELTGQKGAETLIAEVSGQEIPGDQARESDPRGRGVQVLTAHRAKGLEW
DRVIIMGAAEGSWPGNRRGAGLLSAELLDADDPGLAPAPGAWMQQERRAFVLAASRARKE
LVITANLGSGDEQAQASRFVRELGGQVLAVPHDTRRPRSLQGLVGELRRVTADQRSTAGL
REAAAHQLGQLAVVRDDQQRALVPGADPRSWWGLGGLSGRHGTPSPAGVGEPEGPTRDKA
IRLSVTGLQKLIACPRQWFLDVAARGATTGGFAAGVGSVIHLLAEHAVTDHLSEDQLHDA
LDEAWNDLDVHQQGWRTLIERSRAHEMITRFERWQGGQPTEVLGVEVPVRHTFVIGGQPL
ELVGSIDRLERDRTSGRIRIIDFKTGSRAPSRTEAASNLQLAAYQLAVMRGACRELTGST
PAMDGALLVFLRLPAGARDPLLPKVVGQPGLDDHPYPAAEQLANTWLVRGDVDIQGPTMV
DDALAFAVHCVVEEDYPAVEGPPCSYCDHRADCPIWAREASSR
>PFR_JS14_1255□PFR_JS14_1255□Cold shock-like protein CspA□1444479:1444685 Forward
MATGTVKWFNAEKGYGFIAVDGSSDDVFVHYSAIDSTGFRSLDEGQKVEFDIAQGPKGQQ
AEHVKLVN
>PFR_JS14_1256□PFR_JS14_1256□Serine/threonine phosphatase stp□1444851:1445723 Forward
MTNESPATDRDNLRRGPTAWAGGATHVGTKAPPNQDALVVAATPGESHRSAIVAVSDGVS
TSPHSDVASQIAVDVATDHLTSVLTKPHHSDEPSALADDLKAAVVAANDAIVAAAGDDVH
GYACTLVLALVHRGLVVVANLGDSRAYWFGDDATNMLLTTDDSMAQLSIELGTSREVAEA
GRQAHAITKWLGPNAPSLEPQLAGFKVAGSGWLLVCSDGLWNYASAPAELRAVWDSLPAA
PDATAETLAGQLIDWANARGGRDNITVGLVRVEEPDTPAPEQSPAGSTQS
>PFR_JS14_1257□PFR_JS14_1257□Hypothetical protein□1445780:1446064 Forward
MPVAQSPVAGPGRTPGRFECVDIKIGIENVNRELGIETDQTRDEVTAALKEALSNDGVFT
LTDSKGRQLVVPGAKIAYVEFGEEHARQVGFGTI
>PFR_JS14_1258□PFR_JS14_1258□Hydroxylase for synthesis of 2-methylthio-cis-ribozeatin in tRNA□1446251:1446916 Reverse
MGGRELLGVLGQCELVDFEVLSFSGEFAPTLDDRIAVAELATAQFKRFNRVADQLHAHGW
PVGDSLEAFREPLDAFAQATQPTDWPTAQLRSLLVSGLRTDFADKLSAAWPEPMARLISP
GPVAWRIADFANRTLSQSLADDPDLAGSLALYGRRLAAEALGQCQRIAAKEVELTELVAS
AVPRPDDAQTGDMAALGAVSVLLEQLMEGHSRRMARLGLAS
>PFR_JS14_1259□PFR_JS14_1259□DEAD/DEAH box helicase□1447282:1448787 Forward
MTLSTTDPDAAEPAKTTFADLGVAPSIVTALDAEGITHPFPIQEMAIPIALTGTDMIGQA
RTGTGKTLAFGIPILQKVVLKTDEGFDQLDPKDKPQALVMSPTRELAQQVGSDLAIAGRD
RHARVLTIYGGVGYDDQLDALKKGVDVVVGTPGRLLDLVHRGNLDLSHVRIAVLDEADEM
LDLGFLPDVQALLDRTPASRQTMMFSATMPAVIMSLARSRLNQPVNIRAEGRDAQATVPQ
TTQFIYQAHELDKPEMIGKMLQSEGMRKMMVFTRTKRAAQRLADDLRDRGFEAASLHGDL
NQSQREKTMKRFRNDKIQVLVATDVAARGIDVDDVTHVVNYEVPDDPEQYVHRIGRTGRA
GHEGVAVTLVDWQDVTRWKVINKALDLPFPEIEATFSTTPQFLEDLHIAPDTKGRLADAK
PRDEGEHRGDERRDRGKGHGGKGHHDRGRDRHEGHGKKKDGEHRHDAKDKDKGGDAKRDR
PHRKRRRTRNGKPVAAQHKDD
>PFR_JS14_1260□PFR_JS14_1260□Tryptophanyl-tRNA synthetase II□1448925:1450097 Reverse
MESRPSWVVCRLRRMSLTSATEPEESSPDTEARGGSDRQTLVASQARSDAIEADIGVNPG
KYRILTGDRPTGKLHIGHYFGSISNRVRLQNLGVPSMLVVADYQVIYDRDGVGDLQDNVM
SGMADYLACGIDPARTTIFTHSSVPALNQLLLPFLSLITVPELNRNPTVKDEMEHSGGRP
MSGLMLTFPVHQAADILFCKANLVPVGKDQLPHIEVTRLIARRFDERYGRATPDQPVFPE
PDALLSAAPSILGLDGTKMSKSRHNTIQIGMTADETAKLIKKAKTDADRHITYDPQNRPE
VSNLVMLTALATGEKPEDVAARIGDGGGGALKKACTEAINEMFAPIRARRLELEADQGYL
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    RQVLHEGNARANEIADATLRDVLAAMNMDY
    >PFR_JS14_1261	PFR_JS14_1261	PHP domain protein	1450066:1450947 Reverse
    MLIDLHTHSNVSDGTDTPTALVQKAQRDGLAVIALCDHDTFDGLAEAEEAGRRFGVAVLP
    GIEISTHVGSTEVHLLGYGADPWAQPLRRELARMRASRLDRLPKMIAKLHELGMDLSVGD
    VEKQMLGASSAGRPHVADALVAKGYVANRDEAFAKYLDSTGPAYVPRETLALARAIDLVH
    GAHGACIIAHPWIRGTRDVVTSALLASLKADHGLDGIEVDHPDQDQQTRALLFELGGRLG
    LMRTGGSDYHGTGKTGHDLGTCVTRPSALHELALRITARGGSIGGVETLMGRL
    >PFR_JS14_1262	PFR_JS14_1262	Hypothetical protein	1451079:1451555 Forward
    MEFTAEHHYDAEPAAVYAMFNDPQWWRTLVERAGAESSRITAQDATVDVRIELTTPQKAR
    PFAGDTLGLDQTFTWTPTDGGWDGTFRQGTAGKLPAASTGTATIRAGHGGTDVHYTGEFT
    VKIPVMGRKLEAMAAPYVTQIIDLQQKVGTEWLSAHKG
    >PFR_JS14_1263	PFR_JS14_1263	Hypothetical protein	1451614:1451817 Reverse
    MTTRIVLRDHGEAVRLADALRDRGDEVALITQRDGGEDQPASYLVATPVARLQIAQLIPA
    AAEVTED
    >PFR_JS14_1264	PFR_JS14_1264	Hypothetical protein	1451819:1452328 Reverse
    MSTKTSRTDRAPLVFVPLRTDEAASLVTTGTLGGPVSAIAITPGLCETFGVEPDSEDAEL
    AALQVAAVWSLIRGDRRLVMVARVDAHGDADPGEEPNGAVLLPGLPLSAVTAFFTGPHPA
    DEADVARKLAHSDIDGAWQNTDVQALAADAPLLWHDVSELPASVKAKEH
    >PFR_JS14_1265	PFR_JS14_1265	Hypothetical protein	1452409:1452951 Forward
    MLTPMDNAMADLPVPPPQMWATDAGPVECVGVVRQARPPLQLGAGWSRSRPQAVQHRPDP
    AAQRLAITFARMIKEALAGTRPARQLQAVMRADRLEQVVSIQRMGGLTGIRCTHVRADRP
    APGTVEAVACYRWISAEPPPPGGEPAERAFAVAFRLDFRRGRWCCDELQIIASAQPDRAA
    >PFR_JS14_1266	PFR_JS14_1266	Protein translocase subunit SecA	1452991:1455840 Reverse
    MSFIDRLLHAGEGRTLKRLARIADQVNSIEDDYVAMTDEELRGQTADFRERLDNGASLDD
    LLPEAFATVREATKRVLGKRPFDVQIMGGAALHEGNVAEMKTGEGKTIVALAPSYLNALD
    GKGVHVVTVNDYLAQSQAEQMGRVHHFLGLKTGVILAPMAPDERRRAYACDITYGTNNEF
    GFDYLRDNMALTLDDCVQNGHHFAIVDEVDSILIDEARTPLIISGPATENKQWYPEFARL
    AVRLERDTDYEVDEKKRTVSVLAHGIEVTESDLGIDNLYESANTPLIGYLNNAIKAKELF
    KRDKDYVVIDGEVLIVDEHTGRVLAGRRYNEGLHQALEAKEKVEIKDEYQTLATITLQNY
    FRMYDKLSGMTGTAKTEEDEFQKVYGLGVLEIPTNKPMIRKDQSDLIYRSEDAKFTAIVD
    DVVERHDNGQPVLIGTASVVKSEELSRRLRAAGIPHQVLNAKQHAREAAVVAQAGRKGAV
    TVATNMAGRGTDIMLGGNPEFLADQLLRERHIDPVENPEAYEAQWADTLSDLEGQVADEH
    EEVVDAGGLYVLGSERHESRRIDNQLRGRSGRQGDPGESRFYLSLEDDLLRLFKPEAVER
    VMTSMQLPEDQPIEMKLLSRSIESAQKQLEAQNFETRKNVLKYDDVMNRQRHVIYRDRRK
    VLEGADVEGMLRSTVDRVVESAVRMHTQGFSDEWDLDALWNDMRQLYPVSLKVADYDGIE
    NVDELVDDFKADAQDAYDAREVKLGEEMMRELERQVWLTVLDRKWRDHLYEMDYLREGIG
    LRAMAQRDPLVEYKREGADMFDAMRAAFQEEVVGFLFNLDIQVPDAPEVGVQRDENGEEV
    DVRQMLSAGGDSPSGSGAATATATRTAKRAAEPAQAPAVKRAAIKGLERNEPQHMTYSAP
    TETGDVEELRGDEKTDEDDLFAGIGRNDPCPCGSGKKFKNCHGRNPNIR
    >PFR_JS14_1267	PFR_JS14_1267	Putative ribosomal S30AE, sigma 54 modulation protein	1456085:1456681 Reverse
    MDVIVTGRRISINDATRDLVSRRLNDSIVKLKDRVIRTEVEFTANESKGDPSNAIRCEIT
    VRGKGPVIRAGGMAEDKMIAFDQALDRLIAQLRKAADRRKRRRGGQRLADLPVAVEDQSV
    KTAEDTHEVAGMTVDGDGPMVVREKTFETTPLTLAQALDQMELVGHDFFLFVDAASGKPS
    VVYRRKAYDYGVIHLEVQ
    >PFR_JS14_1268	PFR_JS14_1268	Phosphoribosyl transferase domain protein	1456837:1457646 Reverse
    MNLSHVIAAGQDLLLGSECVACGSPGPVLCAPCDRRLDDGPLVREPDGDDLVDGMVPVWS
    GSRYDPIAGKLVIAFKDRGAWTLAAPLSRLVSRALAGLLLAGPGGDASPLWGARGPTAGA
    GGEVPILVPVPADPRRVRARGLDHTTTITRRAAAVCGLEWCKLLRRVSATRDQIGLGSAA
    RRAGQHGTMTIGSPRWCLPRTRRPQLWQARPIVVVDDVVTTGATVREAVRALRAAGARVW
    GVACAAQTELAGSVPRRVGSPLAPGDQTR
    >PFR_JS14_1269	PFR_JS14_1269	DNA-binding response regulator MtrA	1457728:1458468 Reverse
    MTDIEVGGPGLVLIVQDDAERADELHDLLSELGFATRWCASASIALKSFHETRPDLVVME
    VGLAGRSGLDVCREIRRESDVPIILVSTGSATEDIVEGFRAGADDYIVEPFAGAELLVRV
    QARMRRRRNGIQARHTVMVDDLEVDVDNRQVRRHREPINVTPTEFKLLVTLVERPGHVFS
    REELLAEVWGYGHAGDERVVTVHVQRLRAKIEADPDRPRIVTTVRGLGYRLGHTTDVRWI
    PEPLTV
    >PFR_JS14_1270	PFR_JS14_1270	Conserved protein, DUF179	1458604:1459170 Reverse
    MNFSSSPHAGELLVSSEAAGGGFFDQAVIFLLDNDENGAIGVALNKPSTTPVAEVLPAWA
    GELNPPSVLFAGGPVAPNGAICLAKVMDSGEEPPGWRPVLGDVGLLHLDTPVEIAAGAYS
    DVRVFAGYSGWDPGQLSDELDRGVWLRAPARDEDVFGAQAEGLWRRVLRRVGGDAGLLSG
    YADKPALN
    >PFR_JS14_1271	PFR_JS14_1271	Hypothetical protein	1459876:1460517 Reverse
    MPSGSPIPGFTPESFGAAGRDLLDAPITEEQRQRSERYLQDAYAEGRLSHEEFGRRIDKV
    LRARTRRELNAALEGFVKAGLASQVVGQFGAYPSVVVPREVRRSAGRWAGAAAHWSGAFT
    WIVGPAAVYALSKPHSYPHREAAKAFNTQIAIAIVSALVVGFSALLGLGWIPFAVWSALA
    LVLIVVSGLNASDGKDSRNVLQRVLPIRVLDEK
    >PFR_JS14_1272	PFR_JS14_1272	TmRNA-binding protein SmpB	1460607:1461089 Reverse
    MPREKGEKMIARNKKALHDYSIGERLEAGIVLTGTEVKSLRDGRASLVDAFATIDDNEVW
    LRNANIPEYTLGTWRNHSAMRKRKLLLHRQEIKRLERALGDSGGRTLVPLSIYFKDGNAK
    VEIAVGTGKREWDKRQTIRERDMNREAERDLADRNRRHRH
    >PFR_JS14_1273	PFR_JS14_1273	MutG family lantibiotic protection ABC superfamily ATP binding cassette transporter
permease	1461240:1463192 Reverse
    MTAGRPGARQRPPGAAPHRRTGGATRAALMGFLALLMVALGLTAAPQRALAQTSDSFDSW
    TADYTVGTDGTTHVRETLVYRFASDSARHGMYRTLLTREPDGDNKNQDIVYDVSNVQVSS
    PDAPASFTQSDEATKGNPRERFVTIKIGDANKRVSSATATYVISYDVKGALRDAQGVEQL
    YWDAVGDNTPDVNDIRITVAVPGGAQQVQCFSGAVGSDTACTSSSVADQQAVFHQDVKQG
    SEVMTVGVGIASGLVANGTPRLEPAAKSSAAQAAPWGIATLAAAAIVGAIYLVRFRKNSA
    DERFLGVPPGTVPVDVDAAQVGPASKHDVVPVRFDPPQIPVALGGLLVDGQVDSQEMTAT
    LVDLAVRRAIQLRSTTGRHGSSELFGRLIDADKATTPYEKKLLDALFGSVAVGTEVNLSD
    PGSMSDASSELAREVAATATNQGLMKRIGQVGTNRSGAVIGSFVVLIGAWFGGSLLSNTA
    ALASNAAGLTALMIIGALVVVGIITLLIRSSIARRGTRTAMGRAYTDQVQGFEEYLKTAE
    ADQLKFEEGQDIFSQYLPWAIAFGIADRWASLCEQLVAQGRLTETAPYWYYGDPFGFRYA
    YFTSGVLSGVDSGISVPESSGGAGFGSGGSAFGGGGFSGGGGGGGGAGGW
    >PFR_JS14_1274	PFR_JS14_1274	Hypothetical protein	1463376:1464695 Reverse
    MRRMALPRRAWVGLVACSVALSMMPAVSGADDLEDQQASLQQQIGASDSDVYASDAKLQD
    AEKTLSASQQQLADAQAGLARAEADRDAAARSDDDAARALKDAEAALVKAQDDAAKARAD
    VDAQKRKVGTDVRHTTQQNSGLVTIGIFVNNLSTGDMSNRIQWTDQAFRAQQYELDRLQD
    VEQRLEQAEQAMKDAEAAAQRDRQAAADALNSRASTAQAAQDAKAKVDALVSKNAADKSA
    AEQALADAQARNADLKAQSNAVAQRIKDRNAAAAAAAQAAQQADAAAAQAAAAGNSIATS
    TSSVLADPVPGAPITDTYHTRINPVLGYTEFHDGLDLGAGCNAPMYAAAAGTVADVLTPG
    QSGGYGNRLVIDHGLVNGVYLSTGYNHASSYVVSAGQHVDKGQLIGYVGTTGLSTGCHLH
    FHVYVNGATDDPQNWITVA
    >PFR_JS14_1275	PFR_JS14_1275	Efflux ABC transporter, permease protein	1464762:1465679 Reverse
    MRHTLRETWSGLKRNLSMTIAVIVTMWVSLALFGASLMTMAQVNEMKGKWYDKIEISVFL
    CTADSATESAGGNCEAGQDTTASQRDAIRSRLTANPDVSNIYYETKQEAYDEFQRVYKDN
    PIKDSLTVDQMQDSFRVKLKDPQNYKGVVAESQGLMGVQAVQDLHSVLDPFFKVLNGLKW
    GAMGIAGMLLLAAALQIGNTIRMSAYTRRREIGIMRLVGASNGYIMLPFLLEALFAGVAG
    VVLAAASMSALQYFVIDRVRSQLAIQSLGWITWGDTAVAVVWVAVVGVLLSIIPTFVATR
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RYLRV
>PFR_JS14_1276□PFR_JS14_1276□Cell division ATP-binding protein FtsE□1465718:1466404 Reverse
MITFEDVSKLYPRQTTPALRHVSVDIDKGEFVFLVGVSGSGKSTFLRLILREYRPTTGRV
FVAGKDLGRLHNWKVPALRRQIGTVFQDFRLLPGQTVYQNVAFALQVLGRPMREIRQQVP
ATLELVGLANKGERRPEELSGGEQQRVAIARAVVNNPKILIADEPTGNLDPATSVGIMKL
LDRINRRDTTVIMATHDSTIVDQMRRRVIELDKGELVRDQKQGAYGNL
>PFR_JS14_1277□PFR_JS14_1277□Peptide chain release factor 2□1466556:1467665 Reverse
MALDELTEHLSQLNKSLSSIEAVVDVPAKNKQIEELETEASAPDLWNDQEHAQSVTSRLS
RLQSSVEKVQTLRSRLDDASTLLELASEESDADTAQEAEKEIATLADEIDTLEVQTLLSG
EYDERDALVTIRSEAGGVDAADFAAMLLRMYERWAERHAYSYEVYDISYAEEAGIKSATF
TVKSPYAYGTLSVEQGTHRLVRISPFDNQGRRQTSFAGVEVLPVVEETDNIDIPEKDIRV
DVFHASGPGGQGVNTTDSAVRITHLPTGIVVTCQNERSQIQNKAAGLRVLQAKLLERARQ
EREAEMDALKSDGNSWGSQMRSYVLHPYQMVKDLRTGFESGSPDNVFDGDIDGFIERGIR
WRRQEEQAA
>PFR_JS14_1278□PFR_JS14_1278□YqeY family protein□1467760:1468221 Forward
MATLKDQLKKDLVVAMKAHDETAKTTIRMAVAAIMNAEVAGKAHELSDEEELKILTREVH
TREESAETYAAAGREELAAKESAEAELLKKYLPEQLDAAQLQQIVDDVVAQASTDGKPTM
KQMGQLVRAANEQVKGRAEGKAVADLVRKAITG
>PFR_JS14_1279□PFR_JS14_1279□Fructosamine kinase□1468425:1469417 Reverse
MGSNPPVTKAVHCASSRPAPGTPGIGALGIGHWESEPRKGRSRLALPTAVADTIAVRPYV
RGMTTTFTKHNRGTDNLAGEAAGLRWLAQAEPDGGTHIAPVISVDRQELVIGRVQESSPT
SRDAALMGASLAHMHAAGAPWWGAPPAGWPGPDWVGRSRTPLITDQRQAPATWGEFYAQY
RIDVFARCLRDAGTINSDQARTFDAVSRRLRRGDFDVPQPALLQARGQSVARLHGDLWAG
NAMYDGGATGATLIDPMAHGGHAETDLAALSVFGFPRLSEVYAGYDAESALAAGWQERIA
LHQLTMIIMHAVLFGGGYTASALELAGQYA
>PFR_JS14_1280□PFR_JS14_1280□4-aminobutyrate aminotransferase gabT□1469535:1470872 Forward
MSDPVYHLPQERKLITSLPGPSSRKIEARRDAVVAKGVSSSAPFYVDKADGGVIVDADGN
SIIDLGAGIAVTSVGASAPRVVENVQKAVANFTHSSFATTPYEGYVAVCEQLAELTPGSF
AKKTVLVNSGAEAVENAVKVARHYTGRDAVAVAENAFHGRTNLTMAMTSKAMPYKTGFGP
FAPEIYHFPASYPFQEPTPLTGEQAAQRAIDYLETRVGADHLACLVHEPIQGEGGFIVPE
PGYLPALQAWCRAHGIVFVIDEIQSGFCRSGKWFASEYEGLEPDVITTAKALGGGLPIAA
CTGRADIMDSAQAGGLGGTYGGNPISCAASLGAIATMKEWDLPNRAQAIETEIRAKLGDL
VNDPASCVGELRGHGAMMALEFVAPGTRTPDAAKAKQVVSDLLSEGVLMLTCGINGNCVR
FLPSLVIPIPLLDEALDLLVKAIKA
>PFR_JS14_1281□PFR_JS14_1281□Aliphatic amidase□1471051:1471911 Reverse
MSLTVVASQAAPLAIDAPRELFEQACSAMLTKTPDGGMLVFPEMHLFADGQPDRARTKAY
QQAAEPLDGPRVTWLRQLAAGLGVWLVPGTVCERGPSGELFNTALAIRPDGEVAATYRKI
FPWRPLEPFTPGQDFAVFDVPGAGRMGLCICFDSWFPEVSRNLAWLGAETIINVVKTTTP
DRPQEMVMARANAIVNQVNFLSVNAAAPVGRGLSAFFGPEGETLAEIGDDAPADMVCEVS
TQRVRRARAEGTAGVTRPWAFFHSGDQPVELPAYGGRIDPTRWNRD
>PFR_JS14_1282□PFR_JS14_1282□Putrescine importer□1471908:1473299 Reverse
MAMTDTPTAATSAGGPGHTVTFRRELRLHSVLAFGLAYLAPIIVLGTFGVISQKSNGGTA
GSYLIAMLAMLLTATSYGRLSHEVPMAGSAYTYVRKMVSNHLGFLVGWGSMLDYVFIPMV
IWLIGASYLNAQFPAIPDPVWIAGFIVITSGLNIVGIKVADHANLVLLAIEVLVIALFVA
FSIYAVAHHGQQLLSLTPFTGKPFDVLALSAGAATAAYSFLGFDAVTTLTEETVDAKRTI
PRAIMLTALVGGGIFVVATYATELVHPLVQVLDIDSAAFEIAKAIGGAFLSTVFLVGLIV
GQFASGIAAQASASRLMFAMGRDGVLPKRFFGRLSPRTNTPINAILVVAAVGIIGCFLDI
STSTSFINFGAFIAFTMVNVSAISLTRRQIARGEHVNPLTGYVVPALGALVVIYLITELD
LPALLVGGTWLFIGICVLVGLTHGFHRPPPEMTDSTEMEELAA
>PFR_JS14_1283□PFR_JS14_1283□Hsp20/alpha crystallin family protein□1473572:1474024 Reverse
MSTAIYNPFREMDRFFNQVAKTAGPDTRYMPLDLYRDGDQFVAKMDLPGVDPATIDIDVD
DRTLSVRAERKAEQVHKDDKSHWVSRERSYGTYARQLTLGPGLDLSRINADYSDGVLTLT
IPVAEDAKPRKIEVTTSASQPSVESGEQDK
>PFR_JS14_1284□PFR_JS14_1284□Putative ABC transport system□1474274:1476067 Forward
MRSLGRILAHVANLWPWYLGIVICSLASAGTALAVPFVLRSVTDLVVAAVNTHAVDLGAV
VRLAAVLLAFDLANTVTSNIGGYLGDNMAMRLRAGLSKRYFDKLLGLPQRYFDDELSGTI
IGRLSRSITEITQFMQSFSNNFFPMLLTVGAVLVITAHYSVWISLLLLAIFPLYVFFTAL
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SRWWHSMDVVRRGVLNVVFFVIYLIIFLGTARSVYSLGTMVMLVQMVGMARQPATMMSFF
VDQSQRAVAGSRDYFEVLAQPSEHDWRHEDAPAPALIDADAPMISFRDISFGYGQGPDVV
EHISFDVARGERLALVSESGGGKTTLVSLLMGLYRPRQGQILVSGHDTSTLGVTQLRAEV
GVVFQEPLLFSGTVSENIAYADPDVADQQIRDAAKRANADAFIRALPHGYASVVGERGLK
LSGGQKQRIAVARAMIKDAPILVLDEATSALDSRAEQAVQNGLEQLMEGRTSIIIAHRLS
TIATVDRIVTMRGGRVDEIGSPAELAASGGIYAQLLALQASGRRRDRRRLKEFDITH
>PFR_JS14_1285□PFR_JS14_1285□PF11253 family protein□1476102:1476527 Reverse
MGGTTRRAPSSTEGVEQLKLEPGLIVQELGWDDDVDEDLRADIMDAIDGDLVEDSVEAVD
VVLLWQRNDTDVADSLVDAMRDMGNNGYIWLFTPKIGRPGYVEPSELSEGAEVAGLTLTS
AVDVADDWQATRVVRPHHGRR
>PFR_JS14_1286□PFR_JS14_1286□Hypothetical protein□1476532:1476666 Reverse
MPPRRTPPEVSPDPGKGGHSVVKASTRRGAAPRRVEFRGAYVVK
>PFR_JS14_1287□PFR_JS14_1287□Pyruvate dehydrogenase E1 component□1476629:1479376 Reverse
MIPREQPGPILNGLPTNLPDTDPEETREWQDSLDGMIDADGRNRARYVMLKLNEQARARQ
IGIPSLVSTDYVNTIPPAEQVAYPGDEDLEQRVRHMLRWNSAMVVHRQQRPGVGVGGHIS
TYASSVQLYEVGMNHFWRGKDHPGGGDQIYFQGHGSPGMYARAFMEGRLSEADLDGFRQE
YSKPMGGRGLPSYPHPRRMPDFWEFPTVSMGIGPLNAIYQAQFNRYLGNRGIKDTSQQHV
WAFLGDGEMDEPEARGALQLAANEGLDNLTYVINCNLQRLDGPVRGNGKIIQELEAFFRG
AGWNVIKVIWGSNWDPLLEADTDGALVNLMNVTKDGDYQTMKANDGAWVREHFFGKDPRT
AAMVADWSNDQIWSLRRGGHDYLKIYNAYKAATEFNGAPTVILMHTIKGYFLGSHFAGRN
ATHQMKKLAIDDLKGLRDRCDIPVSDAQIEADPYLPPYYKEPDNSDAMEYMMDRRRKLGG
FLPERRTTGKKLPLPGDKAYKSVRKGSGHQKVASTMAFVRLLKDLMRERDFAPFVVPILP
DEGRTFGMDSFFPTIKIYNPNGQQYTPVDHDLMLSYREAKNGQIMHTGINEAGSVGAFTA
AGTSYATHGQPMVPIYMFYSMFGYQRTGDFMWAAADQLARGFYLAATAGRTTLTGEGTQH
MDGHSPILVSTNTALVSYDPCYGYEIAHIVRDGLRRMYGDDPEDISYYITAYNEPMQQPA
EPEDADIEGIVKGMHLINEGDGDANAPHAQLLASGVGVPWALEAQRLLKEDWGVVADVWS
VTSWGELRRDGLECDEQAFLHPELPVRTPFVTQKLAGRPGPVLATSDYMRAVQDQIREWV
PTDYVTLGADGFGFSDTRPAARRHLHIDAASLVVRTLQTLARRGEIDPSKAAEAFNKYQL
LDVHATEEDTAGGES
>PFR_JS14_1288□PFR_JS14_1288□Aromatic-amino-acid transaminase□1479631:1480827 Forward
MSLFAAVEATPNDPIFGLTDKFNRDTDPHKVNLGVGMYQDDDGRVPLLESVRIAEERLAR
AAKPATYPPMDGLPDYNADAQRVVFGADSEAVASGRVVTGQSLGGTGGLTLAADVYGSVS
PNHKALVSTPTWANHIAIMRHAGYDVGKYAYYDGRTGVDIDGLLSDLSGAEPGTMVIMHE
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Forward
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MAAIYTRTGDKGTTGLFGGTRVPKQDPTVEAYGTLDEANATIGEAKARVEDPDMRAALQH
IQQRLFVAAAELASDEAGRAVIANTISPDDVADLERLIDDSMAETGPQRNFVVPGRDLVS
AALHGARTVTRRAERRMLAAAESRPVRPELIHYVNRLSDALYSLARVAEHRFDVARLEGL
VRSVVEKHLAAQSRQPRVAWSPASGFVPADVSATADPATRFGLARYDLDVLQAMAAAAQS
RGAELGVPIVFAGVDAGGHLMLLHRMEDSLLGSLDLASNKAFTAAAFKQPTADLGEASLP
GAELHGIQNSNDGRVVVFGGGLPVFVEGVLCGGIGVSGGTVDQDVTIASFAMSRAKEASR
S
>PFR_JS14_1323 PFR_JS14_1323 Propanediol utilization protein PduN 1518243:1518515 Reverse
MFLAKVRGTVVSTSKDERLVGFKLMLIEQIGLQQEPVGRPEIAVDTVGAGTGSIVIVTKG
SSARFAADRKDAPIDSTIVGIVDTVEIGPA
>PFR_JS14_1324 PFR_JS14_1324 Ethanolamine utilization flavoprotein 1518517:1519401 Reverse
MNPDQLRAIIRQTLVELLAPAPRRALVVFTGGLLGFDECLGGLRALADEGVALDVVQTPS
ARRILDQHKIGALGLPQVDDHLVANHQMLIAPTLTANVAAKVSHGIADCLASNLFSEFIM
SNRLVVASSTAVSPDEAPKRSIYPEMPSGYAELLRANLTALTSFGVRLARSQALARTALA
AFDRRDAAHKDALIAQGIPAQALAACAAPAIPAPAPRPHGGGVSHRGTRVTDTRREPAPR
GPVTGAPSTLKLISQGVVQKLDPGSCLAIRPDTKVTAAARDMAASRNIQITVVV
>PFR_JS14_1325 PFR_JS14_1325 Ethanolamine utilization protein EutJ 1519398:1520255 Reverse
MAMTGMVVTTHVELPEQAIMRFAEQVRTGAIDEPTGQMRLGFDLGTANIVVAVVDAANHP
IAGGWVHSTVVRDGVVVDWAGATSAVRALRADVEQRLGHEFTKASISIPPGISDGDIQVF
ANVIGAAGLDLDEVVDEPVAAARAMGITDGAVIDVGAGTTGVSILEDGKVVLSVDEATGG
HHMTLVLAGSNNIDYDQAEAMKKDPQYREQVLGTIRPTLDKMATIAAQALGSRDVPAVYL
VGGSSSFESAPAIFEARLHRPVVRPAQPLFITPLGIPMPAQEESR
>PFR_JS14_1326 PFR_JS14_1326 Propanediol utilization protein PduJ 1520402:1520680 Reverse
MREALGLIETKGYVGSVEAADAMVKAANVVLVGYQKVGAGLVTVMVRGDVGAVKAAVDAG
AAAAAAVGEEVLSRHVIPRPAADVEKLLPKQA
>PFR_JS14_1327 PFR_JS14_1327 Propanediol utilization protein PduK 1520725:1521342 Reverse
MQLTQALGTIEVLGLPAAITAADVACKAADVRLVGYETTDGMGMVTVKITGQVSAVQSAI
AAARAAASQITSVFAESVIPRPNDQIDPVVLTPVTVGLGASPAARPGGGTSPEAATPEQM
AAAERALDPADPPRDAEPAAPTTDPAPAPDPAPAGPVADDPAATAPAVPSQPKISPSQER
PDKGTAGPSRNRRKAPQAGREAGKK
>PFR_JS14_1328 PFR_JS14_1328 Glycerol dehydratase reactivation factor DhaG 1521359:1521703 Reverse
MNTDKPTINMRVSDQITADQIADICFGMEEEGVPSTVTWQASINPLELAHEASVESRLGV
GIGVALSYAVITTEKLPAERPYIAVNLSRDAARNRAIGANAARLVKRIPLLPMN
>PFR_JS14_1329 PFR_JS14_1329 Putative dioal dehydratase-reactivating factor, large subunit 1521700:1523514 Reverse
MTLIAGVDIGNATTEVALADVAAGAPPRFLASAIVSTTGIKGTQQNTQGVFQAITQALQT
AGRELEQLDLIRINEAAPVIGDVAMETISETIITESTMIGHNPSTPGGLGVGVGTTIRLD
DLGQASAGEPYIVVADHTHGFLDVAARINEAAARVNITGAILQLDDGVLVDNRLTAKIPI
VDEVKLIDKVPIGMPAAIEVAEVGRIVETLSNPYGIATMFGLSPDETASVVPMARSLVGN
RSAVVIKTPAGDVTERHIPAGSLRFLGDRTAEVDVDRGAQEIMHAAESVGTIRDIKGEPG
TNIGGMMEKVRVTMGRLTDRDPAGIEVTDLLAVDTNVPQKVTGGVAGEFSLEAAVGIAVM
VKADRLQMQRIAEEMTEQFAVRVEVGGVEADMAIRGALTTPGTSVPIAILDMGAGSTDAS
VLREGQPARSVHLAGAGNMVTLLIKMELGLDSEEDAENIKRYPLARVETLFSIRHEDGTV
QFFDEPLAPELFARTVVLHPDGMIPLPLRHPLEVIRQVRIHAKQRVFVTNAMRALAAVSP
TNNVRDIAHVVLVGGSALDFEIPQFVTHALAEFRVVAGRANTRGTEGPRNAVATGLVLAW
EAGR
>PFR_JS14_1330 PFR_JS14_1330 Dehydratase small subunit 1523550:1524083 Reverse
MDSEELIRQIMGEVMANLNQDNVAFDKLPAAAPSTTGAAHRVDKSSYPLGEKVPEQIKSA
SGRALSDFTFDKVKSGELTAKDFRIAPETLEMQAQVAESADRDALARNLRRAAELIQVPD
EEVLDVYNALRPYRSTKAELYAIADGLETKYGCTINAAFIREAADVYEKRGRLKADA
>PFR_JS14_1331 PFR_JS14_1331 Dehydratase medium subunit 1524092:1524775 Reverse
MDEKTLRTIIEEVVKEFAAAGDAQGTGAGSATAMATAPSLTEASGDQLEITEEGPAPRGT
NPREVVIALAPAFGGRITKTIIGIPHAEVLREICAGIEEEGLTYRFIRVFRTADVGFIAH
DAAVLSGSGVGIGIQSRGTTVIHQKDLPPLSNLELFSQSPLIDLATFRAIGKNAARYAKG
ESPDPVPVVNDQMARPKYQAIAALLHIKETQMCDLNKKTQALRVEYR
>PFR_JS14_1332 PFR_JS14_1332 Glycerol dehydratase large subunit 1524786:1526447 Reverse
MKSKRFEALDARPVNQDGYVTEWPEVGLIAMNGPNDPTPSIRIEDGVVVELDGKQRADFD
MIDTFIADYGIRLDKAEEVCKTDSRELARQMMDFHVPRAEVVQLTTAMTPAKITEVVGTM
SVLEMMMAVTKMRARLFPANQAHVTNLKDNPVQIAADAAEGALRGFAEEETTVGIVRYAP
FNAIANMVGSQVGRPGILTQCSVEEATELALGMRGFTAYAETVSVYGTEQVFMDGDDTPW
SKSFLASCYASRGLKMRFTSGTGSEVQMGAAEGKSMLYLEARCLYITKGAGSQGIQNGSV
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SCIGVPAAVPSGIRAVLAENLIAMSLDLECASSNDQTFTHSDLRRVARSLMQFVPGTDFI
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AIFRELGLTEVTDEEVEAATYARGSKDMPARNVVEDLKAAEDLMKRGITGVDIVLALDRA
GFEDVANSVYNMLKQRVAGDYLHTSAILNEDFQVISAVNYPNDYRGPGTGYQMTDERWDK
LKTIRQAISPESI
>PFR_JS14_1333□PFR_JS14_1333□Propanediol utilization protein PduB□1526462:1527271 Reverse
MANEQLVDQIMSAVMAKIGNEPASAAPRAAAPSVPASIGRPEATEFVGTSALGDTIGLVI
PNVDPQIHALMKIDPKYRSIGIIGDRTGAGPHIFAADEGVKATNTEVVSIELARDTKGGA
GHGSLIILGAEDVSDARRAVEVTLGELDRTFGDVYGNDAGHLEFQYTARASHALNKAFGA
PVGKAFGITVGAPAAIGVVLADTAVKASTIDVIGYSSPAHGTSYSNEVISCFTGDSGAVR
QAIIAARATGLELLGAMGDVPTSTTTPYI
>PFR_JS14_1334□PFR_JS14_1334□Carbon dioxide concentrating mechanism/carboxysome shell protein□1527286:1527570 Reverse
MQDALGMVETKGFVPAVEAADAMVKSANVTLIGSQRVGSGLVTVLVRGDVGAVKAATDAG
AVAAQNVGELVSVHVIPRPHADVEKILPSFADQK
>PFR_JS14_1335□PFR_JS14_1335□PduU protein□1527897:1528238 Forward
MSDKQRIIQEFVPGKQVTLAHVVANPDPGLYPKIGLPAGTEALGIMTITPSEASIIAADV
ATKASAVSLGFVDRFSGSLVVLGQLSDVESAIENVVAVLCDELGFARPPITRS
>PFR_JS14_1336□PFR_JS14_1336□Ethanolamine utilization protein, EutP□1528235:1528660 Forward
MKRILLVGSVGAGKTTLLQRLHEREPSYAKTETIYTDGTIVDTPGEYLEMPFYKHALRMA
SFEVDLVVLLASAQVSEAKFPPGFTSFFMPPSVGVVTKIDLADQVAIDIATSHLQMAGVT
QIFPVSAMTGAGIDRLAARLA
>PFR_JS14_1337□PFR_JS14_1337□PduQ□1528713:1529843 Reverse
MKQFQLATSLACGPDALTALDRLGGRRVLVITDAFMASSALMDTVRGHLGSAEITVFDQV
QPNPDVQAVARGLRAFLDCAPEALLALGGGSPIDTAKAVRKITLEQGQPLSAGFYVVPTT
SGTGSEVSSFAVVTDPEHDAKLPMTSPDMVADVAILDPDAVRTCPPTLTADSGMDALSHA
VEAYVALDHNDITDALAEKALRLISANLVASFRDGNDLAAREHQQNAATMAGIAFENSGL
GIVHGLSHAIGGSFHVAHGRLNGILMPHVIGFNAGELGFGAATLSPIAERYAQLAGAIGI
DAATRRGLVTGLVDFITAIRRDLDMPASLTDAGVDRAAFRAAIPQLSQTALRDFCTSGNP
RPVTADELAGLLARAL
>PFR_JS14_1338□PFR_JS14_1338□Transcriptional regulator□1529800:1531017 Reverse
MRRTLCHGCDAYGGLQSLAHGTTQIYRCHAGLVDFSVPITSQNSYVGAILCGQDRVPELE
QPDFLMGDSPWRGDPTLEQYYEQVPVVGRRRVQAAAQTLLGLRAGVEGYSGKLRLFLSDD
QASGGVAQSQARGAALRGLSVVPTDIVAGFTPNPNTSSARAADDEADSDAPASDSADILR
TALLAEDFAGTVAEISVQLQAAFDPVPSTDVLEGVQALDEALLAVARDIAPRLAPHLEET
IVRHRRGAGAHPGRYTSQLHAERLATLILDEVLRTRPQRQHNLRDLINDIARNPARALSL
TEAARKLHWSPGHLSKLFKSVTGDTFVSYVMSRRLERAELMLASPQMPVGEIATTLDFSQ
VNYFSRVFRSRTGMSPSEYRRQHSSFDRRPLHEAIPTGHFSRLRA
>PFR_JS14_1339□PFR_JS14_1339□Hypothetical protein□1531024:1531188 Reverse
MTLKRMVDLMDVAALAKTLEDFSEATGFATVAVDAQGVPVTEMCAFTDFCRAIR
>PFR_JS14_1340□PFR_JS14_1340□DNA repair protein RecO□1531352:1532095 Reverse
MPTYRDEAVVLRTHKLGEADRIITLLSRTHGKVRAVARGVRRTSSKFGGRLEPCNHVDVQ
FAVGRSLDIVTQVECLHPYGDPLTRDYVLYTTGETMLEVADRLVAVENEPSLQQYRLLVG
ALRVLGQGTNDGPRPATMVLDSYLLRSLAVAGYAPVLDSCAKCGVMGQQEWFSPSIGGMV
CSGCRPPGSARPEPESWQLLGALMSGDWPATRTVGEGTQREVSGLIAAFSSWHLEHQLRS
LPLIPRG
>PFR_JS14_1341□PFR_JS14_1341□Isoprenyl transferase 2□1532279:1532968 Forward
MDGNGRWATQRGLPRTKGHEAGESALFDVIAGAIEMGIDCLSVYAFSTENWKRSPEEVRF
LMGFSRSVIHRRLDELDAWGVRVRWAGRRPRLWRSVITELEHAEERTRHNDTLQMQFCVN
YGGRAEIVDAARKIAAAAAAGRLDPAHLTEKSFHRYLDEPDMPDVDLFVRSSGEQRLSNF
LIWQSAYAELVFSQKLWPDWDRRDLWDAVSRYVHRDRRYGGTDSATQGA
>PFR_JS14_1342□PFR_JS14_1342□Protein of hypothetical function DUF488□1533029:1533391 Forward
MDIEIKRVYEPASPDDGYRALVDRLWPRGESKVRAELDEWCKDAAPSTDLRKWFNHQEEL
FGEFTTRYRAELDASSEPAALLKRAEASGKSKLTLVYGAKDQKDNQAVVLRDYLNGLQSK
>PFR_JS14_1343□PFR_JS14_1343□2-isopropylmalate synthase LeuA□1533448:1535214 Reverse
MSTTFQPPKSFAAPHVCGLSQPVATPSGMNYERYQPFHPMSLPDRTWPDQRITKAPRWLS
TDLRDGNQALIDPMTPARKRKMFDLLVKMGYKEIEIGFPSASQTEWDFVRSLIEDPEAIP
DDVVISVLTQAREDLIDRTVQSLVGAKRATVHMYNATAELFRRVVFHTTQQGTIDLAQQG
TRWVIDAIEKYLPDTPVGYEYSPEIFTQTPTDFAIEVCDRVMDVWQPDDEREIILNLPAT
VEMSTPNTYADQIEYFSRNISHRDNVCISMHCHNDRGCAVAASELGQMAGAQRVEGCLFG
HGERTGNVDLVTLGMNLFSQGIDPMIDFSDMDTIRRTVEYCTGMPVPARSPYAGDLVYTA
FSGSHQDAIKKGLEDLETRARAESTSIHKIRWEAPYLPVDPQDVGRTYEAVIRVNSQSGK
GGMAYLMKADHHLELPRRLQMEFSGVVQARADDSGHEVTSPVLWDIFDSEYLSRDTPFKL
GEFTVGAAHGQTQITADLDVRGKQTTVTGEGNGPLSAFIDALGQVGAHVRVLDYTEHALT
SGGDAYAAAYVECEVGEGDDTQVLWGVGIDPDITTATLKAALSALDRA
>PFR_JS14_1344□PFR_JS14_1344□Amidohydrolase family protein□1535446:1536951 Forward
MGRMMFRHARLLDLTTGRVGLPHDVLVSGNQVRRGGPAMIAPDDEVIDLEGRIVMPGLWD
CHVHFDLWAASKTRLDVSGCVSANDTLSRLAASITQLPAGAALIAVGARDSQWPDRPDTR
ELDAISGNHPVAVYMNDLHSVWVNSRGLQQWGFRDRVTGTASSGVLREQDAFALEDRLDE
VDRAARSRALIDAQSEAAARGVVGIVDMQTGGHRIDAWRNRAASPDQRLQVRIACWPDTV
DDWVATGLATGALLDDDQWLTAGPLKVIADGSVSARTAWCTESYRRPAPGIDPHGMADIS
AAELSRLMSLAERSGIEVAVHAIGDATVARVLECFAETGAHGTVEHATVMHDADLARMAD
LGLTASVQPAQIIADRLGFAEVWTERPRHVHALASMAAARIRLVFGSDAPVAPLDPWLAI
SVAVTGREPGSADGAWQPDETLSVGQALRASTSGINQLVPGGRADLVVLDDDPFTIQPEA
LAAMRPYLTMSRGHITHRADA
>PFR_JS14_1345□PFR_JS14_1345□Hypothetical protein□1537081:1537215 Reverse
MAKKSQEVTGKKKHKLLRCLLWCTVLSGAVVAAVIYLGRPGTGE
>PFR_JS14_1346□PFR_JS14_1346□Hypothetical protein□1537326:1537934 Reverse
MTLFGRSRRQAWGTKVVYERVDDARGNKVGAAVHDIGSTNVLTLLVVPTPQGGIHEVSSR
IECQNSNPFTWTHSFHIVDGTLLDVGRTDQMPAFCVPMWAEFAVASYLAEHDKHEPIECS
VIDESTGDAHPAVFAWSGHDSVVWSVDGAVRCRHGVTDGEITVSEWPGFTSVRESDEDEL
LRGISAQIRYRVVDFVRGIESR
>PFR_JS14_1347□PFR_JS14_1347□GTPase Era□1537984:1538928 Reverse
MTDQQPAGSQEFRSGFVCFVGRPNAGKSTLTNALVGSKIAITSSKPQTTRHAVRGVLHRA
DGQLIIIDTPGLSKPRSLLQQRLNDLVRSTWSEVDVVALVFPADEHIGPGDVYLATQLAE
LAKPPTLVAIVTKTDLVSPERLAKHLLRVARLQDDLAITFAHILPCSARSGSQVGEVADV
LLSLMPPGPDYYPDGEITDEPDETLVAELIREAALEEVRDELPHSIAVEVDEMMLRDGRP
ADRPLVDIFASMIVERDSQRGIMVGHAGERIKRIGVRARRQIRALLGTQVHLDLRVKVVK
DWQRDAKQLNRLGF
>PFR_JS14_1348□PFR_JS14_1348□CBS domain pair protein□1538921:1540231 Reverse
MTQTDWIFIIVAVVLTVFGSMLAAGETALQTVSRKRAERMVADGIRGADRVLDIEADPAP
TINTAMLLRIVCETGAVILGCLVVFDNFDHDWERIGIPLLVLSIIDFIVWGVMPRTLGRQ
RAEQTAVRAARPLGALTSLFGWLTSGLILVGNALTPGRGYADGPFSSEAELREMVDIAEK
AEVIEHGERDMIHSVFELGDTLVREVMVPRTDVVFIESGKTLRQGMSLALRSGFSRIPVI
GDNLDDVRGIVYLKDLTKRVFDNPEADQKETVDQIMRAAVFCPDSKPVDDLLTEMQATRN
HMVVIVDEFGGSAGVATIEDLVEEIVGEITDEYDAEPDLAEQLDDGRWRISARMPLDEVG
DLFDLELDDEDVETAGGLMAKQLNRVPIIGSEVVWKGLRFVAEKATGRRHQIDTIVVSRE
PEPEPEPSPDQKDDDD
>PFR_JS14_1349□PFR_JS14_1349□Probable rRNA maturation factor□1540385:1540843 Reverse
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MIDLSNESGEEVDTQALIRLARFALDKLRIHPQADLSILLVDVDTMTAYHKQFMNLDGPT
DVMSFPMDELREPADGEAPPRGLLGDIVICPAFTSAQAPGNGRTNQEEIEYLLIHGLLHL
LGHDHAEPDEKAVMFGLNDRIIADWRAEQGSD
>PFR_JS14_1350	PFR_JS14_1350	PhoH family protein	1540883:1541890 Reverse
MHVQRADAGDSDSVRTLTVPASVEMVNVLGPSDTFLRLLESQLDADILVRGNRITLTGTD
ADVELASDVFTEMITITRTGQGLTTDAVERIVSMESADPEVAPSQVLTQNILSSRGRTIR
PKTLNQKRYVDAIDNHTLTFGIGPAGTGKTYLAMAKAVQALQSKKVNRIILTRPAIEAGE
SLGFLPGTLNEKIDPYLRPLYDALHDMVEPERVPKLLTGGVIEVAPLAYMRGRTLNDAFI
VLDEAQNTSPEQMKMFLTRLGFGSKIVVTGDVTQVDLPGGAPSGLRQVESILDGVGDIAF
CQLTNRDVVRHRLVGRIVAAYDRFDSRRNAASRER
>PFR_JS14_1351	PFR_JS14_1351	Inner membrane metabolite transport protein YhjE	1542022:1543404 Reverse
MNHKGRIIVSSLVGTTIEFYDFYIYATAAISVFPLLFFHSSGGNGALLASLATFGVAFVA
RPLGSVLFGHFGDRAGRKATLLASLLTMGVATVLIGLLPTYTSIGIVAPMLLALMRFCQG
LGLGGEWSGASLLAGENSRAGKRGFDSMWPQLGAPFGFLLANGFFFMLTMTMNYDSTQAT
TNHAFLAWGWRLPFLFSAVIVALGLYVRFKLHETPSFQRTKDRGEVVKAPVLEVFRSSWR
DLIRGTFIMLATYTLFYLMTTWILSYAIGKVALGYLGISYHSFLVVQLITICAFALTIPI
SGLLGDKLGRKRFLLVVTVAIIAFGLSFGFFLDPARMGTGSSANLVLMTVFMLIGMALMG
LTFGIQSALLPELFPTNVRYTGSAISYNVSSILGAAVAPFIAAWLAARFGPGSVGLYLVA
MAVLTLIALITTHETRDLDLDAIGRDKPAGEVPESVLVDA
>PFR_JS14_1352	PFR_JS14_1352	Hypothetical protein	1543573:1544064 Reverse
MTTSSEDLSSQGPARMVPEQSTTALVARALRRPKVVGVVLLAAEVVLRLASLLGGRGGNA
DYHDVDFFGAAALAVIVMAMARRHPTAQNQYACGALLIIVMLIGSTHYLRFTGRKMWDDT
FNVLDFTGSIALLVVGVIIMGRTRRIRKAAHPAPNGGAARLAQ
>PFR_JS14_1353	PFR_JS14_1353	Prolyl aminopeptidase	1544120:1545178 Reverse
MSSPQRSTLSPVASGADHDVTAGAVVRPQRVRYPDIEPYDERMLDVGDGQSLHVEQSGNP
DGIPVVFVHGGPGGGIGRDYRGFFDPELFRIIGFDQRGCGLSTPHVSQLHDAAQMASNTT
AHLVGDMERLRTELGIELWGVFGGSWGSTLSLAYAEQFPERVNWLVLRGIFTLRRSELDW
YYNAGASMVYPEHWQHFLAPLRRAGFDLDGDNIVGYHRLLWSDDHELARAAGLAWTRWEA
ATSSLLYSAEHVEESSDPDAALAFARIENHYFAHHGFLRENQLIEQAGRIGDIDGVIVQG
RYDMCCPAATSHELHKAWPRADYRVVMAGHSAFEPNITSELVLATDRLAARG
>PFR_JS14_1354	PFR_JS14_1354	Hypothetical protein	1545260:1545811 Reverse
MSDTDEAIPNDGVENDENTELAQLSPADSLIDRGVADPLDEGYIPPDHWSPAQGFGNTAS
EMARNETIDQRLTQEEPEPDPNAPEHHWNPDHEPRQVGSKRAGRLVAAGGGIDAEDTESE
SVASDVGISGGAASAEEAAMHIIETDDESDDDDDDVQTDDATVNNDPATDGSGTAEKLDE
DQS
>PFR_JS14_1355	PFR_JS14_1355	TRNA-guanine transglycosylase	1545925:1547193 Reverse
MCAAKSCDFSFSVDHVLPNGLGRSGTITTPHGPISTPAFVVVGTKATVKTVTPEQMDQAG
AQAVLANAFHLYLQPGPDIVDEAGGLGRFMNWPGPSFTDSGGFQVMSLGVGFKKVLAMDV
TGMQNDDVIAEGKQRDAQVDEDGVTFKSPLDGSTHRFTAEVSMGVQHQLGADIMFAFDEL
TTLMNTRGYQEDSVRRTQRWAQRCVDEHFRLTDARSGHPYQALFGVVQGAQYEDLRREAC
RGLRQTRAQVPGHEHEGFDGYGIGGAIEKQHLGDIVGWCAEELPDDKPRHLLGISEPDDL
FAACAAGADTFDCVNPSRTARNGAIYTARGRYNVTTAANRRAFVALEEGCDCYTCTHYTR
AYLHHMFKAHEFLGKTLATIHNERFTIRLVDSIRHAVRGGEFDALRTEFLGSFYGGATPG
RA
>PFR_JS14_1356	PFR_JS14_1356	Putative Tat (Twin-arginine translocation) pathway signal sequence	1547313:1548641 Forward
MHGRLNSVHKPFVATDLEVLTITPTSAVISWITRSHRGRSLLPQPAFTDTQLWVGDADST
LRLVHDDPMPRAFHQVTVTGLEPGREYGFRARSGGIQPLPGLYTTNRHTSPERVHRFVTL
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DHPFLVLGGDITYDGTSDQVALARQLLAGYGTSQDDWLAVRGNHDRPRRDGTDPFGDAFV
AYQHMCANQTPEGLRILGIDTTRGGGGGWILPDQLDHIRACLADEPDRPTLVTSHHPVTH
DAALTSPAGPQFMLRWRDRLAVQRLERRAKGVFLHHTGHTHRMRRGKADVQGSHTEYFEN
AACAAYPGGYALLHLYEGGYLLNFWRIATHAAEEWLFRSRWQVMGLMPQLTLGTTNDRNH
VVLKDLSGLHSSGKPVPLELQV
>PFR_JS14_1357	PFR_JS14_1357	Ribosomal RNA small subunit methyltransferase E	1548630:1549379 Reverse
MTDPLFLADIAGAGPGDVVLIEGPEGRHAATVKRMRVGESVLVADGAGAGLRGVIDSVAK
NSVSVRVGELIARRPAALHTVAVQALAKGERSDIAVEAMTELGVDEIIAWQASRSIVRWE
AKAEKGLAKWRSSARAATKQSRRFRIPQVSTAGTPGVVERLARADLALVLHEEATTPLSG
LSVPSAGECVFVIGPEGGISPEELEAFRGAGARLVSLSDAVLRASTAGVVALAQLQALAA
RGGPNGSDL
>PFR_JS14_1358	PFR_JS14_1358	Chaperone protein DnaJ 2	1549376:1550584 Reverse
MSSDYYEVLGIGRDASAEQIKRAYRKKAMQVHPDVTSDPDAEEKFKQVNEAYEVLSDPQK
KSIYDRGGDPAHAGAGAGGGFDPFGGFGGFNGGGQMGFDVGDLLGAMFGAGGTTRGPRSR
VRQGSDQLVRLDLTLAQAAFGTEAPLTLDTYVVCPHCHGQGSANGEEPVTCTQCHGSGSI
TQIQHSFLGDIRSTATCPTCQGYGSVITDPCPECSGEGRVRARRDITVKVPAGVSTGNRI
QLRSQAEVGTGGGPAGDLYVEVNVQPHEVFTRDGDNLEMMLTIPMTAAALGCKVPIKTLE
SELADADPKKSTVELAIPAGTQSGARIAIKGRGVTKLRGRDSKQRGDLGVTIVVQTPTKL
DESQRKLLEELADARGEVGDGIAKTHADDKGFFEKLRKAFTG
>PFR_JS14_1359	PFR_JS14_1359	Heat-inducible transcription repressor hrcA	1550597:1551607 Reverse
MIDDRKLDVLRAIVTDYVASREPVGSKALVERHHLDVSPATVRNDMAALEEEGYLTQPHT
SAGRIPTDKGYRLFVDRIAQVKPLSPAERRAVSTFLEGAVDLEDVVRRTVRLLAVITHQV
AIVQYPESNAARLRHVEVVTLSPEMAIVIVVNSAGTVYQRSIRVPEHSDDDLQFVRDAVN
AAVDGEPPAGAIEALNALAEQPLPRLGSSVVASVLDMLATDEAPRVAVGGVPNLTRFGAE
FETTVKPVLEALEEQMVLLRLVGEAAADHPGDVAVRIGQENPFAPLKTTSVVASSYGSFE
ASANLGIVGPTRMDYPSTMAAVRAVARYVGQFLAEG
>PFR_JS14_1360	PFR_JS14_1360	Inositol monophosphatase family protein	1551866:1552642 Reverse
MDTDQVLGIIKQVSADIVEPRFRALHEDEIDSKAPGDYVTVADREAERELSQQLRAGARD
AVVVGEEGSFVDPGQLDAIGVAPHCFVVDPLDGTNNFVRGSEDFAVMVAELRGVETVGAW
IYQPRAGKAYVATRGGGVYCNGERISAAPIHVPPQGASTFRAWRGFDEQGRIAPVIPASG
SAGIDYPHVVTAAIDFVVYRFPKPWDHLPGQLMLQELGGDVVHLDGRLYRPGSGRMAILS
CRDLATGRRVASGWPRRE
>PFR_JS14_1361	PFR_JS14_1361	PF11296 family protein	1552720:1553601 Reverse
MSAHDRYGHDVLSGDWRHAGKPRTTDMPLSLGLIVEVGSDGYCGEVVGWENGMIVLEDRN
QRRRTFPVGEYGYLVEGRPVALRIPPRRGASQSLRTPSGSRTGSHEQPHVALGSRIYVEG
RHDAELVEKIWGDDLRHVGVVVEYMGGMDDLLGIVAEFEPARGRRLGVLIDHLVANTKES
RVAAQVRHAGYGDYVKITGHRFIDVWQTIKPDVLGIKAWPDVPMDRDFKKGTLAALGIPR
NKPYARIDQADVGRAWQAMLARVSTYRDLDMDFVREVEKLIDFVTQDHIDQDS
>PFR_JS14_1362	PFR_JS14_1362	Putative coproporphyrinogen dehydrogenase	1553696:1554895 Reverse
MSDAAAPGPFPGGHLFPHEELRAPTTRPLSVYVHIPFCAVRCGYCDFNTYTPSQLAGMNM
DDYLAAVHAEIAAAARALGTGRAVSTVFFGGGTPTMATPAQLGEVLADLRDTFGLVPGAE
VTTEANPETLDRARLETLLGSGFNRLSLGMQSADEQVLARLDRHHTPGRALQVARWAHEV
GFPDVSLDLIYGTPGESLDSWRATLDAALGVAPEHLSAYSLIVEEGTALARRIRHGELAM
PDEDAEADEYLLAERMLSTAGLANYEISNWALPGHEARHNLAYWRSDDWWGFGPGAHSHV
HGVRWWNVRHPRRYAALLGEDARPREDFEVIDAPTRHEERVLLELRIADGLPVGELTGTE
RARLAEPLSRGLVTVVGDRVHLTLQGRLLADAVTRDLLD
>PFR_JS14_1363	PFR_JS14_1363	Elongation factor 4	1554898:1556727 Reverse
MSATPGATDPAIIRNFSIIAHVDHGKSTLADRMLQLTGVVDPREMRAQYLDKMDIERERG
ITIKSQAVRMPWHAGDHDYVLNMIDTPGHVDFSYEVSRSLEACEGAVLLVDAAQGIQAQT
LANLYLALDADLTIIPVLNKIDLPSAQPDKFAAEIAGIIGGRASDVLRVSAKTGDGVAEL
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LDAIVEQVPTPQGDPKAPLRALIFDSVYDTYRGVVTYVRVVDGKLSDRERVQMMSTGSVH
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PMVFAGIYPIDGDDFPELREALEKLQLNDAALTYEPETSAALGFGFRVGFLGLLHMEVVQ
ERLEREFDLDLISTAPSVNYRVVMEDGSEHMVTNPSEFPEGKVETVYEPVVRATVLCPAT
YIGAVMELCQARRGEQIGMDYLSEDRVELRYKLPLGEIVFDFFDALKSSTRGYASLDYEE
DGERASDMVKVDILLNGEPVDAFSAIVHRDKAFSYGVEMTNRLRKLIPRQQFEVPVQAAI
GARVIARETIRAIRKDVLAKCYGGDISRKRKLLEKQKQGKKRMKMVGRVEVPQEAFVAAL
TNNELTKKK
>PFR_JS14_1364□PFR_JS14_1364□Hypothetical protein□1557028:1557648 Reverse
MNRSVYRTLLRIVGIVLALVGVAAVFGGVFAHNNVTDQLKKEAISMPTADQVTNLPQASQ
DALKPFFNKEMTTGTEARAFADHYIWNHMQASCKTVKAADGTALDAVPAEQCNYAGVGDV
ATANKSDQTKYTAYTTLRGTLLTGETLRGMLLTSYAFWLIGTIAVFAGWALVAIGIVLAL
VGFVGLRGPGKSAGGAATPAGQTATA
>PFR_JS14_1365□PFR_JS14_1365□30S ribosomal protein S20□1557903:1558163 Forward
MANIKSQKKRNKTNEKARQRNKAVKSALRTHVRNFREAAAAGDKDKATDLAKVANRALDK
AASKGVIHTNQAANRKSAISVKVESL
>PFR_JS14_1366□PFR_JS14_1366□Hypothetical protein□1558297:1558959 Forward
MRTHPTGSTSGPDPVTADGGIVRLGATPGEYLSAFLPSFLGLCLAWLLIAVGGLSRPVRP
VTIVGLVLAAICVVLALLEVRDLPRRTIRWNRGGITLQARRLPTLALPWSELGVVRTVVQ
PDRLWWVLPRTRVWLECQPLDQPAGFDTRHPELADYESPAADEGYSAVRLMVGLGNRRAR
RVDMALRRANPTYRGLRHLPPARRSRPGAGTRQRGARLHP
>PFR_JS14_1367□PFR_JS14_1367□DNA polymerase III, delta subunit□1558973:1559971 Reverse
MFGSVTLVHGSEQLLSERAVAALRKRAMAEEPGLQLVELVGGDMSPADFVEASGGSLFAD
HSLVIITGAESMVPESVDALVAFAGAPSPEVGVIVVHPGGNKGRGLVDKLRKAKAGVVEV
VAPKAWELPKFVQAEARAARVGMESDAAQTLVDAVGNDLRALAGAVSQLASDWAGERLSS
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YLDVRAERMSDIEMSRIVGVPPWKVKTLARQSRLWSETAVARGLIALSRADAAVKGAATD
AGFALEQLILALDHARRDDASGHRRSAGVRRR
>PFR_JS14_1368□PFR_JS14_1368□DNA internalization competence protein ComEC/Rec2-like protein□1560054:1562375 Reverse
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LACTTAHLQAASQGPLAQAGRDRSVVAIQGQVRSDPRELPSRFGSASHVVRIDVSRVDIA
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AATGRRGTGVAGLRQLSVAVWLVVLVDPWLARSWGFALSATATAGILWWAGPWQARMRRW
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VRSQLERAGVEIATASPGQEWAIGEGHWRTLQAGSGDVPGQPTSPGAGSESAENDASILG
LAGNGDLNVLVTGDLEPDGQRNALREVPPQLLRADIVKVPHHGSARQSEDFLAATGARVA
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>PFR_JS14_1369□PFR_JS14_1369□Putative competence protein ComEA□1562494:1563405 Reverse
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TVG
>PFR_JS14_1370□PFR_JS14_1370□Malic enzyme, NAD binding domain protein□1563590:1565344 Reverse
MLMPQPSHGMAMTPEGDCVSQDFEYVREDGEEVVRIAARGREVLAHPMINFGTAFTRSER
EELGLIGLLPPGVTNVYDQVKRIYRQYKTEPNPMARYVFLTALKDRNEVLFYRLVSEHIE
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>PFR_JS14_1371□PFR_JS14_1371□Dihydroorotase□1565362:1566654 Reverse
MSELLLHNVDLLGEGLGDLFVRGERLADPAEASSQVPTVDCSGLIALPALVDPHTHLRDP
GQGNAETIATGLQAAVRGGYGAVFAMPNTDPVADSAEVVEYELDTARQVGICDLYPIGAV
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EAEHGGHLEVGRFANICLVDPDHPWRVDPARLASIAHNTPFKERNYRTSVAATLLRGRAT
YDPGRHFSLA
>PFR_JS14_1372□PFR_JS14_1372□Leucine--tRNA ligase (Precursor)□1566711:1569239 Reverse
MSQGEPKHDAATVSEERSGYDAPAAEAKWQKYWAEHETFKASDAPDDKRQRRYVLDMFPY
PSGDLHMGHAEAYAMGDVLARSWRMQGFNVMHPIGWDSFGLPAENAAIKNNEHPARWTYE
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EQLQAQGTGEQTVTYRLRDWLLSRQRFWGCPIPIIHCPNCGDVPVPDDQLPVKLPDLRGE
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EDVARWAPVDQYIGGAEHATMHLLYARFFTKVLKDLGMIDFVEPFTRLLNQGQVINQGKA
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VTSPLGADPASGDRPLRRATHKAISEITDLLAAGRFNVAIARIMELVNATRKTVDGHNAP
NSNAGSDDPAVREAVEFIAQALSLFAPYVSEEMWEVLGHAPSIADSSWPTADPALLAAEE
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GK
>PFR_JS14_1373□PFR_JS14_1373□Hypothetical protein□1569556:1570614 Reverse
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GCALTTDQVGQADVLADLADMLSTRVGDAMLMVVGYGPARSTDEAVACVEIALGAQQIDI
SLVVSDRRFWVRSAGERVEWSPGHRFDPRASVAATAAVSAGLQVLGGRDQVSALVAGPGA
DDRAIADAWRTARQQASAWSPGQREEFLDDCLTRSVDHAEDLSRDELTQLGALVQCLELR
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>PFR_JS14_1374□PFR_JS14_1374□Hypothetical protein□1570783:1571523 Forward
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SRTDTPAPETPPPAINRFQVRSARGPVVLVVVVALIIVAVLVTLAVRSPKQGAQAASPSP
SAASSARPATSPATPPTALPDSNTIPVDYEGFKGQWTITKSTWDSTGLNLEVEVKGTSGS
LGFSFFALDTDGGSNQYKASGALATGTVTAGGTTTGRVHFNKSHQTTLVILANSYGRQIT
ALTVDA
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>PFR_JS14_1375□PFR_JS14_1375□NADPH-dependent glutamate synthase beta chain and oxidoreductase□1571826:1572746 Reverse
MQTALGANGQIAEELTRELHRNVTHDIRLVSRHPRAVHETDELVSADLRDTRATADAVAG
SDVVYLTVGLPMDSAMWQEQFPVMMGNVIAACRQHHCRLVFFDNTYMYPRTAAPQTEQTP
FEPVGPKARVRAHITTMLLDQMGAGNLEALICRAPEFYGPGRTQSLTNSMVFGRIAKGRR
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RRIGYTTVPTLAFRIGGLLNPTVREVEELLPRYRQDDIFDSSKFMSRFPDFPVTSYRQGI
QQLVEG
>PFR_JS14_1376□PFR_JS14_1376□Hypothetical protein□1572861:1573298 Reverse
MTDSRAEIHDYLTRYAASLAAFDARRAAGLWGTPGMILDDRFAGMLESREAMVRGLEQSY
PLYQQLGLDSVGFELLDHQQLSATVVLVHVRWLFLDATGELLTDAVSYYLLRADDDGLRA
YVCIETDSAEKLAELAERQGITLPR
>PFR_JS14_1377□PFR_JS14_1377□Phosphoglycerate mutase family protein□1573358:1573966 Reverse
MSAPTRLVLWRHGQTDWNLAGRFQGQTDMPLNVAGLSQAEAAAGHVAALGPEAIVSSPLR
RALETADTLAELTGLAVTTDDRLQEINVGQWSGLRAAEVFAQDEIARFRATGQDFRYSPT
GETRCEVGERVAPALREIAAAHPGQTVAVVSHGVAMRMGAARLCNIDYQGAQDLGTMANC
AWSILEPGQGRWHIVDWNVSAS
>PFR_JS14_1378□PFR_JS14_1378□Ribosome-associated protein, iojap family□1573966:1574349 Reverse
MSATEHAVEMTRVAAEAALGKLGEDLVAFDVSEQLAIADVFLIVSGHNERQVGAIVDAIQ
DALIDRGEKVLRREGQGGNHWVLLDYGDLVVHVFRTDDRANYALERLWRDCPEIPLPQET
PTAREQN
>PFR_JS14_1379□PFR_JS14_1379□Nicotinate (Nicotinamide) nucleotide adenylyltransferase□1574346:1575116 Reverse
MTQGRSESASDDEEAGLNLGLVRANTWRRYRLGVMGGTFDPIHHGHLVAASEVAARFDLD
EVVFVPTGVPWQKAGRRVSKGEDRYLMTVVATASNPRFTVSRVDIDRKGNTYTVDTLKDI
RRERGGNLDLYFITGADALASILTWRGASELFDLAHFVGVTRPGVNLGQRDFSHLPSDKV
TFLEVPALAISSTECRNRVAEGLPLWYLVPDGVVQYVAKRGLYDANDGDVLVLDEPVDER
GYTTGTDEPGSDGSNS
>PFR_JS14_1380□PFR_JS14_1380□Gamma-glutamyl phosphate reductase 2□1575190:1576434 Reverse
MVEVYEIASRARTASRTLATLTRERKDAGLRAMAAALEQSSDQLLSANARDVEAAVAAGT
PDAMIDRLSLNPQRVSGMAQGLRDLAGLADPVGQVVRGWNLANGVHVDQLRVPFGVIGII
YEARPNVTADAAGICLKSGNASLLRGSSSALESNRAIVTALREGLVRADLPADAINLVEG
GHETTGQMMRARGSIDLLIPRGGAGLIRTVVEGSTVPVIETGTGNVHVFVDRAADQQMAV
GVVLNAKVQRPTVCNALETMLVHRDIAAEFLPVVVEALGGVGVTVHGDADSVAIDPRIVP
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VLVNASSRFVDGGEFGFGAEIGISTQKLHARGPMGLQEMTTTKYVLTGQGQTRH
>PFR_JS14_1381□PFR_JS14_1381□Hypothetical protein□1576441:1577109 Reverse
MEWTLVVGYLAAIIGAFYVLPQTVHVIRVGSSAGLSPLTWQLQVGASTGWTVHGFLTGQP
NVWACNIVVLCCAAIILIVICRDRKLSWNVWVLSVLVAGALVTVDSVFGAVAYGMLIIVP
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LCLGLYMVKRAGVQLPGLPATSPPCPPAERQMGHGLAPWGPL
>PFR_JS14_1382□PFR_JS14_1382□Glutamate 5-kinase ProB□1577142:1578311 Reverse
MTDQVPSVVPALDTEESVRAAIGSARRIVVKIGSSSLSSARRGLDDARLAALVAALADVH
DAGRDIVLISSGAIAAGLKPLGLTRRPRDVAHQQAAAAVGQGLLIERYTEMFAHRDIRVG
QVLLTPDDVAVRDNYHNALRALGTLLRMGVLPVVNENDTVATQEIRFGDNDRLAALVAQL
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>PFR_JS14_1383□PFR_JS14_1383□GTPase obg□1578304:1579905 Reverse
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QAIVHVIDTATYEPGRDPVRDLDAIEAELHAHGGLDDRPRLIVLNKVDVPDGKVIADMVL
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MGDDRDADWRRIHAAELDKLRAGEGDDGEGVEVNWVGHDPNEDLESYTEGDDD
>PFR_JS14_1384□PFR_JS14_1384□50S ribosomal protein L27□1580054:1580317 Reverse
MAHKKAGSSSRNGRDSNAQRLGVKRFGGQVVNAGEIIVRQRGTHFHPGEGIGRGKDDTLF
ALVGGAVQFGTHRGRRVVNIQPVETTA
>PFR_JS14_1385□PFR_JS14_1385□50S ribosomal protein L21□1580331:1580678 Reverse
MPQAAARYRKWVSVYAIVRSGGRQHKVAVGDVLEVDKMVDEVGASVKLEPVLVVDGKDVT
SDKAGLDKVDVTAEVLGQTKGPKIHIMHYKNKTGYKRRQGHRQQYTRIKVTGIKA
>PFR_JS14_1386□PFR_JS14_1386□Hypothetical protein□1580875:1583661 Reverse
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PQDESPTDQP
>PFR_JS14_1388□PFR_JS14_1388□Hypothetical protein□1584731:1585186 Reverse
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GDWSPQEREMLDRLLSRLLAGLERSAQGDPG
>PFR_JS14_1389□PFR_JS14_1389□Integral membrane protein TerC□1585401:1586657 Forward
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TEMGSEYFAGYITEKALSVDNLFVFLLIISSFAVPRKDQQKVLLVGIVFSIIARTGFIFL
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KLFTVVDGKRMMTPMLLVMVAIGGTDILFALDSIPAIFGLTQSTYIVFTATTFSLMGLRQ
LFFLIDGLLDRLIYLSYGLGAILSFIGIKLILHALHENTVPFINDGESVPVIEITTGISL
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>PFR_JS14_1390□PFR_JS14_1390□Ionic transporter membrane protein chaA□1586654:1587754 Forward
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SAARHSTSRFSALGSGGALATVTALAGICLVLPRFTVSDPSPSYTPSQLAFAGVASLVLY
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FLAANP
>PFR_JS14_1391□PFR_JS14_1391□Radical SAM domain protein□1587818:1589761 Reverse
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STELSYTNLLNALDLAGLPIHAAERDDDAPLVVVGGHCAFNPEPIADFVDVVVLGDGEEA
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RFDGWSEYFDYELWTRCAAEQLAPFGIDLEWFTTRERPQVEVLAWDHLDSGLDRTWLWDE
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>PFR_JS14_1392□PFR_JS14_1392□Hypothetical protein□1589838:1591109 Reverse
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MVLAAPAATNRTNAPRRALASRAPARPARRIADPEGFTIPDAGPDQAPRPARRRAAES
>PFR_JS14_1487□PFR_JS14_1487□Transcription factor WhiB□1705544:1705804 Reverse
MLELPSFDDPSEEDALSWREHALCAQTDPEAFFPEKGGSTREAKKVCQSCPVRTECLSYA
LDHDERFGIWGGLSERERRRLRTQAS
>PFR_JS14_1488□PFR_JS14_1488□Hypothetical protein□1706137:1707219 Reverse
MSEQISTVDQTPKVPRVPWGTRLLRWREPITWASILLTIGFLVGGVVEILLNLFRRGMGF
GRAARALSSSVATGWLVLVVLLVCACAYIKPATGHAKLLARVAALVTSVVVAYDLFLLVA
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QAEEAVGDQWAHPGTPAAPVGVAPGAGGFATSPGQPPDWRSGMQGLSSVFGGAPGATSDQ
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KTPRTPSLIKLDAADPSAMPDNSAETGPVTFTARERADGAQLEQPDEDHGADPGRPAQDS
>PFR_JS14_1489□PFR_JS14_1489□Mannose-1-phosphate guanylyltransferase (GDP)□1707216:1708295 Reverse
MRYAVIMAGGSGTRLWPLSRQGEPKQLLRMIDGKSLLRLAFERVAGAVDPANILICTGAA
YIDEVARQIPEVESRNLLGEPVGRDSLNAVAWPAAVLARRDPGAVTAMITADQIIEPVEV
FRQRLDTAFRVAEQDADALVTFGIVPTSPNTGYGYLHRGTDVPGFVDVSRVTEFKEKPDA
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HDCLLINADVGDSVLAVAGLRDMAVVRTAAATLGCPLKDSQQVKTLVGRVAHEVDAELA
>PFR_JS14_1490□PFR_JS14_1490□Cell envelope function transcriptional attenuator common domain protein□1708421:1709779 Forward
MAEQNDEGGQKADLDWLYRRGPEEAPDPLAGRPARVTSTFNRADVQRHEQEFLAERARRQ
AQQQARPAQAQPGGSAQYVSRGQQHGGYGAANAVSRHAGSGPTGGGNGAPPRRPVPAPVP
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IPGYGRNKVNAAYSFGGAPLLTQTIEGATGLRMDGYMEIGFAGFAGMIDAVKGVQVCLDE
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VANPVRWWNVNEALSKAITRGKDMGPGVALGAGRGMVSVAGGKGLTLQVPVSNSSGWSDD
GQSVVIWDSARASRMFGLLAQGDTKDMDQFAS
>PFR_JS14_1491□PFR_JS14_1491□Phosphoribosylaminoimidazole carboxylase, catalytic subunit□1709817:1710377 Reverse
MSDPHAQGAGAQQASGAAGDDQPLVGIVMGSDSDWPTMQAAAEALTEFGVPFEADVVSAH
RMPDEMLAYGHRAHERGLRVIIAGAGGAAHLPGMLAAVTPLPVIGVPVALKNLEGMDSLL
SIVQMPAGVPVATVAIGNARNAGLLAVRILAAGDAALTDKMVQFQHDLADSARRKGEAVR
SKTVRA
>PFR_JS14_1492□PFR_JS14_1492□Phosphoribosylaminoimidazole carboxylase, ATPase subunit□1710370:1711542 Reverse
MHTVGIIGGGQLARMMYESAIGLGLEVKLLAEGPDVSAAEVIHDVTIGDYTDPATVKAFA
RTVDVVTFDHEHVPTELLSELERDGVAVRPGPKALVYAQDKALMRMKLGDELGLPSPKWR
ICDDAAALAEFGNEIGWPIIAKESRGGYDGHGVWKLDGPGAASIPFTDSLAVSAGEQVQI
LAEEFVDFARELSVIAVRNPDGEAVAYPVSETVQANGICVETTTPAPMMSSDHEAEIQAL
ALHIAKELDVVGVLAVELMERPGGEVVINELAMRPHNTGHWSIDGATTSQFENHLRAVAG
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GADLADVQERARAAAHYLMGDDDVMEDDGE
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>PFR_JS14_1493□PFR_JS14_1493□Peptidase family S51□1711620:1712336 Forward
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SGLGVRTMVLTLWQGAAESVKRLPEADVVLVGGGNTVNMLALWDAHGVSRTLKLMAADTS
RTMVLGGLSAGGACWFEGCLTDAFGDLRGWRGGLGMLSGSFCPHLDGEDRGAIYTQAIAT
GMLPGGYAVDDGVAVHFENGKYTDVLAEREGPTALRLMPSTEPTASGVLTEILEPEVL
>PFR_JS14_1494□PFR_JS14_1494□Putative insertion element ISCmi2 transposase□1712392:1713435 Forward
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RYRAGLPLIDRSSRPTSSPNRLSRKTEHRIVALRFTRRWGPHRIAYHLRLHRSTVGRVLA
RYKMPKLINIDQATGLPVRRPKPTRYEVAAPGQLVHVDIKKQGRIPDGGGWRAHGRGSMQ
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AKPYASEAERAAAYETWLHHYNHHRPHTGIGGQTPSARVHNVTGKYI
>PFR_JS14_1495□PFR_JS14_1495□Transcriptional regulator□1713485:1714069 Reverse
MPKINAPTVREHHERVLTSLIDAAEQVLRYEGPDQFTTSAVSARAGVARNSIYRYVDSVD
DLRGLVVERYMPAWFRAVQEAMDATSDPAQQIVAWALTNLEQATIAGHGWLMKVGDKRLN
QQAAGTVNQAHQNMFAGLGEAWAQISAPNARLGAAMTGGLLNSCMKQVEAGMDSHEVAAG
LERAVRALVEAFRR
>PFR_JS14_1496□PFR_JS14_1496□Hypothetical protein□1714151:1714654 Reverse
MGWRRHLGDDETVIADLRAHPKALVVPVVFLFALAAACGVALAMVPAAVEPWAGWLIAVI
TAGLAIAFVQRPVLAWATTRYGFTGRRLVVRAGLLRRRRSDLPYSRITDVSYARGLLDRL
WGSGTLVVTTASGARLELIGMPQVIALHQAVSQLVAESRPAAPDLPY
>PFR_JS14_1497□PFR_JS14_1497□Biotin apo-protein ligase□1714688:1715479 Reverse
MPTTAPVDPVELEQLLGKNSYWGPIQWRPETGSTNDDLVALAKKGAATGLVVMSEHQVGG
RARFDRVWQDTAGTSVATSVLVAPTPPPLQWGWLSLLVGVAVREGVENYTGAVPGRVTLK
WPNDVLLDERKICGILSERVGDRAVLGWGLNVSMSQEELPVPTGTSLLLAGLPHAKTPLM
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ALVVDDDQGTRRVLTAGDVVHLR
>PFR_JS14_1498□PFR_JS14_1498□Transcriptional regulator□1715629:1716234 Forward
MNDDVVSSISQRTKRAIRAAALELALRDGADKVTVDQIAVAAGVSRRTVFNHFATKYDAF
MPEVAAYSDSALKDFSSGREPDLIRALGDVIGNRIDQVQFTSDQVRAVRKLAQDSPGLHN
AMRGRSGALDARLQAAVMRRLGSTPDDPSTTMTLALARSIWRTTLDAWLTTPDEFNQDSL
RRCLAKSMETLEGLVRSNPGA
>PFR_JS14_1499□PFR_JS14_1499□Transcription regulator□1716248:1716826 Reverse
MAVSTHAEGEQDSAGPSEPRDEQGISEFVSHFGGLMAASGMPGLTGYVFALLLAQPDAEL
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EGSKRLFLEGSRAAGGVGTPAGRRLWLNAKWFTKLGDAIEREMAAWPAEREELLRSLGEL
DDADPHDGPAES
>PFR_JS14_1500□PFR_JS14_1500□Hypothetical protein□1716941:1717459 Reverse
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RALWLSPPAYYFVARARIRRWERGSGRERARSVLTSYVNRATGWFTVAGGASLMALEATW
ELAEIYHWGVAGFWLIVAGLMVASHLNVAIRMWRLMREVPPQGSNPEVSPTS
>PFR_JS14_1501□PFR_JS14_1501□Tetronasin ABC transporter ATP-binding protein□1717564:1718508 Forward
MSPTRVSTAIEINGLVKTFGRVTALDGVDLSVQTGEVHGFLGPNGAGKSTTIRILLGLLR
ADSGTARVLGADPWADVRTLHERLAYVPGDVNLWPNLTGGQVIDLLARLRGDLNPARRDE
LLERFDLDPTKKARSYSKGNRQKVALVAALASDAELFLFDEPTSGLDPLMEAAFDTSVQE
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LGTMPGVSQLRAGGGHVSFVVDAAHLDQAITVLTRAGITSLVSEPPSLEELFLSKYADPV
PTGTPAAPSAGDQR
>PFR_JS14_1502□PFR_JS14_1502□Hypothetical protein□1718505:1720442 Forward
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TRAEEETGRQELIGSAPIARHAPLTAAGLLAGATSVACGLVTWLCVWAGGWPSAGSMLYG
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VTAEEGVWAAPPAHHRPARIGAHARDGEPGSQRHHPHQGVGAIGQ
>PFR_JS14_1503□PFR_JS14_1503□Integral membrane protein□1720254:1721600 Reverse
MIDDSRHDRDFIDGTEAVVRLGSMLLSAGTGAYRVKHAMARAAEAIGMDRHDASVSLTEI
ITTTHKGDNFRTVVREVPRVAVDASRIGALERLARALPDGSTARELEDQLDHIARHVRGR
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WRRSPHAFLSSDAEFAKRDIDYSAPSDE
>PFR_JS14_1504□PFR_JS14_1504□Carboxyl transferase domain protein□1721732:1723306 Forward
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GRHRSTKFGMEKRRPYGDGVIIGVGAIHERPVCVFSQDVGIFGGSLGQVYGEKICKIIDF
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WKSYWRVVRQPLIPAHEGWRGSLR
>PFR_JS14_1506□PFR_JS14_1506□Septum formation protein Maf□1723617:1724345 Forward
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GE
>PFR_JS14_1507□PFR_JS14_1507□Hydrolase, NUDIX family□1724349:1724849 Forward
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APEETAVRECLEETELAVEVERLVMTGVLGPIRYPNGDVCSFVDHVFRCHVTGGRAGTGD
RENTAVRWFGVDTLPADIDPVVVRRIRVAVENPREVVLAGRYPEYA
>PFR_JS14_1508□PFR_JS14_1508□Hypothetical protein□1724940:1725419 Reverse
MQASHPSGSARWCALIVGCLGSALVLSACSAGSGGSSAPVSSSRAVSAAASPISQAPSVD
PSSLGGVTLASLGFVNGPQGFRVPDGLEQRQRVDQTNVVTLVVPGSQGQQLYDYLRNALS
SLGFTLTAASGDSLIFDAPGWEGAFTMDDQLAGLTLRHL
>PFR_JS14_1509□PFR_JS14_1509□Hypothetical protein□1725704:1726336 Forward
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TSATMLLLSRDLKDGLPASDAEAKAISPMLSVTRNASSPNIATNSIMVTARGDWDWTVLG
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TGGGWGDTRSRGYHLRVNGNGVEDAWESES
>PFR_JS14_1510□PFR_JS14_1510□Hypothetical protein□1726333:1726548 Forward
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LSRRRSSEPRS
>PFR_JS14_1511□PFR_JS14_1511□Endonuclease VIII and DNA N-glycosylase with an AP lyase activity□1726699:1727514 Forward
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PIADPIVHIHLGLIGRLSFTELAPPVGQVRVRINDGTWAADLRGPQICRLISEDEEAAAT
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>PFR_JS14_1512□PFR_JS14_1512□Phosphoribosylglycinamide synthetase, ATP-grasp domain protein□1727670:1729451 Forward
MVAVDTTRTITKVLIANRGEIAVRIIRGARDAGLESVAIYADADSASLFVEMADEAFALN
GATPAETYLDIDKIIAIAKRSGADAVHPGYGFLSENSNFAQAVVDADMVWIGPPPAAIES
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>PFR_JS14_1514□PFR_JS14_1514□Genome sequencing data, contig C257□1730074:1731081 Reverse
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>PFR_JS14_1515□PFR_JS14_1515□Pyruvate-flavodoxin oxidoreductase (Precursor)□1731085:1734804 Reverse
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CRAARAELSRRR
>PFR_JS14_1519□PFR_JS14_1519□Puromycin N-acetyltransferase□1738935:1739555 Forward
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>PFR_JS14_1520□PFR_JS14_1520□Hypothetical protein□1740686:1740856 Reverse
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>PFR_JS14_1521□PFR_JS14_1521□Carboxymuconolactone decarboxylase□1740853:1741260 Reverse
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REVLATRGAGAPSAS
>PFR_JS14_1522□PFR_JS14_1522□Transcriptional regulator, MerR family□1741373:1741738 Forward
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QVQEYSQLRHEGDSTVPVRLAMLQSHRGELEARRRRLDEQLAFLDDKIDVYRTKLASQSS
H
>PFR_JS14_1523□PFR_JS14_1523□Hypothetical protein□1741911:1742366 Forward
MKMWTYSYFQANSTNAGLYWRLVVIGAILAALVVLLVLYRHRRSDMRVREMLIIVSLVAA
LAMAMQATDFFESQASLDNSGKMMSFIDNVAQAQYSTTGDIAVSQTNLSTGLIIKVGDKS
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>PFR_JS14_1524□PFR_JS14_1524□PF04239 family protein□1742363:1743007 Forward
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MTMVPYDFWALALKLALGFICLVLQINLSGKGMLAPNSAIDQLQNYVLGGIVGGMIYNSA
ITPIQFLIVLLLWTLIVLGAKFGSNHVRLVKHVIDGEPTEVLRDGRLDVAQLARLGVSAH
DLALKLRNSGATDMAKVRRAVLEQNGQLTVTMEGDDLTQFPIILDGQIDEYALELTGKNQ
EWLDDQLGRAGTTLRQVYMARYVNGQLHVSAFTD
>PFR_JS14_1525	PFR_JS14_1525	Silent information regulator protein Sir2	1743026:1743949 Reverse
MSSEAISRFARSHVRRATSGWQPSTNLRGDVDQARELISGAAGVVVLTGAGMSTGSGVPD
YRGPDSIRATPILYHEFRHDPVARQRYWARNYQGWAVMSRARPNEGHRALSRWEHTGSPS
PLVGVISQNVDGLHEASGTRQLLTLHGRGADVICLDCARMFPRADMQQWMAALNPGVPMN
DHLGPAELRPDADAEVENWQGFRVPPCPACGGMLKPDVIFFGEPVPRGRVAAAFAWCDAA
DVLLVAGSSLTVMSGLRFARHMNKAGKPVIIINHGATRADEFATVRLDEDTTRVLPELVG
FGGTDRR
>PFR_JS14_1526	PFR_JS14_1526	Methionyl-tRNA synthetase (Methionine--tRNA ligase) (MetRS)	1744177:1746123 Reverse
MPVGRSVSSARLSRRQACDLLPAPLGPRAAAGPAGPRACVDTNAVPTILGAMCAHILATA
AWPYANGPRHIGHVSGFGVPSDVFARYMRMSGNDVLLVSGSDEHGTAIQVKADAEGLTAQ
ETADKYHRIIVEDLQGLGLSYDLYTRTTTLNHEAVTQEVFRTLYDNGYIIEKTQLGAISP
STGRTLADRYIEGTCPICGYEFARGDQCDNCGNQLDPIDLINPHSRIDGEVPDFVETTHF
FLDLPALAEELMTWLNSRKDWRPNVLNFSYNFAKELKPRAITRDLDWGIPIPVEGWENDD
MKRIYVWFDAVIGYLSGSIEWARRTGDPDAWKAWWQDPEARSYYFMGKDNIVFHSVIWPS
MLLGLNGEGSRGGTPSKWLGKLDLPTEVVSSEFLTMKGSKVDTSHGVVIYVGDFLREFGP
DTLRYYIAVAGPENKDTDFTWDEFVRRNNNELANEWGNLVNRSLSMAFKNNGEIPPAHEL
LNVDAELLASSKAAFITVGKLIEECKFKAAITEAMRVVATANQYISQQEPWKLGDDTDRR
DTVLNTALQVVSDANTLLTPFMPHSAQKIFEMLGGTGVWAAQPEIREVSEGEGDQEHSYP
VLMGDYDSAQAVWQSLPIKVGTPLTKPVPLFRKLDEALAENGPEWAKL
>PFR_JS14_1527	PFR_JS14_1527	Enoyl-CoA hydratase echA9	1746164:1747096 Forward
MADGDVQFEVREGTGYLRLMRPTALNALSPQMIAVITEQLSAWRDDASVQALDISGEGRA
YCAGADVRWMRSTMIENGVQSALEFLADEYAMDAVVAQFGKPVTTHLHGVAMGGGLGLGM
HGATRVATADLAMAMPEVGIGLWPDVGMLFEFSRLPGEIGTWLALTGLTIDANTALAAGL
VDQVDLMSAKPDLDLAWVDDYFVGDDAREIITRLEASSDERAVQAGELIRTRSPLSVAVS
LAAIRRAATLHSVGDVLDQDLAIARALLPDPQCDFVEGVRAQLVDKDRQPHWSVARIEDI
DPDKARAIVG
>PFR_JS14_1528	PFR_JS14_1528	Hypothetical protein	1747172:1747684 Reverse
MGHTVIQVPVPALETVVRPHVLASRPGVKLPDDVVCAHITLLGPFVDKTDVTAELVATIR
QVFNDVHRFEFELTDFRGFADGLVYLAPEPAEPFKQLTERLVEAFPAWQPYGGQFDEVIP
HLSLGTSLPAYEIMALLRKLPVEEVADRVTLTWWGDDEITNLEEFPLLAD
>PFR_JS14_1529	PFR_JS14_1529	Ribonuclease H	1747761:1748792 Reverse
MIVAAADGSSLNNPGPAGWAWFIDKDNWACGGWPHGTNNRGELMALLQLLTATAGAPDEP
LKVLCDSQYVINSVTKWMAGWKRRGWVKADKKPVQNVELLKAIDQAITGRTVSFEWVKGH
AGHPLNEAADTLAHGAATAYQQGKLPDPGPGFRGSGPVGVPGEPARGNASGPARGDASEA
ARGRVAPEPASTQEHRSVLGAPSPTVDPDAEPDLFSIADDPADDFAEVVRAEQSLLTDEV
RSDPARLRVLLHPDFVEYAASGRIWTRARLMAQIGPLPRRVTFEVMGQTRLSADTVLLRW
KAIDSASTSLRSSIWVRDGTLGRPRWRLLFAQGTVQAPGAPRT
>PFR_JS14_1530	PFR_JS14_1530	Basic membrane protein	1748864:1749808 Reverse
MSGANGFDDQGASRAASQGLDRAVAQLGVQSDRAEAHSVGDYPAAIQSMVGAGCTYILGA
SPDQSDALAAAARANTDLHFALVGATKPVSEKNLKLVRFQSSQVGFLAGYLAAASSSSGT
VGTFGATNAPAVTLYMDGFSQGITYFNQKASKAVKLVGWTMGSQSGDFLGGADPYSDKEG
ARARTEDLIGQGADVVMPVAGTADTGAVQAVNAHQGTRLVGTGSDLCASYVDACAATLGT
AAAGVDQMVFDAIEEAGVGFTNTTLVGTLANGGVTMVGVGKGAPVAQNIADDLTAVSQGI
KDGSIKVTSPSSVS
>PFR_JS14_1531	PFR_JS14_1531	Phosphotransferase family protein	1750058:1751347 Reverse
MNLERRAPRRERQRARRALTPDPDGLRLLTSTDGVDFARAAVGQCGGEVISARLDHIDHQ
PGRGTSVLYSCDVNWPGSRRLELVGLTWRAGGLNPADLDAEVFHDDNHEVAAWIYPEDPD
LPGLARATVVDQVLALLLEHRLVPVSCDASQLSLQMVSYRPRARAVVRASLRAAGSNRPA
MVFYLKAFTAADGPRALRRLEMMGRAGLPVARLLAATDDQLLVLAALDGQPMAHHIFDES
PAVSGDQLVGLLDELPAGLLDLPRRPAWADAVGHYADMVAGQLPAAGDRAREVARVVGAA
ADTAPADEPTHGDFHEGQLFLSGGRVSGLLDVEAAGPGRRVDDLACMIAHLSTVQHMDAG
QAARTEVLIRRLLASFDARVDPVQLRLRAAGVAISLASGPYQEQAPDWKHQTLGILAGAE
DLIRRAEQL
>PFR_JS14_1532	PFR_JS14_1532	CBS domain pair protein	1751411:1752931 Reverse
MPIWGSIAVIFVLFFIGGVFSAAEMALVSLRDAQIEQLSTRGKRGRAVKELTSNPNRFLS
AVQIGVTLAGFLSSAFGTDSLAGAWVAPAFARWGVAPGLAGVLAVIVVTALISFFSIVIS
ELFSKRLALQRPETMALVLAPIVNGLAKVFRPVIWALGASTNALVRLVGFDPKAGKEGVS
DEELRSMVVNAHSLGAEEKHIVDEVFSAGDRSLREVMVPRTEVDFLPGNMTVDQAIREVQ
GAPHSRYPVIDGSPDRVLGFLHVRDLMGVGSTPRNTPISKLVRPVLSLPETVRVPRALSD
MRRAHSHLAIVLDEYGGTAGVVTLEDLVEELIGDITDEYDVVDDDTRKHRQLSEIDGLTT
LEDFEDATGHVIPEGPYDTVAGFFMTERGEVPTVGDSIKVSLDSDAPVSDDDEDEEKLRG
DDYELTVTQMDGRRIAWLRLRALSDTAELGAGVIEPAAAQAATKPATELAADGDPNTVAH
LTETLARNKVATDVGKADPGGNAQRP
>PFR_JS14_1533	PFR_JS14_1533	Predicted branched-chain amino acidpermease	1753254:1753892 Forward
MYGISFGALAVTAGLTVWQACALSALMFTGGSQFAFIGVIAGGGTGAAAWGAATMLGIRN
GIYGMRIKALLRPSSRRIPLMAQITIDESNATATSQDILAEQHRGFWTAGVGVYVLWNLF
TLVGALAGDAMGDPKQWGLDGAACAAFLGLLWPRLKSRDPIAIAVVSAAITVITIPIVPP
GIPVIIAALVTAVVWEWRHHGDGATPDEGATP
>PFR_JS14_1534	PFR_JS14_1534	Hypothetical protein	1753889:1754200 Forward
MSLTAWVLIASASAFVIKLAGYLLPRSVLDRPQVIALAKMMTVGLLASLTIMNTVSSGQR
LTPDARLVSLLVAAIALKLRAPFIVVVLLGALAAALGRLAGLP
>PFR_JS14_1535	PFR_JS14_1535	Isocitrate dehydrogenase [NADP]	1754361:1755578 Reverse
MAKIKVEGTVVELDGDEMTRIIWKLIKDELILPYLDINLDYYDLGIEHRDATDDQVTVDA
ANAIKKHGVGVKCATITPDEARVKEFGLKKMWRSPNGTIRNILGGVIFREPIVISNIPRL
VPGWKKPIVIGRHAFGDQYRATDVKLPGAGTVTLTYTPDDGSEPMEMEVVKMPEAGGVAM
GMYNFNKSIEDFARASFNYGLNRHYPVYLSTKNTILKAYDGQFKDIFARIFEDEYKERFD
AAGLTYEHRLIDDMVASALKWEGGYVWACKNYDGDVQSDIVAQGFGSLGLMTSVLLSPDG
KTMEAEAAHGTVTRHYRKYQAGEETSTNPIASVFAWTGGLRHRGELDGTPGLVAFADTLE
NVCVKTVESGRMTKDLASLVGGDQGYLNTEDFMKALSDGLAEALR
>PFR_JS14_1536	PFR_JS14_1536	Malate dehydrogenase	1755756:1756742 Forward
MSTTPVKVAVTGAAGQICYSLLFRIASGSLLGDTPIELRLLEITPALPRLEGVVMELDDC
AFPNLAGVEIGDDPEKVFDGANLAMLVGAMPRKEGMDRSDLLGANGKIFTGQGKALNKVA
ADDVRILVTGNPANTNALIAKDNAPDIPDDRFSALTRLDHNRAKSMLAKKLGVNVGEVTN
MTIWGNHSNTQFPDLFHTKVGGKNAYELVNDEAWYENTYIPEVAKRGGAVIKARGASSAA
SAANATVEAMHDWAVGTPANDWVSMSVVSDGSYGVPEGLISSFPVTCKDGKYEIVQGLDL
NDFSKKKIAATVDELTKEQGEVREMGLI
>PFR_JS14_1537	PFR_JS14_1537	Hypothetical protein	1756924:1757247 Reverse
MTPAPPSSTKQPVAAPLKLDRLRAQWPLLLCLAFFVAGMAVTAAAHWRRGAVLMGAGLGL
AGVLRLFLPPRLAGLLVVRRRWFDVLVGIVGGTTMCVLAILVPPLER
>PFR_JS14_1538	PFR_JS14_1538	Bifunctional protein FolD	1757253:1758113 Reverse
MTAQRLDGKAVAAQIKIELKQRVDALREQGVIPGLGTVLVGDDPASQIYVNGKHRDCEQV
GIESYRVDLPADATPEQVERSIRVLNDSTMCTGYIVQLPLPPQIDPNWALELIDPDKDAD
GLTSDNLGKLVLGRSGVLPCTPRGIVELLRRYEIPLDGAKVCVVGRGTTVGRPLGLLLTR
RDVNATVTLCHTGTKNLAEETRQADIVIGAAGHPGLVTASMLKPGAVVVDVGVRRIEGKP
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VGDFTADVWDVASYVTPNPGGVGPMTRAMLLVNVVERAEQIAAQEQ
>PFR_JS14_1539□PFR_JS14_1539□Bifunctional purine biosynthesis protein PurH□1758187:1759740 Reverse
MTDPTRAPIRRALVSVYDKTGLEELGRALAAAGVEIVSTGSTARKLSEAGVEVVPVEQVT
GFPETLDGRVKTLHPAVHAGILADRRLESHRRQLDELGIKPFDLVVSNLYPFSQTVASGA
DFDECVEQIDIGGPSMVRAAAKNHPSVAIITSPDQYSQLTDALAQGGFTLAERRVLAAKA
FAHTAAYDASVASWFAEQTTDEGLPGFIGQAATKLHDLRYGENSHQRAAVYAAEGAAPGL
VGAEQLGGKEMSYNNYTDADAARRAAYDFSGPAVAIIKHANPCGIAVGSDIADAHAKAHA
CDPVSAYGGVIAANQIVTLAMAQQVKPIFTEVIVAPDFEPAALELLQTKKNLRILKAEDF
HFDKFLWREISGGLLASDPDRLDAPGDQTSGWKLVAGPAADAAMLSDLLFAWKACRSVKS
NAILLAHDGASVGVGMGQVNRVDSCRLAVSRAGDRAKGSVAASDAFFPFSDGPQILLDAG
VSAIVQPGGSIRDEETIEAASKAGVTMYFTGNRHFFH
>PFR_JS14_1540□PFR_JS14_1540□Phosphoribosylglycinamide formyltransferase□1759862:1760473 Reverse
MAYRVVVLVSGSGTLLQALLDAQAAGALDARIVAVGSDQPGCRALARAQDAGVDTFVVPM
TTLLPRGSAARQAWDEEFARAVDACSPDLIVLAGFMKLLGEPFMRRFAGRVINTHPAMLP
AFPGAHAVRDALTAGATTTGSSIFWVDDGVDTGSLIVQEPVPVHPGDDEDTLHERIKVTE
RRLLVATVNELARRAPAGDPTSV
>PFR_JS14_1541□PFR_JS14_1541□Hypothetical protein□1760484:1761962 Reverse
MARRRRTRTAVLETHAEESETSVRDRARTLPWRATTALSAVGTALASWIIVTAFCSLGWL
SQSQSSYAQVLEFGTHAWLLGHGVPMTIEGVRVSVIPLGFALLVMLVTTSFVMTIARHLA
TRAFGGRARTERQDAEARGLALRMTVWFTVPYMAILAVAASATGESAQIGRALIGGLVIC
GPITLITTGRALGWSVISFNQGGWIRGVIAGVWSAVAALIGVAALVLLIALIARHGQVGA
LHNALNPGGLGGAVLAIGQAAWVPNAVLWTAAWLLGAGFTVGDDTLLTPLVSRLGPTPDF
PILGALPSGAAPSSAGLAWLLVGVLAGALGAFVAVRARHNNATQALPPRRMSIEAAALCG
VCIGVLSGLLACVLIAFSDGSLGVERLRRVGPMMARVVVLAPTLMGAGGLLAGYGAMHVF
KLIARRGAAAPSPAPQPAGTRAKRPSLRALLRRRGEATVPTASRPDDNDTTDAAPTTDSG
SGAADPVHGDEG
>PFR_JS14_1542□PFR_JS14_1542□ATP-dependent DNA helicase PcrA□1762056:1764545 Reverse
MTDQTPPDLFSAFDQRLSALGAPGSGEGFAPHTPHDAHDDAEALLHGLNPPQEQAVVHEG
SPVLVVAGAGSGKTRVLTRRIAWLIAQRGVHPGSILAITFTNKAAAEMRSRVAELVGPRT
RTMWVSTFHSACVRILRTELAEAPELGLRRNFSIYDDTDTKRLMTLVLRDQNLDTKKFPP
RTVMGWISNAKNELLGPGAAAEQADNGNEELYAQAYEEYQRRLRAANAMDFDDLIMITVQ
LLHDHPDIREKYRRRFRQVLVDEYQDTNHAQYLLIRELCAPNEDQIDAPRVDPPELLVVG
DSDQSIYAFRGADVRNILDFEQDFPGARTILLEQNYRSTQTILSAANAVIQHNSGRPVKK
LWSDAGDGDKIIGWVADTEHDEARWVAEKIDELHDHQQAAYSDAAVFYRTNAQSRAFEEV
FIRLGLPYRVVGGVRFYERREVRDALAYLRAIANPADDVSIRRIINVPKRAIGARAETAL
EMFAVSQSIPFSQAVDRAAEVPGLATRSRHQVESFASMMAGFRGLVAAGSSADEVVAAVL
KDSGLLDELKDSKDPQDETRVENLVELVAVAQEFVAQAHTLDLSAGLRPDAPGDQDAPEL
ADELVAGMPEADDSLGAFLERIALVADSDQIPDSDPDSAGVVTLMTLHTAKGLEFDNVFL
TGMEDGIFPHMRALADPAELSEERRLAYVGITRARRRLFMSRAAVRTVWGQPQYNPPSRF
LEEIPAELIDWQRTGADLTSWGSSASARTASARRQTSTGGPVFGSGHGDLPRTKTVASLE
PGDRVLHSSFGMGTVVAAAGSGNNATADVDFGSAGVKRLALRFAPLEKL
>PFR_JS14_1543□PFR_JS14_1543□Phospholipase D domain protein□1764682:1765935 Forward
MRLPPATGRVVRNALLGILGAQLGAAGVLVAADNVRKHRAGPARFPRSAVTQARADDDLV
SVYSYGEDLYNDMLTAIRRAKHTIFFETFIWKNDPIGQDFKQALIEAANRGVAVYIVYDQ
FANMVVRPSFFRFPDNIHVKRHPLVQSVAFWNLRNSGRDHRKILVVDSRVAFMGGYNIGS
RYARTWRDTHARFEGPSVADFENAFVDYWNLRPVHLLSSQRSSMPELPDTSQRRWDGSVR
LSRNTPRWAVFPIRNMYLEAIDKAQRNIWLTSAYLIPDDDLRTALARAAQRGVDVRIIVP
AQSNHVIADWLSRGYYTGLLRDGIRLFLFHNAMVHAKTATIDGHWSTIGTANIDRLSLAG
NYEVNAEITSPQVATALERIFLTDQSNCTEMDLARWERRSIVAKGTEWLLAPWRPLF
>PFR_JS14_1544□PFR_JS14_1544□Fe(3 ) dicitrate transport ATP-binding protein FecE□1765992:1766747 Reverse
MIALADVLKKYSPEVCIGPVDLHIPDGGITALVGPNGAGKSTLLTMIGRLLGLDTGVIEI
AGYDVARTKSADLARVVSVLQQENHFVTRLTVRQLVGFGRFPCTHGRLSAADEELVDQAL
DFLALRDLEARYLDELSGGQRQRAYVAMVLAQDTEYVLLDEPLNNLDMRHSVQMMRHLHR
AARELGRTIVIVLHDINFAGRYADHICAMKDGRVAAFGPSDEIMDSAVLTEVFDTPVDVV
QGPHGPLAVYY
>PFR_JS14_1545□PFR_JS14_1545□ABC-type cobalamin/Fe3-siderophores transport system, permease component□1766744:1767862 Reverse
MADTQTEAVGRGRPGPAGGVGGPGSDMVVDTPTRETPPVRTHTGAFATRAARRRYLVVVV
GLAVAAVAASFGLLAWANPMPVGSRGFWKIAQRRLASLVVIAVVAFSQALATVAFQTITN
NRIITPSIMGFESLYRAVQTSAVYFLGVAGVVALQGVPQFLIQVAVMVALAVALYGTLLS
GRHANLQVMLLIGIVIGAGLGSVATFMQRMLSPSEFDVLSARMFGNISNAEASYLPVAVP
LCLAAGLGLWVRSQRLNVMALGASAATGLGLNHRRETMLGLTLVSVLIAVSTALVGPMTF
FGFLVATLTYSLAGTHDHRRIFPVAVLTGFVVLAGAYFVMRYVFYAQGMVSVIIELVGGT
TFLIVLLRKGRL
>PFR_JS14_1546□PFR_JS14_1546□Petrobactin ABC transporter, permease protein I□1767855:1768886 Reverse
MTLPDATPVRRTRHGASGGPPRPGPVPDRKLLDPKLLVGIVVVAGLLVLSLTTGVYDVFG
ASDGSRMFQITRVPRTVALVLAGAAMAMSGLVMQLLTQNRFVEPTTTGTTEWAGLGLLLV
MVIAPNASIGTKMAVAVVAAFLGTMVFFAFLRTVTLRSSLIVPIVGIMLGAVVSSISTFI
AIRMDALQSLGVWFAGSFTSILRGQYEILWVVAAVGVAIFLVADRFTVAGLGKSVATGVG
MNYERIILMGTGLVAVATGVVTVVVGNLPFVGLIVPNIVSLARGDDLRSNLPWVCLLGIG
LVTVCDPLGRVIIMPFEIPVSLILGIVGSVVFVVLLLRQRRRG
>PFR_JS14_1547□PFR_JS14_1547□Iron compound ABC transporter, iron compound-binding protein□1768883:1769899 Reverse
MSSTRFTNRGTLAVVALSAALLAGGLTACSSGAGSDTSPATHSAAALSSIEITDNNGTHT
VTTPPQSVVALDNRTFETLSQWGVGLKAAAVSLMPSTISYTTDKSIVDIGNHREPNLEAI
VAAKPDLVINGQRFTQYTDEIKSLVPDTTILDLDPRDGEPFDQELKRQTTVLGEVFGKQA
EAKKLNDDLDGAIARVKKAYKPADTVMAVNTSGGEIGFIAPHVGRALGPVYDFAGLTPAL
QVQGSSKDHKGDDISVEAIASSNPTWILVMDRDAAISADDPSYKPASELLKNSQALAGVT
AVKEGNIVTMPADTYTNESIQTYTEFLNDFAAALESRA
>PFR_JS14_1548□PFR_JS14_1548□Hypothetical protein□1770190:1770441 Forward
MGLISWIILGLICGTIAKAIIGGRAGWISSLIIGVVGGLGGGWLGSLLFHRPLSGFFSPW
TWLLSVVGSCLVLWVYNKVSSRS
>PFR_JS14_1549□PFR_JS14_1549□Response regulator□1770678:1771376 Reverse
MTSLPGPLTTDEPRPEGPRRVVLVDDHDIFRAGVRHELTAAAPDEIDVVGEAGDVEQAVK
VITGTTPDVVLLDVHLPGGGGAEVVRQVHQIDPKITFLALSVSDAAEDVIAVIRAGARGY
VTKSISTADLVEAIGRVATGDAVFSPRLAGFVLDAFSGSISVESIDEDLDRLSQREREVM
KLIARGYTYKEVARELFISIKTVETHVSNVLRKLQLSNRHELTKWATDRKLV
>PFR_JS14_1550□PFR_JS14_1550□Sensor histidine kinase□1771373:1772716 Reverse
MGSTRQRGTSSEPPRTGMNAPGGAVPSWPDGASGHPAGRGPRWPAGLARRMRGSWLGGVC
TGIADYLGSPVWPVRLCFVLLAMTAYLGVVAYAALWAFLPIKDEAAEQARAVRPARKPRS
SRRQDLEVWLSIGLVLLLCLGLLVLSRLFGLGSIHAFFWPVVLAAVGIGLVWRQADQPEE
EPDRLVPRWMAPLVSSSKWATVLRMGLGMTLVGASVLLVAYTQVDGPYLPAVLGMVALAL
AGFGVLTAPWMNRMRSNLARAHEEKLVADARADMAAHLHDSVLQTLALIQRQADDPKAVA
SLARRQERELREWLYGEAPGPRDFRAALRDAGAQVEDSSGVRVEVICVGDATLNDGLSAM
ILAAREAMMNSAKHSGADHIDVYAEVDDDHVELFVRDRGVGFDAEQIRADRMGVRRSIIE
RMERHGGTAQVRSAPGEGTEVKLEIAR
>PFR_JS14_1551□PFR_JS14_1551□Possible stress-response transcriptional regulator protein PspC□1772958:1773248 Forward
MGTKQLVRRHDNRWIAGVAGGLADYWGIDALAVRLGFIILGLVTFGTAFWAYLICWLLIP
DGVDGSKGLDAVKRTINGFRDKNDGPQDFNPYDDTK
>PFR_JS14_1552□PFR_JS14_1552□NADPH:quinone reductase and related Zn-dependent oxidoreductase□1773545:1774489 Forward
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MMLAMVLDHPGGADTFRPEERPIPEATATHSVLEVMAFGVNHAELITRAGGSPDVRFPRV
IGIEAVGRVHATSPASGLEVGQRVVTLMGGLGRDFDGSYQEYALVPNSQLYPVGIEMAWN
RLATIPESFYTALGSLDRMHLTAGDALLIRGGTSSVGLAAMQLAKSFGVRVTSTTRSPGK
IARLEALGADEVLVDAGTLPGTERFDGVLELVGAATLDDSMGHAAPRGCVVVTGGLGGQW
TVPDFDPFSIRGYLTNFQSTEVNPALLRHMLTLVAQQGLSLPIVGEFPLPDVGRAHEALE
TSTEMGKIVVSVAH
>PFR_JS14_1553□PFR_JS14_1553□Protein containing DUF1963□1774540:1775427 Reverse
MSQDLKQALFGVFDAVQKNAIKLDFGADPEPGEAGQSRLGGRPDVPRDFEWPRFQDKDDD
SADANRPLTFLAQVNLADATRYDTEGLLPTAGVLSFFYEMETQEWGFDPRDKGSARVFFF
EDPATLRPASVPDDLDDWFPDGQAISYRNMVDLPAWLGFTELPEEVRRTNPLPVPLTDIE
WEDYDAMREEYGAPSEGDDAVTTKLLGHPDVVQNPMEAECEMVTRGMADGAEGEEISQEL
RDDIEKASRDWTLLFQMGTDSGLEFGDVGHINYWIKKQDLARRDFDKAWLILQCG
>PFR_JS14_1554□PFR_JS14_1554□GMP synthase (glutamine-hydrolyzing)□1775632:1777056 Reverse
MVAKKPTAIILSGGPASVYVPDAPKVDPALFSTGIPVFGICYGFQLMAGALGGTVEHTGT
SEYGRTSVAIDDTGVLLHDLDDISSVWMSHGDSVTAAPAGFASLARTAGAPIAAFEAPER
KLAGVQWHPEVAHTERGQEVIEHFLFDFAGCKPTWTSSSIVDDQVSRIRAQVGDKRVLCA
LSGGVDSAVAAALVQRAIGDQLTCCFIDHGLLRKGEAEQVKHDFVQITGVDLVVADESER
FLSALAGVSEPEAKRKIIGREFIRSFEDVARQIAGDKGIDFLVQGTLYPDVVESGGGDGA
ANIKSHHNVGGLPDDLQFTLIEPLRALFKDEVRAVGAELGLPDSMVWRQPFPGPGLGIRI
VGEITQDRLDLLREADAIAREELTAAGLDREVWQMPVVLLADVHSVGVQGDGRTYGHPIV
LRPVSSEDAMTADWSRLPYDLLEKISTRITNQCPEVNRVVLDVTSKPPATIEWE
>PFR_JS14_1555□PFR_JS14_1555□ABC transporter, permease protein YjfF□1777480:1778508 Reverse
MSAQTLNAAVPTRALPSWLKIDRKRIPTLASVVIFLIMIIYGQAAYGQTLTMSTASNLLI
NNAHLIILAVGMTFVILTGGIDLSVGAVIAFSSVLGAQLLNAGWNPVLVMGIIVVVGGLF
GLASGVLVQYFRVQPFIATLAMMFLARGLASILSTTPIRLDDASGFRTLATQWKVIDGPK
VNDLVITPNVLIAVVVVVAGFFILHRTRTGRTVYAIGGSEPSAELMGLPVNRTKYLIYVI
SGLCAGIASVVYTSKLGMAQNVTGVGWELDAIAAVVIGGTLLLGGAGYVLGSVLGALVLG
LMNVLIARDGSIPPEATTIITGAILLLFVLLQRAVVKRDHND
>PFR_JS14_1556□PFR_JS14_1556□Permease component of ribose/xylose/arabinose/galactoside ABC-type transporters (Precursor)□1778505:1779563 Reverse
MKAIVKNQYFWGIIALLLLIMVDVIKDPSFVRITVNNGNLYGSLIDILRGSAPVLMIAIG
MTLVIATAGIDLSVGSLMAVSGAVSMEFLASAAHSGSTGAVLTALGLSLLVTVLLGAING
LLVSVVGLQPFITTLIMMMTGRGIAKVITGGQNTSARSDGFAWISTGTVFGFPVAFVIAI
AIVALVALVVRRSALGMTIESVGINQRASRMAGIKPLYILFSVYVISGLLAGMAGVFATA
NVMTVEVSKTGMDMEMDAILAVVIGGTSLAGGRFSLGGSAIGALLITTLNRTVTFLNVPS
AATPAFKAAVIIIVCLLQSERVRNLFKTLKRSRRVVEAAPARVEEVKEVVAA
>PFR_JS14_1557□PFR_JS14_1557□Sugar ABC transporter ATP-binding protein□1779560:1779910 Reverse
MRPPDPEKLIKNLSGGNQQKVLLARWLATEPRLLILDEPTRGIDLGAKSEIQEDVVKLAS
EGMSVIFISSELEEVVRLSQRILVLKDNRAIETITNGPDVSANTIVDIIAKDGQAA
>PFR_JS14_1558□PFR_JS14_1558□Monosaccharide ABC transporter ATP-binding protein, CUT2 family (TC 3.A.1.2.-)□1779968:1781092 Reverse
MTEPTARIVEMRGISIEFPGVKALQDVDLTLYQGEVHALMGENGAGKSTLIKALTGVYSI
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>PFR_JS14_1559□PFR_JS14_1559□Periplasmic binding protein/LacI transcriptional regulator (Precursor)□1781230:1782210 Reverse
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>PFR_JS14_1589□PFR_JS14_1589□Glycosyltransferase, group 1 family□1818038:1819183 Forward
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VSMPQYPAVRIATATTSRLTKLLDDFAPDVAHVAAPLVLGRAALRATRRLGIPSVALFQT
DFPTYLGRYLPRALSPARAEPLAWGIMRRVHAPATLTLAPSTATRQELVRHGFGRVAIWG
RGVDTTRFAPTRRDEALHRRWAPGGECVVGFLGRLAPEKNVADLSALSTLPGIRCVIVGD
GPLRDQLAARLPSAVFTGAMEGSEVARHMASFDIFVHPGELETFGQTLQEAAACAVPVIA
PRRGGPIDIVREASTGFLYPPGDLAAMRSQVARLVADAPLRHRLGDQAHRAMATRTWPRL
VGQLVQHYRTAIRLTAQAESR
>PFR_JS14_1590□PFR_JS14_1590□YjeF protein□1819212:1820630 Reverse
MRAIATVQQIRDAEQAWFDAHPGEDLMAEASAHVASTALQMVGDHARVLVVVGTGNNGGD
GLFAARDLANAGCDVAVWCTGSRWHEAGRAAAEAAGCVFADAREAVEGLAEASLVIDAVL
GIGGRAGLREPVAEFARACADVGVPVLSVDLPSGLAADSVGARDTISFRATRTVTFGALK
LCQLANPARQACGLGELAPIGLQIPSPRMWATELVDIAAHWPFPGVDSDKYSRGVVGLDT
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GSERYPGAGVLSTTGALFSGAGMIRFCGARRSAELVGAAMPSVTFGPGRVEAWVLGCGWG
ARDDAASVIAERLATGVPAVLDADALRDLPDTVPGNCLLTPHAGELARLLGRDRAEVEAD
PVAAARTAAARYGATVLLKGSTQYVAEPSGRVTLAVEGPAWTAQAGSGDTLAGICGTLLA
AGLSARWAGVLGASIQALTAAAKPGPYPPDALAHRMPGVLAKLAGRAAGARD
>PFR_JS14_1591	PFR_JS14_1591	Holo-[acyl-carrier-protein] synthase AcpS	1820632:1821099 Reverse
MIVGVGIDVCSVSRFDAMLERHPGIVERLFNPAETRVRGLARSGRSLSARFAAKEALSKA
LGAPGNLSWRDAEVVSDDNDRPSMKMRGSVARRAAELGITRVHLSLSHDGGIATAIVIAE
RDEPASDGPGGDEPGNEPGNSADLDEAERDEPGRN
>PFR_JS14_1592	PFR_JS14_1592	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 2	1821140:1822990 Reverse
MGMCGIIGYIGPEQATGVILDGLRRLEYRGYDSAGIAVQDNGRLEYRKKAGKLANLDAEL
AERPLPESHAGIGHTRWATHGVPNDANAHPQLSNDGRVAVVHNGIIENFATLRAELGAEG
VEFTSDTDTEVAAALLGRAVNRGNDLTVAMREVSKQLHGAFTLVAIDSQEPDVIVAARRN
SPLVVGVGQGENFVASDVAAFIDHTREAIELGQDQVVTITANDITVTDFDGGPAETRAYH
VDWGTTAAEKDGYDWFMRKEIFEQPKAISDTLLGRYSPQGELTLDEIHISPETLRRVNKI
IILGCGTAHYAGMVAKYAIEHWVRIPCEVELASEFRYRDPIVDSQTLCVAISQSGETADT
LQAIRHAREQGAKVIAICNTNGSTIPRESDAVIYTYAGPEIGVASTKGFTTQLIACYLLG
LYLAQVRGMKFGDEIRTIMDELEAMPAKMQSVLDHADQIYTLAKGMEDEEDFIFIGRHVG
YPIALEGALKLKEIAYLHAEGFAAGELKHGPIAIINPGMPVFAVVPPQGRDQLHDKVVSN
IQEVRARGARTIAVAEQDDNEVDQFAEVVISLPKVSTLLQPVLAVVPLQLFACEIATLLG
NDVDQPRNLAKSVTVE
>PFR_JS14_1593	PFR_JS14_1593	Pantothenate kinase	1823139:1824221 Forward
MSNPDGAPGAASGSPFRAAYATAHEQALAKALAARGVDEPDVTASPSQGTTPDSPWIELP
RAKWSQLAHDSHIALDQATVERLRSRQDPTDERDVEEVYLPLAQLISLRLKNRGRLFSAQ
NDFLQLDAERTPLIVGVAGSVAVGKSTAARLLQELLSRDAAHPNVALVPTDGFLYPTAEL
ERLGLLARKGFPESYDRRALLKFVVDVKSGCPDLSVPVYSQVLYDIVPGELNRIHNPDIV
ILEGLNVLQPAVVGPDGHTGLTVGDFMDFSVFVDADEADIERWFVERAVAFRASADDPDS
FFKTYAGLSDEEYRSEARKVWEAINGPNLRDNIAPTKPRATAILRKASDHRIESVRIRKI
>PFR_JS14_1594	PFR_JS14_1594	Phosphoglucosamine mutase	1824358:1825701 Reverse
MRGVANDDLTPELAFKLSVAAAHVLGEAGAFDGRRAVAIVGRDTRISGELLQASVMSGLA
SAGVDVIDVGVIPTPGLAYLVESQGVDVGVMLSASHNPMPDNGVKFFQRGGVKLDDKIED
VIQERLDEDWVRPVGAAVGRIKPDSSLIQTYISHLVGSLRGVSLKGLTVVLDCANGSSSV
TAVPAFSSTGAQVLAINGQPNGLNINENAGSTHIEGLQKRVVAEGADMGFAFDGDADRCL
AVDADGHVVDGDQIMAILALALKDEDSLAEDTLVATIMSNLGLIHAMRAHGVKVDQTKVG
DRYVLEDMVANGFSLGGEQSGHVIMSEFATTGDGVLTALHVASRAAQTGKSLAELAGVMH
RLPQALVNVPNVDKLRAALDPVIQSEANAANKKLGNSGRVVLRPSGTEPLVRVMVEAATQ
DEADEIANALAKVVAERVGLSKAGRAS
>PFR_JS14_1595	PFR_JS14_1595	30S ribosomal protein S9	1825853:1826404 Reverse
MSAPTNEDSTVSQTTNDDVETGTTPFTDENNREIAYRADSTGAAPNASTSRSAVIAPGIG
LGRRKEAVARVRLTPGTGKYTVNGKTLEAYFPNKLHQQLINEPFVVSGSADAYDVVARIV
GGGISGQAGALRLGIARALNQIDEEVNRPGLKKAGLLTRDSRAVERKKAGLKKARKAPQY
SKR
>PFR_JS14_1596	PFR_JS14_1596	50S ribosomal protein L13	1826401:1826844 Reverse
MSTYSPKPGDITRTWHVIDAEDVVLGHLAVAAATLLRGKHKPTYAPHMDTGDFVVIVNAS
KIAISGNKREGSLRHRHSGRPGGLHTTSIGELLDSDPRKAVELAVWGMMPKNKLSRQQMS
KLKVYAGPDNPHKAQNPEPYEIKQVAQ
>PFR_JS14_1597	PFR_JS14_1597	Uma4 protein	1827192:1828499 Forward
MSHPTFTTPCLTTFCGLDELGLEAVGQRLDPDRAVIECRVVEPDRWCRECGCEGAPRDTV
IRRLAHEPFGHRPTTLLIRVRRYKCCGCGRVWRQDTTAAAPVRAKISRGGLAWGLAGLVL
DHLSVTRVAAGLGVSWSAANDAILAEGRRRLIDDPARFEGVTTIGVDEHVWRHTRHGDTY
VTVIIDLTPVREKTGPARLLDMVAGRSKAVFKTWLAARPKPWREGIEVVAMDGFTGFKTA
AAEELPDAAPVMDPFHVIRLAGDALENCRRRVQHDVFGRRGMKGDPLYQARRTLLTGAGL
LTDKQQARLDALFVEDRHVEVEATWGIYQDMITAYRDKDRGLGRFFLAHTIDKISASVPE
QLVEIRKLARTLTQRASDVLGYFDRPGTSNGPTEAINGRLEHLRGTALGFRNLSHYIARS
LLEAGGFRPALHPRS
>PFR_JS14_1598	PFR_JS14_1598	Elongation factor G fusA2	1828580:1830676 Forward
MRTVSSPTDLRNVVLVGSAGSGKTTLFENLLRARIPGYRGERDDAERASALTLATIGNHN
DTAGSDVVINLLDAPGHPDFYGDLRAGLRAADGAVFVVSAADGVDPITAALWAECAEVNK
PRAIVVTKLDTDKADFFATTELIHEAFGAGTHPAYLPLLREEGGEVIGNISLLTGHVHDY
SSGQRVTRDTTPLERAEMDAFRADYVESIITESEDEDLLERYFNGDDLETGKVVEALFRA
LYHGTFFPVIPVLMDGIGVEELLGMIHRGFPMPNRRVLPAITTAGNDLVEPELGDPAGPL
VAQVIRTVADPYAGRLSMVRIYSGTLRTDATVHVAGHREAMTGRALDHYPDHDDEERVGQ
ITVPVGTDTAVQDAAIAGQIVYVARMAHAQTSDTLSDTDAPMVVEPWPLPRPLLPLALHA
TSRNDDDKLSNALQRLLVEDPTVSVERDPATDQLVLWTMGQAHLDLLLARLTGRYGVNVE
REEIKIPLRETFIAETVGHGRHVKQSGGHGQYALANVRIEPGERGSGFVFAEEVVGGSVP
RQFIPSVEKGVRTQLDRGVLSGYPVVDVKVTLTDGKAHSVDSSDMAFQAAGAAALRDAAS
AETVALLEPFDEVTVVCGNEYVGAVMTDLGSRRGRVTGQHGGDDGRTTVTALVPASELTR
YAIDLRGLSHGTGRFEREPAGYELMPPELAQQVLDERG
>PFR_JS14_1599	PFR_JS14_1599	PF03733 domain protein	1830808:1831203 Reverse
MPKPLATLLNVIWLVLGGVWLALGYVVAGVIGCVLIVTIPAGIASFRMARYVLWPFGRTV
VPKPGAGAGTAAMNIIWMIVAGWWLALLHIISALAQAVTIVGIANAVVSLKMIPISVMPF
GKQIVSTTSNR
>PFR_JS14_1600	PFR_JS14_1600	TRNA (guanine-N(7)-)-methyltransferase (Precursor)	1831416:1832285 Forward
MSDNSRVHHAMADGAAGGRVGPGGTNADPSGTSHSSTGHSSADPINGHRGVVSFVRRSPR
MNESQRQALAAHSSEYLVEVPHDRLSTSVRHGATMSWPQVFGRQAPLVAEIGSGVGDSLV
AMAGARPSDNVIAFEVYLTAVASTMGKLARADVHNVRLVVADGGEGLRELVRPGELSELW
TFFPDPWPKKRHHKRRLVQPGFAELVADRLAPGGLWRLATDWADYADQMREVLDAEPGLT
NVYSDRPGGWAPRPDRPFTRFEKRGLDAGREVRDLAYRRVHPEGDGENG
>PFR_JS14_1601	PFR_JS14_1601	TRNA pseudouridine synthase A	1832278:1833156 Forward
MGDRRFRLDLSYDGSHFHGWAMQPGQRTVEGELATWLTRIAGTAQPVRLVVAGRTDAGVH
ARGQVAHADLPATMDAAELKRRLLRALPPDIVVRRLTVAPPGFDARFAAIWRRYVYRLWD
LSSHPDPLLRGMVTTKSLDLDPELMTAAGSRLLGLRDFAPFCRRREGATTIRTLLQCEAH
RVADGCGTIELTVRADAFCHSMVRSLTGALVAVGSGTQSMDWLDEVAAGPTRAGSVTVMP
ARGLCLEQVAYAPDHELAQRARAAHARRTLPAGPETTTGPVDSDDCGCGFEG
>PFR_JS14_1602	PFR_JS14_1602	Methyltransferase small domain protein	1833194:1833793 Forward
MTQYFVNPEGPAKYHQLHATIWGHDYEFRSSNGVFSQYRLDLGTSVLLRTLDPPVDRPAR
FLDLGCGFGPIAVALATECPRARVDAIDVNERAVELTAMNAKALGVASQVSASAPDQVPA
DVRYDEIWSNPPIRIGKPALHELLDTWLNRLTDDGVAHLVVAHNLGSDSLAKWLTGQGWQ
VDRLGSAKGYRVFDVTRRH
>PFR_JS14_1603	PFR_JS14_1603	Hypothetical protein	1834072:1834623 Forward
MKSSPTLAVAALGLCAITALAGCSSSTSGSSSSPSNTATALSMKDCTSQGKVWLVVQTDQ
DKTLANQCVGTPSTGTAALEAANVAIGRSSDGKMICTLGDYPNPCPATFTGAYWQYYTAT
PNGSWTYSDKGADDSSPKAGSIEGWCYGTTCTPKLDGVSAAPSASQSTEASATSSSTSSV
SGS
>PFR_JS14_1604	PFR_JS14_1604	Cobalt transport protein	1834669:1835769 Forward
MVAAPASVHRMARRSTHPWAWWCWAIGAAAAVSLTHNLALIVLVCAAVITVVMVRRSDAP
WARAMGLYITLALVIVTIRMLFQITIGGIRYGRVLFTLPQLQLPGWMAGIRLGGPVTLEG
LVYTAADAGRLGAMIICLGAANALANPKRALRSVPSALYEVSTALVIAMSVAPQLVESLL
RIRRARRLRGGTVRGLRGLGALVIPVLQDSIERSMSLAASMESRGYGSTRDKARVGRGAG
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FAMLASLALLCFGAFSLLSLANGAVLGISTLGAGVVAAVIALRSSGRQLAVTHYRPDPWR
ARESITALCGLAVIGVTVQLGIIAPKVLTPPAQPATWPALDPLMIVIIGLILAPIAATTT
PPAGEA
>PFR_JS14_1605 PFR_JS14_1605 ABC transporter 1835766:1837382 Forward
MIEFRDVSFTYTGASDPVLHDVSFQIPEGDLCLLVGRTGTGKSTLLRSINGLVPWFDGGR
LTGTVQVDTMVTSQHRPRDLARVVGSVGQNPLAGFVTDKVEDEIAYGMEQLGVAQPAMRR
RVEDTLDLMGIADLRHRPLTDLSGGQQQRVAIAAVLAAQPRVVILDEPTSALDPTAAQDV
LSSITTLVHEVGLTVVVAEHRLERVMAFADSVAWLPGDGSVQVGPAGDVLARADVRPPLV
GLAQALGWSTVPLTVRDARRRVKAEHIVLTDPPQAPAPDGPVVLTATKLVVDYGETRAVN
AVTTAFRAGEITALMGRNGAGKSSLMWAMQGAVASSGTLEVTGADPRTVSAEKARELVTL
VPQTAADLLYLPSVGDECRQADKESGRDEGTTAGLLSELGVALDMGRDPHDLSEGQRLAL
VLAIQLSSRPRVVLLDEPTRGLDYTTKAHLATMMRSLASRGVCIVVATHDVEFAAASTDR
TIVMAEGDIIADDTTREACTASPTFSPQLAKVFWPQPILTVADVRRGRGQQADGATRP
>PFR_JS14_1606 PFR_JS14_1606 Substrate-specific component CbrT of predicted cobalamin ECF transporter 1837379:1838230 Forward
MNLLTRHRGPATAGGYLMPLEPRKRLSARTSVMLALTAVLGLVAFCWPLFVRPGAVLGSD
ASGRTATPFVMGAIMAVVLALLIAELSNEDLDVKALAMLGVLAAVGTAVRPVGAGTAGIE
TVFVLLILAGRVFGPSFGFMLGILTMFSSALLTGGVGTWLPYQMLGAGFVGLLPGLLPRR
RPRPGSVGEIVVLCLYGFVAGFGYGYLLDFAFWPFTTGLGMGAPGFDPEASPWRNLHTFF
VLDTVTSAGWNMGRALTNAVLIALLGRPLMRILRRTSRQARFD
>PFR_JS14_1607 PFR_JS14_1607 Putative integral membrane transport protein 1838245:1839837 Reverse
MVGTLAKLQLTLAWRGVRSSTGRIIGTVIMGIYGLGLTALLVFGLVMMRTPAMDAWRGPV
LTLAFGLVTLGWPLITMFTAGSNELLDPGRFALFPVTARQLIPGLFAAAMLGAGALDTAL
LALGTVISWSGGLGTAVAAAVGAVLGVATCVISARALTALMSRVLASRRFRDVGGVAFFA
VIMAVSFGMQFGSRIFADSGAPQDVIFIAARITSWTPFGWAWALPWDVAQGAWLPAAAHL
VLAAALVWALLRLWERSLARALVSPLDSAAVGGTVKSGRFDFLAPRGPIGAVARRDLRYW
RRDPRRLIQLLAVIVVPVFMFAPGLAQGMSQGSNFAVDFAAVLGGVIVASTLAWSISYDG
SALWMQVLSGVTGREDRIGRCWSVTIVTAPYLLVVLFGSLFLTGDWQLLPGLIGALITAF
GSSLGVGSLVGALWQQAMPAPGGNVFSRGSGTTAENFLGSMIAMIAPIVLTAPNLALAIV
SWWKPWAGWAAIVVGLVIGSLACWAGVRLGGRHLDKHWPEVLNKVKETHA
>PFR_JS14_1608 PFR_JS14_1608 ABC transporter domain-containing ATP-binding subunit 1839807:1840847 Reverse
MSEQTPPPGGTSGPDPAREEPVISAFTEPQESATTPSGAHIPTPVPMPGFAPPPPMPAPT
AAGIIGDDPSLDEPVPTSVAPGRTRPVRPPGPPALSIVGLRKAFGAKLAVADLSMAVPRG
CMFGLVGPNGAGKTTTLSMATGLLRPDAGQVLVGDVDVWADPARAKALMGVLPDGLRLFD
RLSGRELLKFVGQMRRMDEATITDRSNQLLSTLGLSEDANTMVADYSAGMTKKIGLACAL
IHRPRLLVLDEPFESVDPVSGETIREILHEFVAGGGTVVLSSHVMELVETLCDAVAVMAA
GRLLAIGDTDDVRQGKPLQQRFLELVGAHHLEGGGLSWLGRSQSSN
>PFR_JS14_1609 PFR_JS14_1609 Superoxide dismutase 1840943:1841611 Forward
MKGAPRKTRYVKATQLKEDNMAVYTLPELPYDYSALEPYISGEIMELHHDKHHKAYVDGA
NTALDKLAEARDKADFGAINKLEKDLAFNLAGHVNHSVFWKNMAPKGSAPERPTDELGAA
IDEFFGSFDNMKAQFTAAATGIQGSGWASLVWDPLGKRINTLQFYDHQNNLPAGSIPLLQ
LDMWEHAFYLQYKNVKGDYVKSWWNVVNWDDVALRFSEARVA
>PFR_JS14_1610 PFR_JS14_1610 Resuscitation-promoting factor RpfB 1841906:1842991 Forward
MKNGLKTLLIGGVGIATLAVGGVGTAIADNEVSLNVDGQQKTVHHFGGTIADMLDKQGIQ
LGDHDQVIPDASQKLHDGENVTVRFGRQITVTFNGQTHTLWTTSTNLAEILAQLGVSDDA
KLSVDRSMNVGREGLTFTAVTPRHVKVIADGRTVEVSSTDPTVGGLLKGLGIEVGGDDVT
SAPLESLPVEGMTLTVQRGHVDEKTVDEPIDYDTVRQEDPSIPSGTTKVKTAGVEGARTV
TYRIKTLDGKEAQRDVLSQTVHKQPVSKVVLVGTGQAASGGATDTANSGIWDRIAQCESG
GNWSINTGNGYYGGLQFAASTWAAYGGTAYAPTANLATRDQQITIANKVYAASGLSAWGC
A
>PFR_JS14_1611 PFR_JS14_1611 Glycosyltransferase, group 1 family 1843101:1844342 Reverse
MRGTDRVFSRPGPGAAGGAYVAGLRPGDHNGPMRIAQLANFVAPHSGGMRVALDGLGREY
VAAGHERILIVPGLRDAEVETASGVVCQIASPRVSGTYRMIVRPGAVRRALRRFRPTNVE
CSDKWTLAWTGRWATHHGVGSVLFSHERLDDMLAGWLRARRPMRRMVGFLDRRIVPRFDR
VVVASQYAAEEFARWSPRVRVVPLGVDLSEFRPLPPTPRDAGAPLRLVLVSRLSREKDPQ
LAIDAVLELHRRGVPVRLDVFGSGPDEEALRSRARGGPITFHGFIADRGELSARLGAADL
SLSVSPKETFGLVVLEALASGTPVLTSNRGGAREIITPGAGVVDEPASGHVPWGAWAPSR
PTALAEAIEQLIGRLGPGMRRAARQRAEQFSWQDCAHRMLQVHQETLGDGGRQ
>PFR_JS14_1612 PFR_JS14_1612 50S ribosomal protein L17 1844383:1844970 Reverse
MPKPTKGPRLGGSPSHQRIILANLATQLFEHGKITTTQTKARRVQPFAEQLITKAKRGDL
HSRRLAAKTVKDKFVLHRLFDEIAPTMAEREGGYTRVTKIGNRKGDNAPMAVIELITEKP
SVKAAPKAADKAADVKADIETKAEKKADKANEASSEKVEAVEEKAEEAKAKSAEVKEAKK
AERTVQESVEKSDHE
>PFR_JS14_1613 PFR_JS14_1613 DNA-directed RNA polymerase, alpha subunit 1845014:1846033 Reverse
MLIAQRPTLSEEVVNDFRSRFVIEPLEPGFGYTLGNSLRRTLLSSIPGASITSIKIEGNQ
HEFSTLPGVVEDVTEIILNLKGLVLSSEEDEPVAMYLRKSGAGEVTAADIAVPTGVEIYN
PDLHIATLADDGSIEMELVVERGRGYVSSTLNNNPDAEIGRIAVDSLYSPVLTVSYKVEA
TRVETRTDFDRLIVDVETKPSIRPHDAVASAGKTLVELFGLFRELNVEAEGVEMGPSPVD
EQLAADMALPVEDLNLSVRSYNCLKREGIHTVGELVSRSEQDLLDIRNFGSKSIDEVKEK
LGDLGLTLKDSTPGFDPLAAADRFEDEDDGADYAETEQY
>PFR_JS14_1614 PFR_JS14_1614 30S ribosomal protein S4 1846158:1846763 Reverse
MARYTGPMTKKSRRFGTDLVGNDKAFERRPYAPGVHGRGRTKDSEYSLQLKEKQKARYAY
GVLEKQFHRYYEEASRRPGRTGDLLLQILESRLDNVVYRAGFASTRRQARQMVSHGHILV
NGKKVNIPSFRVTPLDIIDVRAKSQEMTPFVIARETFGERDVPGWLTVKPNKMRVLVHQL
PTREQIVLDVNEQEIVELYSR
>PFR_JS14_1615 PFR_JS14_1615 30S ribosomal protein S11 1846794:1847201 Reverse
MATTSRKAASKTKVRRKVKKNVVTGEAHIKSTFNNTIIAISDPNGAVIAWASAGTVGFKG
SRKSTPFAAQMAAEAAGRRAMDHGMKRVDVFVKGPGSGRETAIRSLGAIGLEVGTISDVT
PVPHNGCRPPKRRRV
>PFR_JS14_1616 PFR_JS14_1616 30S ribosomal protein S13 1847247:1847621 Reverse
MARLQGVDLPREKRLEVALTYIFGIGKTRADAILEATGISPDIRVKDVTDAQLVELRDFI
DANYEVEGDLRRSVDADIRRKIEIGTYQGRRHRAGLPVRGQRTRTNARTRKGRKKAVAGK
KKAR
>PFR_JS14_1617 PFR_JS14_1617 Hypothetical protein 1847874:1847987 Reverse
MKVRPSVKRMCEHCKVIRRRGVVRVICTNPRHKQRQG
>PFR_JS14_1618 PFR_JS14_1618 Translation initiation factor IF-1 1848080:1848301 Reverse
MAKKEGALELEGTVVEALPNAMFRVELDNGHKVLSTISGKMRQHYIRILPQDRVVVELSP
YDLTRGRIVYRHK
>PFR_JS14_1619 PFR_JS14_1619 Hypothetical protein 1848681:1848965 Forward
MAFFAVNYTYDPAKDVEAVRPRHREFLRGLAERGVLRASGPFPGLEPQRSLLIFEADSAE
EVATLLDQDPMHTEDILKVREILEWNPVIGIFAV
>PFR_JS14_1620 PFR_JS14_1620 Hypothetical protein 1848995:1849381 Reverse
MSQLPIGSRPPRDPQRPVADAQRDDLTQRLNTAYERGDLSLEDYQGLLAQLFEAHTTGDL
VPVVQALPAQYRVPSAPQGAEVDTNLAPGEVNQSRKRADLSLPMAKVGIGIAAVLAIIVV
AIVIGVAL
>PFR_JS14_1621 PFR_JS14_1621 Methionyl aminopeptidase 1849407:1850237 Reverse
MERIEVKSLDQIKAMRVAGLVVAEGLAAMGDAVRPGITTGEIDQIGRDVLAAHGATSNFL
GYGTEWGLPPYPGVACISVNEVVVHGIPGSRVLQPGDIVSIDYGAIVNGWHGDAARTFAV
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GTAMHQAPDIPNYGKAHRGPKIGPGMCLCVEPMVTLGMDDTAVLDDEWTVVTVDSSRAAH
WENTTAVLPNGLWVLTEPDGGRAQLEAHGASYAGLD
>PFR_JS14_1622 PFR_JS14_1622 Adenylate kinase 1850249:1850809 Reverse
MGAPGAGKGTQAVGIATHYGVPAISTGDMFRDNVKNGTPLGKQVDAIMKAGDFVPDELTE
QIVADRLDQPDAQGGFLLDGFPRTMHQVDALDDYLDKHGHSLDAVISLDVDPEDLIARLL
KRAELEGRADDNEETIRHRMEVYTSSTAPLLDAYKSRGLLVAVDGNGTVDEVGARIAAAV
DAKVGR
>PFR_JS14_1623 PFR_JS14_1623 Protein translocase subunit SecY 1850821:1852134 Reverse
MISGFLNAFRTPDLRKKMLFTLFILVIFRIGSTIPAPNVNIAAIQKCASDATTGDQAGVY
AMINLFSGGALLHLAIFALGIMPYITASIILQLLTVVIPRLEALKKEGATGQETITKYTR
WLTIVLGVLQATSFTMMAVSGQLYRTCTESVVYSDGVFPIIVMILTMTAGTSLIMWMGEL
ITDRGVGNGMSILIFTQIAARFPSSMWSIKTAHQGNQGWLLLVLVVAVGLLVMAGVVFVE
QAQRRIPVQYAKRMVGNRLMGGSTTYIPMKVNQAGVIPVIFAASMLYLPMLYAMFRPEGA
AATWIATNLNGRGDTVWYNVIYVAMIIFFTFFYVSITFDPVEVSDNMRKFGGFIPGIRAG
KPTEDYLAYVLSRLTAPGSLYLALISLIPTVAIVLLGADQNFPFGGTSLLIMVGVGLDTV
KQIDSQLHQRNYEGFLK
>PFR_JS14_1624 PFR_JS14_1624 Dipeptide/oligopeptide ABC superfamily ATP binding cassette transporter, permease protein 1852434:1853507 Forward
MTPTRGLADNATESDAAEQSRTARRPRGAGVIKYLLRRVLGWIGMIFLATNLTYFLANLF
LDPKANYLERNPPIPDDQIDRMLHPYNLDPTVSLIDRWWTWLQDVLLHWNWGMSPDGQAV
NTQVAFRVWNSAQLMLGATILACAVGIAVGVYTASRQYKLGDRIFQAISIVAMNTHIVVA
SMVAVIVAIAINGAAGQRIFFVTGSASIGVHGFFPVLLDKAQHLILPTLCLLFINYASYH
FMQRSLLLDNINADYVRTARAKGLTKPQAIRRHALRTSIIPVATQVAFAIPGIFTGAVLT
EKIFGWQGMGDYFVTTIAKNDIHGVVAVAAFAAAMTAVGAILADIFVVLLDPRVKVS
>PFR_JS14_1625 PFR_JS14_1625 Oligopeptide transport system permease protein OppC 1853509:1854495 Forward
MSQTPDQLVPDELGYVATADGDQNLNLPAHRTRRMRLYVRRFWRNKPAVVGLGVFAFLVL
CSLVGGRFTPFRYTDMDFGALGAQPGTPGSVVRPDGTLVNATHLFGTNSGGIDVFAMLMH
GIGRSMTIAVSVSLVTTLFAAFISALAAYLAGLTERIVLAVINFLLILPSFLLMALIANH
YSGAWQMLIVVMIVFGWMYPARVIWSLSTSVREREYISAARFMGARGPSVVIRHMVPNIG
SLLVIQFTLGVVSTVMTETGLSFLGFGVKIPDVSLGTMLQSGVSAISSTPWLFWFSAGTL
TLLTVSVALISDGLRDALDPNSAAGGRA
>PFR_JS14_1626 PFR_JS14_1626 Oligopeptide transport ATP-binding protein 1854492:1856591 Forward
MTDPILSVNDLHVSFPSEAGVVDAVRGVSFDLYPGRTLGIVGESGSGKSVTSLAIIGLLA
DSAKVTGSVTFDGTELLGLSDQQMTRHRGNDIAMIFQDPLSSLTPVFSVGDQIIEALKAK
NPHISESDARARAIELLGLVGIPNPATRVKSFPHEFSGGMRQRVVIAIAMANNPRVIIAD
EPTTALDVTIQAQILDLLKVAQRETHAAVILITHDMGVIAGSADEVLVMYAGKPVEQAPV
YEVFSHPRMPYTLGLLGAIPKVHHNDNAPLVPIKGNPPILINLPDGCPFAPRCPVAVDHC
RTREPALEVIDTIDQTVSHPDTAPGEAELVHSSACWRSGEIHGGEIDGKPVFPVPPRPAS
DIRETPRDERATTIKVDHLVKTFPLIKGALLKRRVGSVYAVDDISFDVRAGETLSIVGES
GSGKSTTLLEIMAMNHDTVGEIELDGKRLKTLSRAQRRAERRNIQMVFQDPMGALDPRFT
VYDIIAEPLHTLGFPRDGIEARVNELMNLVGLDPAHIDRFPGAFSGGQRQRIGIARALAT
NPKVLALDEPVSALDVSIQAGVINLLAELQAKLELSYLLVAHDLSVVRHISDRVAVLYLG
GIVEIGDVDAVFDESRHPYTQALLSAIPIPDPTVERTRSRVVLKGDLPSPTDNEPGCRFA
SRCPLFQTLPEQDRARCLHETPALHGGEGADHLVACHFR
>PFR_JS14_1627 PFR_JS14_1627 Oligopeptide-binding protein OppA 1856662:1858380 Forward
MRSTTTKAFAGVAVLALALAGCGSNSGSSTKSADSNAKLSYSINEQAATNLKDGGNLNLS
IGEITPQLNMFQANMTVDTSTLWNWYNPQLIKFTPSGDMKLDKNYLESVNSELKDGKTVV
TYKINDKAKFNDGTDLDWTAFQATWQANSGKEQEYNANTIDGYDQIDSVKAGDNAKTVVV
SFVGPYPWYSSLFNNVLHPAVNSADIFNNGYTGGTLASAHPEWGAGPYALTGFDANAGVV
TFERNPNWWGDKGKLDKITYTVRADVQAQVNAYKNGEADTVETSTSELLTQVTSVADTDI
RRGTRAANYLLTMNSKSELLSDTAVRKAIATGINRAQLQQVLFQGLDYSEAIGGSLTLYP
FQKGYQDNLSKVVAKTDTAAATKALEEAGYAKGSDGTYAKDGKALSLRLPLFSSSTTSKA
MYQAFQTQMKAVGIDVQIIQKSSKDFSTTVKNRDFDLLISGWASTDPNGVAFFCQKFCSD
STLNKSGTGTAELDNLIKGPGGLTSLQTAEDQESKANELEVQALGTFGILPIYNGPEIFA
VKKGLANVGAGVYATTRAQIGDFPENIGWQKD
>PFR_JS14_1628 PFR_JS14_1628 Putative luciferase-like monooxygenase, FMN-dependent, CE1758 family 1858632:1859828 Forward
MDTTENRVPVQIGIFSVSDLTPDPTTGITPTEHERLKNYALIVKKAEEIGLDAFALGEHH
NPPFVSSSPTTTLGWLAAQTSKITLSTATTLITTDDPVKIAEDYAMLQHLADGRVDLMLG
RGNTGPVYPWFGKDIRQGINLALENYNLLHRLWREEVVDWQGKFRTPLQGFTAIPRPLDD
VPPFVWHGSIRSPEIAEQAAYYGDGFFHNNIFWTMNHTKRMVDLYRRRYEHYGHGRYDQA
IVGLGGQFFMRKNSQDAIKEYRPYFDNAPVYGHGPSMEEFTEYTPLTVGSPQQVLERTLS
FKDDVGHYQRQMFLIDHAGLPIKTVLEQLDLLGEILPEMRKGFLEGRPDDIPDAPTHASL
VAARDAAGVAPVEHVKVGADDVTGTSDAPEPPDSVFEK
>PFR_JS14_1629 PFR_JS14_1629 FMN reductase 1859939:1860586 Forward
MKVLAISAGMGQPSATRMLVDRLAAATVKHAGAAGLELDEPIEVIELRDIATELMSSEIS
RVPSPRVAGAIESVEAADTLIVVSPIYNTQPAALLSLFFEVADDAILRGKPVLLGATGGT
ARHSLAIDRALLPLFHYLHALVVPTSIFAATDDWGSPASLDKRTEDAAGSFVGLLAMRAG
VPNTDELSGSDTDKASHGDDDFELENDFETMLKSI
>PFR_JS14_1630 PFR_JS14_1630 50S ribosomal protein L15 1860943:1861386 Reverse
MAIKVHHLRPAPGAKQTKHRVGRGEAGKGGKTAGRGTKGTGARKNVPENFEGGQMPLHMR
LPKLRGFQNPFRVSYQVVNISRIADLFPAGGAVGVDDLVKAGAVRDGQLVKVLGDGDITV
KLEVTADKFSASAKEKIEKAGGSVTVQ
>PFR_JS14_1631 PFR_JS14_1631 50S ribosomal protein L30 1861388:1861570 Reverse
MAQLKITQIKSTVAEKPHVRSTVKALGLKRIGDVVTKPDRPEFRGMAQAARHVVTMEEVK
>PFR_JS14_1632 PFR_JS14_1632 30S ribosomal protein S5 1861570:1862181 Reverse
MNTQAQGRGRGQGNDRRGRDDRRGRDNDRNRDQYLERVVTINRVAKVVQGGRRFSFTALV
VVGDGEGTVGVGYGKAKEVPAAIAKGVEEAKKNFFKVPMVQRSIPHPVQGEKAAGVVMLR
PASPGTGVIAGGACRAVLECAGIQDVLAKSLGSPNAINVVHATVAALKMLEEPEQIAKRR
GKSVADVTPAALLRARQEVEVKA
>PFR_JS14_1633 PFR_JS14_1633 50S ribosomal protein L18 1862204:1862587 Reverse
MAININHRRNLAQRKASQMRRQKRVRKHIFGYPERPRLVVTRSARHMFAQVIDDVAGRTL
ASASTMETELRGMSGDKTAKAEKVGELIGQRAKEAGISQVVFDRAGNQYHGRVAAVADGA
RKAGLGL
>PFR_JS14_1634 PFR_JS14_1634 50S ribosomal protein L6 1862590:1863132 Reverse
MSRIGRLPITVPSGVEVNLDGQKVAVKGPKGNLDWNIPEPITIKKNDEGQLELSRPDDER
EHRSLHGLSRTLVNNMIIGVHDGYQKDLEIIGVGYRVISKGPTQLEFALGFSHPVTVDAP
EGITFEVKTPTSFTIHGIDKQVVGEIAAKIRKIRPPEPYKGKGVRYAGEHVRRKVGKAGA
>PFR_JS14_1635 PFR_JS14_1635 30S ribosomal protein S8 1863163:1863570 Reverse
MTMTDPIADMLTRLRNANQAFHDETSMPSSKIKAGIAEILKQEGYIADYAVKDPEADEVG
KKLVVTLKYGDDRKRSIAGVRRISKPGLRVYAKSNQLPKVLGGMGVAIISTSQGLMTDRQ
AHEKSVGGEVLAYVW
>PFR_JS14_1636 PFR_JS14_1636 30S ribosomal protein S14 type Z 1863730:1863915 Reverse
MAKTALKVKQARKPKFAVRAYTRCQRCGRPRSVYRKFGLCRICLRTLAHAGDLPGVTKSS
W
>PFR_JS14_1637 PFR_JS14_1637 50S ribosomal protein L5 1863924:1864586 Reverse
MARKNADAGLAVAEVAQATAPEMPRLKKKYREEIVKALHDEFNYDNPMLIPGLTKIVVNM
GVGDAANDRKILDGAVKDLTAITGQKPQTTKARKSIAQFHLREGQAIGCHVTLRGDRMWE
FADRLLSLALPRIRDFRGLNSNQFDGHGNYTFGLTEQVMFLEIDQDKIDRVRGMDITFVT
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TARNNEEGRALLKHLGFPFKATDDAKVPSARDFRRNGNRK
>PFR_JS14_1638PFR_JS14_163850S ribosomal protein L241864586:1864957 Reverse
MAKMKLKKGDRVQVIAGKDKGVVGEIIAVDPANERVTVQGANIVRRHTRDSADASGAQVK
GGIISVEAPLHVSNVQLLVKDGSKDVLTRIGAQRQKVSKRRADGSEYEGTRGVRIARKTG
KEI
>PFR_JS14_1639PFR_JS14_163950S ribosomal protein L141864959:1865330 Reverse
MIQQESRLKVADNTGAKELLCIRVLGGSKRRYAGLGDTIVCTVKDAIPGGSVKKGEVVKA
VIVRAVKSHRRVDGSYIKFDENAAVILGGTTSEPRGTRIFGPVARELRDKHFMRIVSLAP
EVI
>PFR_JS14_1640PFR_JS14_164030S ribosomal protein S171865461:1865736 Reverse
MSQTDSTTERAGRKVREGVVVSSKMDKTVVVAVEDRVKHGLYGKVITKTIRLKAHDENNE
AGEGDRVRIMETRPLSATKRWRLTAVVEKAR
>PFR_JS14_1641PFR_JS14_164150S ribosomal protein L291865733:1865981 Reverse
MAKTESLKAADLRAQSRGDLNDQVVKLKEELFALRFQAATGQLENHSRLREVRKDIARIY
TVLQERNLGIVDDPDREGKAEA
>PFR_JS14_1642PFR_JS14_164250S ribosomal protein L161865983:1866402 Reverse
MLIPRRVKYRKQHHPNRRGMAKGGTELAFGEFGVQALEPAYMTNRQIEAARIAMTRYIKR
GGKVWINVYPDRPLTKHPAESRMGSGKGSPEFWVVNVKPGRVLFELAGVTPDVANEALRL
AIHKLPFKARIITRDEGEI
>PFR_JS14_1643PFR_JS14_164330S ribosomal protein S31866408:1867226 Reverse
MGQKINPIGFRLGITTDHKSRWYAEKQYSELVGEDDKIRAWLVKNLERAGISSVEIERRS
DRITIFLYAARPGIVIGRNGAEAERVRGELEKMSGKQIQLNILEVKNPETDAQLVAQGIA
EQLGARVAFRRAMRKAQQSAMRSGAKGIRIRCSGRLGGAEMSRSESYREGRVPLHTLRAD
IDYGFYEARTTFGRIGVKVWIYKGDVTGTRAERAAQKAARQAAPSRQRSNRRPGRGERGG
RRRADAAREQAPRSDAAISAPAAAPATENAGA
>PFR_JS14_1644PFR_JS14_164450S ribosomal protein L221867229:1867714 Reverse
MSNTTQRPSRRVALLGDRPGSYAIARHVRMSAQKVRRVADTVRGMDATQAIATLRFAPQA
AAEPVRKVIESAVANAETSEGLHNEQLVISQIYVDEGVTMRRIRPRAKGSASRILKRASH
ITAVVEPAETAGHPPLKKASSAKNSSKATAADTTSDDTKEA
>PFR_JS14_1645PFR_JS14_164530S ribosomal protein S191867740:1868021 Reverse
MPRSLKKGPFVDGHLQKKIDVQNENGTKTVIKTWSRRSMVTPDMLGHTIAVHDGRKHVPV
FITEGMIGHKLGEFAPTRTFRGHVKDDKKARRR
>PFR_JS14_1646PFR_JS14_164650S ribosomal protein L21868039:1868875 Reverse
MAIRKYKPTTPARRGSSVSDFNEITRSTPEKSLLAPKSKTGGRNNSGRITTRHIGGGHKQ
AYRIIDFKRYDKDGVPAKVAHIEYDPNRTARIALLHYADGEKRYIIAPQGLEQGATVYAG
VGADIKPGNNLPLRNVPIGTQVHSVEMRPGGGAKLGRSAGASIQLVAREGQYATLRMPSG
EMRMVDVRCRATIGSVGNAEYSNIHWGKAGRSRWKGIRPTVRGVVMNPVDHPHGGGEGKT
SGGRHPVSPWGQKERRTRSKNKASSKLIVRRRKSGKKR
>PFR_JS14_1647PFR_JS14_164750S ribosomal protein L231868914:1869225 Reverse
MSDFKIRDPHDVLISPVVSEKSYGLIDENKYTFIVDPKANKTEIRQAVEAVFGVKVVGVN
TANRKGKKRRTRYGVGRRPDTKRAIVTVAENDHIDIFGNAPAE
>PFR_JS14_1648PFR_JS14_164850S ribosomal protein L41869222:1869923 Reverse
MNETTSIDVVNAEGKKAGSVELPGELFDAQANVPLMHQVVTAQLAAARQGTHSTKTRAEV
SGGGKKPWRQKGTGRARQGSIRSPQWAGGGISHGPQPREYSQRTPKKMVATALRGALSDR
AREGRIHVVSEFVGGDKPSTKSAAKVIAGLGDYGRVLVVLERSDENNWLSMRNLIGVHVV
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>PFR_JS14_1649PFR_JS14_164950S ribosomal protein L31869920:1870579 Reverse
MTTEHKVKGLLGTKLGMTQLWDENNRLVPVTVIQAGPCVVTQVRTPDTDGYSAVQLGYGA
IRAKSVTKPAAGQFARAKVTPRKYLAEIRTSDASEYTLGQELGPDTFSTDDVVDVTGVTK
GKGTAGVVKRWGFKGLGASHGVHRKHRSPGGIGACATPGHVFKGLRMAGRMGNARKTVQN
LAVAGVDADKGLILVRGAVPGNKGALVVLRTAAKKGEAK
>PFR_JS14_1650PFR_JS14_165030S ribosomal protein S101870591:1870902 Reverse
MAGQKIRIRLRAYDHEVIDSSARKIVDTVTRTGAKVAGPVPLPTEKNVWCVIRSPHKYKD
SREQFEMRTHKRLIDILDPTPKTVDSLMRLDLPAGVDIEIKLP
>PFR_JS14_1651PFR_JS14_1651Aminotransferase, class IV1871337:1872209 Reverse
MIISVLGTGVVDSNAPIAMADDLALTRGEGVFDSTVVYRQVTGPRILHLDWHLARLERSA
QGMGIECPSRDAWRRAIDDALDVWHGHNAVIRLILSRGREVVTDDPAQHLAYVLLSDIKG
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>PFR_JS14_1652PFR_JS14_1652Glutamate--tRNA ligase (Precursor)1872256:1873650 Reverse
MALFDKAWAVRTGGQFVLRIEDTDRNRLVPGSEQQIVDSLNWLGLTPDESPEQGGPYAPY
TQSQRLDTYRPVVDKLLASGHAYHCWCSQERLAAMREEKAAKKQDTRYDRLCYGMTKEER
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>PFR_JS14_1653PFR_JS14_1653Acetyltransferase, gnlAT family1873935:1874624 Reverse
MAWRPAYCRGASKFVTAIACRGAYGHDCRVSDRDRAGDGGRTGDPGSGREHAAPRGPRAA
TPGHIPARAEVEIPTARLVLHGVDPAQAEQLARGISPLPCVAGYPHADSDTAARMQRHAL
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LTAWAHAHGASTVLAEVDPTNHASRGVLAKAGFLPVRSDGPKLRLRHQG
>PFR_JS14_1654PFR_JS14_1654Membrane protein, PF09852 family1874666:1876096 Forward
MVTAPQRHPQLWLALICLIALAAYLVTSIVKFNRLRDGMDITIFDQAIRSFAQGHAGYTT
LKAPGMPIFGDHFHPIILTMVPLYWLWDDPRMLLITQGICIAWAGWLLGRLAIRRLGPGT
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PLWHEWTIGRCRDECRVFPAALAQLPAGSRVATDVYLTSHVAAHADVSQWRPPDYLDDRG
QPVTPDWLLLDRETISYQNKDSHWVDQFLADPVVRGTRYEVVWQRDPMVILRPAHS
>PFR_JS14_1655PFR_JS14_1655Translation elongation factor Tu1876290:1877480 Reverse
MAKAHFERTKPHCNIGTIGHIDHGKTTLTAAITKVLADKYPQWNSFEAFDDIDKAPEERQ
RGITISISHVEYQTEKRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTHE
HVLLARQVGVPAVVVALNKCDMVDDEELIDLVEMETRELLTAQEFDGENCPVVRVSAFKA
LQGDEKWAEQIMKLMDAVDDYIPQPERDTDKPFLMPVEDVFTITGRGTVVTGRIERGVIT
TGETVELVGLADTQTTTVTGVEMFRKILDEGQAGDNVGLLLRGTKKEDVERGMVVTKPGT
TTPHTEFKGSVYVLTKDEGGRHKPFFSHYSPQFYFRTTDVTGTVVLPDGVEMVMPGDNTD
MEVELQKPIAMEVGLKFAIREGGHTVGAGRVTEIVK
>PFR_JS14_1656PFR_JS14_1656Translation elongation factor G1877715:1879814 Reverse
MAIDLQTDLAKVRNIGIMAHIDAGKTTTTERILYYTGVNHKIGEVHDGAATMDWMEQEQE
RGITITSAATTCFWNNYQINIIDTPGHVDFTVEVERSLRVLDGAVAVFDGVAGVEPQTMN
VWRQASKYNVPRICYINKLDRTGASFDWCVQTIRERLHAVPVLLQLPIGAEADFIGILDL
IDMDAKTWRGETELGEHYEVEEIPAELAEKAKATRAEMIETVAENDDTFMELYLGGEDWT
NEDLKAAIRRGVLANAFTAVVCGTSFKNKGVQPLLDAIVDYLPSPLDIPAVVGFKPGDES
VEIDRHPAKDQPLAALAFKIAADPHLGRLTFVRVYSGVLTTGESVLNSTKGNKERIGKIY
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QMHANKRQEVEEMPAGMICAVMGLKNTGTGDTLCDPQNPIALESMTFPDPVIEQAIEPKS
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NDLRAKTSGQATYTMEFESYGIVPKGIADEIIAKAHGTE
>PFR_JS14_1657□PFR_JS14_1657□30S ribosomal protein S7□1879985:1880455 Reverse
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>PFR_JS14_1658□PFR_JS14_1658□30S ribosomal protein S12□1880455:1880826 Reverse
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KEK
>PFR_JS14_1659□PFR_JS14_1659□DNA-directed RNA polymerase, beta' subunit□1881286:1885176 Reverse
MLDVNTYDTLKIGLATADQIRGWSYGEVKKPETINYRTLKPERDGLFGEQIFGPTRDWEC
ACGKYKRVRFKGIVCERCGVEVTRSNVRRERMGHIELAAPVTHIWYFKGVPSRLGYLLDI
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>PFR_JS14_1661□PFR_JS14_1661□Hypothetical protein□1889079:1889705 Reverse
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TGVPTAASSSSNAVSTDSRAYSELVRLSDQGWTATQPLTNQWVAELGSSVVVPPSQPTPT
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ADDVRNWCSDQFGSAPPDRCDPLQLHPR
>PFR_JS14_1662□PFR_JS14_1662□LSU ribosomal protein L7/L12 (P1/P2)□1889976:1890371 Reverse
MAKLSTEELLDQFKDMTLIELSDFVKAFEDAFDVKAAAPVAVAAAPAAGAGEGEGAADDA
NAEVDVVLDSIDSSKKIQVIKEVRALTSLGLKDAKDLVESAPKIVLEKVNKDTANDAKEK
LEGAGATVSFK
>PFR_JS14_1663□PFR_JS14_1663□50S ribosomal protein L10□1890388:1891035 Reverse
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>PFR_JS14_1664□PFR_JS14_1664□Lipoyl synthase□1891405:1892355 Reverse
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CPNIFECWEDREATFLIGGEHCTRRCDFCQIESARPTGYDRDEPRRVGESVKQLGLRYAT
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>PFR_JS14_1665□PFR_JS14_1665□Octanoyltransferase□1892352:1893224 Reverse
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>PFR_JS14_1666□PFR_JS14_1666□50S ribosomal protein L1□1893391:1894101 Reverse
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TINLPNGTGKTARVLVFAQGAKATEALEAGADEVGGDDLIARVNDGYLDFDAVVATPDLM
GKVGRLGRVLGPRGLMPNPKTGTVTMDVTKAVSDIKGGKIEFRVDRHSNLQFIVGKLSFT
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>PFR_JS14_1667□PFR_JS14_1667□50S ribosomal protein L11□1894223:1894651 Reverse
MPPKKKVAAVVKIAIAAGSATPAPPVGTALGPHGVNIMEFVKAYNAKTEAQRGTIVPAEI
TIYEDRTFDFITKTPPAAELIKKAAGVQKGSGQPDKEKVGTITSDQVREIAETKMPDLNA
NSVEQAMKIVAGTARSMGVTVK
>PFR_JS14_1668□PFR_JS14_1668□Transcription antitermination protein nusG□1894761:1895648 Reverse
MTQTPDEGDNKPLEETELNLGSNDDQGDTDTGINLDFADFSDDDAKSGAELNLGPLPTEE
GEADKAEPAADQDAEKPDEPDEKAPSQEDEAVAKALEELHDDLVVKPGEWYVVHTYSGME
NRVKQNIDNRVKSLNMEDYIYETVVPTEDAVEMRKGQRKKVTRVFMPGYVLVRMEMTDES
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WSTVRHTPSVTGFVGQGQTPAPLDLSEVEHMLTPSVTAQVVASGEAKAGADQEKVEVVDY
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>PFR_JS14_1669□PFR_JS14_1669□Putative SecE/Sec61-gamma subunit of protein translocation complex□1895668:1896255 Reverse
MADRSERAKRRAEQAQSGPVKRHRSTGEHMEADDLPGSMLPEANGEPDPAVIDDADAEEL
TNADDTVDSTPDKGDPDDVRIDDESQLDEAERRADEAQDEKPTPIVRKHSTSPVRKAGGA
RAKAGKPTQAKKGHKRAGPITFTKQSVGELKKVVWPTGEQTGQYFVVVLVFVLFIMAVVA
GLDFGLTRLLLWLFG
>PFR_JS14_1670□PFR_JS14_1670□Hypothetical protein□1896688:1898172 Reverse
MATRASSRLLEWGTSALVTALFVVLWWRQRAVSPATHEEASSLLHAQLGVGGLWTATAHA
DRSWFAYWLCLVPMGSGPDALTVARTFSLVCAAVMVFALAATAGRLWGTGGALVAGGFLV
ANPAIVTLALSARGEMLGLALLALASWLLVALLESYQDLGLGPGIVYGLLLAAMVVCDLT
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YARATVTHLECAAS
>PFR_JS14_1671□PFR_JS14_1671□UDP-N-acetylenolpyruvoylglucosamine reductase MurB□1898194:1899327 Reverse
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DEVKRADEAGEPLLVLSGGSNMLVSDDGFNGTVLQIATRGVEGEISGCGGAVMNIAAGEN
WDDFVQLAISREWRGVEALSGIPGMVGSTVIQNVGAYGAEVGELVYRVRTWDRQEKSYRT
FANADCKFSYRNSIFKQSRLPGSPTGRYVVLEVTLQFLLGNMSMPIRYAELAHRLGIEVG
EHAPAQKVRDEVLALRRSKGMVIDPDDHDTWSAGSFFTNPIVTSQVAAGLPEDAPRFDAG
GGMVKTSAAWLIDHAGFHKGFGEGAATLSGKHTLALTNRGHATAADMVALARQIREGVHQ
AFGITLVPEPVLVGLSL
>PFR_JS14_1672□PFR_JS14_1672□MaoC-like protein□1899397:1899828 Reverse
MSAFDPAAVRAGDVLPPLTLTITRGGIVRYAGASTDFNPIHWSDCKARELGLPGVLAHGM
WTMGASLRIITDWCADPRRVLDYQVRFTRPVQVPDDDRGVQVQVSASVTGVEAGVATVAV
DVRIDHEGKPVKVLGNARAHIRL
>PFR_JS14_1673□PFR_JS14_1673□UPF0336 protein□1899825:1900259 Reverse
MPIGPEHVGRTYPSTAPYRVSRAKILEFVKSLGDPNPAYLADDDTPFTAPPTFAAVIAAS
AWGAMFDDPDLGLSLQRTVHADQRFDIERLMREGDDVTATLTITKVHNRGLTDMVTIAVK
LDTVDGEHLCTATSTLLNTREAAE
>PFR_JS14_1674□PFR_JS14_1674□50S ribosomal protein L33□1900407:1900577 Reverse
MAKKAGDVRPKITLACTVCKERNYITKKNRRNTPDRLELSKFCPRDGRHTLHRETR
>PFR_JS14_1675□PFR_JS14_1675□Alkyl hydroperoxide reductase, F subunit□1900976:1902631 Reverse
MAVLDAALISQLNQLMDRVTHPVELVMSLDDRPESAQISDMLEQVAALSANITVRRDDSA
HDRRPAFSITRPGSDISITFAALPTGHEFNSFVLALLQVGGNPVKLDEKVVAGARAITTP
KNFVTYISLTCQNCPTVVQAINAMAVLNPLITNTVVDGSLFRDEVEAEKIKATPTMYLNG
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AVIGGGNSGIEAALDLAGVARHVTVVEFMPACKADEVLLDRVDQTTNITVLTNSAVTEVV
GDGSQVTGLHYDDRATGEHRELALDGVFVQIGLMPNTDWLKGAVKLDAHGQIVIDDRGAT
NVPRVFAAGDCTDVPFKQIIVAEGAGAIAGLSAWESLIREQSTAAPKGSDAASTTGSQDA
RKGEPQAAMAR
>PFR_JS14_1676□PFR_JS14_1676□Alkyl hydroperoxide reductase, C22 subunit, thioredoxin-like (Detoxification of
hydroperoxides)□1902855:1903418 Reverse
MSLVGTQILPFKASAFHQGEFVDVTDEDLKGKWSVIFFYPADFSFVCPTELGDLADHYDQ
FQKMGVEIYSASTDTHFVHAAWHKESEEVKKVQYVMLGDPSGQLATNFQVLREGQGLADR
GTFLIDPDGVIQLVEVSADGVGRDASELVRKVRAAQYVRQHPDQVCPAHWDETGDTLTPS
LDLVGQI
>PFR_JS14_1677□PFR_JS14_1677□Hypothetical protein□1903942:1904436 Reverse
MLRHTGGMAREPQVFHADGPVRRTWASKLAATLAVLVVVALIVGPVVVRAVHRSNADAAE
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GLADQAYSWSWAAISLLVTVVACAFTFMPPRPLTTRKDARRPVR
>PFR_JS14_1678□PFR_JS14_1678□Exodeoxyribonuclease□1904515:1905456 Forward
MLRLATYNVNGIRAAQRRGFAGWKQRCLPDVACLQEVRCPYEALPMEAFAGFHVAYDAGE
LKGRNGVAVLSRTPFDAVRVWSDQAMFISPAGDARMAGADELSVPDYPLARPLRSFNHEG
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HLTRARRAAHAAGREFLVVGDFNIAHTRLDVKNWRPAQKASGFLPEERAWLSEQLSPRTL
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VSDHAAVVVDYDL
>PFR_JS14_1679□PFR_JS14_1679□Hypothetical protein□1905515:1905901 Reverse
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YLALLIGILQRRGWAVTLVRFFAFCTVAQIIVSPNYPTTARFLTTLVFLACVVTLLWSLK
GFRTVRRT
>PFR_JS14_1680□PFR_JS14_1680□Mannosyltransferase MptA□1906068:1907657 Reverse
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RRAEGLPSKLIGTAATMAGLLLIMSAWYRLRPGARGGAPGDATGPAAYLTLKHWAVLAWW
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ARKRPATFISWGYLVVAIASPALHSWYMLWGGLTLPLAQPRRRLVAVAIWVNLALLCYDA
VDMAWRNDGVAIGVAAVAASVFMTWIHQASVRVTRHPGHATHLELPATS
>PFR_JS14_1681□PFR_JS14_1681□Ferredoxin oxidoreductase, alpha subunit□1907829:1909718 Forward
MNPGQQTPQRQRLNRVVIRFAGDSGDGMQLTGDRFGAESAEHGNDIATLPDYPAEIRAPQ
GTIAGVSSFQIQFADEDIVTPGEHVDVLVAMNPAALRANLADVVRGGLVIVDKHSFAKRA
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GRPTEDTVHWLGETFASRPSVRDANIAALRAGENYGENTEQFAVRYEVPPAPVPAGRYRR
ITGNLATAYGLMVGAARAGMTLFVGSYPITPASDILHELSKRKAFGVITVQAEDEIAGIG
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KVRGQPLPVGELTQYLAGHLDEIEQEARR
>PFR_JS14_1682□PFR_JS14_1682□2-oxoglutarate ferredoxin oxidoreductase subunit beta□1909715:1910794 Forward
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RENTMVVSGIGCSSRLPYYLNSYGIHSIHGRATTLATGLAVTRPDLAVFVVTGDGDALSI
GGNHLLHALRRNVNITILLFNNRIYGLTKGQYSPTSAVGQVTKSSPMGAPDRPVNPVSYA
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VIPLVAGEQIRFGTDRELCVVPDANGGVRIAKVSEVKEADIVVHDPTNPDPTRAFALSRL
TDSGVMHRAPMGIFRDISLPSYDDQVRTQITQATHGEANPSSDPALQNLINGTDTWLVE
>PFR_JS14_1683□PFR_JS14_1683□Peptidase family M13□1910924:1912897 Forward
MGSLGQVSTPAFHFEDFDKSVAPTTDLFRHVNGTWLKNAVIPDDRSNWGAFAILRENSEK
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AVHEIVEGLEAGDDPTTEQAKIANLYASFMDEETIEALGVSPLAPILARVDAIASVADLA
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DLSAQSFEFYSKGLRGVPKQRARWKRGVSVTEGVLGEAIGKRYVAKHFPPETKAAADRLV
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MSPLEAIKSCFRNYVNPNGRSGRAEFWWFLFFILVVDSVLGLLAVLTGDHTTLADDGWFY
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IGGTFGPNRYGPGRYDPRAAFDPDTPLTPTR
>PFR_JS14_1686□PFR_JS14_1686□Polyprenyl synthetase□1914848:1915825 Reverse
MTQAEDEAFEAYVGDQLDAVERRLSAITLTAANPFLAEAAEHIIAAGGKRFRPMLVAVTS
QLGPQPNDAAAQIAAVVVELTHVASLYHDDVMDDAALRRGVPSANAAYGNSTAIMVGDWL
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LDLLPDGAATRALSRLCDEVVSRSN
>PFR_JS14_1687□PFR_JS14_1687□NADH-quinone oxidoreductase subunit N□1915839:1917395 Reverse
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>PFR_JS14_1688□PFR_JS14_1688□NADH dehydrogenase subunit M□1917399:1918940 Reverse
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FGGFVLLLGVIGMYAVSAGAGKPSLLTADLAGLSMGQGMERWLFVAFFIAFAIKAPMVPV
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>PFR_JS14_1690□PFR_JS14_1690□NADH-quinone oxidoreductase subunit K□1920873:1921172 Reverse
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>PFR_JS14_1691□PFR_JS14_1691□NADH-ubiquinone/plastoquinone oxidoreductase chain 6□1921169:1922038 Reverse
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>PFR_JS14_1696□PFR_JS14_1696□NADH dehydrogenase subunit E□1927720:1928451 Reverse
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VGK
>PFR_JS14_1697□PFR_JS14_1697□NADH-quinone oxidoreductase subunit D□1928507:1929880 Reverse
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ELAKHLRDDEALRFEICVSVSGVHYPEQTGHELHAVFHLLSMTYNRRIRLEVEVSEDDPH
LPSLVPVYPMANFHERETWDMFGIIFDGHPALTRILMPDDWVGHPQRKDYPLGGIPVEFK
GAVVPPADDRRSYNR
>PFR_JS14_1699□PFR_JS14_1699□NADH-quinone oxidoreductase subunit B□1930641:1931198 Reverse
MGIEEKLPAGIFLTTVEQVQGWMRQASFWPLTMGLACCAIEMISYGGPRADCSRWGQEIF
RASPRQADLMIVAGRVGQKLAPVVRQLWDQMPNPKWCIAMGACASSGGVFNNYAVVQGVD
HIVPVDMYLPGCPPRPDMLIDAVFKLKKGKVQHTTMGAHRVQEVAELEQKALAAPATIEQ
KGLMR
>PFR_JS14_1700□PFR_JS14_1700□NADH-quinone oxidoreductase subunit A□1931217:1931582 Reverse
MNAYIPVIGLVALATLFVVIAAIVLSPLIGPHRYNRTKYDSFECGIQPTPQTLTGGGRFS
VKYYVTAMLFIIFDIEIVFLYPWAVAFDHLGSFGVIEMITFIIVVFVAYTYVLRRGGLNW
D
>PFR_JS14_1701□PFR_JS14_1701□Geranylgeranyl reductase family protein□1931639:1932970 Reverse
MVHGEVQMGDAPALASAQLSTADQDSFATEADVIVVGAGPGGSATAAFCAMRGLSVLLLE
KSQFPREKVCGDGLTPRAVRMLTRLGIDSTETAGWARNKGLRVYGGRTEPFELPWPELAD
FPDYGLVCPRSRFDDVLAGHAMKLGVTLHTGVNVTEPITADDRIVGVRDNQGREFRAPIV
VAADGNSTRLAVAMGRQRDEARPMGVAVRTYFESPRAQGEWMESWLELWDGRPGESNQLP
GYGWAFPMADGTVNVGLGMLNSSSAFGHTDYRALMRTWLATTPPEWQFDEAHQRGEIRGA
ALPMAFNRKPAYADGLLLVGDSGGMVNPFNGEGISYAMEAGELAADAISEAHSRGVGTPG
AERALHAYPTALSSRFGGYYRLGTIFVKLIGNPQIMHLCTTYGLPHRSLMKLVNKLLANL
TDEHRGDAMDHLINTLSRLAPPA
>PFR_JS14_1702□PFR_JS14_1702□Chorismate binding enzyme□1933316:1934554 Forward
MIINPGSSRLHASTIAIDDPGALTQYVDGHGAAFLRGEDGFVAMGEVARLDGATMSEADQ
WWTQLAADIEKESEMPGLVGTGPLAYGTFTFDPEHTAAASAFIVPETIIGRRDGVSWLTQ
LGYDRVNPQMPEVQPAPQPPAELFFEDGQISGADWLALIARTSAALRASGAEGVVLARDL
HAIAEQKICPAWLLHQWRRNYGGSTCYLVDGLVGATPEILVHRRGGLTTSRILAGTTQRL
DNVDEPAEIARLLSSQQRMHQHRLSVESAVTALGAHMSGIHVPEAPFVLALPDMLHLVTD
ICGVTEGTFSTLALAAAVHPLSSVTGFPTDQARTILANSGFDRGRFCAPVGWIDAQGDGD
WFVALRAAQLSPDWKGVTLYASASVDPDTAPHNKLVSTEMKFALMRQFLAGD
>PFR_JS14_1703□PFR_JS14_1703□ABC transporter, permease protein□1934600:1936405 Reverse
MSSRNKRRNRSRKERAAQPAARPPQQRRPAPTDDPDFEGFDPDYPFVDVGFDAQGMVDER
QLLLLVKDWRKGRATRRLRDVITDAYVAMFTVVVVAAMIISGLLSAQNQASTCTSDGCVT
ARKLLPWLVVAGLWVGALAISRIFGPIVASAAEGFWLLDAPLRRSSVLARRMWGMIFAAG
GVAAVVAALVTVLVGLPLPTVGAWTAAAAFTTAAWMAFTAAEQGAERTIMVRVAQIVVGG
VAVVVLVAVIASASGWLSVGLGGTGSFELAIVVAAAGLVLAILASLIARRRLDNVGRAKL
ITGGELVSGMQGAAFALDFALMRDILIERRNHLRGHVKPARGHWRGTRALVWRDLQRLVR
SPGPLVGFLVSLIVPYALESLGVGSLTPILSALIMVAVMVPFMDSMRVLTRTKGLARLFP
MTDSELRTATTIVPASLALIWTIVVTPAFLLNLNGQAASVSVSNTLWYGVITAAAGLLGA
MRWVSAKSANYNMPMVATGAGAVPPGLMFNLIRGIDVAVLVTAPLVLNWPPIVSAIIAMI
AFMVLRSGGINQQELMEKSEEQRKELAAQKEAARGGGGRTRPKQVISRSGTPARTRPPLR
K
>PFR_JS14_1704□PFR_JS14_1704□Heme ABC exporter, ATP-binding protein CcmA□1936402:1937094 Reverse
MEVMARRSTVLKISNLVKKYGDHTVIDHFNLQVYESDAVALTGRNGSGKSTVLRCIVGSD
KPTEGTIEVLGEKAKDTEISFRRNVATVIDDLDFFPDLSVVEHLDLLARAHGLEDTDELV
DSILEEVQLVPQSGQLPGTLSSGQRRRLALATAFVRPKKLLVLDEPEQRLDQEGIDWLGK
RLRHEKEHNGLAIIMASHEPSLVEAVGARIVRIGGGLEETQSLAEPEQLA
>PFR_JS14_1705□PFR_JS14_1705□Demethylmenaquinone methyltransferase□1937262:1937909 Forward
MFDDVAPRYDLLNDVMSMGQDRLWRREVVRAVDAQPGDYVLDLAAGTGTSSAPFAAAGAH
VFPTDLSFGMLEVGKQRQPDLTFVQGDATALPYRDDSFDAVTISFGLRNVEDTAKALEEL
RRVTRPGGRIVICEFSTPTWAPFRVLYQRFYLPRVMPLLAHLGSNPDSYSYLTETIAAWP
NQQALARLMSDAGWKRVEWRNLSGGIVAMHRGFAD
>PFR_JS14_1706□PFR_JS14_1706□Nuclease, RecB family□1938036:1939805 Forward
MLDSYAARSCPVKTRNRFDRTVRLPVNTSSDIAIRASTDAMQELFTGSTAFKKEVMDALA
AHPDAVDLRSLMDEDWSERSAATADAVAAGALLIIAPVLPLDVAGHRAGQPDVLVLGPPA
PDGDTGYYPVIIKRHRVLEASPRGRRQPCTPLSGGQRLLRVAGCGVRTHREGDLLQLAHY
RRILEATGWCSGGVPVAGIIGTDEILIRQGRPVLGRNRTHRPGDLKHLVISWANLGAKRL
RTFARTASSGWRYRSSLERYDHEFAFRLRIAEIAARRTGSPDDPDPRVRPIVVHECESCP
WWVACKPQLNDDDLSLRIDKARLDVHEITVLRSMGISTITDLACTDVEQLLPTYLPEVQH
RPGAENRLRLATERADMLAHGIAVKKTSVGPIELPAQGYSIDLDIETSAAARVYLWGFLV
NDPDDDSGPHYVSFSRFEDLDHAGERALAEEAATWLVEQLTAHPEAKVYHYSDYEVVHIR
RIARKSASPSLRELAQNWTRTNFFDLFPVVQKNFFGVHGLGLKKLAHNGAGFNWRDEDPG
GLNSQCWFAEAVHGPSHEVRAGFATRVLEYNEDDVRATRALRAWMRTLS
>PFR_JS14_1707□PFR_JS14_1707□1,4-dihydroxy-2-naphthoate octaprenyltransferase□1939822:1940703 Reverse
MATASEWLEGARLRTFPTAISPVVAGTAIAWWHGRAPLGIAALCLVVALALVIGVNFAND
YSDGVRGSDENRVGPQRLVGSGAANPSAVKRAAFACFAVSALAGLVAVLVTGHWWLLIVG
VACILAAWFYTGGRHPYGYLGLGEIFVFVFFGLVAVGGTSYLLSARVGAPGWLTAAGIGV
LACAVLVTNNLRDIVGDTASGKRTLETRIGDRATRVLYAVLVGVAALTVVGVAALTTWWA
LLGLACLVFLAPACRVILGGARGMALVATLKNTGLGELCYALGILAGVAISMI
>PFR_JS14_1708□PFR_JS14_1708□Hypothetical protein□1940884:1941138 Forward
MARILPVLVLLALTIFAVVDLTQTDPYDVPYMPKWMWLLVVIFLPAVGPVAWIVLSRLHG
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MNDGSRDGGGAPPPDDNEDWLRKL
>PFR_JS14_1709□PFR_JS14_1709□Transporter, major facilitator family protein□1941475:1942761 Forward
MRRMFASLAVPNYRIYFTGMTVSNMGQWMARTAQSWLVLTVLTDHSATALGTVTALQFLP
TLFLMPIAGKLADRFPKRRILMLAQLVGLIDAAVLSTLVITGVAELWHVYLIATIDGVGS
SFDSPARQSFVSEVVSGRQLSNAISLNSASFNMTRLLGPGLAGVLIAIIGTGPVIAVNTV
SFAAMIICLALLKTRDLATPARAKDGGSIHEGLRYVRRRPDLMVLLAIGFAVGGLGFNFQ
ISNAVMTTGIFHRGSDAFGLLDSIMGVGALAAALWSAARHGPRIRHMIISMAAYTVLGLV
AAFSTNYWVFALLQAPIGLATITALVTGNTLLQSHTSASMRGRVLSLWMLMITGITPVVS
PVVGHLGDWLGPRATVMFGVICVGISTVIITWVIMHTDSLRLRFDSHRRGWWYLERRRVT
DEITMPVK
>PFR_JS14_1710□PFR_JS14_1710□Hypothetical protein□1942924:1943322 Forward
MADDNYDDLYNSDVVASDGKKIGGVGQVYLDDKTGQPTWVTVKTGLFGTKENFVPLVHAD
IANGEIKVPYAEEVVKEAPTVDPDRHLDADEEADLYKYYGIETVPAPGTDRDEADADQAD
ADQAGTGPNATQ
>PFR_JS14_1711□PFR_JS14_1711□Cytidine and deoxycytidylate deaminase zinc-binding region□1943348:1943812 Reverse
MATIEPGQEITVPSWDEYFLGITQAVAARAKCTRRRVGAVLVGPDHRIIATGYNGAAPGR
PDCLEGACPRGRLSYDEIPGLGDYDRPGTPGFCIAIHAEMNALLFATRDTKGATAFITDE
PCPGCRKALAAAGIVRAVWPEGEFDGDQIVDFGC
>PFR_JS14_1712□PFR_JS14_1712□Cation diffusion facilitator family transporter□1943841:1944809 Reverse
MARVTNVTSTEKASPMRETIAGRYAAPVDLSKFAWLSIAAAVVTIVLKSGAAWLTGSVGL
LSDALESVVNLVAAIFALVALKVSIKPPDSNHPFGHSKAEYFSAAFEGIMIFVAAVVIIY
SAVERILNPRMPEQLGFGLLISVVASLINGGVGFLLIRAGKQRRSATLSADGRHLMTDVV
TSVAVIIGVGLVALTNLQVLDPIVAILAGINILWTGWRLIRSSSEGLMDIALPPEDEAKI
EGVLDRFRADGEIDFHAVRTRESGNRRFMEMHVLVPDEWSVKRAHDLAEDVIDELVKVEP
DLRVSAHLEPKSDPRSYEDIDI
>PFR_JS14_1713□PFR_JS14_1713□Phospholipase, patatin family□1945000:1946589 Forward
MSRPAWFGVLPFLGRHASTRQETPAVQGLVIAGGGARASFQIGALRYLYEREHIAPSVIT
ATSAGAILGSLLAQSKDPAEQLASLRGIEKLWLAMTQPSDMFTERSWFTQLKSHADALDV
LRQVEEKAEHDDPGHQPGLWSRFGWGTRQAAAKQEGDAKQAGATPTHQVTGGAATGAGES
PDAPDAAPTSTDNALSPQERTLALAMSEEPGEPLGWTPNMFFQLAAGLPQLGRASADLTA
AWRGLERNRSLFKPGPILRRLLSRDFFHSEQVTSSGMTLRCAFVGLNSGELRYMREDGHI
VDRDDKVLAGNPFDISMGVLASCSIPGVFKPVEMNGEWYVDGGIRENVPVEGAVSNLGVT
RPYVIVSGPSGLNYDAQVGSGDLISILFRIQSIQSDESERDEVAYARSSGAVVIEPELSV
HETMEFDPGTLRINRDYGWMRAAEAMHEADAATQQVNREIIETRLQAWKRERQMKPGSPH
EFDQAMLNEVGQLKLHLQSLLGSADKDLLPPDAQQWWTRSEGDDAPAAS
>PFR_JS14_1714□PFR_JS14_1714□Hypothetical protein□1946695:1947042 Forward
MSSTDRGYDHLYGARVIDRDGAFVGDVAQVYTDQVNGEALAVTVRTGLFGARRLLVPLIN
AAVGWHRIDVPYLRAHVNSAPPAGTPVRSARDAYPHLSPVTEAEIAAHYELTTLR
>PFR_JS14_1715□PFR_JS14_1715□Hypothetical protein□1947163:1947822 Forward
MTWFAVGLGLAGLILGIIAIMQARQANRAAHDTRANVNAAVQAAFSAAADAQKSHQELVA
RSRAAVLHDTQDNGPAFPGTQERGRFNWVMEISRDEKGLVTSLRAVSEGSHIAHDVTFIV
NSDEHAERSVHFDVIRPGRPVDLRAEQTVAMHRDRVAEATKQQAANTAGIATDMPRKLGP
IDTHLRLSIIAVTEDGTPQAYVIERTLRTTEHGSVLVYA
>PFR_JS14_1716□PFR_JS14_1716□Transaldolase□1948021:1949103 Forward
MNPRLKALSDAGVSIWLDDLSRARITSGGLAELIKDSSVVGVTTNPTIFAGALSNGADYA
AQLTELGDVSTAEAIKQLTATDVRDACDLFAPIYQSSEGYDGRVSIEVEPGLAHDTEATT
KQAAELYKLVDRDNVLIKIPATLAGLPAIEATIAAGISVNVTLIFSVERYRKVMDAYMAG
LEKAAAAGKDLSKIHSVASFFISRVDSEIDKRLGALNHPELAGKAGVANGLVAFGAYQEV
FASERFQKLAAKGANLQRPLWASTGTKNAAYPDTLYVSDLVARGVVNTMPEKTMQAFADH
GELGEPIDGRAAEGQATLDKIAAAGVPLAEVFDQLETEGVDKFVASWAELVESVASAMKR
>PFR_JS14_1717□PFR_JS14_1717□Hypothetical protein□1949357:1949794 Forward
MGMMMDTQQSHSRQSHSRMMWRRAVPVAMMGMVALTAAGSLIGTESARGESASRTAATTQ
QATSQGITQSIAVDACGQRAEQTIAKAAPALAVKAHDTLDTATLQRDADRWQVQIGVRIG
QKQHLAHCTVTGSATSPAIANFVYW
>PFR_JS14_1718□PFR_JS14_1718□Zinc-binding dehydrogenase family oxidoreductase□1950112:1951137 Forward
MRGVIMESAGVVRVEERDDPRIIEPTDAVIRITTTCICGSDLWPYRGVVPVHHQVMGHEY
LGVVEQIGLAVTTLHVGDHVVGSFCISDNTCEICRAGYQSRCVHGEFVSQHIGTQAEKAR
IPYADGTLVAMPGKPDADLIPSLMATSDVLGTGWFGAAAAGVGKGSSVAVVGDGAVGLMA
VLAAKQLGAERIIAMSRHPERQQLAREYGATDIVEERGDAGAERIKQMTGGLGVQCAVEA
VGTEQSLMQAVDATRPGGHVGFVGVAHEGVALPMDKMFAAEVHLFGGPAPVRRFLPELIQ
LVWDRKINPGKVFDLTLPLERAAEGYKAMDERTAIKVLLTL
>PFR_JS14_1719□PFR_JS14_1719□Ketopantoate reductase protein□1951134:1952099 Forward
MTHPSSGSAGRRPRVALIGAGAIGMAVASGLLRAGRAVVVCGGHAPIHRIEVTEHGTTSA
WAVEHTDDPTTLGDVDTAIVAVKAQQTDSAADWLRAVARPQVTVLVAQNGVEQRERVAPY
LGQPGAGASPTDAPQVVPAIVYLNVERLAPGRARVNHVGDVDLAFPVGEAARELADELTH
GGLRVRLEDDFAAAAWRKLLTNISANPLTALTGRRAEVLHEPAIRQAAGQLMAEAVTVAQ
AAGIHLTHADATAALDWLATIPGDATTSMLSDRLAARPLEYDALTGAVVRTAARVGVEVP
ANKLMLALLSALPSGEGPHRR
>PFR_JS14_1720□PFR_JS14_1720□Aspartate/tyrosine/aromatic aminotransferase (Precursor)□1952162:1953328 Forward
MTVSHRARNAETFHALDFAQRAADLEAQGHHVVKLSIGEPDFGAPPAVLAAGRDALDGRP
LPYTPPLGLPELRSALSDFYRDRHGVQVPAERIAITMGASAALLLATAATTDPGDEVILA
DPSYPCNRELVQSFGGTVVALPTTAATRYQLDADMVERAWGDRTTSVMIASPSNPTGTSI
PFDELAAICELARSRGGWRIVDEIYLELSDASPAHTVLEVDPDAIVTGSFSKYFGMTGWR
LGWAVLPPQLVGPVERLAMNYFLSASNPTQQAALACFTPETLEVCERRRRELGARRRLVL
EGLARIGLPVPVVPDGAFYVYIDVSGTGLGAWQFCEQALDVAHVALTPGRDFGPTTGETH
VRLSYAASRGELDEGLSRLGHFLASRRG
>PFR_JS14_1721□PFR_JS14_1721□Heavy metal-transporting ATPase□1953466:1955337 Reverse
MTTVTGSTSRTTIRPQAGASLWSRIDRTDLARTLFVAACTAALALGLDWPSPTVPLLAVI
GLVVGCWPVVVEAWHDIRQRRMSMELSMLLAIIAAGVIGEWTTSLLITTFVLAAEILEDL
SMDRGRDALTALMSFLPTTVTLREGHITREILLDDVAPGQVLVIGPGERVPVDGVVDKGR
STLDQSRITGESMPVDVAVGDPVYAGSINQVGALEVRAERVGANSSYGRIVTAVREAQSS
RAPVQRMADRFAAWLVYLSIAGAIVTFLVTRDLSATISVIIVAGACGIAAGTPLAVLAAI
ARIARVGAFVKDGAHLEALSVVDTVVFDKTGTLTRGVPTVTDVRTAPGVSTQQLLAWAGA
AEAYSEHPLGRAIAAHVRAAGVAPGTAQSFDYQPGRGVSVEVDGRMIAAGNARLVPDAPA
SAADGVATPVHISVDEHYAGTILLADQVRDSARSVVAELRHRGLRVMMITGDQPATARAV
ADELGITEVRAGLLPDEKLRAIDVERAAGHRLAMVGDGVNDAPALMRATVGIAMGSGTDI
ARDSADVVLISSDLNDLAATLHIARRARRIVMFNFVGTIVVDVIGMVLAAFGLLGPVLAA
VFHVGSESAFILNSARLIPGRRH
>PFR_JS14_1722□PFR_JS14_1722□HTH-type transcriptional regulator CmtR□1955334:1955759 Reverse
MREDTKACTFNVESQYVDLAAEVFSLLSDATRIRIILALRDGELSVGDLADRVRKSPTAV
SQHLAKLRWGKIVQARQEGTRVFYSLIDEHARKLVAQAVFQAEHVVGGVPPHHLNGEGVP
AAPAASDATETASATDPGQRA
>PFR_JS14_1723□PFR_JS14_1723□Transcriptional regulator□1956301:1957068 Reverse
MAEPDEGSDIGSALSSLSAALSQLSSAVVNQTSDEINARVTDPLRRASEQITDVAERLGS
GSSARPRGIEATREALLDAAAQLFAEKGYEGTGVSEIARRAGYTKGALYANFASKQELFK
ALIERELARSHEDLESSLTGASMPLGADREAVQRQVLLTLEANLYAIRHPQMRDEVLADT
RGQLRRIAEVIARTHGEALAEGQEPAQDYLDDAMVVAAVESFAALGTMLSDDPVAAEAVT
RSRDRIIGRILGSQD
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>PFR_JS14_1724	PFR_JS14_1724	ABC transport ATP-binding subunit	1957237:1958277 Forward
MNTVLDVRGLHKHFGKGAHRVEANAGVTMAAHAGQVVGLLGHNGSGKTTMVNQIVGLTRP
DSGTITVGGIDATTHPALARRLVSLQAQANVPITGLTPRRAIELVGRMRGAPARAMRSRA
RELIEALDIGPWADVASQKVSGGIARLTAFAMCLARPAPLVVLDEPTNDVDPVRRRLLWT
QIRRLADAGHAVLLVTHNVRETERVVDRLVVLNHGQVLAQGTPATLVHDRAGMLTLEVDQ
APGQPPHWPAGITATPVGDHRSRAVVASDRAAALVAWAADELRTGAIERYELSPVSLEDA
YIDLVTGHHPAAAGADADQPDAAPLDEPDTTTESTNDPAAGQEHTA
>PFR_JS14_1725	PFR_JS14_1725	ABC transporter, permease protein	1958274:1959080 Forward
MSTITSIRATPNSATTGTTMAPAGVARWRQFGLVFQWQLRRNLTLMPLYVVVQLVLSVAT
VVGYGLLIGDPAPDAARYLVTGAPTISLVMLGLAMTPQFVAQSRTEGSLDWMRALPISRP
VFLLADLAVWTMVALPGLVLSIIVGALRFHLDLSMSWLIVPAALLIALTSASIGYAIANL
CPPTLAQLISQVLVFVILLFSPLSYPADRLPQWGQAVHHWLPLESMGEIMRHTILSADFA
APLSAWLLLAAWCAAAVTGASWALGRRS
>PFR_JS14_1726	PFR_JS14_1726	Hypothetical protein	1959518:1961263 Forward
MNPFVKTARVAITSTLVAGSLATASLVFAPLAQADYSPLAATATVNVRQGPDTSSSVLAT
LSSGDTVTQRGAEQDGWLPITYNGANAWIQAQYVASTTAATQKDQISTAELTADAYVRTA
ANANAWVLGTAHTGDKVGITGQASGDYTPVNFYGRAGWIATKLLSAADASVTSIKITTAI
SSDYLWVRGGESTAAQSIGMLYPGDRVDVTGDPVGGWVPINFNGKTAFVAANYSRYLTDP
TVVTLSTKTDVTNKDTATSTGTDSSTAGGSTATTPTTTAPTTTAPETKPTTTPPATTAPT
TPPATTQAAASTKYTTADVNVRVGPGIDQQSVTVLKENSQVAATGKTSGDWTEVSYDGAS
RWISSQYLSDTKQAEAPAPAPAPDPTPAGPTGSRWTTAALNAYGSSTQPKPATTVVPEGT
QVELTGKQADGRSEYTWNGTTYWSATEYLGTNAPATNTSANTAKPGANAVETAINFAMSK
LGGPYVWGGTGPVGYDCSGLMQAAYAAAGVTLPRVTWDQVNAGKQVSVGDLQPGDLVFFY
DNGHVGMYIGNGNIVNALNEDAGIVVTPISYMPISAAVRIA
>PFR_JS14_1727	PFR_JS14_1727	Domain family protein, hydrolase, alpha/beta fold family	1961982:1963064 Reverse
MTAWLPDLLVTGYQAHTWVIPGAKRLDNEPEGPLTATLVRRGAPRHERAVLYLHGWDDYF
FQAHVADWFDAHGFDFYAVDLRRYGRNLHEGLYAGYVSDLRDYYQELDHSVELIRHDHPG
VPITFMGHSTGGLVGALWAAERPGLLNGMLLNSPWLDMQGSPVFWRVMAPLAGAVAAINP
LMELAITDLGLYKRALHVSGEGEWNWDTDFKSNPAFVPRFGWGRAILAGQGAVAKGLHID
TPVLTLISTRSDFSRTWNDDMHGSDLVLDVRRIGAAALHLGDLVTIRRVRGAVHDVMLSR
APVREVIFDEIDRWLDAYVRPEGASALYWQRLGRPAATADPAVPGTPQESDGKGDVAATQ
>PFR_JS14_1728	PFR_JS14_1728	Hypothetical protein	1963316:1963546 Reverse
MGRGRQKAKQTKVARDLKYRPVQTDFASLERELRGESAHDPDDQGHDAIPDNYLDLAKQY
DPDSADAGAADDEKHR
>PFR_JS14_1729	PFR_JS14_1729	Phosphoribosylformylglycinamidine cyclo-ligase (Precursor)	1963780:1964841 Reverse
MSDSAYARAGVDIEAGDAAVELMKAHVARTKRPEVLGGIGGFAGLFDASKLAAYRHPLLA
TSTDGVGTKVAIARAMGVHNTIGWDLVGMLVDDLVVCGAEPLFLTDYIACGHVVPERIAA
VVEGIADACVSAGCALLGGETAEHPGLMEPDEYDIAGATTGVVEADELLGPDRVQPGDVA
LAMASSGLHSNGYSLVRHVLLDEGGLSLDATIPQLGRTLGEELLEPTHVYAGQVMKLLDR
VSVHAMSHITGGGLAANLVRVVPQGMRVDVDRATWRPAGIFELVQATGDISQADIEATLN
MGVGMVALLPPDQVDAAQRVLDELGLNSWACGQVSATPGQPATVELSGSHPLS
>PFR_JS14_1730	PFR_JS14_1730	Amidophosphoribosyltransferase	1964838:1966379 Reverse
MELRPGCPVSPESQTDAEHDDVPHDECGVFGVFAPGEQVSKLVYYGLYALQHRGQESAGM
AVSNGQRIMVFKDMGLVSQVFDESTLNSLRGDLAIGHTRYSTTGASVWKNAQPTFKPTPS
GGLALAHNGNLTNTDELEAFARARVGVGGEVPHKSSMDSTNDTSLVTTIMASYDEPLEDV
AMELLPKLVGAFSLVFMNENTLFAARDPQGVRPLVLGRLHSGWVVASETAAIDIVGGTFV
REIEPGEMIAIDAAGLRSRRFAPARPKGCIFEYVYVARPDTVIAGRRIHNVRVKVGKILA
REAPADADLVIPVPESGVPAAIGYAAESGIPFGMGLVKNNYVGRTFIQPSQTLRNLGIRL
KLNPLRDVIEGKRLVVVDDSIVRGNTQRQLVRMLREAGAAEVHVRISSPPVEWPCFYGLD
FATRAQLIAPGLTNDEICRSIGADSLSYVSLEGLIQATHVPKDNLCRACFDGIYPIEVPP
GQSAEMGLDAPEAPACGGYENVEFDRINHKEAS
>PFR_JS14_1731	PFR_JS14_1731	Hypothetical protein	1966480:1967319 Reverse
MSDDPTAGDPYRNDPYRGGANPYGANQYGGAYRGGQPDGSYPGYPPPGMGDTAPIPVVNE
DDPDPDDKRPSRIPTILVTLFLGPFGAIAAAVSAGRAHDRGFPRATYWLSFIFTWAVHLL
IITALVVAWLLGAFDGVLKSSSTPSPSSSPVASATPTPSATATPTPTTTSAAPTATSARP
SASATASASATPSGVSNLADFPAGAAKMCGASIAANSATTCDFATAVADAYLRSGSFGQA
ATVQATSSTTGQTYTMNCNMDARAITTCTGGNGASVYMR
>PFR_JS14_1732	PFR_JS14_1732	UPF0237 protein	1967589:1967858 Forward
MIAIVTVTGLDHTGIVAAVSTRLCELGINILNITQTIMGDYFTMIMQCELDESRHGIGEV
ADELRRTGESTQVDVRVQSEAIFHAMHEL
>PFR_JS14_1733	PFR_JS14_1733	UPF0210 protein	1967862:1969211 Forward
MDTTHDILETIEMIEDNRLDIRTVTMGISLLDCADHDPRVAQRKIYDRITHQARDLVTTA
QGIETELGIPIINKRITITPMSIVAAGSEVDDYTGFAETLDRAAKEVGVDFVGGFSALMS
KSSTAADRRLLDSIPAALAATEVVCSSINIGSTKAGINMTAVARTGEVIQELAQATDGIG
CSKFVVFCNAVGDNPFMAGGFHGVEEGDCCINVGVSGPGVVKRALDKVPEATWGEMSETI
KKAAFKITRMGQLVGTMAAERLNVDFGIVDLSLAPTPAVGDSVAEIIETMGVGTVGGHGT
TAALALLNDAVKKGGLMACSHVGGLSGSFIPVSEDAAMIDAVRSGSLSLAKLEAMTAICS
VGLDMIAIPGDTPASTISGIIADEAAIGMMNNKTTAVRVIPVPGATVGDEIDFGGLMGGA
PVMAVNPSSAEHLISRGGRLPAPVHSFRS
>PFR_JS14_1734	PFR_JS14_1734	Chloramphenicol phosphotransferase family protein	1969270:1969839 Forward
MLIAMAGLRATGKSELAEQLATRMKAVLVQVDALEEAIIGAGIWRNEATTTAAYDAAAAV
ARANLRNGLDVIVDAANYKAETRALWVGLADELHVDHMFLVTTCSDQAEHQRRIEHHRAN
GDGSQLTWEQVIERNMKTAFWGDEPRLAIDTSKGLDVDHVMALVASFASDNQPVRISKGP
RRGARRAQA
>PFR_JS14_1735	PFR_JS14_1735	Formate-tetrahydrofolate ligase FTHFS	1969941:1971617 Reverse
MKSDVEIAMEATLKPISQVAETLGIQPEEYDPYGRDKAKLSLSLLDRIADRPDGKLVLVT
AINPTPAGEGKTTTNIGLSMALNRLGKKAITTIREPSLGPVFGIKGGAAGGGYAQVLPMD
DLNLQFTGDMEAIGAANNLLCALLDNSLHQGNPLGIDSQRVELRRVLDMNDRALRNIVIG
LGKRSDGVPRESGFDITVACEVMAILCLTAGMDDLKARLARMVTSYNGDFDAVTAEQLEA
TGAMALLLKDAIKPNLVQTIDNTPAIVHGGPFANIAHGCNSVLATRMALKLGDYTITEAG
FGADLGAEKFFDIVCPSAGFQPDGSVLVATVRALKYNGGQGVKELGTEDLDALGRGMANL
ERHVENLRSYGVPVLVAINRFPADTEAELALVRERCTAMGVRVVDSEVFAKGADGGIELA
NAVVEMCEHPTQPARFQPLYRPEQGLRASIERVAREIYRADSVHFTSLAESQLARLTKAG
FGGLPVCIAKTQYSFSDDPHLLGAPTGFEITVRELSVRAGAGFVVAFTGNIMTMPGLPRH
PAAAGMDIEADGTIIGLS
>PFR_JS14_1736	PFR_JS14_1736	Hypothetical protein	1971748:1972236 Reverse
MAEDFTPRYESYPDRLIREAMERGDFADNPLRGKPVKLGRPGEQKSWIQERLEREDLSGI
LPPPLQLRREKARIARTLANVPTEQQARQIIDALNERIRDANLNPATQPRVVISLLDAEQ
ALSDWRDAHPGAPSHGPKRGPSGPADGRADRPGDRPGDSGQR
>PFR_JS14_1737	PFR_JS14_1737	Peptidase dimerization domain protein	1972236:1973582 Reverse
MASGRDQEVIDQVREVLPGVLDDLRSMVRIPSVSSQAAHAGDITAMADQLVGYLKMLGWD
DVRIIEAGGKPAVLAHYPAPEGKPTVCLYSHYDVQPTGDLDAWTSDPFVAVERDGRLYGR
GTADDKGGLGVHLAALRAFKGKPPVGVTVLFEGEEEIGSPSLDALLDKYTDELEADAYLI
CDCGNWEVGTPAFTTSLRGVVDCVVQVSTLDHAIHSGEYGGVAPDALTALCRLLATLHDE
RGNVAVEGLVSGHAPEQLEYPDARMRAETGVLDGVEFIGDDSFVDRMWNKPSISVIGLDT
TPIAVSSNVLIPSASARVSLRVAPGDTAENAREKLFAHLRSHAPWGARVTLSNAEAGEPA
SLPFEGPIAEEARAAFATAWGTEPVLNGTGGSIGMIASFQRAFPQATILGTAVSDPHSRM
HGIDESLHLGDWRKAAASEALLLDRLAR
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>PFR_JS14_1738□PFR_JS14_1738□Phosphoribosylformylglycinamidine synthase 2□1973587:1975851 Reverse
MVDTVENARTTPDVVQPWEALGLKADEYARIRDLLDRRPTGAELAMYSVMWSEHCSYKSS
KIHLKRFSELPQTTPRGPLLAGIGDNAGAVDIGQGYAITFKAESHNHPSYVEPYQGAATG
VGGIVRDIMAMGARPVACMDALRFGPLHSADTKRTLPGIVAGVGGYGNCLGLPNIGGELV
FDSSYYGNPLVNALCVGVMRHEDLHFAKATGSGNKVILYGAATGADGIGGASVLASETFE
ADGPAKRPSVQVGDPFMEKLLIECTLELFHAGVVTALQDFGAAGISCATSELASAGDGGM
HCELHLVPLRDPTMTPEEILMSESQERMMAVVEPADVDAFMAICGKWDVQATVVGEVTED
DRLIIDWHGETIVDVDPNTVAVDAPRYDRPQLRPEWLDGVQADHANNLPRGHDGAALAEA
VVAVATSPNLADKSWATSQYDRYVRGNSVLSQPEDSGMIRVDEQTNLGVALSMDANGRYA
YLNPYFGAQLALSESYRNVATTGAQPVAITDCLNFGSPEDPEVMWQFTEAIKGLVDGCKV
LGVPVTGGNVSFYNQTDGINILPTPLVGMLGVIDDVRLRIRQGFAHAGDTVLLLGDSKQE
LGGSAWEDVMHGHHLGGLPPFPDFDAEIALGKVLQAAAKQQLVSSAHDLSEGGLAVALVE
SCLHGNHGVSFTLPTDLDPCAELFSETQARAVVSLPPQSVAEFTTLCADAGVPVRELGEV
RGDQLLEARGFFTVQLDELRPQWQSTIPEAMQGA
>PFR_JS14_1739□PFR_JS14_1739□ATPase BadF/BadG/BcrA/BcrD type□1976152:1977108 Forward
MVDPGDSEGTVLCLDAGQTITRTQFRRNGTVIGESEHAGVLTDRPLLPQLATAVRSGLHA
ADSTVDVAAIGVSGLVDNADASELLDMLAGTGIREVLLAHDSTTSYLGAIGDELGAVVAA
GTGSVTLAVGATRTARVDGWGYLIGDAGSGFWIGRAALDRAMQAHDGRGAPTALTAVVRR
DFDDLEEAYLELQADELKVSRIAGYAQTVAELAATDMVCRRISEEAADLLAHAVFAGLRR
VGQAEREDPMVGAVGNAFRNTVLRDRFEQVLRDQLPKLRFVEGRGNGLDGCYRMTLVAPD
SALRQRINRATASERPQD
>PFR_JS14_1740□PFR_JS14_1740□Transcriptional regulator HspR□1977267:1977701 Reverse
MSEPWLPQVIDPDAAIFTVSVAANLTGMHPQTLRGYDRMGLVVPKRAKGRGRRYSPRDVT
RLRLIQRLSQEEGINLNGIRRIVGLEKELDDMRQRVSEITDLMRQMTDMQQQVQRIFTAG
PTGVQPGRHRREYLRALESGPTDL
>PFR_JS14_1741□PFR_JS14_1741□Chaperone protein DnaJ 1□1977794:1978966 Reverse
MSTKDYLEKDYYKVLGVPKNAKPEQIKKAFRKIARENHPDQHPGDKKAEERFKQASEAND
VLSDPAKRKEYDEMRSLGGPGGPGGFRFNRSAQGGGPGVNVNDLFRNMGGAGSMGAGGLG
DILGGLFGQGGTGTSTRVNATPRRGADVEGQASISFRDAVEGTTVKLRMLSDDPCPVCHG
TGAEPGTMPRVCPTCEGSGVQVSMNGTTVPCPTCHGRGLIVDHPCHACHGSGRAEGTHTM
QIRIPAGVTDGQRIRVRGKGASGENGGPRGDLYVKVQVAPDRVFGRSGDNLTVKVPVTFP
EAALGTEISVPTLTSGSVRLRIPAGTPSGRTFRVRGKGVSKVKGGHGDLLVTIEVSVPSH
LDKKATEALKAYAGVVNEPNPRDAATSDES
>PFR_JS14_1742□PFR_JS14_1742□Protein GrpE□1979028:1979678 Reverse
MTDKPAEGNGDEQPEGDFSNLTPEEFLAKTADGTAKEAAAGARANAAHDALGQAKALAAE
RTEDLQRLQAEYVNYKKRVDRDRDVARAKGVESVVRDLIPVLDAIHQAEAHGELTGGFKL
VADELESLAAKHGLVIFGQAGEEFDPRFHEAMYQVPTPGTGEMRIHEVMQKGVRVGDSLI
RPARVAVSVPNGEPAGDDTIADQDDNASGDDKAPDA
>PFR_JS14_1743□PFR_JS14_1743□Chaperone protein DnaK□1979843:1981717 Reverse
MARAVGIDLGTTNSVIAVLEGGEPTVIPNAEGSRTTPSVVAFAKNGEVLVGDVAKRQAVT
NPERTIRSVKRHMGTSWTTKIDDKEYKPQQISGFVLQKLKRDAEAYLGEPVTDAVITVPA
YFGDAERQATKEAGEIAGLKVDRIINEPTAAALAYGLDKAEKEQTVLVFDLGGGTFDVSL
LDISDGVFEVKATKGDPKLGGDDWDQRIVNWLIEQFKAKNGVSLEKDKMALQRLQEAAEH
AKIELSQTQTTDINIPYITATQAGPLHLEETLSRAEFQRMTQDLLDRCKTPFNAVLKDAK
IGVSGIDEIILVGGSTRMPAVQDLVKELSGGKEPNRSVNPDEVVALGASLQAGVLKGEVK
DVLLLDVTPLSLGIETKGGVMTKIIERNTTIPTKKSEIFTTAEDNQPSVMIQVYQGEREF
ARDNKSLGNFELTGIMPAPRGVPQIEVTFDIDANGIVHVYAKDTATGKEQSMTVTGGSAL
SKDEIDKMVKDAEANEEADKKRRESVDMRNEADMLTLRTDKLLDENGDKLSDDVKQPVVE
AVAKLKEALKGTDNDDEVKAAMDDLNQKASAMGQAVYEASQQQQAAGAAAGEQGAPASGE
ASSNDDDVVDAEIVDDEDKKDDSK
>PFR_JS14_1744□PFR_JS14_1744□6-phosphogluconate dehydrogenase, decarboxylating gnd2□1982125:1982985 Reverse
MGRNMAERISRAGHDVIGYDRDPQVSQVADLPALVDALELPRVVWVMVPAGEATRAVIAE
LAGLLAPGDLVIDGGNSHYTDDRPNAETLGDKGIHYLDCGVSGGVWGLDNGYGLMVGGDD
ADVARAMPIFDALRPEGPRDEGFVHAGRIGAGHYAKMAHNGIEYGLMHAYAEGWELLEAA
DDLVTDVPGCFKAWTRGTVVRSWLLDLLVKALEENPGLEGVSDYTTDSGEGRWTLDEAVA
RAVPMPVLAASLFARFSSRQETSPSMQMVAALRGQFGGHEVHRKGE
>PFR_JS14_1745□PFR_JS14_1745□Gluconate permease□1983174:1984517 Reverse
MTLHLILAALAGIATIVVLIVWLKVHPFLALMGGSAVMAVSAGVSYTDMFASFTKGVGST
FADVGLLIVMGSIIGTLLISSGGADVIVDTILDKTPVKRLPWAMALIAFVVGIPLFFEVG
VVILIPVVMYAAHRAKLPVILLGIPALAGLSVLHGLVPPHPGPLIAISALNANIGMTMGL
GLLIAIPVLIISGPLLGRVMAKWVPITAGDDYVQKEADAVHADDRKPSFAISIMAVLLPV
VLMLARTVAELAHIDKTTAGRFLVFLGTPLIALLITAIFAMFVFGYLLGRTRDMMNKLVG
SAFGPVAGILLIVGAGGGFKQTLVDSGIAKMIGQGLADANLHPLFAAWLMAVLIRLATGS
ATVATITAAGIMAPMVGSLPPVEGSLMVLAIGAGSVFLSHVNDAGFWMVKEYFGMTVGQT
FKTWSLMETVISVTGLACVMGVSLIVL
>PFR_JS14_1746□PFR_JS14_1746□GntR domain protein□1984866:1985630 Forward
MSEEATNQPKFMSVDRELGIEIIDGVWAVGEARALEEIQERFNVSRTVAREAARQLEAMG
LARPRRRLGLVAQPQENWRMLHPVLINWRLHSTQRMAQMRAVVQLRQAVEPMAAANAARI
APIPDRGRLMSLAAEMRQFSDANDEESFIDCDNEFHEVMLACSGNELFAALGELVGIVIR
ARVDFDAPHPARQPTIIAHEAVAEAIFKGNADGAHAAMSTLLSDACHDFSGVNISLPTPT
EAPTTPRQRPAATK
>PFR_JS14_1747□PFR_JS14_1747□Cobalt transport protein CbiM□1985940:1986647 Forward
MHIAEGVLPPVQCAIWFAAAAPFVVHGAVQVVKQIKHHPENRLLLATAGACTFLLSSIKL
PSVTGSSSHPTGTGVGAVLFKPPVMAFMGLIVLIFQALLLAHGGITTLGANTFSMAIVGP
WVGYGAYVLNKKLGGPLALGIFLAMFLSDLSTYCVTSFQLAFAYPDPSSGVLGAAEKFLG
IFAISQIPLSVAEGILGILLFRFLFKVAGPQLQALGVRLGNKRTANAEVPEVAHV
>PFR_JS14_1748□PFR_JS14_1748□Cobalt transport protein CbiN□1986640:1987140 Forward
MSEATITNPGAGAPNPTTPASDTSGHGLFAADRKWVTPVLVVALVVIFVGSLIIGGIRTA
GQDETFVGTDSAATEAAEEAGAKPWFQPLFEPAGEVESGLFAIQAAIGSGIIFYCLGRMS
GKKAARKQEAAIGVTAAAADASTSPAAAISPDGSTPGPTAPGSRNA
>PFR_JS14_1749□PFR_JS14_1749□Cobalt ABC transporter, permease protein CbiQ□1987144:1987938 Forward
MSGLHIGALDDAAWGSPWRRRRVGEKVACSMGLVLTALLAPTWPGTLLVAVAAIALIVGA
ARIRPRVLLAAMSAPIVFLILGAISVLFSVGAAPADAWWHAAFLSVGPTSVAQAARLFAH
GLSGTLAVMVLATTTPMVDLLTWLRRFRVPDPLLEIASLTYRLLFVLAETTANVLAAQRC
RLGDNPVGRWNGLSRRWHNTAAAVGAIGLRAWDRSSRLTEGLAHRGFETSLVTLPVPRVA
SPRLITATVVVLAAIWSISLVVAR
>PFR_JS14_1750□PFR_JS14_1750□Putative ABC transporter ATP-binding protein in CobA 5'region□1987935:1988828 Forward
MSALLAAHDLVAGFPDRPRVLDTVNLAIGRGTRLALLGANGSGKTTLLSCLAGSLKPTGG
AVERDGAPIDWGRKGLREHRRHVQMVLQDPDDQLFSADVSQDVSFGPMNLGLEPDEVHAR
VREALTLLGADHLAERATHQLSYGERKRVATAGAVAMRPDVLMLDEPTAGLDPLGVHQMR
DALDRLTDAGTTIVMATHDVALALDWADEVAIVCDATVHQGAPEALLSDADLVARSHLDT
PWPLALAAALGLSSRPRNLDEAVAALAPALGEFAATHDAAASVPGSDDTTNTDEETR
>PFR_JS14_1751□PFR_JS14_1751□Putative uroporphyrinogen III methyltransferase□1988825:1989598 Forward
MTTTLLPGTVTLVGAGPGDPELVTVAGLRAVQQAEVILYDRLAPQDLLSEASDDAELVPV
GKIPRGHYVPQEEINQLLVAHAREGRKVVRLKGGDSFVFGRGGEEWQACAEAGIPVRVIP
GVSSATAGPALAGIPLTHRHLVQGFTVVSGHVSPSDERSEVPWRQLAKDRLTLVILMGVA
HMRDIAPELMAGGLPADTPVRVVSNASLASQESWRTTLGDAVADMDAHHVRPPALVVVGT
LAGVDLSHPDHRAPSDH
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>PFR_JS14_1752	PFR_JS14_1752	Putative ATP-dependent helicase HrpB	1989637:1992258 Forward
MACGRETLPNVFDLDRIAAELPVGGRLDELAAALTAPDARLVVQAPPGSGKTTVVPPLAA
RRHAGRVVVTQPRRIAARAAAHRLAELSGTALGREVGFTVRGESRRSDATRVEFVTTGVL
VNRVLRDPELAGVGTVILDEVHERRLDTDLAFAMVHDVADLRDDLALIAMSATLDAQRWV
SLLGTGTPAPVVDVPGALFPLRIEWAPPPSGVLPTYGGHLDNAFAAHLARVTAATLAQHH
AADGAPASALVFVPGARDVDQLIGLLRHEPGLAGDIEVAGLYGSMAAREQDAVLRGGGRP
RVIVSTAVAESSLTVPGVRIVVDAGLSREPRLDATRGVTGLVTVRESRASADQRAGRAAR
LGPGVAVRCFARDEWAGMSAEATAEASVSDLAGAALTLACWGSARGQGMTLPDPLPSDAL
DRAIATLRGLGALDARERPTALGRRLSTLPLDPRLGRALLVGAARIGPSRAGKVMAMLAS
DERVPDGDLMVQWRALSSGRSPAARRWRHEATRLERMARGSDGRPGSASGAPLSDQAAVG
LLAALARPDWIARRREPGGRAYLTASGTGVDLLRESSLVHSEWLAISELTRLDTRTGPAR
AAHASGSLVRAATALGEQTALDAGADLLDEQDTATWDPATGRVQTRRQRALGAIVLSSTP
VRTRAAAAAGAALAALPQVGLGIDEPGLLRWSDGAVGLRNRLAFLHSVDASAWPDVSQPA
LVARADTWLARPLHTTGSTFDVDVTTALRTLLDWRQLAELDRAAPERLPVPTGSQVRVRY
PSPESGEQKPVLAVKLQECFGMRTTPRVSGVPVLMELLSPARRPLAITDDLESFWVNVYP
QVRAENRRRYAKHPWPEDPLTAPPRRGTTRSGR
>PFR_JS14_1753	PFR_JS14_1753	Membrane protein, PF10081 family	1992349:1994208 Forward
MPKHHGRARGAGNQNPRRLLTTLGTSTLGTWTRQARRHAQRLNIPLPAALGGIAGYALAH
TTSLLPRTPLFQGVVAAVNASVGYELGMMAADVAALRRAPKATPGVNPAPTTASPIVPNP
LTGVPTPRPGNGSLRSGLAAAALGATLIGVPLAALRSQRRTAEFCQVPGPRVRWAPASAA
ASVAILGFFTLCWRISEMLLDWLSHHLGQRLAWRLAARALATLVVLAGTAVLFDQVILRG
IRLAGRTVADRLDHSTPAGVTQPDRAVRSGSPSSGETWDSLGLQGKRFVSGGPDAARIAR
VLGSPAQDPVRVYAALDGRGLAGIARAVLDEMDRTNAWQRRVISIVTTTGRGNANEWSAS
ALEYLLAGDCCTIATQYSGLPSAITLFTSREQPVAATRVLFEAVQGRLAAMPANERPQLF
LAGESLGAYGSNGIFTDVDDMVAHIDGALWLGTPNFTPMHRELTRSRDAGSSAVAPVVDR
GRHIRFAGRSAQLSADEAGRPLDAWQSPRIAYLQNETDPVVWWGTRLLYRRPEWLAERRP
ATTPMGRMHWFPFVTFWQVCADMPVCRNVPEGFGHKYHASQITPAWAGVLGRDPRADYSA
IEQALIQDVTIPPIKVFGI
>PFR_JS14_1754	PFR_JS14_1754	Azoreductase B	1994260:1994871 Reverse
MKIAIFGATGMVGSRLVDEAMARGHEVTAVTRNGRAIPGTTAVAMDFTDTPAVVELANAS
DVVIISIPPDRSRVEPIEVNLHAHQRLIDAVPSARIIVVGGAGSLKVAGTYLRDRPGFPE
AAMRNSTWGISMLERYQASPPALDWLVVSPSPLIEPGQRTGHYVLGIDEPAGQRVSAENF
AVGILDEIEDPDHHRMRITFADK
>PFR_JS14_1755	PFR_JS14_1755	Azoreductase B	1994877:1995488 Reverse
MRITIFGATGHVGSQITAEALRRGHQVTAVSHSGKTVADTTPAQANFDDTPAVVELANQA
DVTVISVPPSRTADEPIEVNLDAHQRLIDAAPDTRIVVVGGAGSLLVDGVPLRDTPGFPD
AYRREATWGIELLKRYRQAPVGVDWLIVSPSPEIGPGERTGQYVVGTDSPVGDHITTQDF
AVGILDEIEAPAHHRMRITLADK
>PFR_JS14_1756	PFR_JS14_1756	Hypothetical protein	1995725:1995955 Reverse
MNIDWGALALVSVVTLIGTVVVVAAVSTAALLLDLSRARAHAGTPAPAMRVGAYAMMVVC
FAMLAFGLWLIIPYFH
>PFR_JS14_1757	PFR_JS14_1757	Phosphate transporter family protein	1995952:1997223 Reverse
MTLTLVIIVVVVALVFDFTNGFHDSANAMATSVATGAFGARQAVAVAAVLNVVGACLSTE
VAKTISSGIVDNSLVNPQTVLAGLAGAIVWNLVTWLVGLPSSSSHAMFGGLIGAVLVTAG
MAGVHWGVVVSKIILPALVAPVVAGIAAALSTWISYKITSPTAHHASRIFRHGQRLSASM
VALAHGTSDGQKTMGIITLVLIGAGYQQSGTHPHWWVIALAGCAIGLGTYSGGWRIMRTL
GKGLVEIKPAQGFCSETASTVAILASSHLGFGLSTTHVCSGAILGSGIGRRGAEVHWGVA
GRMGIAWLLTLPAAGVVGAVASFAASKGAVGLVGVLVMLIGAAIVVLAVARHTKVDHTNV
NDSHEVTVRLSPEPEVAAATPAPVPVQATVADLLKPAAEKPGGHHREGTDGSNPRMAGSG
AGR
>PFR_JS14_1758	PFR_JS14_1758	VPDSG-CTERM exosortase interaction domain protein	1997435:1998181 Reverse
MDWSGFAAQLGAHLRASVAGVHPDEGWWIAAAVGAALVAVVVRPVWRWTRIAVTIVHELG
HAVVGLLSGRKWQRFVVHPDMSGEVSTLGRPTGIGRVLTTAAGYPAPAVVGAVGIWAALA
GWGPLVLLALALMALGALVRARSAFTVLALLVVLAGDLAAWWFGDVQLVAALVCGVGAFL
VLGAWRQLLNVARSGDPGQDPVVLGMLTHLPRGGWIAVFVLVVGAFSAWSLMMLWPVLGG
WLGLFAGR
>PFR_JS14_1759	PFR_JS14_1759	Transcriptional regulator, MarR family	1998577:1999236 Forward
MTAVVSHNGGASDLVLPVLELSSEVTSATEAIIYRHQLTPAWWQVLATVLDTAHTVPDIA
RRLNRTRQSVQRIADIIVDNEWARWDANPKHRRSQLLASTLSGRQAAAELEGGLQDWADS
VGEGLTVAEMDQFRSLLDRILHGSRDYRAQPLSEKGPDLEDHWGPNRRTRARVARCNGAA
RHVGPPQPDAAGLPVRAPVGVKVSRGAVQSGVQFSRGAP
>PFR_JS14_1760	PFR_JS14_1760	Hypothetical protein	1999217:1999360 Reverse
MTGPDRVRVDWAVAGRAADGHVFALSGHDDATVDQHGHIQTLTVRPD
>PFR_JS14_1761	PFR_JS14_1761	Hypothetical protein	1999332:1999592 Reverse
MAAATNPGITTLNRYFELSNTAGQNQRDLDELLGLFARDAELESARGEIANGEEGLKDFF
RTFFRPQRGVAPCVEHRDDRPGPCSR
>PFR_JS14_1762	PFR_JS14_1762	Putative monovalent cation/proton antiporter	1999609:2001567 Forward
MGDGSHPPTVTLPRPPVGPADADNGVAIGCDNEPVSVAILIFVVAMLLIAASDRLAEHTG
VVAPVALLALGIIVGFTPWVPDISVDPQMIVAVILPPLLYATATSMPTMDFRRNLTPIAV
LSVLLVAVSAVVLGFIFEKMVPGIGLAVGIALGAVASPTDAVATSIVRRQGVSNRLVTVL
EGEGLINDASALVIMSSALAAVAAHVTAGEVIGHFAQEVIVALLIGWLAGEVMVWVRARV
GSVTADTVLSLVTPFVAYLPANALHGSGLVAAVIAGLVVGREAPERLHSSHRVAAGQMWA
TLQLVLESTVFGLMGIQLPGILHDVARGELHFKLAAIVAGVGLVATIVVRAVMVVPLVLG
SSRRNNRREQKRPRLEMMNEMAGKMTEKVKDGPTTVSRGGRSMTITPERASTFRHRVWRA
LADIDYFTEQSFGPREGAVIVWSGMRGAVTLAAAQMLPESTPHRSFLILVAALLASASLA
IQGSTLSLLVRLVKPTKTRPVTRAELRDIYGRMREAAQDVPVPPKLMAMLNAQGEDDSEV
TGDIRGPAVSLAWNLTSRMRESGVTLTQAQRNQVTALSFRYALDVIAAQRKALLAVRDTG
KFRPQALDDVFATLDADEMALELHAGPLLTQGIEEPGAPADQDPDDRLAPLE
>PFR_JS14_1763	PFR_JS14_1763	Pyruvate oxidase	2001711:2003468 Forward
MTKVNASNAMLQVLKDWGVDTIYGLPGGSFDSTMNAIHDFRDDIRYIGVRHEEVGALAAV
AEAKLTGKIAVTFGSAGPGAAHLLNGLYDAKTDNIPVLALIGQVPTAMMNTDFFQELNEN
PMFADVSVYARTVTTAEQLPQVVDTAIRTAYSKRGVAVVIIPKDLGWAPIEDNYVSSANA
FTPADWNLAARDADVARALDLINEAQRPILYYGQGAKGAGDEIRALSELLGLPMVSTYLG
KGIVADDDPGYMLPTGRVAGKPGVDVGKTADLVLLAGSNYEFGGHMFSPTATFIDVNLET
SVIGARHAAALGVRADAPTFLRQLLELARQQGDARNDHADWLAAAKQDKAEWTTWVDAKA
ADDREPIRIEPIYAEINKHAKPDAIFGIDVGNVNISSGRFLKLGGDKRMVTSPLYATMGF
GLPAGIAAALKYQGRQIWTLSGDGGFAMVVQDLATQAAHNLPVINIVFTNKSLGYIEAEQ
DDTRQPHSGVALTDVDFAKVAEAFGVKGYTVRTLAELRRVLDEVSDTKVPVVIDIKVTND
RMLPVEAYPVNRADRPDFDDFAAHYEATPLRPFGEILAGHGIHLG
>PFR_JS14_1764	PFR_JS14_1764	Hypothetical protein	2003610:2003981 Reverse
MEIGSLAEWVTGFAEVLAVSVALFLPSWERRRATREKRLRTLRTIRRLTPRLLTLPATSD
ERSGDLRMLQTFLMVTDMMNIDPGVEDVIDTGQQIASMVHQGQPVSDHDAAAIRALLDSL
PSS
>PFR_JS14_1765	PFR_JS14_1765	Hypothetical protein	2004223:2004408 Forward
MVVVDAAEAIWIRPRKGQPDLSEEEIEDRIRRTNAVTAEVFGPRFAARNRLRRPGRPNGD
V
>PFR_JS14_1766	PFR_JS14_1766	Hypothetical protein	2004467:2005438 Reverse
MSLLGRLDELATQLSTLSGELAEHSHADAALRERIQQAKQRAEGFSPIMAGLDLWSAMTL
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ELSTLVAKVTDEVEQLRASCAATRFRIALARLHCDQVGYFTVELIDQTPDWQLAAPGIVL
LCRALSQGVAETAGAVQGNAQLAAKVASDINEMAQAVSIPRTLLASWQTMAAGRELSDDL
RELMPQVGSTIETTAEQIERIGRVAEECRRNAQPHDITAIREHVMALSEAASVVAAESAP
TPHADPQPVDSPEVDRQYDEPPAPPSETVAPAAGAPGSGVPDAGQPGGEQSPVPSPTQAF
PPPPVQQPFRPEQFPPPQAPMGR
>PFR_JS14_1767	PFR_JS14_1767	Hypothetical protein	2005439:2006128 Reverse
MSAQTADTGWRDVARKVSAPDPNGTEQQLGLNDVFFSTTDRKGVIEQANEVFVRISRYPR
EVLVGSPHNIIRHPVMPGAAFRAMWDYLLDDQPFVAYVHNLAADGSLYTVLATVTPLDGG
FLSVRTRPERADLLGAADSIYGTVRHLELEWEAAGLGAPAAAAQGLGVLAKQLTAAGIPD
YTAFMQTVLPAEVQARIAAGATVPQRPWAVGRLADMAVHQRRLTEELDD
>PFR_JS14_1768	PFR_JS14_1768	Adenosine deaminase	2006311:2007528 Forward
MPDVARRDLNLLPKAHLHLHFTGSLDIPTLRELSAWEGLDEAEQLIDDDPLSVPATKRGW
WRFQRTYDIARHVVISERALRAVVDAAARNDAAQGSRRTEIQVDPTSYAPYVNGLVNALE
IILDEAALASRRHGIQMGVIVAASRLHHPLDARTLARLSARFAGRGPGGVIGFGLSNDET
EGNTVEFGPAFRIARRAGIPGVPHGGEFRGPHHIAQVIDELHPTRIGHGIHAAESPALLK
RIVDAGITLEVNPASNVSLGVYPDYSKVPLRTLLDAGAQVALGADDPLLFLSGLTDQYRI
AHDYLGLSDAELAELARMSIRGSFAEQADKARWLAEVDAWLAAAPESGPVLPAAGVAPVP
GGLVARPSGLLVPERGLVAPPGDGGAESADAGQGVPDARNVRPGL
>PFR_JS14_1769	PFR_JS14_1769	Nuclease SbcCD, D subunit	2007479:2008759 Forward
MRAKASRMPAMSDPASNLVAMRILHTSDWHLGRTLRGVDLSDAHAAFLDQLVAVARSERA
DAVLVSGDVFDRALPPLDAVNMLNDALARLTEVAPVVLIPGNHDSPQRLGLNAKLLRDQL
HIRATLADIAHPVVLPDSTGHDGLVVYAIPYLDPDMTRDRLGELAGVDGDGRIARSHEAV
VGAALSMVHRDLARRRAANGTRIPAAVMAHAFVTGAQPSDSERDLRIGGVDSVPAALFAD
VGTDYVALGHLHGAQAVAGSRDPASDHDEDAVMRYAGSPLAFSFSEQHQHKSTALVTFDE
AGPVTSVELIPTPVPRRLSDVRGSLQQVLGEDFAAQRDDWTRVVVTGEDRPADLSRTVKK
AFPHALEIRFESTLREREVRATVSAQADPLEVVGEFIADVSNRRPDAAELTVLRTALERA
TKQGDR
>PFR_JS14_1770	PFR_JS14_1770	ATP-dependent dsDNA exonuclease SbcC	2008759:2011923 Forward
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SSGDRMVSTHRKAASEPYVDLVVDTSRGLYRVRRTPQFTRPKKRGEGLTSVNATIRLWKL
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QIFGTELFERAQQELTAMAADYKARADQARTQIRSLAERFAHSAWPDEAPTPDGSPASEA
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ARPLAAARRAASALSTATTEWEVVAAEIAATDDGVLLEQVRPHAVGNLGSPDGSDDAALS
TLRDEITRLGTTRGQLGQLAQLEAGLPARHARLDADNARLAEITARITTTQQELAELIAG
RDELSQRHGQLPPTDDALTSASLAQQAATRTLEAAQAAEQDASQLVALRAAEQEAIDAAD
LAEREYRTARAGWLDGLAGTLAGELVDGDECPVCGATSHPHPATPAEGAATRDDVERLAQ
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ELTARIADADRQVTTTRSTLAELQASASGLKGAIATATTQLDDDHHQIDRHREDYPDIAG
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IAALRQSITDFDTRRARIAAQLERAELVAAVASPVPDLESLDTKLADAEQAQEAAELALG
RATAHLAQSRQAAEELEAASLALTRMAPEAAPVVRMAELATAGDRNLRKVTLPTYVLLRR
FEQVIDQANDRLESMTHGRYSLQRTDEKEGRSRKLGLGLVVIDHLPVDTARETQTLSGGE
TFLASLAMALGLSDTVTAEAGGISLDSLFVDEGFGSLDPESLDMVMGQLEKLRAGGRNVG
VVSHVTEMKQRIAERISVRKLPDGSSTLTTTVDD
>PFR_JS14_1771	PFR_JS14_1771	Hypothetical protein	2011948:2012130 Reverse
MLAPGTTIAVDSSSWTPLDETGAMVRIEVTVPGTAPTPYTAVMVKEADGTWKVMGTVAAQ
>PFR_JS14_1772	PFR_JS14_1772	Carboxylic ester hydrolase	2012444:2013775 Reverse
MRRRTTIAALAAVLSFSPLAAQAAPASADGGTSSTPRSVATSTSSAGVDPASACGDLVQL
APVLSSDHTPDGKQITPKPTADGRRVPVIIVHGWVSYDTHSDARDHLFSQYVDRTADPAG
GTGYLLAQSQYRSSLIGMLQQVPGAEVYTFDYSQVGSRWVTDPQIGPKLSQAIECLSDSY
QQKPVLVTHSMGGLVARQALSNNDSKGRPISGRVSNVLAVGAPNNGSDSAQMIASALTIG
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WPDNVKVTAYVGDIQMGGISLFGLNSPRLLDLGDLLVSVDSAKAGSQRSRQVNCEYGIIS
TKSAETGLVRLMLAGQGNSVEQPADLLSSPCFHEAMLHETTITGDLQRDLTEVLGANTAW
HDPATAGEQSAGATTVSAVRESR
>PFR_JS14_1773	PFR_JS14_1773	Acyl-CoA dehydrogenase type 2 domain protein	2014160:2015308 Forward
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QTALAKAAPATALAINMHQIIVGMARYLVAHGNDKGRQVLHDAAAGELFGFGISEPGNDL
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GFYVKPDWDTLGMRATQSNTTVLDGAHAPADQVLARITPGPNADPVVFGIFSHFSAFIAA
TYQGIGERAIEVAAEQVATRHSVKNDDVYAHDPDIRWRLADAAIAMNGSAAQLRDIVRDL
DDDADRGALWMPQLSAVKNACVEATMHAVDQAMRSVGGRSYYTSNELSRLYRDAVAGLFQ
PTDQESLHAAWANVVLGPITKG
>PFR_JS14_1774	PFR_JS14_1774	FAD linked oxidase protein	2015471:2018257 Reverse
MSSATTEKAVGTTRLIDRVGMAHDASHYLLIPEVVITATDTAQVANTMAQAYRENRTVTF
RSGGTSLSGQSLSDSILLDVRKNFRKVEVLDGGARVRCQPGATIRNVNAHLARYGYKLGP
DPASEIACTIGGVVADNSSGMACGTQFNTYNTLESMVLVLPSGTVIDTAQPDADAKLHRA
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GTLGFVAEVTFRTLPVQKHAATALLIVPELSVATDALEDLVRNGALCLELMDAASLRVVQ
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RNNLWQLRKGLYTSVAGARPAGTTNLLEDIAVPVGSLTATSAELQDIFAKHGYDDAVIFG
HAKDGNIHFMVTSDWRNPVDVEKYRDFTEDMVNAVLRHEGTLKAEHGTGRVMAPFVERQW
GAELYDVMKTVRRLGDPHGVLNPGTLLTDDPEGHMHHFKMMPPVDDFVDRCVECGYCEPT
CPSADLTQTPRRRIALLRSAEELPPEQAKELRKDYAYEAVDTCAADSLCLLACPLRIDTG
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KDVIPKVGNDLPGGGPKRPEPESTSQDDFVFFPSCMGSLFEPAKGGYKDGAAGAFEKLVA
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VKDVEACALAVSDDVTVPVDAGCCAFAGDRGLLHPELTASATKRETAEVTQRTYDEYVSG
NRTCEMGMTRATGHTYHHVLEMLAQHLV
>PFR_JS14_1775	PFR_JS14_1775	UPF0214 protein YfeW	2018651:2019928 Reverse
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DLHYDLASITKVFTAITVLSLADEGTLAMDEPIAALLPAFRTSPERRRITALHLLTHTSG
LPPVWPGWQDAGMRSRSREAILADIVAMPLRWAPGERLDYSCVGYITAMALAEQATGQGW
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SVTDDVDLTMVRGTVHDETAQVIGGVSGNAGMFSTLADLARLAGALSSGLPGVLGRESFA
MLWGDQLPRLLGGHADAEAARNGYRHGAGLCVAQTRAAGPDAPWLRSHTGFTGTSLVLNR
AGDYAILLSNRVHPTRQAPDLAPVRVALTRAAGLVEPGGLAERGGLAEPGELAEPGELAE
PGGQA
>PFR_JS14_1776	PFR_JS14_1776	OmpA family membrane associated protein	2019925:2020710 Reverse
MRRLRAGVRPELPAAGRHRQAAAGRHPRSAAAARPPAPAARPARCAGAAALAVVTVLTAI
TAGCNVVVHAVAAGRRRAPGQLHAGVTPGTAMVLGAGVRGQRPTPYLAARLDLAVRLWRE
GAISRILVSGWAEAPDDAAGLRYDEPAVMADYLVAHGVARGAVLRDPAGLDTWTSAVRAR
QLHGLDAMVVVTQAYHLPRALAAARMAGIDAFGVADTTRDHNAKWWRYRLREVPACVKLV
GEWALSRTGLRAAARARRGDQ
>PFR_JS14_1777	PFR_JS14_1777	Glucose-6-phosphate isomerase 2	2020714:2022396 Reverse
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QQLTMESNGKSTRWDTSPVTTETGEIFWGEPGTNGQHAFYQLLHQGTRVIPADFIGFARP
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QDSSTMSLIRAYKAMRAGNR
>PFR_JS14_1778□PFR_JS14_1778□Hypothetical protein□2022588:2023592 Reverse
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SAQTTMTLPVITVDAVHAAKSSAKPHRRVSLPVAAVALTSALGLGATLLPQTVAAAPDNG
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YLGNGQVVHAADYGTGVIVGTVSSMPVSSVTHIG
>PFR_JS14_1779□PFR_JS14_1779□2-keto-3-deoxy-6-phosphogluconate aldolase (Precursor)□2023818:2024516 Reverse
MMNTVTNSSSRLALPDALTTTRGVVLMPPDEDSGALMPVLEVLVQEGLTAIALPCPRSDE
TADDEGADTPQDPSAELTGLMAMYSFRATVGIHGVRTTADAQLAIRAGARFAFCLFPEPG
VLDALRVASIPAIVTALTPTEVEQAWQGAVSAVHVRPAEVFGTGYAQGLHELVPDASLIA
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>PFR_JS14_1780□PFR_JS14_1780□DEAD/DEAH box helicase□2024653:2027205 Forward
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SGKSLIATAAHFVALSDRGRSYYTAPIKALVNEKFFALIDIFGADLVGMVTGDASVNPDA
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>PFR_JS14_1781□PFR_JS14_1781□Putative kinase inhibitor protein□2027239:2027703 Forward
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LEVPADAKPAAVEELLKAHALASATLTPVFTSTI
>PFR_JS14_1782□PFR_JS14_1782□Cutinase□2027849:2029087 Forward
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>PFR_JS14_1783□PFR_JS14_1783□Hypothetical protein□2029609:2030307 Reverse
MRQSGGVGEAFAGIAGLGIAGFDPLGALALMAAMALGARRRAIATLLVTTVATIVVTGFV
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PLPARTGRRPIWQRTGVIVSALVGGFFLLVAGGTSAATAPTRATSPATSPTASATLTPSP
TPTPTPTPTPTPTPSKSPTPTPTPSPSPRPAPAATQEQEQPAQVPQQQQANPAPAPVQQQ
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>PFR_JS14_1787□PFR_JS14_1787□Hypothetical protein□2034424:2035233 Reverse
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>PFR_JS14_1791□PFR_JS14_1791□Phosphoribosylformylglycinamidine synthase 1□2039094:2039771 Reverse
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GAIARFAPVMDSVIDAANKGMPVLGICNGFQILCESHLLPGALMRNEKMKFICREQRLRV
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LKTAPPEDQIVKVS
>PFR_JS14_1800□PFR_JS14_1800□Hypothetical protein□2048863:2049555 Reverse
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GRDQDDQLIGSIRDGLDVLRAHGWFSDELREVMESSVDASRAVFERPGGNLAGTPLVVHG
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YAINDTLFHWQSQSATTPGSSSGRRLLGEHAQSFDLALFVRQRGNDDLGKGAPYTFLGLV
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>PFR_JS14_1831□PFR_JS14_1831□Hypothetical protein□2091248:2091547 Reverse
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>PFR_JS14_1832□PFR_JS14_1832□Hypothetical protein□2091728:2091928 Reverse
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DPDFLV
>PFR_JS14_1833□PFR_JS14_1833□Hypothetical protein□2091915:2092334 Reverse
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>PFR_JS14_1834□PFR_JS14_1834□Hypothetical protein□2092727:2092903 Forward
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>PFR_JS14_1835□PFR_JS14_1835□Hypothetical protein□2093136:2093450 Forward
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QQRQSTVRKDSEDGQDRSPREDQPTVGPDAQIARHTHRAEPPSA
>PFR_JS14_1836□PFR_JS14_1836□Hypothetical protein□2093680:2093853 Forward
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>PFR_JS14_1837□PFR_JS14_1837□Hypothetical protein□2093894:2094826 Reverse
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ASSIEELATY
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>PFR_JS14_1839□PFR_JS14_1839□Hypothetical protein□2096419:2096973 Reverse
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DVQA
>PFR_JS14_1840□PFR_JS14_1840□Putative zinc transporter ZitB□2097454:2098404 Reverse
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GHMLSDVASIGVALWAMTLAARPARGRWTYGFKRAEILAALANGVTLLVLGLVLAVEAVR
RLITPPQVHAPPVIVVAVVGIAVNFLATWLLARANRTSLNVRGAYQHILTDLFGFIGTLV
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LEPGAHAQHEPGMHHH
>PFR_JS14_1841□PFR_JS14_1841□Amino acid permease□2098521:2099915 Reverse
MSTTAADPAPAGLRRSLRNRHIQMIALGGAIGTGLFYGSAESIGQAGPAILLCYIVGGAI
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TVFLYVISIALIAGIINWTMIVITDIKFRKRIGPEGVRKLAFRMPGHPVTSYVVIAFLAM
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>PFR_JS14_1842□PFR_JS14_1842□Hydroxyethylthiazole kinase□2100343:2101203 Forward
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>PFR_JS14_1843□PFR_JS14_1843□Thiamine-phosphate pyrophosphorylase (Precursor)□2101236:2102051 Forward
MPRSDAQPDAQFDRQPGAGRRRSVDLSVYLVTDTEQCGGVDGVVRTVREAVPAGVTLVQL
RDHHLSDDDFVALGRRLVDVLDGTGVPLLIDDRVHLVGPIGAQGAHVGQDDMPIDRARAM
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GHTAGNPVGQASPASQDPSASPNPSPDKAAR
>PFR_JS14_1844□PFR_JS14_1844□Phosphomethylpyrimidine kinase□2102048:2102914 Forward
MMSTPPAPDTTAPSGATAATRPPVALTIAGSDSSGGAGIQADLKSFSALGAYGMSVIVAL
TAQNTTGVTGVLATPPEFVTAQLDAVTSDIRLDAVKVGMLASAELATTVRDGLAALRAAT
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>PFR_JS14_1845□PFR_JS14_1845□Putative hydroxymethylpyrimidine transporter CytX□2102993:2104309 Forward
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GALLLGGAAGIGAHTGTPSMVGLRGLLGRGASVVPTVLNIAQNIGWAMMEIIVITSAATH
IVGAAWHWPFVIVAGALCTLMAIRPLGSVKILRTVMLWLVLAGSIYLFVMVLRQPSHTIG
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WSPTLAWFIGFVAYQLIYPGSIPGWSDLWAGLAQALGFVAPGWLGSTLGSIVVSAVAAAG
LGAIDTAVHRRRAEGGGA
>PFR_JS14_1846□PFR_JS14_1846□Putative unusual protein kinase□2104437:2106134 Reverse
MSSDRPLRARYRRILGFFARLTVQMWFFDVVLPRVGLRRLAARGRTRRFQKAAARFHALA
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SRRVLTLSDVSAIKVDDIEALNQHGIDPHEVAYAVADAYIKQVFEDGFFHADPHPGNLFV
TPVPDAMVGEVGRRWKLTFIDFGMMGEVPGDLRGQLKDVIIAIGLRDSQRLVRCMEELHM
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LIMMGVSLVPLAYAVFGGLFRRFRV
>PFR_JS14_1847	PFR_JS14_1847	Transcriptional regulator	2106177:2106749 Reverse
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RKVYSILAQD
>PFR_JS14_1848	PFR_JS14_1848	Hypothetical protein	2107044:2107706 Forward
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TAFAAPNTPTAVAAAAANGTVASNDAAAEASSLVINDSDFAQGAYTDAHSNDKIQLYSQI
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>PFR_JS14_1849	PFR_JS14_1849	Hypothetical protein	2107779:2109395 Forward
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GDTSLVPYTGAFLATVKSKDGSKYTTVPSLQQYMPKAENGVNYWVNNFRVAAASGASDGL
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FHDVPADNMYYKDIEWMASTAISTGWPDGTYRPLADTNRDAMAAFIHRAVTAGVLTVK
>PFR_JS14_1850	PFR_JS14_1850	ABC D-methionine transporter, permease component	2109519:2110175 Reverse
MNWDTIGPVYGKAIVETLIMVVITLVIGGFAGLLLGLGLYSTRRGGVMSNSGLHTVLNVV
VNIVRPIPFIIFVTAIGPLTLLVMGTTIGTTAATFALCVAATFGISRIVEQNLVTVDPGV
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>PFR_JS14_1851	PFR_JS14_1851	Methionine import ATP-binding protein MetN 2	2110172:2111437 Reverse
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A
>PFR_JS14_1852	PFR_JS14_1852	NLPA lipoprotein	2111434:2112399 Reverse
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KSQADLQAILDKLETQIKEKK
>PFR_JS14_1853	PFR_JS14_1853	DNA-binding response regulator TrcR	2112950:2113678 Forward
MAGPNAPELLTRPDGTPIRVLAVDDENSLTELLSMAMRYEGWEPTTAATGSDAVRAARDT
NPDAIVLDMMLPDFDGLEVMRRVRAEQPDVPVIFLTAKDAVNDRIVGLTAGGDDYVTKPF
SVEELMARLRSLLRRSGATSKRSESELIVGDLVLDEDSHEVTRGGDEIHLTATEFELLRY
LMRNPKRVLSKAQILDRVWNYDFGGQANVVELYISYLRKKIDAGREPMIHTMRGAGYVLK
PA
>PFR_JS14_1854	PFR_JS14_1854	Two-component sensor kinase TcrY	2113659:2115524 Forward
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NANASFPRQPDATATGASGAAPVSGATGTVPVSPGTVPTAAGQELLTQTTNGMARARKAP
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PPEIADKVFERFARADVARTHDKEGSTGLGLAIVAAVMAAHGGTAALDSSDGHTTFTLRL
PLASDDSGRPAGPPPQADLSH
>PFR_JS14_1855	PFR_JS14_1855	PfkB family sugar kinase	2115759:2116751 Reverse
MSDPSSSAPEVRAAARAARSALERVTNRRGRVGVLGSLNADLTVTTRTLPGPGETVVGDP
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IRIEAADA
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>PFR_JS14_1858 PFR_JS14_1858 Protein of hypothetical function DUF299 2123042:2123935 Reverse
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>PFR_JS14_1860 PFR_JS14_1860 MATE efflux family protein 2125615:2126979 Reverse
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>PFR_JS14_1865 PFR_JS14_1865 Isochorismatase hydrolase 2130842:2131459 Forward
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APTVPQIMNELPGVDQIDRTGVNAWEDPEFRAAIEATGRRKIIMAGLWTEVCLAFPALDM
IEAGYEIYPVADAVGGVSQVTNDRAFDRMIQAGAHPTTALALGCELMRNWARPGTDDFRR
IFNWYFHQQRSLGLLDAKILPSVGR
>PFR_JS14_1866 PFR_JS14_1866 Hypothetical protein 2131597:2132937 Reverse
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AFYLVLAYLALPRFHRILTALYVPDYYIGRTRTGDGLLGDPVNLALLGDGVQIRQAMEDA
GWVEADPVNLNSALRIIAGSVMRRSYPTAPVSPLFLFGRQQDMAFQQEVDGSPSKRHHVR
FWRCPPGWLLPGGARVDWLAAGTFDRAVGLSLFTLQVTHKIEPNIDVERDHIVATLEHAV
PQTKVNVLENFSTGYHTRNGGGDTLRTDGALPVIDLSAVPVHAEAPHEEQHQMLSDVGKR
PVSLILAFLLILIGIGITFSEVAVDAFHDVAGQVAASGGTRTEVIVANVVALVVLTGLQV
VLSTLVFKGFNWARVLLLAVTSVTLVTRLAGAIVRVPGSMDIVQMSVDVLIVYALTSLSA
RTWTHDRRTLRRELRRKRRDAKALGA
>PFR_JS14_1867 PFR_JS14_1867 Uncharacterized conserved protein UCP033563 2133250:2134440 Forward
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AAALLRQWISEGVMVYDDQPSFTIYRMAFTDATGAHRVISGVLGGLEVVDEGAGGVLPHE
RTTKKAVTDRLDLTRATSTNGSPVWGLSLAHGLTDALAAPGEPVGEITVDGVRHSVERVV
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>PFR_JS14_1868 PFR_JS14_1868 Succinate CoA transferase 2134564:2136087 Forward
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VAEGFMGKLDFAVVEAVRITEDGNIVPTSSVGNNKTYLDMAEKIIIEVNSWQSPDLEGMH
DIWNGYLTPPNRPIIPINNVGDRIGDTFLTIDSDKVVAVIETTDRDRNSPFKPIDDDSRA
IAGYLLDFYANEVKHGRLPKNLLPLQSGVGNIPNAVLDGLLHSDLENLTSYTEVIQDGMV
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GMIEADIYGNVNSTHVMGTRMMNGIGGSGDFTRNAYISAFVSPSTAKDGAISAIVPMVSH
VDHTEHDVMVIITEQGIADLRGLAPRLRAQKIIDNCVHPDFRAQLQEYFDHSLATSKAKH
TPHDLRHSYDWHLNFIENGTMKLSHYR
>PFR_JS14_1869 PFR_JS14_1869 2-deoxy-D-gluconate 3-dehydrogenase KduD 2136315:2137127 Reverse
MAKDLPNDTTPTTAPSVTSLFGVSGRRAIVTGGDSGLGHGQAEALLEAGAQVVIMARTRS
KVDAALAGWARRGLEGHGVVADLSDAASRGRGFDEAVATLGGLDVLVNTAGMITRHRAED
YPLDEYRAVLAVNAEAPFGLSQRAARIFIAQGHGKIINMASMLSFSGGANVPAYAASKGA
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LKGITVFLASGASDYLNGAVIPVDGGYLGR
>PFR_JS14_1870 PFR_JS14_1870 D-isomer specific 2-hydroxyacid dehydrogenase family protein 2137167:2138216 Reverse
MADHLTVAVATPLSEELCLLIEAREPRCELIRDQSLLPPMRYPGDHAGDPGFRRTARQEE
AFRAMLTHADASYGIPGESPQLLAWTAEHNPGLRWVHTTAAGGGAQVRQAGLSREQLDRI
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GLPNVIISPHTAGLDAHEDRSIAELFARSATLILDGREPLNRVNTVEFY
>PFR_JS14_1871	PFR_JS14_1871	Pyrophosphatase PpaX	2138295:2138948 Reverse
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>PFR_JS14_1872	PFR_JS14_1872	Hypothetical protein	2139456:2141012 Forward
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RDGQIYVRNIGDKQWREAPMPSCLAGQVVGISLNEDLLIALDSQGWIYTMGNLLSDPSKW
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FVGKEGAFGARPAGLVNAVPRNYAAAIEVPYETMLASISDPVLGQFIERDLANQRMHEVF
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VPVSPRTGEPVRRRSIVATQVAFWTSALCAGIGYSWYWFQAMHKGQFHTASWVTGWLHPR
PGGMWSLMLACGLAAAVAAMVALPCVTAYQAWTGHRFARTLSWWALGGSLLGVLFNWWAV
AAIPCALVGVVLLRLGSSRDYFTEWDTLRTPPPQPELPTDVFYGPLPRFQ
>PFR_JS14_1874	PFR_JS14_1874	Starvation-induced DNA protecting protein	2142560:2143087 Reverse
MTNTISAIHQAEVSTTNLQNAESGFVASDILRDSLQSVLVDLIALSFSGKQVHWNIVGPN
FRDLHRNFDDVVEIAREGSDTIAERMRALHVAPDGRTDVVSATTTLPELPAGEILSSDAV
DLVVKSIEATTRTIREVHDAVDSADPSTADLLHELINKLEQQAWFIAAEKRQPQD
>PFR_JS14_1875	PFR_JS14_1875	CAAX amino terminal protease self-immunity	2143245:2144276 Reverse
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NPLLGVLSPLMMYTPAAAALFVVMVVQRVRGRAVLASLGMWPIRPLKRTLLLSLAALVGT
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LLMIVSCVILGTLFGWLRIRSGNIWPSVFGHAALNGTAGFLGLVVAAGESPSVLATSPLG
WIGWTLVALVVVVLALAGQFRGKDQWAVNVAKAPAVGPSPFQP
>PFR_JS14_1876	PFR_JS14_1876	Hypothetical protein	2144464:2144682 Reverse
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EGLKGVFNKDES
>PFR_JS14_1877	PFR_JS14_1877	Putative long chain fatty acid-CoA ligase VraA	2144852:2145910 Forward
MNTSVIDTGPVCVLGEGPGVVHQFWQAHRRGRLIGLRTSGTTTGAGRVIVRSTDSWVDSL
DAVAQRCALTPHDRIWIPGPMGSTMNLFAACLAVHNGVEWSSDKPECATIWQLTPARLSS
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PVRAWAREHLTGADRPRRWQWVAHPPLTLSGKVDLRALALELGGPTDRPDSP
>PFR_JS14_1878	PFR_JS14_1878	Acetyl-CoA C-acetyltransferase vraB	2145907:2147061 Forward
MNTLADNPVIIEALRTPIGTTGGVFADQTTTDLAAPVLGELDARLPAGTGFSEVVLGNVR
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LAAISIGGGQGSAMVVEAVHPRGN
>PFR_JS14_1879	PFR_JS14_1879	Sugar phosphate antiporter	2147440:2148888 Forward
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DQLGLTTTQLGTIGFGFSLTYGFGGLILGFFADGHNTKKIISALLIASGVVAITIGITLA
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IFGHSLHGWGSTFTVLFVSAGVGLVCLVAVALFEERMIRADREFSKEHPAADAGISEGAD
DE
>PFR_JS14_1880	PFR_JS14_1880	YktC (Inositol monophosphatase SuhB)	2148881:2149732 Forward
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TSRTGYPVLGEEGHGVDSFAGRVWVVDPIDGTMNYVETRRDYAVSLALVSDGQPLIGVVA
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DLKEIRAMPRLVAALVESRGHRRYGSAALECIEVASGRAGAFVHLWVSPWDIAAAMVICA
EAGVTVTRLDGTPLDVRHKGSILAGAPRAHAELLARLVSDPTH
>PFR_JS14_1881	PFR_JS14_1881	Permease, cytosine/purine, uracil, thiamine, allantoin family	2149910:2151430 Forward
MTTAATSTTPAPDERLLEAPIEHGVLSHVEQRGIEPVPADKRNGTPGQLFWIWFAANISI
LGIPLGATLIALGLNLWQAVLATAIGAFGSFAVVGVISVAGRRGGAPSLTLSRAIFGVRG
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YWYWHGISLAGTGSWLIGLVVGLLFMSAKISDTEVWFAGPLSHTWIGTNGLAWLVSLVVA
AGLYALFGGLRRKDDAAAALAAGAAA
>PFR_JS14_1882	PFR_JS14_1882	Carbohydrate kinase, PfkB family	2151427:2152431 Forward
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SPDFFGAVGTGPMGDILRGAMRRIGVAAQGPTIAGLDTGYCVAMTEPDGERSFISVSGAD
AQMGPDEFAGLALRDDDLVYLCGYSFMSPGTRTAVERFAAARTEWTQAGGRVLFDAGPMV
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DGAWFADGDAARKVPTPRVGAVDTNGAGDAHAGVLGAALLEGIPRDRALVLANCAGALST
TRPGPATCPDRLAIEDAADKLVGSADSLVGSTDS
>PFR_JS14_1883	PFR_JS14_1883	Modification methylase (Cytosine-specific methyltransferase)	2152580:2154238 Forward
MPRFVELFAGCGGLSLGLRAAGWEEAMANELSPMAAQSFAFNLLGVDLDRTSFWSQPIAD
RKVLWINSQLPPQQGDRLQENPYGTERPRYNDLSQVGNIPMDSSRLIVGDIRALNDWMRD
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SFPDNFVFRSWETTGGKRRSFQVPQYTQVGNAVPPLLGKALGETMSALLALSQRRSVQPI
SLPTLQKQGATP
>PFR_JS14_1884	PFR_JS14_1884	Hypothetical protein	2154235:2156346 Forward
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SAY
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ARRARVA
>PFR_JS14_1890□PFR_JS14_1890□Sn-glycerol-3-phosphate transporter GlpT□2165062:2166480 Reverse
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>PFR_JS14_1891□PFR_JS14_1891□Mg2 transporter-C, MgtC family□2166769:2167497 Reverse
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SA
>PFR_JS14_1892□PFR_JS14_1892□Putative secreted calcineurin-like phosphoesterase□2167504:2169186 Reverse
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>PFR_JS14_1893□PFR_JS14_1893□Putative metabolite transport protein YaaU□2169179:2170567 Reverse
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>PFR_JS14_1896□PFR_JS14_1896□Putative UDP-GlcNAc C4 epimerase□2174441:2175415 Reverse
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EHCDAARSSGGASKGFLTLDEEIDAVETVRALSPRTPVMMSINWGRSAIDTRNAGGPLTQ
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AGDHLLFDGVTFAVMPQWTPSQERLRYVRGLLSVMPRGHLSVAF
>PFR_JS14_1927□PFR_JS14_1927□Dihydrolipoamide acyltransferase□2213149:2214495 Reverse
MPEYNMPDPGEGLTEADIVEWHVKVGDQVKVNDNLLDIETAKSLVELPSPFAGKVTRIYA
EAGTTVAVGAPIVFIDDGTGPAPEHDGGAPAQGAEPGAQSSPAQASSAQSSSNQSGPAQS
SAPAPAAQGPAKAAPAAARPDADEASAQRDLDGGMTGERLLSLDELPASKPTQQTVRQML
VGYGPADESTPSSTERRRRAHQVSRRGANERALRDEEIPVDTVRRLTARNVVHSRTSKVH
TTAWVSTDVSGTMELVANLRKRREFKDLHVTALLVWCKAVCLAMRNNPMLNASWEDGSER
IILHHDVNIGIAADTPRGLMVPVIKQAQNRDLLSMADELTRLVNLAKAGTLQPSDYRDGT
FTITNVGGLGLDAGTPIINGSESAILAMGAITRQPWVVGQGDDEKIVPRWVTTLSISFDH
RLIDGAIASRFLRDLAALVRDPAMAMAY
>PFR_JS14_1928□PFR_JS14_1928□Transketolase, pyridine binding domain protein□2214506:2215480 Reverse
MTTLTLAKGLNQGLHDAMDEDPQVLMMGEDIGKLGGVFRITEGLLDDFGADRVIDTPLAE
AGIIGTAIGLALRGYRPVCEIQFDGFVYPGIDQIINQLARYRSRTHGRQSLPVVVRIPFG
GGIGSPEHHSESPESHFVHTPGLHVVACSNPHDAYWMIRQSIACPDPVIFFEPKRRYYAK
GEVDTSAPDLPLFSARIVRPGADLTLLTYGPMVQTCLDAARVASAEGRDVQVIDLRSLSP
FDMATIRDALKRTRRAIVVHEAHRTLGPGAELAARLDEELWGELDAPVLRVTGYDTVYPP
SRSEKGYLPDAERVLDAVDKSFDY
>PFR_JS14_1929□PFR_JS14_1929□Pyruvate dehydrogenase E1 component, alpha subunit□2215477:2216589 Reverse
MDSDDPTQPLQLLTPDGTLVDNPRFPWEGSDEDLVDMLRQMTTARRFDVEGAALQRHGEL
GLWAPLSGQEAYQAAVTKVMKPQDMVFGTYREQSIALQKGVPLGDILAVWRGSSLSRWIA
SDAQVAPYYMIIGAQPLHAVGYAMGVARDKAKHPTDPANDAVTLTIYGDGASSQGDVNEA
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GLIDYAWTEKLNADLDTFGALVRDTCRALPNTPMSEVFDAVTADPGLYLSEQRADCLDWL
ATPPSEGAAE
>PFR_JS14_1930□PFR_JS14_1930□Methyltransferase type 11□2216734:2217456 Forward
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PGRSLDLGCGEGADAIWLATQGWQATGYDISQTAIGRAQQAAAEKNVADTTHFEAVNLDE
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PPEMASQGDFPKPEEDLKALDPDPRFFEVKLAETRRRPATDPTGKPATMNDAVILIQRIR
>PFR_JS14_1931□PFR_JS14_1931□Lysine--tRNA ligase (Precursor)□2217642:2219222 Reverse
MVSEQRPEKAPQSPGNQSRKNEPRKNEAADVEQDLPEQMRIRAEKRQRFLDEGKQAYPVD
LRRDHTLAEVRATWGHLAAGEETQDEVTIGGRVIFIRNSGKLCFATLQDGFTPDQDAERL
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EDFLNALEQGCPPMGGLGLGVDRLVMLFTGAGIRETILFPLLRPLN
>PFR_JS14_1932□PFR_JS14_1932□VarM□2219363:2221057 Reverse
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RLIAGELTPTEGSVHVAGSCSYLPQDVTGAAGTSVADQLGITAIRQALVRIEAGSVDVHD
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SKGERDFLANRAEKNTGGKKLMHNARLHDAEAARAAADAAARQPDVIRIPLPDTAVAPGK
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TVPTGVLSQRTDELDRFDTCIDALLDVAAQRTAGEARELLARFLITGDKAFQLPATLSGG
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LHFNRSWQLRRTDEGTVIEEQLGG
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>PFR_JS14_1933□PFR_JS14_1933□SAM-dependent methyl transferase□2221347:2222279 Reverse
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ASMGKRVLRPGGLHLTHEMLEAAAPHAGDRIVEFGPGVGLTAAELLAARPAFYVGIEPNT
EGRAKLDAVLSGRPARVVTAEASASGLDAGSADLVVGEAMLTMSSPQQRRAIVAEAARVM
AAGGRYAIHELALADTAPDPDRRTGRGEVSREISATIKVGATPVKLAVWRALLTDAGFDV
VWQGTAPMRLLEPSRLIADEGPIGFARFATNMIRRPEARRRVLAMRNSFRAHKADLSAVA
MVAVKRPTQH
>PFR_JS14_1934□PFR_JS14_1934□Conserved protein, contains double-stranded beta-helix domain protein□2222279:2222638 Reverse
MAQQTPVTQAGVFTNLASELPVVPKSTTSRVVLDNDLIRVVEFTFDAGELLTEHASPRAV
VVQLLEGTMSFTVDGAESTLHVGDVVYLAPGTPHALVATTACRMSLVMVEAGAHLAGEN
>PFR_JS14_1935□PFR_JS14_1935□Amino acid permease□2222802:2224304 Reverse
MSNQPDRPRGARPTTGGGATGQRVPSGAPSGLDDDPTTQPGLRRGLKNRHIQLIALGGAI
GTGLFYGSGQSIGQAGPAILLCYLVGGAAIFMVMRALGEMSVDTPVTGAFSYYAWRNWGE
RAGFVSGWNYWFNFVAVSMAELTVVGKYVQFWAPGVPAWVSAAAFLVVVTLVNLVSVKAF
GEFEFWFAIIKVVAIIAMIVLGALIITTGLGNGGHPIGVENLWVNDGFFPKGLWGVLLGL
VIVMFSFGGVELIGITAGEAENPRTTIPRAINQVVWRILVFYVGAVFVMLCLFPWNQLGT
SESPFVTIFDKIGITGAANILNLVVLTAAASAYNSGLYSNGRMLYSLARQHNAPRALMKV
NRFGSPWVGVLVSSAVTAVAVVLTFLFPDTVFLYVMSIALMAAMTNWVMVVYTDVKFRQR
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VKRWRDKHGIEAVSEDRWRM
>PFR_JS14_1936□PFR_JS14_1936□Dihydropteroate synthase□2224557:2225447 Forward
MQQRPSPLRLGTRVFSTAAPAVMAIINRTPDSFYAPGRFTELDDALAALDRCIDQGADIV
DVGGVRAGQDGPWVGEAEEITRVRPFLAAARQRHPGTLFSLDTWRAGVARACAGLIDLVN
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LPVDQRLEGSLAATAVAAWQGAILFRAHDVQATRRVVDMVASIRGDRPPARAERGV
>PFR_JS14_1937□PFR_JS14_1937□Transcription regulator□2225525:2226217 Forward
MTRAAPLPAEQRRESIIAAARPLLLAHGDGFTTKQVARAAGVAEGTIFRVFSSKQDLLNA
VVADVLDPTPVIKALDEMAPDASLDERVHHIIELLHRSISDVRAFFAAIHAIPAHGKLFR
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DQLSVDLATAAGFLRSVTFATIHPFLMNGAPPMTPDQLSALLLHGLKKES
>PFR_JS14_1938□PFR_JS14_1938□ABC transporter□2226217:2227950 Forward
MLVRLIWRYLRHYKAAAAIVIAAQLVATVSSLLLPNLNAKIIDQGVSTGDTGYIWRTGLL
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SIARALVKKPDFYVFDDAFSALDVSTDARVRAALAPTTKDAAVLIVAQRVSTIRHADQII
VLDSGHIVGRGTHAELLESSDTYREIVESQMSALEAA
>PFR_JS14_1939□PFR_JS14_1939□Bifunctional ABC lipid A exporter□2227947:2230010 Forward
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YESQFSAAEQPEELAGSATSGAKRASS
>PFR_JS14_1940□PFR_JS14_1940□Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase□2230244:2231200 Reverse
MKGQGPYVDWFGVESAIQQAARRQAADHPGASVGQYLDHIRRDRFLSRVFADPESGWLLK
GGTAMLARVPTGRHTRDVDLSTTRATLDEAVEDLAHRVAVDMGDHLRFQLESERPGLAVT
QPGVLVARLSFACITDTGKRFDNVAVDLAVGPPPVGHIEHTRPADSPDRPRLISPPYAMF
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MEWTVGTGSPAAGPHRGV
>PFR_JS14_1941□PFR_JS14_1941□Hypothetical protein□2231197:2231844 Reverse
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VYRVCGAPATDFQEITATWLALSNPGRRLTAAGTTAATLYGIGDFLRTVPEFIVAGDPST
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>PFR_JS14_1942□PFR_JS14_1942□Hypothetical protein□2232099:2232299 Reverse
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ERTRSA
>PFR_JS14_1943□PFR_JS14_1943□Hypothetical protein□2232385:2232756 Reverse
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LPAGVSAADIKAYRRAHRGATISDAIRALGGDAPGGPDRDGGPDRHDEGGGNGDDGRPPG
AGQ
>PFR_JS14_1944□PFR_JS14_1944□Hypothetical protein□2232828:2233037 Reverse
MRGSTKMIIVGAVLVVAIMVAGEVWGAGSSSGGTTLWAALNPVTRFGLLLGTMLTAVGVG
IRVWMRRTK
>PFR_JS14_1945□PFR_JS14_1945□Hypothetical protein□2233072:2233371 Reverse
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ALTAVAIGLKVAAGGDARAVLPDLDDELDDEIALGRGPA
>PFR_JS14_1946□PFR_JS14_1946□Putative aminobutyraldehyde dehydrogenase□2233922:2235346 Forward
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>PFR_JS14_1947□PFR_JS14_1947□Dihydroorotate dehydrogenase 2□2235594:2236742 Reverse
MSINYGSDALAAAAASAAAKSVAGNATTDQLMAPREVNAQVTVPNTTDLSSNYMGLPLRN
PVVASAGPLAQTVDSIKTLEDAGVGAVVMHSLFEEQLRYESEQIVQQTEEQSESFAEALS
YFPVTAIASVGATLSSQYLQVLEDGAKALEIPLIGSLNGASGGTWTAEARRMQDAGASAI
ELNIYLVPGDTSITGREVEDRHVEILRAVKDVVNIPVAVKLSPYFSSFGEVATSLCDAGA
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DDIVKGLLAGADVVMTTSALVRHGAAYAGRLIDGLRDYLRRSDLTLDQLRGMLAVPSDAS
ASEYERSGYVSAIEKAKRRYGV
>PFR_JS14_1948□PFR_JS14_1948□Pyruvate-flavodoxin oxidoreductase (Precursor)□2236744:2240511 Reverse
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IAYSHCISHGYNLRKGLDQQYKAVASGHWPLIRYNPEVRDSGGNPFLLDSARPRISLMDY
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>PFR_JS14_1949□PFR_JS14_1949□TRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA□2240517:2242151 Reverse
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IPEK
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>PFR_JS14_1952□PFR_JS14_1952□Drug resistance transporter, EmrB/QacA subfamily□2244071:2245768 Forward
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KMYGTLGFISADMSNPLNMVTASSSPLTLKLMTWFACFLVPVVLAYQAWSYWVFSKRLST
KEMPEHEHEPNVAEVHV
>PFR_JS14_1956□PFR_JS14_1956□Cytochrome D ubiquinol oxidase, subunit 1 domain protein□2252519:2254021 Reverse
MDAQVLARWQFGITTVYHYFFVPITLGITWLLAILQTLWVRSGNDQWLRLVKFFGKLFLI
NFAAGVVTGIVQEFQFGMNWSEYSRFVGDIFGAPLALEALIAFFLESTFVGLWIFGWNRL
PKGLHLATIWLTALGSFISSIFILAANSWMQNPVGAVYNAATGRAELSDFLALITNPVFL
ATLPHTIGAAFMTAGALLLGVSGWWLAKKRRDAQPADSLDTSTWRKSARFSAWVLILASL
VTFISGDFQGKVEAEYQPMKLAAAEGLLETQESAPFSVVAIITTEGSGQDKTYHKVFSLD
VPGVLSILAKNDPNAKVQGIQDLRESYLQEGYATDNGTQNALQSQFADELKAMPVDPVPN
VMVNYYSFRLMIGLGVLAFIIGIATLVQTRRDHLPKGGKFYAVLMACLPFMPLFANSFGW
ILTELGRQPWIVNGVLPTWTAASPGNGAGAMWLTMILYTLVYAVVAVIVLKLFIKTIKEG
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LPALVKVEKPTDDAPLSFAY
>PFR_JS14_1957□PFR_JS14_1957□DNA polymerase III, epsilon subunit□2254373:2254984 Reverse
MAGYAVLDLETTGFSPARGDRIIEIGLVRLDPQGHVDDEWSTLVNPRRTVRATRVHHITS
ADVAAAPTMAELAPGLVDKLRDRVVVAHNSSFDVGFLTAELRTAGMTIPPEPIPSVCTMR
QSTRFLHARSRRLVDCCEAAGVSLRDAHSALGDARATAELFGHYLRAAGGELPWQDVVDR
ARRYPWPQALFVEPQTHLVQRPE
>PFR_JS14_1958□PFR_JS14_1958□Panthothenate kinase□2255137:2255760 Forward
MRTMTVSQSLTAAHELAKHGERHLLGLTGEPGVGKSTLAALLAADLGAAAVAVSMDGFHL
AQKELERLGRASRKGAPDTFDSWGFLSLMQRLTTNDAPAVYAPEYHRELHNPVAGAIRVD
KHVPLVIAEGNYLLLPGRPWGLAHDMFDEIWFLQTNQDLRHKRLINRHMAFGKTAQHAER
WTLGPDERNARTVRAQIGRADAVIELS
>PFR_JS14_1959□PFR_JS14_1959□Peptidylprolyl isomerase□2255834:2256208 Forward
MTNPNKPEVTLPDEAPDDLVIEDIVEGTGPEAKAGDLVDVHYVGVALSNGQEFDSSYGRG
EPLSFQLGVGQVISGWDNGVQGMKVGGRRRLVIPPQLGYGARGAGGVIKPNETLVFVCDL
VGIH
>PFR_JS14_1960□PFR_JS14_1960□Hypothetical protein□2256342:2256575 Reverse
MARKTYTGPEVDVTFDGEVCRHAAECVRGMPEVFDIDKRPWINPTVADTPELAQHLRDVV
SRCPSGALRIVEHPVEA
>PFR_JS14_1961□PFR_JS14_1961□Hypothetical protein□2256664:2256891 Reverse
MLSGDKLIVFTHTEVEPNFEGQGVGSKIARFALDDVRDDGSRSVLPLCPFIKGWILRHPD
YKDLVYRAKPSNVKD
>PFR_JS14_1962□PFR_JS14_1962□Membrane protein containing DUF1211□2257141:2257686 Reverse
MVLELRTPEGNGFSDLVHETGLGFLTYVLSFAYVGIYWTNHHHLFQLVEKVNGPVLWANL
NLLFWLSLLPMTTDWMDASDLSRVPVLIYGVDLLLAAASYWLLSHTLVRSQPSESLLNQA
LGDDRKGFWSPILYGIGIAAAAGADYLPGHLGVGIAIAMYLLTGLLWVIPDRRVERLVAL
S
>PFR_JS14_1963□PFR_JS14_1963□Carboxylesterase type B□2257879:2258586 Forward
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DAPRDMAGNPVQFEPGNSPAPSTIERMQVQDTDSGRLRVPSVGLDVPLGSMLAVDNVINP
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GHDYIAQSWRAISKKQLPAAQDLWDPVPGRLVLITCLEQPDGNSPDNLVVVAQLR
>PFR_JS14_1964□PFR_JS14_1964□ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein□2258732:2260051 Forward
MPRVKQVSDWFGAHPMFADSVWAGFIAVVSLLGAASISGRWDSAGSGPILDILYIVWALS
YAVPMIWRRTRPVLACWLLLIPHLVQLMVITQPMPGNITVPMMMYAVAVHGSPRAGRIWL
GVGVLAAAAAALRWSYRGNGAEQYWTVAVFNAFALSALVVASWLLGAFNRERHATVASLR
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VEQARGALDTIGQTARTALRDTRALVGALRDGESVEMAPQPQLDDIPQLVASTANSGLPV
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DGQGTLDNDGLGHGLIGMRERVASSHGTLTARNRLDGGFEVIATLPVGDQSAAAQAAGPR
PDTHRRGNDNGRRGEDNAR
>PFR_JS14_1965□PFR_JS14_1965□Response regulator receiver domain protein□2260020:2260727 Forward
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QAPDVALMDIRMPVLDGVAATSEIVAGSDTRVLILTTFDLDEYVYSALQAGASGFLLKDA
GPTELLAAIRAVASGDSVVAPSATRRLLERFVPTLPTAQSGGDTKKRLEALTDREREVLT
LVGQGLNNTEIAETLFLGGATVKTHIGHILAKLELRDRVHMVVFAYDAGLVHPRG
>PFR_JS14_1966□PFR_JS14_1966□ABC transporter□2261082:2262020 Forward
MTTMTQPTTAAVRTVHLTKIYGQGDTQVTALDDVSVEFIRGQFTAIMGPSGSGKSTLMHC
AAGLDTPTSGQVFIGQVDATSLSDTNLTLLRRERVGFVFQAFNLLPTMTAEQNILLPLKL
AHSKPDRQWLDTIVKVLGLQDRLSHRPAELSGGQQQRVAVARALITRPEVIFADEPTGAL
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NGTGLKRQAGDA
>PFR_JS14_1967□PFR_JS14_1967□ABC transporter associated permease□2262020:2264473 Forward
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VGVTLITLLTVGASASQASLDRYLSATYPQDAVVSAVKSVDEQTLTRIKATDGVQDAALV
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TAGTTVQLTAKVSDDYAPTLIVSTTVLNKIDADAPDSAWVQYKAGANVNTVTTDLGKAIG
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VRLVIIGLIAVAAGWLASLIPASRANRISPSAALATE
>PFR_JS14_1968□PFR_JS14_1968□2,5-diketo-D-gluconic acid reductase A□2264796:2265638 Reverse
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VGKAVREAGPDRAEIFVTTKFSKQWHSRKGVHEALEHSLERLGLDYVDLFLMHWPMPGEG
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LDNHDIVTEAWSPLGRGADGVLNAPAVLDAAKKHGITPAAAVLAWELNQGIVTIPKSANP
EHQRTNLEAIGVELSAQEMKAIDALADPNAKVDDSDKTGN
>PFR_JS14_1969□PFR_JS14_1969□3-carboxymuconate cyclase (Precursor)□2265743:2266792 Reverse
MSTQLCYVSGRRDGLITTVRFDDKAETAEVVSRLNLGPKPMPLELNRERRLLRVATGADP
LRVSTLKLLPDGSCQVLSEVNCPLSATYLSFTPDDRMAFVVSYHASRLAWAPVWDNHLID
DSAWHVEQVGEQPHCVEPSPDGRHVYVVELGANRVQGFRVSDGELVADEQIGVQFEHGTG
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TPSLDDQTLRHWGAELALDPQRHWILASERRASTLNLQALNDDGSFGARLDHVPTEKQPR
GMGLIGDHHVIAGAELGDTATIYRVDDQLEPVAEVEGLGGPVWFASIGS
>PFR_JS14_1970□PFR_JS14_1970□Shikimate 5-dehydrogenase aroE□2266879:2267697 Forward
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VTAPLKEALIEFGRPDQQSSELQSANTLIFGHPNRLFNTDVTGLRDAMASYDVIMPGTAV
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VHQAIDQVRLMTGEEPLAEPLIEVCRAELANR
>PFR_JS14_1971□PFR_JS14_1971□Glycerophosphoryl diester phosphodiesterase family protein□2267796:2268515 Reverse
MTAVWAHRGASAAAPENTLPAFQAAATLGADGVELDVQRTRDGQLVVCHDETIDRTSNGV
GNLADYTLSQLKEFDFSAGHPEFTNVAIPTLAEVFDVLGPTGLMINIELKNSVVPYEGME
AQVLALVHAAGWDDKVFYSSFNHRSMRRLAERDYPVGLLYDSVLWRAAKYAAELGASALH
PSGRAVRVNPGVVRAAHKRGLSVNVWTIDKPAQIQALLDLEVDAIITNVPDVALGVRDA
>PFR_JS14_1972□PFR_JS14_1972□Oxidoreductase, short chain dehydrogenase/reductase family protein□2268512:2269195 Reverse
MAERRAVLITGATRGIGRAIADELADDWHVLVGGRHPDQVRKVVQALPSAEPFIADLTDA
GAMQAAVEQIGHLDAVVHSAGAVVMGPVSELSRQDWRDLYEINVVAVADLTAELLPKLRE
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VDIQRQLGVQYQPERYLQPADVARAVELALTMRPGANVDTVSVRPAL
>PFR_JS14_1973□PFR_JS14_1973□Hypothetical protein□2269328:2270683 Forward
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>PFR_JS14_1974□PFR_JS14_1974□Cell envelope-related transcriptional attenuator□2271659:2274256 Forward
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APSTPADPTPTGGSSRRGMGTNEPHVSKWGTRESTPEPTASATPRRSWSRRRAESTGDQP
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NPGNPDYNAIRNRISGAITASDNGTTPSAPASASSSPMATGSAGSASSVASAAGSGSTSA
SAAGAAATPSGTAENMSGACDYHPN
>PFR_JS14_1975□PFR_JS14_1975□Membrane protein without function□2274705:2275142 Reverse
MSSYILRPRIPRRAFVLGSAATVVGLVLVVIGLVQNWAILAIIVLAALLAVGLLTLLMVA
YSMVNHRIHIDLDAKGYRVHGPGMDRRGTWAKVTRVAVTPDGSRLMIASGPVKRTYISCP
KGGDDPAMQALIKEISAHLPEHSRR
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AIKPGNQTQVPMAHASKAHELLESGDNTGKIILVV
>PFR_JS14_1977□PFR_JS14_1977□Argininosuccinate synthase□2276525:2277961 Forward
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>PFR_JS14_1978□PFR_JS14_1978□Putative CONSERVED PROTEIN CPSA□2278616:2280325 Reverse
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DEVLGDKA
>PFR_JS14_1980□PFR_JS14_1980□Probable thiol peroxidase□2281440:2281937 Reverse
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>PFR_JS14_1981□PFR_JS14_1981□Putative periplasmic or exported protein□2282298:2282945 Forward
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GVEELKGADARTLVDKLEATPLSQRRTDLRASVRADELQLSDTSGNKASVKMPADQFYLS
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ITGTLTVSYDGKSASQQISTAKADDPTCLTTLHLA
>PFR_JS14_1982□PFR_JS14_1982□Two-component system, sensory transduction histidine kinase□2283007:2284296 Reverse
MSEPRTPDRPAGTHPATPSAPDVPRDAALGDGRDAAGTGDRRDSRDSGAGVRRWWHVLTR
RSIARRFLTGAAVVVGVAVVTIFVVDALVSPAIFHAHLMQADLSNPETVLRHVEEGMRSS
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FTVTVPVLH
>PFR_JS14_1983□PFR_JS14_1983□Putative OmpR family two-component response regulator□2284293:2285012 Reverse
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LDLGLPSLDGVEVARRIRTFSDCYILMLTARADEVDELIGLSVGADDYLTKPFSPRLLIA
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>PFR_JS14_1985□PFR_JS14_1985□PTS system mannose-specific EIIBCA component (EIIBCA-Man) (EII-Man/EIII-Man)□2286653:2289640
Forward
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NRYQVVIGGAVESVYNDIMALPEMKEGGSATGTQKSGSNADVKSAAKEKGPRGRFTWLDS
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>PFR_JS14_1986	PFR_JS14_1986	Phosphoprotein 3 (GPP34)	2289780:2290460 Reverse
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>PFR_JS14_1987	PFR_JS14_1987	Seryl-tRNA synthetase SerS	2290581:2291855 Reverse
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KASGDERNALLSRTKELAAKVRELDASAHEADEHYTEVVKQFGNIVFEDVPEGGEDDLFV
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DEILDSKELPLRYAGFSPAYRREAGSYGKDTRGIFRVHWFDKFEMFTYCRPEDAVAEHER
LLAHEKEFISALGIPFEVLDVASGDLGLSAARKYDCYGWVPSQDKYREITSTSNCTEFQA
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TPKG
>PFR_JS14_1988	PFR_JS14_1988	Diacylglycerol kinase	2291982:2293607 Forward
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PPSPMADAITYQGSSYPSLHMAMAAATAAVVVGVTTTTRQPRWAVVLWRLVGFAFVVAMG
FDRWLMNAHHFTDIIAGVLLGAAVVSAVMLFARVRMLPLIAPRHPANAVRPRGGLCAVIY
NPAKMRDEMVFRRQLVSELAGAHWEIPLWLPTTIAQPGAAQAREAIARGADLVVAAGGDG
TVREVSGALAGSGIPMGIVPSGTANLLAKNVGIPIDMEDAISVAVGGEPTPLDLVRLVVD
AQADKPLYFAVMAGIGFDARLMQRTNESLKKALGAAAYVFSAMPELFTKPHRVEISVDGS
KQTRRNAVLTVMGNVPSIGGGVELMPDADPTDGRMEMVVGSPVGLSAWARATAQVLTRMG
ADPTLEQYAGVAMSVEVDEPMPYELDGDLVGSGSLFEAEVDPGALMIMLPPRPSSQAPAA
R
>PFR_JS14_1989	PFR_JS14_1989	Prephenate dehydratase	2293487:2294473 Reverse
MLGYFGPEGTFTHQALLSVSEDEATPFSTVAAALDAVRAEEIDAAMVPIENSVEGSVSAT
IDNLGSLDAPRLQIMQEVLVEVTFDLCARPGTTLDQVHRIITHPHAAAQVRDWLSLHLPD
AEVIERGSTAAAAQAVSDPDSGFDAAVCAPIAGRLYGLVPLATDIADNDAAVTRFVLVGR
PGRPALATGADKTTLVAYMRHDEPGALLSILQQFAVRGVNLCRIESRPTKTTLGNYCFNM
DAEGHLDDFRVAAALMGLKRVCKDVIFLGSYARADQQLPNVPVGAKDSDYRAAGAWLEGL
GGNMIINAPGSTSASNNDPDPTRSPSNS
>PFR_JS14_1990	PFR_JS14_1990	Hypothetical protein	2294896:2295510 Forward
MSQPMPPDSSGQNDPEGWVRDPTAPGGWAPIRGYQPRPGGQPGQGQYQAPPPLQARQPMP
PQHPQAPMPQQRPQAPMPQQPQGRPQQPPRYSDEARNDARASLEAFGEMGPQYSDAVIDS
FLARVDSQLGAQHQQNAEIEKRKAKQEDKRRSGRTAALSISLGIAIPLTAIASDYGLVGM
AMAWVGVLLVAFITTGFKWGRDDK
>PFR_JS14_1991	PFR_JS14_1991	Branched-chain amino acid aminotransferase protein	2295802:2296755 Reverse
MTESQPADDASDGPLTPGGAELSGVVRRPFTPRALVWNGEAFVDDVRAIEPALDILAADS
WRSSHGAAAHFDLHCLRFEAGVARWALDAGLPIPGAREWASMRRAMIAAILTAHHDTHRD
AGLETGQDLFPRIGWEMIGGHAGPVFVLRIRACPPMRDDTTLLWTGLTDPRLHPTVKGPD
IERLGKLRGVAASRGCDDAILADPNRTVLEASTGSLVWWYEGKIVLPAHRERVLPGVTET
MVARRAASLGMQVVRANARTDDWGSGQGVWFLNSVQGISPVTRVVIGSRAMHLAPFVATA
EWRHWWGSQFRPYSPSL
>PFR_JS14_1992	PFR_JS14_1992	Aminodeoxychorismate synthase, component I	2296748:2298481 Reverse
MAHSKHGPRLQLHVRSVRPAPGASPWDVEALFRRLSDGANAAFWLDSAQSVGAQSAVAQS
AVAQHVGPRPAGTTSDRGRFSLLGTDAGDLSEVLRYCRHDDAGHTRLQRGHGAGRVSQTL
DGDILDVLAERLAARPIGEVPEGIPFAGGYIGYLGYEAKALVFPDDPTRHSPTPEGYWLR
PQATIVIDHATNVAHLLVLTAEGDDDAAARWFGRLEDVLGRAGTTPSSPVPSRAAPTPTA
PTATPPRVAGSWRLTRADYEEHVRRAQDFLRAGDSYEVCLTDTFEGPYPAGIDALDLYGV
LRRINPAPYAAYLRFDTFGDHLEVLSASPEQFLKVRDDGLVSSKPIKGTAPRSADPAEDQ
RLAAELATDPKSRAENLMIADLLRNDLGRVCVTGSIRVPALMQVESYATVHQLVTTVQGM
LRDDVDLVGLLRATFPGGSMTGAPKQRTLQIIDALEPGPRGIYSGALGYLGYGRRAELSI
VIRTIVRNHDRLSIGAGGAIVLDSQAPAEFDEKELKAAALLSALRRAGTPAGRPAPYGGS
STHDANSAPGAGHDDTGVHRAARDAHAADHQGGEPDD
>PFR_JS14_1993	PFR_JS14_1993	Hypothetical protein	2298719:2299708 Forward
MKYAVIGAGAMGYRYGVLLQENAGVDVDFVDTWEPNLAKVAEQGGVYVSRDHEGRHLVPI
NLYSPEDYKGNPDVWIIFVKQMQLEGVLERCAHLFNDKQVVFSAMNGYGHFEKIQKYFSD
DRIYGGTAMIATVLNGPGDVDFIGKSGAGEMHMCAYTEKVTDIEKKIAEDFKAANLNPII
TENFMGTCMAKVIFNSVVNTLCTMYEITMGQFIEFDGAMAMAKQLIDEAYDVCDRAGIRL
IESRQDELKSIDYVSRVGNPLHYPSMYQDMSKGRPTEVDYINGYIAKLGRENDYPARTHG
FLTRGVHLAELAWHIHKEEAEKVEAEQAA
>PFR_JS14_1994	PFR_JS14_1994	Hypothetical protein	2299597:2299821 Reverse
MKEPGALRSRLPWLCPGPLQPREVFRLQLTGGRSGLIAQAACSASTFSASSLWMCQASSA
RCTPRVRNPWVRAG
>PFR_JS14_1995	PFR_JS14_1995	ABC transporter inner membrane permease YbhR	2299909:2301096 Forward
MRALVVKEFQELVRDRRTLAMLLLLPLLLLVIFGYAANFSVSKVSVTVIGRDAPTLADDL
SRYPVAGQNLDISTAAGATDPEQLLRERRADVVVQAVEESTSATPSSAPISERMHVYADG
SRLFAAQAAQRAFTTLVAQDTQQHLARIQASAAAGASGGSATQGSAAAGGAAQAASNPGS
VVTVLFNPDLKTSWVMVPGLIGLILTFIGTVITSIGLVRERETGTLEQLAVVPLRSSSII
LGKIIPYFLLALFDMVLITAVGVWLFGVPFRGSLLLFAAAAVIFLFVVLGFGVLISTASQ
TTGQAIQLAIMTVLPQVLLSGLIFPLDSMAAGVRWIGYCLPLTWFNQIAQGIMLRDAPAG
SLLWPFVILAAMAVVFFGIATLQMRFSLTHGGARA
>PFR_JS14_1996	PFR_JS14_1996	YbhF	2301093:2302910 Forward
MITLRGASVHFGARAALDDFSGSFAPGQVTALVGGDGAGKSTLLRVLTGRVAATPAQPGA
VTPRTQLGYMPADAGVWNNLSVAQNIAFVARVFAMSSEQTRERSQLLLARAGLAQVGDRE
AGKLSGGMRQKLGFVLATLHSPSVVLLDEPTTGVDPVSRGEIWSLIAGAAAEGATVVFAT
TYLDEAERCDQLFLLDQGRLVASGTPDEVIASCPGTVWQAPASATGAADDVPRATSWRRG
DQLFVWTPSDREAPAGFTASVPDLENTSIALLLAGGATLGADNLDDAATAPGHPRASDAP
VVLASRVTKTFGDFTALHDVSLAVHPGEIVGLLGGNGAGKTTLMRCVLGLEQVASGRVLL
FGQVPSIAVRRRLGYVAQGLGLYPTLSATENLRFTARVFGARSGGREFSAARGARDGVRL
GERALAYAHDLGRGPVGALPLGARRMLAYLCAIEHDPELLVLDEPTSGMDPLSRARLWRE
LREVADRGVGILVSTHYMAEAAQCDRLEMLTAGRVSASGSVADITAGRRSLVVHAPQWQR
AFALLRDADLPVALDRRMLRVPGASRDEIARVLDGLAGGYSVTEAASTLEETMMLAERGG
DAGGK
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>PFR_JS14_1997□PFR_JS14_1997□Type I restriction-modification system, M subunit□2302964:2304532 Forward
MTESTKESERAELHKTIWRIANDLRGSVDGWDFKSYVLGMLFYRFISENLTAYINKGEHA
AGDVDFNYADLPDSDAAMALRETVDEKGFFILPSDLFENVRRDAPHNPNLNETLANAFAN
IENSAAGTSSEGDLKGLFDDLDVNSNRLGNSVMQRNEKLVKLLDAVGDLPLGNFGEHTID
LFGDAYEYLMTMYASSAGKSGGEFYTPQEVSELLTRITVVGKTHVNKVYDPACGSGSLLL
KFGQVLGQGGVRKGYFGQEINLSTYNLCRINMFLHGINYSDFDIALGDTLTEPKHWDEEP
FEAIVSNPPYSIHWAGNYNPTLINDPRFSPAGVLAPKSKADLAFTMHILSWLAVNGTAAI
VEFPGVLYRGGAERKIRKYLIDNNFVDTVIQLPPDLFFGTTIGTCIIVLKKSKRDNSVLF
IDGSAEFVRPGNKNKLDDANRQKILDAFTAREDADYFAKLVPASEIADNDYNLSVSSYVE
PEDTTEKIDIIELNARIAKIVARQSELRTQIDAIVADLEDAQ
>PFR_JS14_1998□PFR_JS14_1998□Type I restriction enzyme, S subunit□2304529:2305194 Forward
MSKIEELIERLCPEGVPHHPLGEVGTFTRGAPFQKRDFTEEGFPAIHYGQIHTFYGPWTA
TAKSSIPRDLAERIRKAHPGNLIIATTSEDDQAVAKATAWLGDTEVAVSNHIYIYDHSMN
PKYVSYFFQSKAFQDQKQRYITGTKVRDISTQSLAKVMIPVPPLEVQHEIVKILDTFTDL
EAELEAELEAELEARRAQYEHYRDRLLSFNETPPRRSGGSL
>PFR_JS14_1999□PFR_JS14_1999□Hypothetical protein□2305464:2305781 Forward
MKAVQPKSDIDPKYLHYALLSSQEKLLRGARKRGGSVTSLDSKKFFKFKIPLPPLEEQNL
LAVTIDSFDALVNDLSSGLPAELNARRQQYEYYRDKLLTFKELKS
>PFR_JS14_2000□PFR_JS14_2000□Type I site-specific deoxyribonuclease, HsdR family□2305778:2308816 Forward
MTDSPAAPHYAPIAISKRSTVVAEYVPESTDDEGYESEATLEARFIKLLQQQAYEYLPIH
SSEDLVANLRKQLEALNQLTFTDDEWARFFAESIAGHHDGIVEKTRRIQHDHIQLLNRDD
GTTKNIYLLDKRHIHNNRLQVINQYATDSGARSNRYDVTILVNGLPMVQVELKRRGVNIR
EAFNQINRYQRESFWADSGLYEYVQLFVISNGTLTKYYSNTTRATHVDQASGSKRSRSQV
SNTFEFTSWWSDAANKTILDLAGFTRTFFASHTLLAILTRYCVFDSNNQLLVMRPYQIAA
TERILNRIETSTNAGQVGTVNAGGYIWHTTGSGKTLTSFKTAQLATEMPTIDKVLFVVDR
KDLDYQTMVEYERFQKGAVNSNASTRELKRQLDDPGAKIIITTIQKLSRYIGGNPESRVY
AGHTVIIFDECHRSQFGAMHKAITKTFRNYHIFGFTGTPIFAQNSSSAGSPVLRTTEQIF
GDRLHLYTIVNAIADHNVLPFHVDYVDTIKVKAGIVDREVAGINSEAALLNPQRINGVVD
YVLSRFDQKTKRQQSYTLKEQRVRGFNSLFATASIDAAKRYYAAFKARRAELPAAEPLKI
ALLYSFAPNEAQPDGLLGEEDFETGHLDQSSRDFLDDAIADYNAMFATSYDTSAQQFGDY
YKDVTRRLKNRELDMAIVVNMLLTGFDAKTLNTLWVDKNLRQHGLIQAFSRTNRILNSVK
AFGNIVCFRDLQEQTDEALRLFGDDNAGGVVLLQPFDHYYDEYKETADRLLNEFPIEERI
ISEAEKKEFIGLFGVLLRLVNILSTFDEFEGRELLSPRQMDDYKSQYLALRDEFANHLDA
QKESIDDDVVFEIELVRQVEVNVDYILMLAEQYLEVKDGPRDKEIRAQINRAASASPTLR
NKRDLINDFVDSLNVDSRVGEEWQEFIDRHRTAELDSIITDERLKPGPTQHFMHDAFVDG
AITTTGTAVTRILPPASRFSKTNNHEQLKDRVLAKLQAFFDRYAGLLNDVRD
>PFR_JS14_2001□PFR_JS14_2001□DNA polymerase□2309097:2310425 Forward
MARRQAPSDPTTDTSFVPAQRTATPAAGFPPVPPAEPVMVPAKPITIPVELVVEPAHPVT
DPASQQFGTATPDASGWYMPTYGERDISDWVPEVSRLKRSGELEAALSLATGCMDAMVQA
AERNPANVMEHYVIEVVRIQHKMARYSDEVDTIESWLGREIPASRDDHRLDLRKRLAKAR
ELVARSEGRDSSAHHAQWKRLVALQKASKQQGAPASTPPAPQSPRAQVIPERVAASRQPA
PSRARVGSSRRRPSRFIPALDEFLAQPFVAADFETANRSSGVSACQIALVRVEAGRVVNR
FNTLLKPPSGFDDFEFTYLHGISARDTRTAPSWPDIIPAIRGFAGDATVYAHNAPFDSRV
WRQLDEFFHTRSLPDHFFCSYLTARRMMPGLDNYRLPTVLERCAPHFVLDHHKADSDAEA
CALIVAALQSNPELYARLEAHR
>PFR_JS14_2002□PFR_JS14_2002□Appr-1-p processing, ADP-ribose-1-monophosphate processing activity□2310540:2311493 Reverse
MTAISAVVGDITTQDVDAIVNPTNTEMRPGGGVDRAIHDAAGPGLLEEVRSRFPTGLAVG
DAGWTHGGRLAARYVIHTVGPLQPTSKKSEQLLASCYRRCLQIADELGIQTIAFPVIGVG
SYGWPGNKAIPIEARTLMESPSSVSRIMIIASDEVIRDQVLACLINKAWLRLLQGVRVLH
ERGFEGVRVWAGFGPVGGWRIQITDVDYMKKLPDSEIYIAREYRSDRVYWNRWGAQVGKT
LITNLTTPGEVADLLLGEVPYLAQKKSDPEYVVWYQALVSVCEGLEAQPWTSSDWVTPPG
WGIGQKVVFPYPPAPKG
>PFR_JS14_2003□PFR_JS14_2003□Transposase IS6110□2311583:2312470 Reverse
MDGRRLGVELICRLLQVAPSSYYAAKTRAPSARALRDEELIPQLVEIWEANYRVYGVRKL
WKAARRGGIMIGRDQTARLMRVAGIEGARRSKRVKTTRPDPASSRHPDLVKREFTATAPN
RLWVTDLTFVPTWAGVAYVCFIIDAFSRMIVGWRVASHMRTEMVLDAIEMARWSRGAHHE
DLRCHSDAGCQFTSIRYGERLAEIGATPSIGTVGDSYDNALAETVNGYYKAELVRGPTRS
GPWKTVEDLELATLGWVHWHNTQRLHGYLGDVPPAEFENAFYAVPNDSNLLIGIK
>PFR_JS14_2004□PFR_JS14_2004□IS3 family element□2312503:2312847 Reverse
MPKELANGKPTTRRYSVEEKAAAVRMVRTLRAELGVTQGTVQRVATQLGYGVESVRMWVK
QADVDDGVVPGVSSAEEQRVKELEQENRELRRANEVLKRAASFFGAELDRHYRK
>PFR_JS14_2005□PFR_JS14_2005□Hypothetical protein□2313521:2314327 Reverse
MVANQMHTLRVRVRGLSRGYIRGVLSALAVVPADWSGVRGLVLGGLHIDIARGSAHIECT
AGRDVPDEPTARLVRQWSSTTMDELDGAFTPEGFSTAWGARYAGLDAGYERLLVGSARWM
IDARQERALHTSYILDVLDVFDVVPVPAQEFSTTFESLLRAAHLRHEEDGGPDGSAVGPR
MVLLGRAGTVALDHFECSELDGRYAPDQLRERAGSRAEGYRKRWQTILAYASDAAAGEGI
ADAPAGRITFDDVSDEQARRRLQGRLGR
>PFR_JS14_2006□PFR_JS14_2006□Gluconokinase□2314505:2316040 Reverse
MTETMMPGNQTTEIPEARPVPFARAIGPFVLAMDIGSTSTRAALYDAMARPVLEQNAVAE
HHFVEGADGTSEIDADQMADEVAETITGALAGLEPGTVSAVAMDTFAASLICVDAQGRAI
SPCMTYADSRSAPQLAELRKVLDLDEAQQAVGVRLHTSYHPPRLLWIKQNHPDFWARTAR
FVSLGEYVFTKLAGVDACATSTMAWAGMLNRHSGQLDDYLLSVTDTRADQYAQIVDPDQP
QTPDPGLINDRWPALSGAKWFPTIPDGYASNIGVGAVGAETVALSAATSGAMRVIVPGTP
EKLPSGLWAYRVSRHESIVGGALNDVGRVMTWLTTTFAPVDATERDTALRAAPRPDTPLV
LPFLTGERATGWSGNARAVFCGVTAASGPWDMWRGTVEGVAISYRRIFEQLRSIDVNIER
ILASGGVTHHFPATLDVITNALGYPVHVVNMERMTMRGTAMMALGVINPEGKFATAPQHS
VNNPDPSQAPYYDDLRKRFEEVYDEVIAGKE
>PFR_JS14_2007□PFR_JS14_2007□Hypothetical protein□2316063:2316200 Reverse
MGPVWRAFAPGAFGLVVAAIVLVTKPAPREGLVVREWAREWGTSS
>PFR_JS14_2008□PFR_JS14_2008□DNA-(Apurinic or apyrimidinic site) lyase□2316332:2317195 Reverse
MPELPQVEALADFLRTDLVGSVIERLEVGAISALKTFDPPPDALVGRTVTAINRFGKHLD
VDAGGLHLVFHLARAGWLVWREKVPSTVIKPGKSRIALRVRLQGGAGFDLTEAGTQRKLA
VWIVRDPQQVPSIASLGPDPMAPGFTPAVFRQILAGAGRAQLKGILRDQHVIAGIGNAYS
DEILHDAKLSPFKPAANLTDDEVERLYAAIRDGLAAATERARGLAARDIKADKRAQLRIH
GHAGDPCPVCGTPIASVNFADSSLQYCPVCQTGGKKLADRRMSKLLK
>PFR_JS14_2009□PFR_JS14_2009□Leucyl/phenylalanyl-tRNA--protein transferase (Precursor)□2317188:2317913 Reverse
MLAHVFGPEASWPSQDLVGFTEQIDAGLTMAAYASGLFPMPLHESEFHGMGWWSPMQRGI
IPLPSLRVSHSLRQALRRYRTTIDTSFDEVLAGCADPTRPGSWIDDDVKAIYTGLFERGV
VHSVETWDDDNRLVGGLYGVGLRGLFAGESMFHDREHGRDASKVALVRLVDTLSARPDGK
ALLDTQWLTPHLASLGGVEIPRHRYLELLDDALDAPETAWPAPGVFTRGRALPPALGGSH
A
>PFR_JS14_2010□PFR_JS14_2010□Hypothetical protein□2318288:2320462 Reverse
MTQDNSGSAEKPFRLGTNYQVETPLGHGVIGTTWRGTGAGGAELAFTVLNKRFASNPQVV
RHLLAQRPVLATVRGDHVVPVVDMVADSDVVAVVSPYIKGTDLRSRLDDEGTLPPAEACR
IISETAQGLATLHATGLTHRDVKPSNILLDDTQQPASAKVTDYAVGGIVEEWAGGGHSAV
LASTPAYLSPEVIAGDPVTVQSDMYALGVVLYESLCGVTPFAPLQPEGTMQAILTLDPGR
PRGVDDALWEVLSMLLNRDPRQRGSADALSWRLSELQNALADAPKLPKLDVSPSPTPLPQ
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AAGAVIGAAAAAVPTQQAAAQPTQAASGPSDAGQVAGGQTAAGQAGPAQGQGGQGQPVQG
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PQPVPHQVAASQPGGAPQGAPAQQPTAAFAAQQAPTQELPAQAAAQMGGAQTPPPVPPAP
QRAHPEPEPQRGQPLRRRPKFIVGLVLVIVIGLAAAAAIAVAVTRLSSSSSSSSASQSSV
TPTPSETPTPTPTPTPTPTPEVWPPDANAVICTSGGTMAVKRGTTYCTFGTTVQQALAAG
TLTAPSAAPGAAGTPATGTTPAAGGPTVSLRNTQTGTSVAVSCTSGATITTCSGNDGSVV
WVRR
>PFR_JS14_2011□PFR_JS14_2011□Putative cell wall catabolism protein□2320774:2321382 Reverse
MSKTLSRIASVASVAALAGSITVIAGQNASADSVNWDAVAACESGGNWGTNTGNGYQGGL
QFSSSTWNAYGGGQYASSANQASRDQQIAVAEKVLAGQGIGAWPVCGANAGSAGSYTSTN
TGGTAASTSNAASSTTRSTARTESTYTPARAASTGGSYTVQSGDTLSTIAAAHGTTWQAL
YAANKSNITDANLIYAGETLNV
>PFR_JS14_2012□PFR_JS14_2012□Citrate (Si)-synthase□2321593:2322897 Reverse
MGETAKLEIDGEVYELPVVQGSTGEKAIDISKLRNTTGLITLDEGYANTGSCRSAITHID
GEKGELSYRGIPIETLAEHSTFIETAWLVIFGRLPTELEREHFSELLSQNAALHTQMRAH
FAAFPEQAHPMAILSAMINAISTHDRPKIAPDDDATLERYAANLMSKVRTIAAGSYKTSI
GEPLIYPRRDLLYTQNFLHMMFSLPYQEYEASPQAVHALNLFWLLHADHEQNCSTSTVRM
VASGEANLYASCSAGVVALWGGRHGGANVATVQMLQRIRNEGLSPKQFLAQVKDKESNIR
LSGFGHRIYKSYDPRARLLEKAATDLLDATDSKDPLLPLAQELAAEALSDDYFAERSLYP
NVDFYSGVILRAVGIPLNMFTVMFAIGRMPGWIANWREINNDPNGRIYRPRQVYTGPPYV
QWREYADRISQPGE
>PFR_JS14_2013□PFR_JS14_2013□EcsC family protein□2323417:2324220 Forward
MPTRKRSNTGSTVGAIGATVVAMAPTIAPGPSANLLRRLADYAIDGVGPLPGARIAAGHA
LEHKTGDVEAALDSLVRNHVAMAGAQGFVSNLGGVVTAIAAIPANLAAVAVVQTRMVATI
AHLRGYDLSDLRVREAIWMTLLGRHDVDDLVAAGKLPSTPLGVATAPVLDSALEQRIAEQ
VLATLVGRSGGKQTLAMMSKRIPLVGGGVGMATDGWFTWTVASYARDVFAPRRLPELPGP
EQVVDEEQPAPQPESDVRDAEWSEEDD
>PFR_JS14_2014□PFR_JS14_2014□Hypothetical protein□2324331:2325200 Reverse
MVLLAIVNLAAAVLLIAMGVLGQRHALPRNGWAGIRTATTMTNDDTWDAAHVAAAPAFVI
GGLVQLLLAATALVLAGNDDLNGAGVAIVFTVVWLVTLTAAVAMAAVVGVRASKAVLVRQ
QQQLVAVGAHGHSASASDEVLGAEPPGEWISRDPARTVAAIVMALVPAALMMVLRSSVFA
DLPAKVPQHWGLSGPPDAWVSSNTAFWLGFVAACVLGVAAISVLLVARTARARRGYYSLF
TIMAFIASGGWLASALYGIGIAIGGWQSGLIIAAAAVLGLVARYIVPDA
>PFR_JS14_2015□PFR_JS14_2015□Putative subtilisin BPN□2325379:2326995 Reverse
MDGWMHRIGSARRARTGRSRGGRRLAGWVLAALCALTVGLSSSAIARADDGLWYLDQFGV
RDAHAQGLDGSGVTISVIDSPLVSDYPALSDANISYDTVPQSTRAPGGRSEGYDACYQNG
QKIVASFKSGQAMDPDAPGDPIFITHGTEMTSRIVGNGKGYGSDPGFEGIAPRAAVKFFA
NSGGIGSGDVADNSCEGPDGSALGTDLATTGLGIARAVGAGARVVSMSFLTSVDADDYPG
FLSALQHGVIMVSARDNSQEPGLPDMVGDPSRLTGLPGLVTVNSIGPSGPLAPSSDTTDG
SVAILSPGNEVLIAPAMDTRVLDVANGGTSSAVANLSGMLTLALQKWPDATGNQIMQSLV
ANTRDSDGTATLDEGHERGFGVVDLTKLLAVDPTGYPDVNPILDQEVTRAAEHGETADMY
DAQCAADSAQTTEYQFGDVTMKVPCQAGQFKQELVRQQDAWAAVQQCRADGGADCMRLSA
TNTAPAVSKQAGAVQAPAAPVRTSTHAGVWVAAATGALAVVAVATGGVILHRRRRSSH
>PFR_JS14_2016□PFR_JS14_2016□Alanine racemase□2327005:2328153 Reverse
MLYTTHLEIDLDALRHNARAIKQLVGDRKVLVAVKADGYGHGAVPIARLFQREHLADWLG
VATVSEAMALREGGVTLPILKLSHAFPEELPTAIDADIALTVVDEQSADEAAEAAKVVGK
PVNVHLALDTGMRRIGAEPEHAVALARHIDEDALNLQGIFTHMPVSDTTQGYDFTVEELA
RFAKAVDDVQADRATRGLPAVPLVHAAASAGVLGHDLSGLTMVRPGIAIYGAYPDAQTPR
TAALRPVVTMRSKVSFIKRIRAGETVSYGRTWTAPTDRWIATVPVGYADGFNRLNSNRGR
MLINGRSFPVAGRVCMDQTMLDLGEADDHGVHRGDDVIIIGASGDEYISTDELAELAGTI
SYEVTAVIPPRVSRQYFDSAAE
>PFR_JS14_2017□PFR_JS14_2017□Hypothetical protein□2328326:2329879 Reverse
MTSASSTHSRERHILLGVTGSIAAFKAAQLASDWVKQGHQVRVLMTAAAAQFVSPLTFQS
LTHQSVRIAMFDDSGASQTATDDGMHVGITHIDDAKWADVFVIAPASADVIARIAAGMAN
DHLTATLLAATCPVVLAPAMNTRMYDNPVTQRNMTTCRQLGMSFVEPSSGLLACEDVGKG
RLAELSDIEWAVDEALEGMSAPRFDADVAGPGRSGAARAEAPRPTSDVESAGATPSDAGS
SDAGPIDAAVIDAAMADAEPSTTLVVPDSVTSDVVVPDAGAMPPLRAGGPAGGAEGLLSG
VRVLITAGPTREPIDPVRFLSNHSSGRMGYALASAAHDLGAAVTLVSGPVSLPEPAGVTM
VQVQTAAEMFDAVTARFEQADLVVMAAAVADFAVAAQADQKIKKRGRRALTLQLEATPDI
LAWCGEHRHPGQVLCGFAMETTELVAHATEKLARKGADMIVANSLTTPGAGFGTDTNVVT
ILTATDGEPHRDDLPMMTKRELAGQILARMAALRVSA
>PFR_JS14_2018□PFR_JS14_2018□MarR family protein□2329923:2330267 Reverse
MTASHDDCALESLLILNQCIPLFETLKDPERQSILVRLIEHGPLTVNEVAESSSLSRPAV
SHHLKILERNGLVSMTKEGTRRICRAETQTGLSLLKRLVSALEADLAEVPGVAH
>PFR_JS14_2019□PFR_JS14_2019□Possible FMN oxidoreductase CC3083, imported□2330270:2330917 Reverse
MRFLTQIYRAMRDALGDDFPIGLKLNSSDGVEGGFSEQDALSVIETMAAMGLDLVEISGG
TYTKPPVDVVDGVDPRRGTIFFLDFARRLQGRVDIPVALTGGFLAAPDMEEVLASGAADM
IGIGRGLVVSPDLPNKILDGGSHETVSLPRVTTPVSAVDRALGSILVISWYEHQMCRLAE
GKQVASSGDATVALMSTLRSHGLGALAPRRNSGRK
>PFR_JS14_2020□PFR_JS14_2020□Uma4 protein□2331041:2332348 Forward
MSHPTFTTPCLTTFCGLDELGLEAVGQRLDPDRAVIECRVVEPDRWCRECGCEGAPRDTV
IRRLAHEPFGHRPTTLLIRVRRYKCCGCGRVWRQDTTAAAPVRAKISRGGLAWGLAGLVL
DHLSVTRVAAGLGVSWSAANDAILAEGRRRLIDDPARFEGVTTIGVDEHVWRHTRHGDTY
VTVIIDLTPVREKTGPARLLDMVAGRSKAVFKTWLAARPKPWREGIEVVAMDGFTGFKTA
AAEELPDAAPVMDPFHVIRLAGDALENCRRRVQHDVFGRRGMKGDPLYQARRTLLTGAGL
LTDKQQARLDALFAEDRHVEVEATWGIYQDMITAYRDKDRGLGRFFLAHTIDKISASVPE
QLVEIRKLARTLTQRASDVLGYFDRPGTSNGPTEAINGRLEHLRGTALGFRNLSHYIARS
LLEAGGFRPALHPRS
>PFR_JS14_2021□PFR_JS14_2021□Hypothetical protein□2332608:2332943 Forward
MTWSPSSMLSRTWGYLPLGAKHAGEPIPEVARLGRTLKAWKREILAYWHTDRSNAGPTEA
INNVIETTRRIARGFRNFDNYRLRILASASGQRPYRQPPKLVKQGQPNHAE
>PFR_JS14_2022□PFR_JS14_2022□Restriction endonuclease PvuRts1 I□2332962:2333900 Reverse
MEKLEYLARTLSRTSRKDYENYVVNAVWNRLDDSEVQPVSQKLVAIDPRSRYFIDLYFPQ
LNMGIECNEPYHATRSEQDAGRTITIFDVLHQVQPNSGYQQLDIDVFVRDHTGNVQWAPL
EAVDNAIDDVVGKLRARIETLRQSGGFSPWVIEPDDPFAYFQNRDEISMADDIGFANIAT
VCNSILGSSYSLESRGPRKSCFVPSSLRSIYGSEYLVWFPKKAVAGHAVSRGWNNMLSDD
GLSLDEYNEDWNAIDSATGQKRVVFIQAVDPVTRVRAYRFAGVFLRDGVSEIGGVPRKHY
RRISDKFTVVHG
>PFR_JS14_2023□PFR_JS14_2023□Uma4 protein□2334210:2335517 Forward
MSHPTFTTPCLTTFCGLDELGLEAVGQRLDPDRAVIECRVVEPDRWCRECGCEGAPRDTV
IRRLAHEPFGHRPTTLLIRVRRYKCCGCGRVWRQDTTAAAPVRAKISRGGLAWGLAGLVL
DHLSVTRVAAGLGVSWSAANDAILAEGRRRLIDDPARFEGVTTIGVDEHVWRHTRHGDTY
VTVIIDLTPVREKTGPARLLDMVAGRSKAVFKTWLAARPKPWREGIEVVAMDGFTGFKTA
AAEELPDAAPVMDPFHVIRLAGDALENCRRRVQHDVFGRRGMKGDPLYQARRTLLTGAGL
LTDKQQARLDALFAEDRHVEVEATWGIYQDMITAYRDKDRGLGRFFLAHTIDKISASVPE
QLVEIRKLARTLTQRASDVLGYFDRPGTSNGPTEAINGRLEHLRGTALGFRNLSHYIARS
LLEAGGFRPALHPRS
>PFR_JS14_2024□PFR_JS14_2024□IS1096, TnpA protein□2336409:2337191 Forward
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MNQLLTRDVVISALARDLQVGWRTLWKAIEGPLQERLKEISDQASVEALGLDEHVWRHCG
PHKNRMITGVVDHTRPKRGKDGKTKPFARLLDVQVGRSGAVAEDWLASQGKEFASKIRIA
AIDPYRGYANAISATLKEADMVVDIFHVTKLASQALDEVRRRVQQDTLGRRGHAKDPLYR
ARRLLLTGANHLTEKMATKLDALLQEGDPNWEVTITWTVYQKLIDAYQQSDSHDMVTLID
ALKDLGVPPAWSEARGGADS
>PFR_JS14_2025	PFR_JS14_2025	ISPsy26, transposase orfB	2337410:2337973 Reverse
MWVTGITYLRTRAGWVYLCAIKDACSRKVIATAMSTTMTTDLVEEALRRARIIRPNAPRK
VIIHSDRGTQFTSEQMYEYCRELHLDQSMGRTGVCWDNAMIESQWSVLKAEFYDRYEWDT
PQQAIQGVEEWIYDFYNTKRLNSAIGYQTPVEFEAQHAAALTRAAWTNPTVRNLRVTPIQ
RGLVVLA
>PFR_JS14_2026	PFR_JS14_2026	Hypothetical protein	2338382:2338726 Reverse
MWRGLVALGEGVVMSTGNEKTRRQRRKFTAQYRHEAARMVIDSGRTIAEVAQELGLGPQL
LGRWVKAEKETMTPSTLSPDEREELKRLRKENADLRMDNEFLGKAAAFFAAKHQ
>PFR_JS14_2027	PFR_JS14_2027	Hypothetical protein	2338847:2339335 Forward
MSRRRLVGLSIGQLGGPQWEYKDDDREIARRVLNTLGDRRLLWRDFSLEIEEHCVSSANE
IRRQLGDHLDNPEIGHDLAVQIRLMQKLFRDFVSEVGPSGDEWGRRMTPIATDPLSVALG
RLRGLMGVQIGILAAKYGLEVSDELATIVPDQEGWFWERFDS
>PFR_JS14_2028	PFR_JS14_2028	Transposase, ISlxx5	2339686:2340720 Reverse
MARVGLSFSDRSEISTASKAGWSVRRIARHLGRCPSVILRELHRNSTKTRGYQAVTADVR
AQRRRARPQQRKVAGDPVLQARVEADLAASWTPNEIAGRLRLEATDPTVERMANSADARG
RTVSGEAIYQYIYAIPKGELARKGIFLQSKRTKRRPRTTGRTRGGPIVGMVPIAERGEDA
AQRRVPGHWEGDLIIGKNGTSCAATLVERMSGFTGLLALSSKHAEPTADAVIEFFNDLPE
MMKASLAWDQGSEMAQHAKVSLATAMPVYFADPHSPWQRPSNENTNRLYREYLPKGTVIP
DHQPYLTTIAEEINNRPRRRLGYLTPTEAFARLLAGEPHVASTP
>PFR_JS14_2029	PFR_JS14_2029	Triacylglycerol lipase	2340879:2341994 Forward
MMNSRTRSHISKKVLGVLAMTVAAVTFAASAPASSFAASDSNGGPTIQNPGGIEETHSPG
GVPSGAVGPERGSGASEAINAILYAYTHPGAAVKGVNDFSCKPAKGTRPLVLVPATLSSV
YMNWAYYAPKLKAKGLCLYSFNYNPLVLSKANNTQIEGAGFTGDIKSSAAFMAGFVNKVL
ASTGAKKVDLLGHSQGGGPLPRAYIKYFGGNKKVHSLVGMNPSNKGSTLYGLSTFLKWLE
DRHLINGVYTGDDPAVIDTNKLFEDINFQGEWQQAQGSPFLTDLNDEGMTVKGIKYTVIA
TRNDEVVVPWTNTFLDGASANTTNIVVQNVCPDEKSGHIGAAYDPVYFQLAFNALYPNQA
SKVECGSGMPF
>PFR_JS14_2030	PFR_JS14_2030	IstB domain protein ATP-binding protein	2342331:2343089 Reverse
MSTIDIETKRKLREMGAADLLGALEAQDDQLAIGLPFGERIRLAVDDAHAAFTDTKITGL
MRRAGLRYPNADLRSLDLVEARGLDRSVIAELGTCGFVTTHRNIVLQGFTGSGKSYLASA
IAKAACTHRYRAHVIRMPDLAEAWQTAGDRPQGASKFIKKYTAFTVLVLDEWLLDRPDES
MRAMLLELMERRYDTGSTIFATQYAKKDWHTRLGGGVHADAIMDRIVHNALWINTGDINM
REHTAQAGTTTT
>PFR_JS14_2031	PFR_JS14_2031	Transposase subunit 1	2343086:2344651 Reverse
MVNRIPAKRVLRLRAQGLSGRAIATSQGVARKSVAAVLEAADRLGVGWDDVAEREDAEVY
ALLFPGRGEHVSVFVQPDWAEVHKQLARVGVTLKLLHGEYTDKVAAGGGVAMSYDRFCRG
YEHHVAITGVDSRVGHKAGRTVEVDWSGPTMELIDPATGEVSTVYLFVACLPFSRYAFVE
PALDMRQATWLRAHVAMFEFFGGSVPRIVCDNLKTGVISHPRDGEIVLNDAYRELATHYS
AAVLPGRVRAPKDKASVENTVGHIATVVIGALRDRTFTSLDDLRAAIRERLEAYNAAPFQ
KRPGSRSSVFITEEQPLLRPLPAVAFEVSTWVRRRRVGRDGHVTWARNHYSVPWTHVGEH
VDLKLTASTLEVWSADQRLASHQLLPATAVNQYSTRQADMPPGGGWQPWDQDRLLAWARR
IGAATTAVIERIFASVPVAEQAINPALAVLRLSHRYSAARLETAARMGLEAGIDSPRYGH
LQPLLAVGRDKTGGSPGGEASIEDPGAGFVRGASYYAGDQQ
>PFR_JS14_2032	PFR_JS14_2032	Hypothetical protein	2344838:2345023 Forward
MRTADPLLSADTSDERSGTVPNVVFPTAIEEIDGQQFVFYGMADSKIGTARLYRRSPQET
Q
>PFR_JS14_2033	PFR_JS14_2033	Peptidase C60, sortase A and B	2345239:2345886 Reverse
MNHTSRPGRRWITILGVLAAVVLIVAGIMGYTGSFDRTDPGAATDMNGRPVHLDTGATPD
PQASATPDGTGRFQVPAVGLNVPLGSLNAVGGTITPPGFTSAYLVRNRGVTPARASRGTV
FVVTHSIHGGGTAPGNYLVDVTHQRSRLAPGVRILVDNVAYTVTGSRQITKTRLGSDPAI
WTNTPGRLVIITCMLGQHGQLSPNNLIIQATQATT
>PFR_JS14_2034	PFR_JS14_2034	LPXTG-motif cell wall anchor domain protein (Precursor)	2345894:2347114 Reverse
MLAHADQGSFNPMAAYSAWNIVSFGDASITAESEGAVAAAGNVSFTGTNVATQHSATVDG
KPVSLLTGGTIDLADSTGTLQVHNGGMRVGDASDLSLLDTDSNGASVAWRAVAKGAGYDS
SPRAELTEQGSDYTAAEDPDGFSSQFSQDAAVTTSEKVADSASCAQQADVTIEGTTATVD
LQTGTNYWSVSADQLSTLTQITFAGNPPSAANGTFLVVNVTGTPVTLNMTLAGSRDPSAI
LWNMPDATSLTQSGDSIDGSILAPKAQYTKSSANIQGTVVSQSASLGGSEEHYWPFKGQI
GTCTTTPTSPSTTPTSPSTTPTSPSTTPTSPSTTPTSPSTTPTSPSTTPTSPSTPGSPAT
TPSGGVVQTGGTAAGQSRTAGWLGLVGLGVAGLIGLSAYSLRRRRS
>PFR_JS14_2035	PFR_JS14_2035	Site-specific recombinase, DNA invertase Pin	2347437:2347850 Reverse
MRQIAARLGRSLIDVLNTVDLLQNRGVTIRSIRDGIDPDTTTGRLMLGMLATLAEYERDL
FGERVAAGIAAARAQGTRFGRPPADPEVVDRKLAIAAERARGRTAEQAARLVGWSRATLY
RHQHEAELRHAVTPSRT
>PFR_JS14_2036	PFR_JS14_2036	Hypothetical protein	2348130:2348576 Forward
MLTDLIHMGPVQTLLIAYIAMAAVWAIVLFGMHTVAWVVSDDDSRMTKVSAALLFASPAW
PVAIICCAVYGTVTLIHLIISSWPTYRHHADHVIGTTGARRPAHARRVASARRRLATEAP
VGTRQPRTDVGASRRRRRQAIRVTRLDC
>PFR_JS14_2037	PFR_JS14_2037	Hypothetical protein	2348587:2348973 Forward
MAVPTRMTSIIVPLEQLLESTTEPVAERTPQPVAEPTTEPETGSVSGDRGTIIITAAVPT
IIMTPAEIHRISKQFSRSARLFHSGSLAGAEPGRVVHDAVHDRVSVDPSAETVVPVLLGV
PGTEDQLR
>PFR_JS14_2038	PFR_JS14_2038	Transposase IS4 family protein	2349155:2349679 Reverse
MVGEEPATHGIGRSRGGLSTKIHQGVDGRGRPLATVVTGGQRNDGIMMADTFDDIKVPRI
GPGRPRTRPDAVLADRGYTSGVNRSYLAGRGITAVIPQKSNEITARKKKGSKGGRPPAFD
VQAYKGRNVVERWFNLAKQWRGLATRYDKLATTYRAAVMLAAVITWLRHITDTT
>PFR_JS14_2039	PFR_JS14_2039	Putative IS like-2 transposase	2349690:2350079 Reverse
MSQPSRFEAFTDHQWARIEPLLPSNEGHRGRPFTRTRQIVNGIVFRYRTGIPWRDLPRDR
FGPWQTVWQRHRRYAEQGTWDEVLTHILAAADASGLIEPNVSIDATIVRAHQHATNTRRP
EVTTGGRIE
>PFR_JS14_2040	PFR_JS14_2040	Hypothetical protein	2350168:2350929 Forward
MSYFGCLDAGEFEDALEQVLSKGRTFKPIMSLPDWEGAAGCYIMVFDHYKQFYVGTTGNI
RQRIKQHWSARKPFDRILFGTPYDSVFPVDELRPLDTTRLYAARSRNPFSMEERVEKAAD
RRFCLNRMAGGEPTPLMVALTILDPRSRPLVPGVAPMTSEEYQRALTGVHDVVASAVALP
PADAGEALASMDMGIRAVTLSSGELGFWSRRDEVGRAVVRGDLDTVRYSAFLEALGEHVF
WPKADMQRNSVEG
>PFR_JS14_2041	PFR_JS14_2041	Hypothetical protein	2350947:2352002 Reverse
MDEILADLDEDQGGIGWWRGYVGWQVSAELGEYLLSACGGVSEALIKASLAIQEYRESSC
ARDHALTQAWCAIAKRGGSRDELIGAQQALGDAGQRREDRLDAWLEQTIVSLGQALDRVA
AVIVIVAGIKCDVIRTDWGELQKVAVKALKNGRGQGLRQGVLADVGTSGRERQNALLSDV
LKPEDHGPEDWLSWLIAQRNTMVHRAPRMSLIQMVGTRARPTGVINPLPSQPDWVGTRAM
IDAGKAGTMSSMFLVSTPQTVLEGLRGSMCTFLDQLLKETLYLWGARRSDPRLIVQPGGS
WQPVPKSGTLSFPGYGEPASMVTKEIAVHPSMGRRLRAARLMDDQVHLWEA
>PFR_JS14_2042	PFR_JS14_2042	Hypothetical protein	2352085:2352243 Forward
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MPGVVVAVLWALIALILFLVGRSQIKQVKGVPQTVDTLKEIPETLKRNEENR
>PFR_JS14_2043□PFR_JS14_2043□Hypothetical protein□2352240:2352803 Forward
MSDSPDEIRADIERTRHDLGRDVDALADEVSPSKIVDRQVDKVRGAFTSVRERVMGAADD
AGSSLTDAVSHAGDLKDRAVAKAEGNPLAVGLIAFGAGLLAASLIPASSKEKDLAATVKE
QAQPLVDEVTDAAKEIGEHLKEPLQASVESVKSSAQDSVATVKDEAQGAASDVKDQAQHA
RDNISDS
>PFR_JS14_2044□PFR_JS14_2044□Ribonuclease BN□2352866:2353960 Forward
MTSTAPSTPRNAPDPEASGKPDSPDDLHKRSWKYVLRKTIREFSSDQCTDIAASLTYYAV
LSLFPCLIAIFSLLGVVGQGKAASDAVLGIIEQVAPGDTVDTIRGPIEQIAESPGAGFAL
ITGILLAIWSASGYVGAFSRAMNRIYEIEEGRPFWKLKPAQLLVTVITIVLLVIAAIILV
VSGDVTKAIGDALGIGDVPQTIWSIAKWPLLIFIVVLVVAILYYATPNAKQPKFRWISMG
ALLAIIVLALATAAFGFYVGNFSNYDRTYGSLAGVIIFLLWLWIANLALLFGAEFDAELE
RGRQLQAGIAAEEDIQLPSRDTRKSDKAAEKERQDIEKGREIRQNADPDDTAKDATTPGP
AREH
>PFR_JS14_2045□PFR_JS14_2045□Hypothetical protein□2354007:2354261 Forward
MSVFDLAQTDPIEGAEPIPENPADAHQLSGDDPAGIAEAVTDWLTGQGWAIEHNQLGAGL
NGYTSPDDKRIVIGLFSDEGVGVV
>PFR_JS14_2046□PFR_JS14_2046□Transposase of ISAar20, ISL3 family□2354185:2355540 Reverse
MPDATFTRPDLTTFTRLDGLGLEVTGQLLEPDRSVLACRVVEPDYWCRRCGCQGVPRDTV
SRELAHEPFGWRPTTLVLTVRRYRCKECSHVWRQDTTAAAPPRAKISRAGLRWGLVGIVV
GHLSMARVAEGLGVAWNTANDAVLAEGRRLLIEDPTRLDGVKVVGVDEHVWRHTRRGDKY
VTVIIDLTPVRDGTGPSRLLDVVEGRSKKAFKDWLAERDQAWRDGIEVVAMDGFAGFKTA
TTEELPDAVTVMDPFHVIRLAGDALDECRRRVQQELHGHRGRKGDPLYTARRTLHTGADL
LTDRQHERLDKLFAGDRHVHVECTWGIYQRMISAYRHPDRAAGRVEMSSVIDALAEGVPE
ALVELRKLGRTLTRSACDVLAYFDRPRTSNGPTEAVNGRLEHLRGLALGFRNLTNYIARA
LLEAGGFRPHLHPHLRRARSRFACRRGWCSR
>PFR_JS14_2047□PFR_JS14_2047□NADH oxidase□2355507:2356295 Reverse
MSSNHASADILATRQATLADPLTLPSGAVIKNRILKGAMNEALGDRGAHPTEPLVNLYRH
WASGGTGLLLTGNVMVDPRQLGEPGNVAVEDETDMDMLRQWAQAGTENGAALWMQINHPG
KQSPRTINQHPVAPSAIGFGGKYERFFSMPRELSRGEIEAIVGRFARTAVIARDAGFTGV
EIHGAHGYLVNQFLSPLDNHRTDEYGGSLENRLFTDEGVAVVRPGAARRCRGEGRGLPMM
GVLTQPVRKTSTCLTLPSRALT
>PFR_JS14_2048□PFR_JS14_2048□TDG/mug DNA glycosylase family protein□2356579:2357178 Reverse
MAKGFTRAELQAFRHQTVPDLLPEPLRLLFVGINPSLWSAGVGVHFAHPGNRFYPALAAA
GITSHVIDASHGYPPEGLSELERGGVGISNLAREATTKADELDNQQFVDGLARIREMVRR
YHPKVVAFLGIGAYRVATGDRHAKVGEQALRLDWGDGTGSSAHVFALPNPSGLNAHETVE
SLGRDYREAAEAAGVPLFH
>PFR_JS14_2049□PFR_JS14_2049□Ornithine carbamoyltransferase□2357182:2358186 Reverse
MAVDLSGRNFLKEADFTPEQWAEFLRLAAELKAAKKSGTERPTMVGKNIALIFEKTSTRT
RCSFEVGAHDQGAHVTYLDPSGSQLGHKESVEDTARVLGRMFDGIEYRGFGQSRVQTLAD
YAGVPVWNGLTDEWHPTQMLADQLTMTERSTKPLREVSVAYVGDARFNEGNSHLVSGALS
GMDMRIIAPKELQNSAEVIATANEIAATTGARLTVTDDPNAVEGVDFVSTDVWVSMGEPK
EAWAERIDLLRPYQVNSALLARTGNPKVQVLHCLPAYHNLGTAIGREIYELTGMDALEIT
DDVFEANADVIFDEAENRMHTIKAVMVATLGERG
>PFR_JS14_2050□PFR_JS14_2050□Hypothetical protein□2358325:2358705 Forward
MLWRTVVNAAAVGVATWLLPGISFIGNDTTGQRALTLAIVAIVIGLLNAFVKPVLTLVSS
CFVVTTLGLFLWVINAAVLMFASWLCGAMGVGWHVAGWDSAFVGALIVSVVAMLLGGNRD
NYGGRN
>PFR_JS14_2051□PFR_JS14_2051□PtpA□2358702:2359166 Forward
MSAFDLLFVCLGNICRSTMAEQVARAQAADRALGLRIDSAGVSDWERGNPLDPRAAKCLS
AHGYPVGDHRAHLVTDAELGSGLIIGMERSHLDDLASMGAPGDRLALITDFVPGDHADGL
PDPWYGDMSDFEFTLKVIEAAMPAILDDAASLRR
>PFR_JS14_2052□PFR_JS14_2052□Cyanophycinase□2359222:2360136 Forward
MTLFLVGGGPSQATGPIYDSFVEQARGRGPRIALAILGAPEQAGASVGMYADPIRQRWPE
AQIEPIWLIDEDEGTVEWPTDPEQLGGLVVAGGWAPGYLDALTPLRDEIVRIVRGGVPYM
GFSAGAQIVAKHAIVGGWQSHGRAVGPEIAGDGSTEIVVRDGLGLIGSAVDVHIDSQHLL
ERAISALLDHDISSAIAIDEDTALVVDVASGRSDVVGSGAVHWLNNEGHEVRVRRTQGPQ
AQPVVEDDTESTSDAGSTGDTASPEDTASPEDTGSSEDTASTGADASADTASPGTESEPP
TNEK
>PFR_JS14_2053□PFR_JS14_2053□Response regulator MprA□2360143:2360835 Forward
MAMQILVVDDDQAVRDSLARSLHYSGYEVETAEDGLEALAKLSNLHPDAVVMDVMMPRLD
GLETTKMLRANGNDVPILVLTARDAVGDRVDGLDAGADDYMVKPFSLEELLARLRALTRR
SRPESQQANEVLSFADMTLDPQTREVTRGGRRISLTRTEFALLQTFMEHPGKVLDRSWLL
NEVWGFDFPATANSLEVYIGYLRRKTEQEGEPRLIHTVRGVGYVLRETAP
>PFR_JS14_2054□PFR_JS14_2054□ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein□2360832:2362259 Forward
MIRPLRRAVLGRNGEPRTLQQRFAAMTAAVVALAVAVVGMIAYVSTSRSLYGQVDDELVS
VAGYMVTPIASDVTGMGGLNSSSLQAANVNIVLVKSDRSIVRVQDEKVSIQPDAPEVAVA
RMKFGKSTRTVSLGPDGQRYRLVAVPMEAKDNSSYALVLARPLEPLVDTLDQLRAILLWL
GIGFTIIAAAVGYTIGRRVMQPLRQLSDAVAHVTETDELVPIGSTRADELGDLSRAFDTM
MHSLASSRNRQKYLIADASHELRTPLTSMRTNVELLVADEKSGMLPEGARAEILGDVAAQ
LGEFTSLVGDLVQLSRDDVVLPSPEPLDFAEVVESAITRAKRRGSSLNFDVSLEPFYVVG
EPDTLERAVTNLLDNAVKFSPRGGTVHVHLAGDTLTVSDEGPGIAQDDLPHIFDRFYRSN
KARNTPGTGLGLSIVAHTVKAHGGWVHADNAPGGGAMFTVRLPAAPPEVVAQMDH
>PFR_JS14_2055□PFR_JS14_2055□Membrane protein mosC□2362288:2363547 Reverse
MASGMESPETAHETAHGASHKAGRVPTRLRLARLGVLLIFFVNGATFASLVPRYPEIIER
LHVSNTLWGLALGIGPIGGIALGWLAAPLMRRYRSRNVAALAQIASSGALVILALAGSIE
WVFVAMFAMSAFDAVTDTSMNYHGLRVQRLYRRSIFNSFHGWWCIGAVVGGFLGSAAAGA
AMAVPTQTYVVTVGVLLCCVVASWAMMLPGEDREQVAGTEVATGRAWLRPRTLAVLVGLGL
LGALAGGIELGGSAWSPLYMTDQFAATPFVAGLGFVALMVFETLGRLTGDVLVDRLGLVR
TVVWGAVVCLAGMALALAVPTPVTALIGFGASGWGIATMIPNAMNAADGLPGVPAGVGLT
ITTWVMRVGFVLFPIVIGALGDAVSLRLALLVIPLSAVLIMALSPLLRPRPAPQAAATG
>PFR_JS14_2056□PFR_JS14_2056□DNA glycosylase□2363547:2364545 Reverse
MAGARSGAAGSPAQRTVLGAAGRLDMALGRLAKGPADPTHRRVGAQHWWRATRTPDGPAL
LELFDHHADVVTRAWGEGADWALDQVPRLLGEQDDPSGFAALAADCDLLRRAHHDHPQWR
IGATDNLTEALAPAVIEQKVTGPEAFGGLRSLLAKYATPAPGPAATPDGPAHGMVVPPTA
EQWAHIPSFEFTRAGVDGRRAAALVRAMRRVPSLERALGRATDGAERSRLLQTQPGIGPW
TAAKVLQWAYGDPDAWSVGDYHAPALISLALTGQKGDDAFADEALAPYAGHRYRVELLVT
PLVAHAARRGARRTLPSHVPGVGVNRRRSWRR
>PFR_JS14_2057□PFR_JS14_2057□Putative insertion element ISCmi2 transposase□2365339:2366013 Forward
MPKLINIDQATGLPVRRPKPTRYEVAAPGQLVHVDIKKQGRIPDGGGWRAHGRGSMQDRH
AGVARDKAARAGAAGSRGYRYLHHAVDDHSRIAYSEILDDERKETAAGFWTRANAFFAGL
GVTVTAVMTDNGSCYRSGAFADALGDEVKHKWTRPYRPQTNGKVERFNRTLAVEWAYAKP
YASEAERAAAYETWLHHYNHHRPHTGIGGQTPSARVHNVTGKYN
>PFR_JS14_2058□PFR_JS14_2058□Transcriptional regulator□2366206:2366982 Reverse
MEQQPATSRDVRIHDVLQVVTREGTIAVKELADELGVSPMTVYRDVAALETSGLIQRSHG
RVTAAPFSMAEASSLMRMGTELDAKQRIADAALPLLAPGSTIAMDDSTTCRHLFPGLGEL
APLTVVTNARFIADAVRDSAELELITLGGSYLRWADAYAGPMTEAMIDQVSPDVCIMSTT
AVTGGVCSHPDEAMAAVKGRLMRAARQRILLVDRTKFSRNALHRFLPLSEVDVVITEKSL
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  DPAHLATLRDQVERVITV
  >PFR_JS14_2059□PFR_JS14_2059□NAD-dependent glycerol-3-phosphate dehydrogenase domain protein (Precursor)□2367072:2368124
  Reverse
  MPTITVLGAGAMGSALCRPLADAGWDVRLWGTWLDDHLLDAVEAGKPHPRTNVPLAPGVA
  TFRSAQLEQALDGTQVVVMSVASVGVPRVAELALPGIAKADALWMTSKGFSEADDGRIGL
  LPEAIRSIAAAKGVALPPLVAIAGPVKANECAQALPTATIFGCRDREVSRSYAAQAATAN
  YAIAHTDDETGVEVCAPMKNVYAIALGVADGLEEKTGVPHHNLKAAAFAQAIAEMSLLGA
  QLGADPATAYGLPGVGDLEVTGLSGRNKVYGVRLGRGEQPQEALAEMDRLEQTVEGVPAT
  ALAVRFVEQIGGGLAERMPLLAAVNRLLNDAGVDPMTEVARAVLPVKPTL
  >PFR_JS14_2060□PFR_JS14_2060□Carbohydrate kinase FGGY□2368177:2369733 Reverse
  MSERQRTQQGPLVVAIDSSTTSTKAIVVDTNGTVWATARRPIPLLTPAMDHYEHDPALWW
  RTSHETIGEVLGGLSQADRDRVAAIGITHQRESFAPFSADGTPLANGILWLDGRAAEQIE
  RHGSAHVHELSGKPAGVTPAIYKMAWVTQHHPEWFARADKVTDVLGAIVFNLTGRWASST
  AAADSLGLFDIQRRDWSDELLQIAGVRRDQMPELVAPASPIADIRPELAAEWGLARPIPV
  IAGLGDGQAAGIGAAAVDPGVGYLNMGTAVNAGVESGSYIYNPAFRTHVSGIPGNYVLEV
  LQSSGSYLAGWVRDTFGDPDHPGDPDVERDNAAAAAIAPGADGLVTLPYWNAVQSPYWDA
  LARGAVVGWRGTHTRAHLYRSVLESICFEMRRNLDELADGTGTPITQLRIMGGGARSGVW
  RQIMADVTGVPLTVCLEEEISALGAAVLAMAAINAHAEPLADGSPDVASSAKAMASFGET
  VHPDMELHERYRRIAAVHARLYPALRETFQELAALSQD
  >PFR_JS14_2061□PFR_JS14_2061□Hypothetical protein□2370162:2370482 Reverse
  MGEARLMGEAQLAGEARLMGEAQLTGEDRLTGEDRLTRGPRSEGADPMAGPADGPKVNYL
  CRGYRHFFTAIDAPMRYLAACVLSGRDPARVMPWARQYRILVSPGT
  >PFR_JS14_2062□PFR_JS14_2062□Chondroitin sulfate/heparin utilization regulation protein□2370475:2371602 Reverse
  MNVMDSPSIGPGGAPAPVRGPLRAQRGSRGVRPAPHVMAKPAGPTCNMECTYCFYLDKQA
  LFPRSSLRMTPEVVRAVLQDAIDASPDTAIQFCWQGGEPTLRGLDFYREAFAVARRIVPP
  GRHFAWSMQTNGVLIDERWAEFLARHDVLVGLSIDGPRDVHDRWRVDRGGRGTWAKVMRA
  ARLLHEHGVRFNTFTTVHPANQHRGAEVYRFLRDEVGSDFHQYIPIVVPDPARPGHVVRG
  LSVDPGAWGEFQVDVFSQWLHRDVGQVFVMNVEWALAAWCGDEPASCMFREHCGDAVVVE
  HDGSVYSCDHFVDPAHRLGRVGDDSLAAMVADPRQRTFGDAKADLPARCRECPVLFACHG
  ECPKNRLMGGGPVDG
  >PFR_JS14_2063□PFR_JS14_2063□Sulfonate ABC transporter periplasmic sulfonate-binding protein SsuA□2372217:2373218 Forward
  MHKKRLFHIPLALFSALLLVLTSACSASTDDGSGTRANAGASASTQLQTVKIGAVPTLIL
  GFLQVGEQQGYFAKQGLKLDITPADSGPNIISSLAAGQYDLAYTAYAPALVAVAGGQDLR
  LVDHLDNVSAAGHNAGLLVKSDSPITRWKDLEGKKIGANAPRSQLVLWIQAAIKADGGDP
  GTLQIVPLPLNQIADNVAQGKLDAGSVTEPYLTQAHNSPALRDLGDPATAGFSQGTPSGG
  VFTSEKTLQAKSDVITKYRAAFAQTIDYANGHVDEVRAQGAKLVGLSDAAAKTITIDPIS
  TDVKAQDFGPFVKALTELGWTKTDVDIERFLSR
  >PFR_JS14_2064□PFR_JS14_2064□Hypothetical protein□2373527:2374216 Forward
  MGLRILNPEIVPGVGATLAELVRLVGLPGFYVTLGQTLLSAGVGLVLALVIAVPVGLALA
  SSAWLRRLLNATIDALRPIPPIVLLPLAILAIGGGLGFKVTLVLQGALWPLLLQTSYGLR
  AVDPLQTDVAASFRIDPLRRLFLFRIPAAAPVIFSGLRLAASTAFGVSVMTELVGGERGL
  GSILAIAQSGNNVPRVYAITIITGLVGLAIAFFFGRLERLLLPWQEATR
  >PFR_JS14_2065□PFR_JS14_2065□ABC-type nitrate/sulfonate/bicarbonate transport system, permease component
(Precursor)□2374332:2375105 Forward
  MEPAFAPDLVPVLVPALLVAIYQLISGSSPYLPGIGEIAAASRQMWTGAGFSANVVPSLT
  NLAVGYLAGLVLGLAVGVALGRAVVLRELLAPVIAFGLNLPGVAMLPVFLIAFGIGPRMQ
  QGVIAFAVFFVVVINTTAGVRNTDPLLVDMARVYRLPRWRRICQVILPAASVSVLAGARV
  GLSAALLVMVVGEMVGASNGIGAQTLLAQQNFDYAQMWAGIVLLAALGIVLNLGFLAAER
  RLTHRLRLPAANLQETS
  >PFR_JS14_2066□PFR_JS14_2066□ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component□2375296:2375895 Forward
  MEVAGQPVAGQPPEQVGLVFQDYGRPLLPWLSITGNVALPLRSKGVDRAGARTLALGALD
  AVGLAGRGKAHPRELSGGMQQRVAIARALAYEPQLLLMDEPFASVDAQTRMDLEDLVLPP
  RDQFGITVVIVTHDVDEAVYLSDRVIVLTPPPSVVSRIVEVDLPKPRDQQRTKDDVRFAR
  LRGEVLDLVRGREPEARAA
  >PFR_JS14_2067□PFR_JS14_2067□N-acetylgalactosamine 6-sulfatase (GALNS)□2375931:2377583 Forward
  MTEGPRAQDPVTQDPGGQDPGGQDPATQDPTAQDPTAQDPPPTALFDRRTRDAAAERPFR
  GSGRTARRPNIVFILADDLGWGDLGCFGSLHNRTPSLDALASQGLRFTHGYATSATCSPT
  RLGLYTGRYPGRLTAGLEEPLGTRDEHHGIPADHPTLPSLLVDVGYRTAMIGKWHCGWLP
  WFSPLKAGFQTFYGNLDGAVDYFGHFDTSGQPDLWDGEEPVTEQGYYTEIIGRHAAAYIR
  EAGDDPFYLQVNFTGAHWPWEGPDDEELSRHIADEPADTHEESLRRLFHADGGSLAKYGE
  MVAALDASIGEVLAALDAKGLRENTIVVFASDNGGERWAFMWPFVGEKGDLEEGGIRVPL
  IVRWPAVIDAGQVSDLPNATFDWTATLLDAAGATPDADHPLDGTSLLGWLTGTQGAPQRD
  LLWRTREQGAVRRGHYKLLVDRHGHSVWHNLFGTDGRPSYRLFDLSADGREKADVADQRP
  GLVAELKAVWRSFDEELLPYPDASAWDASADGASSRGASTSGRSTPGQSTLGRSTPGRST
  TGGQCPGLPD
  >PFR_JS14_2068□PFR_JS14_2068□SDS hydrolase SdsA1□2377660:2379678 Forward
  MTEIDIHTHTALSDAEAVVRHADGGLDDATKPATGFTRQLNAGVAERLGIDLDDASNSEY
  EVARAHLVRPADTLEILDDQGRQVWNVRKFDFLKDPQVPATVNPSLWVHAKSDRLAGLFE
  VVPDTIYQVRGFDISNLTLVKSKTGWIVLDVLTTTETARAALKFAEEGLNADIANNIRAI
  LISHSHADHFGGIEGIIASERIGRTEDGLVPIYAPAGFLEEAVSENVYAGTAMSRRSDYQ
  FGTAAAARAHQGSLPGLSQITPKGTVNLPRPTHVIEHDQTIVLDGVEVFFQLTPGTEAPA
  EMNNYFPQFRALWLADNTLATLHNLYPIRGAQVRDAKAWVNYILDLVHRFGAQATVAFQA
  HEWPHENTAEQPNAVREYLLNTAAVYKYIHDQTLHLANQGYTADEIGRRIEVPDQLLKHW
  YIRPYYGSVEINAHAVYNRYLGYFNGNPINLFPLAEEQFARKFVEYGGSADQVLQRAQAD
  FDAGDYQWAAYAANQVVFTDPDNQRARYLAADALEQLGYQSEPSIWRNAYLQGAEELRHG
  VDSSQQLIGNKGALLSHVSVESVLDYLAISLDGQKAASDDFELELTVEHPDTGQDAESYL
  LYLRGGALLYHRIEGSDGTRPHATLLRSQLGALIAGRPVPVGIERDAHDLLGRLQGYLVN
  LAASSRFNIIEP
  >PFR_JS14_2069□PFR_JS14_2069□Hypothetical protein□2379607:2380407 Reverse
  MRSQRHPVCAPGDGPACLRRPPLSSTTQLVSDGPICLRRPVWSVLPGTIHFAPAGPIRGI
  HPFRKCVRHTYSVHCVRGGRPRCALWTSIRDALGRVLRRDGVLRYETNTTVSVWDCPIAA
  PCKKWVRRTHSPARRYGGLPRWWCRFKRRDWEPDTTAPASTEAPAFQLLPSSRSAGPKSG
  HARWFWWFRRPQWFREPPRARKPRGPRSYDSGSRGSALGASTVSAGREPRAAGRWGLSRE
  RAVLRLDDVEPRGSGQVHQIALQASQ
  >PFR_JS14_2070□PFR_JS14_2070□Hypothetical protein□2380484:2380795 Forward
  MPVTVRNITTREFRDNLSEQLSRAAYSGDRIQILRNGQPIAMVVSMDDAEELRELDYYKD
  AADYRRAVAERNGDPLAMPTRNDVIVADGASARNDLARRLGFE
  >PFR_JS14_2071□PFR_JS14_2071□Multidrug resistance protein YcnB□2380805:2382169 Reverse
  MGSGMELNWTTRLVVAAVLLAAAFTGLLNQTLMVTAMPMMMHDFGISLSLAQWLTTGNVL
  VVGVVTPVSAMLYERFSTRALFLWSTGLFIAASVLGFVADNFWPVLAARLLQAVASGIIM
  SFAQIALLRITSPRRMGTVLGLYMMVVSAGPAIGPVMSGVILEYLSWHALFGAGVLMMAV
  VFAAAVFTLPNIKAARKIAIDWPSFVLSFVGMGLFLAGISTVQEAPLVGVSMMVAGLLFV
  AWFARRQWSSAQPLLNLRLLKGATFRRMTVGVMLAFGVFLGTETIIPVLLESHAGRSGFA
  TALVMLPGAVSNVIASPLTGRVFDARGLRTIWAWGSGITVVSAVALLAVSPASAPWAIAG
  AYLLRVVGTSVMSALPTARALKGLTGEDISHASALLNSLRQVAGALSNTVLVWAVAVVPD
  FTDGFRLAMAITAAATVVMVVVFARQARLDRAGA
  >PFR_JS14_2072□PFR_JS14_2072□Hypothetical protein□2382519:2383484 Reverse
  MDMELAAVIAVAVIVGIDKSLLPGAGTLAIGILANVIPARQASGLSLALIIVADWCAIWA
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YRKDVDWGVLRRLLPNVVVGIGVGAVFLALADDTATGCTIGVILLVFIIWNLLAMARKRR
RAALGGGLAGYGVSGAATAGSVPAEPPAVSSPGDRGAAASAGGDGELAGDGGAAGGGESQ
PAGFVSARSGGTSSEGWWARTRARFSWRGFGFGGLTGFTTMVANAGGPVTTMYFLAEGLS
VTAFLGTTAWFFLVVNLIKLPISLSLGMLQTSSLPLVAAMVPVILATVLFGRWLAHRINP
SFFRTVVVALTFVAAIALVIS
>PFR_JS14_2073	PFR_JS14_2073	IolE protein	2383853:2384806 Forward
MTQTTTPATQKARNTNDPKYSKLAIGVCPDQWGVWFPDDPKQMAPRQAMQEMAEAGFEIL
ETGPYGYFPTDPKELKSWTDEFGLKVVAGTGWGILHKAEAWAETERHFRQIAETHAAVGA
EYIVHLPPLYRDDKTWEFTDDRVLSPEAWHLYVDNANKLGQIMLDDYGLKMVLHPHGDSH
IETPDEIARIFDATDPRYVNLCLDSGHVVYGGGDPVELVHKYPERITYVHIKAFDPKITK
EAHDKDWPFGEAVTKGASVRPPAGLPEMHAFIDALAELDKDIYCICEQDCYPCPPDFPKP
NAIKMRDYLAECGLGLK
>PFR_JS14_2074	PFR_JS14_2074	Inositol 2-dehydrogenase 2	2384878:2385888 Forward
MTVRIGLIGAGGMGRAHVERIQNELAGGEVVAVADVNPDAAGYAESIGARYFPTGPELIA
DPGVDAVIIATFGKVHAPDVIAAIRAGKPVLCEKPLATTAQDCLDILAAEQEAGRKLVTV
GFMRRFDKGYNEMRAQLTEGQHGYATMVHCRHRNPSVPATLYTTRNMIDDTAIHEIDICR
FLLDEEITTVRVDTPRRSSNAPQGLQDPLVLVANTASGVRIDDEINVNIKFGYAIECELV
MESGTVRLADQDHTILRDIEGDRHAICRSHIDRFHDAFNAEVQQWIRAVERGEHAGSTSW
DGYAATCVVDAAIESLEHQGREVAVQMIDQPAFYAG
>PFR_JS14_2075	PFR_JS14_2075	IolH protein	2386108:2386974 Forward
MVDIALDPNMYYASMSTAQTLFKAAELGFDYVELSPNTEFHFWHRYPKADDDFVAGLNKA
QKDSGVTVRTLNPVFNWSSTDEQERAAQVRNWRRLLELADQINVREIVSEFSGNPNTPVR
CEEQWYKSIFELAPDFEKYGITLSMEAHPYDFVERHDDAYSIVRGTNLDWIGYEFCCPHT
FHLDDGVGDVERMITSCAPKLREVHVADTLNHRANDGNRYIINPPGVDARVHQHSEIGKG
EVPFDKVFETLRAVGFDGVLSLCVFGFHEQADEINRRMLERVRSEFGA
>PFR_JS14_2076	PFR_JS14_2076	Transcriptional regulator	2387123:2388157 Forward
MAGGSRPTQADVARLAGVSRQTVSLVVLDDPRVSPRSRAAVTSAMAQLNYRPNVAARALV
SHHTGFLGIVFSDLANPFHAELAEALRAAADRLGFVPFISPVGQSADEEKVAINRFTEMA
VDGLILVSPLSDNTTLEALGAQVPTVIVTRNSGPANVDLVHADDRASAAQVTQHLLAAGY
DPVVFLGYERRIEGDSSLARIDGYRAAMRRAARPEQVQIVTQGGVPQIVGGLAASLTRGF
GLVCHNDLIALEAWAALAELGLEPGPDVGVAGFDDTGMARFPGVGLTSVNNGTTGFADTA
VEMISQRLAGRTARREVVLPTHLIVRRSTLRDQPDRPPRPAQQR
>PFR_JS14_2077	PFR_JS14_2077	S33 family lysophophospholipase	2388402:2389340 Forward
MAIQEVTFPSSNGRDTIYGWIYEPTQPARGVVQIVHGLGEHSRRYLHMITALLDAGFVVA
ADDHAGHGKTSTESGVWGDTGENGVTTVISDEYSLHKLVRDDHPDLPFFMFGHSWGSMIA
RGFASAHGATLSGLALCGVAAQIDGVETKLDRVGLDAALAAGPGTASGEEFVGQIFEDFV
SRYTDVRTPNDWIALDPDVVADHARDPFNNYYKPMSLRFVHDFVTLYDQVNAPDWYTSIR
ADLPVLVLAGDQDPVANYGEGAYHVANQLEASGHRDVRTHVYTGYRHEVHNEPQTRADVE
SELTVFIDGHLQ
>PFR_JS14_2078	PFR_JS14_2078	Glycerophosphodiester phosphodiesterase family protein	2389555:2390364 Forward
MLTAGNHTPDKEVTMAATRATQHVPTFNSTIFAHRGLPSRAPENTLAAFDLAADEGATWI
ETDVDIIADGTPIIIHDTALDRTTDHRGKLYDIATAEELAGIDAGSWFAPEFASERVITL
DALVDLLNRRKLNANIEIKANEQGAERTIVLVDAIASSLARLDPEREIIISSFSQPVLMT
FHARHPEYAIGVLYETAALYDDWLSVLELCGASYIHPEDAGLTRERVQAFRDAGYGVNVW
TVDARDRANELLNWGATGVFTNIADQLIR
>PFR_JS14_2079	PFR_JS14_2079	Transporter, major facilitator family protein	2390559:2391923 Forward
MATSTSSTRRFSLPVFLRKGRIGPFLAVVMSGQIIYSAFEAFKGSLMIPLQQMLGITQTQ
FGILMSYIGIAMFLYVPAGWINNRFKVRTIILWSLGWRLATYLVLFLLTPPFAVMSVIAV
SWGVLDAIVWPAVVNGVSILSQDQDKEGKGLAMGLLESIRRLTEFLMNGLVIVILMVWSD
HTVGIMRIAAIVYALLIVPMMIAVARLVPDTKIAQEQGKSDSLAALTGLFKVIARPRVWL
AGIAALTVYWSYINLMYTSAPYLTQVFGVSAGLAGAFGIFNTGLVGIFAGLLSGLLADYV
FKSSTKMMAISLGAVAVACVIVMALPVRSSMIWPIMIMLIVVAIATFLGKAVILAPVAEL
NLPEGISGSAMSVGSFLAYASVFWAYTLNGHLIDANAGNPQAGYRLIFVITAVVAVIGCV
AAGLLTVINRRVKAHQQVAAAEGGTDAAPAPRAE
>PFR_JS14_2080	PFR_JS14_2080	Transmembrane ATP-binding protein ABC transporter	2392291:2393007 Forward
MPRVQDFTLQVCATHEAGPYTRLRVRCPELLNPRKSDELLPTAWLRLLVPDGGRQHQRGY
TLVECDHGTGEASIYMLHHDPAGPGSRWARSARPGDRIGAQLLAGQLYLQPPPDAGALYV
GDLASAPAIAGAIAAAPASCDIAVVLQAEPGSWSPVPHTACTLTIVSPDAGEDALIEAVT
TIPGRDYAWLALEASAAQPLRAALIAAGLPRDAVQYQGYWRRGTPMGRTVETSARAAA
>PFR_JS14_2081	PFR_JS14_2081	Putative insertion element ISCmi2 transposase	2393004:2393678 Reverse
MPKLINIDQATGLPVRRPKPTRYEVAAPGQLVHVDIKKQGRIPDGGGWRAHGRGSMQDRH
AGVARDKAARAGAAGSRGYRYLHHAVDDHSRIAYSEILDDERKETAAGFWTRANAFFAGL
GVTVTAVMTDNGSCYRSGAFADALGDEVKHKWTRPYRPQTNGKVERFNRTLAVEWAYAKP
YASEAERAAAYETWLHHYNHHRPHTGIGGQTPSARVHNVTGKYS
>PFR_JS14_2082	PFR_JS14_2082	AP endonuclease, family 2	2394254:2395288 Reverse
MTSSTTTNASAPSPLNLGAYTACLHNYTLEEALDILAADGLTGAEVNVGGFIPSPHCPVD
LLIGSQTARDDYLATFEAHGMRLAGLNTSGNVLSPLPDQGPKHAYDLRRAIELAGKLGVG
EIVCMSGTPGTDPDGKYPAWVVNPWDGTQLEVLEYQKSVLDPFWREMDLRAQDAGVQLAL
ELHPHNVVFTPVNFLEFADRIDAKNVGVNMDPSHLMWQGMDIVESIRLLGSHIKHVHAKD
TKLFPGVGTRGVLDSSFGPVPADPALRTPTGFDHYVSTWPADPAWRFVTVGEGHDVPWWT
EFLKALVEIDPQMNINIEHEDAAFGQLEGVELGAKNLIAAADAR
>PFR_JS14_2083	PFR_JS14_2083	Oxidoreductase , NAD-binding Rossmann fold family protein	2395412:2396599 Reverse
MPENTLSVAVIGAGMAGRTHANAWRQVRTVFGTRGVPQVRLAAICDAYLPFATDAANSYG
YERATSDWHEIVEADDIDIVSIVVANKLHREIALALMAAGKHVLCEKPLSDNLDDAAAMA
AAAADASVVSGIGFGYRRHPAIAEIAELANSGALGEILHFDGRYWCDYGADPQVPIAWRY
RGPMGSGALGDVGSHITDLAEFVAGPIASVSGGSFATVIAKRPPAVEGLAGGRGAAGDAE
ATETVENDDIAEFNMHFASGAIGSISVSRVAFGMPNALCFHVLGTQGRASFDLARSGEIK
LDDTNSPAGLRGPKQVLTNPSFPYYKGGSSMDFAGVGNTQIEQFTYQARAFLDQVIGLDE
GLPPVPSFAHGYRAMRIQDAVATSAGRGGASVEIK
>PFR_JS14_2084	PFR_JS14_2084	Periplasmic binding protein and sugar binding domain of the LacI family protein	2396731:2397774 Reverse
MAADPTQRDVARAAGVSRGLVSLALSGSSLVADDTRERIVQVAHELGYTRNLGAASLASK
RSPVVGVVLPDLRNPFFESVVDNLQHEADGLGLLPLVATSADDRSRETTVLQRFRELRAA
GIVMVSPVEGPEAFTRIGSQLPLVLIGAALAGDGFDSVHVDEDAAAALIVEHLRSHGWRR
IVAVSFVSGLGEVWVAHRHRALARAAAAAGMPLERVEVPRGEALAPQLGGVLAAQADQRV
AVVTHNDLTAADVLAFVRARGLRPGHDLAVIGFDDTHMARRPEFDITSVSQNTGELARLA
MVALQGRAEWMGARALRRHPDAAEGDDEPLRGREFIVAPALSVRSSS
>PFR_JS14_2085	PFR_JS14_2085	Thiosulfate sulfurtransferase	2397801:2398619 Reverse
MTLIDPATLRAKLASDNPLVVLDARWSGPAATVDEGHKDFEAGHIPGSLWVSMNKEMSNP
DVPGGRHPLPDPGAFEAEMRRKGLNEDSSVVVLDGGNSLAAGRLWWLLTDGGLTDVQVLN
GGFAAWKAAGYPVETGPTWSSKVGDIMLRAGHLERVDAQHVLANGGTLWDVRSPQRYRGD
EEPIDPKAGHIPGARNLPATEAQEPDGTFKSPDELKKVFAAVKPGDAVYCGSGITASQAL
LAMHVAGINGVKLYPGSWSDWISDDSRPVERG
>PFR_JS14_2086	PFR_JS14_2086	Glutamate decarboxylase	2399032:2400444 Forward
MNDPARHPAYSIDRSQLGAVEINPVFARPAEATEFSKFRLPASESLPETAYQVVHDEAML
DGNARLNLATFVGTWMDDYANRLYAESADKNMIDKDEYPKTAEIETRCWTMLADLWHAPD
PDNTIGTSTIGSSEACMLGGLALKRRWQHARKAAGKPTDHPNMVMSSAVQVCWEKFCNYW
DIEPRYVPISEDHKVLDGTNLADYVDENTIGVVAIMGVTYTGMYEPVKQIAAALDEIQER
TGLDVKIHVDAASGGMIAPFIQPDLEWDFRIERVASINTSGHKYGLVYPGLGWVVWRSVD
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DLPADLIFKVSYLGGDMPTFALNFSRPGAQVLLQYYMFLRLGMDGFRRVQANSHDVAKFL
SSQIGAMDDFELWNDGSDIPVFAWRLKDRPNRKWDLYDLSERLRTRGWLVPAYPMPADLT
DVTVQRIVVRNGLSHDLADAFLESMRAEVAYLDALPAPMPSQHKQSGFHH
>PFR_JS14_2087□PFR_JS14_2087□Amino acid/polyamine transporter, family I□2400637:2402034 Forward
MAMLTLVTVASLRSLPAMAEYGLASVALFIIPAVLFLVPTALVAAELATGWKGGIYTWVR
EAFGNRWGFVAIWLQWIQNVVWYPMQLAFIAVCLTYVFGVNIGNNGFYVAAVIIVFYWAS
TLLSLAGKGLFAKVGSWSGIVGTIFPAVLLIVLGALWLTTGAPVQTDMHASAMLPPWTGI
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HSKLGLMDSVNLAFQEFFNHWHIAWATPLISLLIAAGAIASVIAWISGPSKGLLAAARTG
LMPVALQKRNKEGVQSHILFAQAGIVTVLALLFVVIPNGDTAFATLIGMASALYLIMYML
MFAAAIRLRHTKPDVKRTYRTPAMNLVAGVGFVACAAAFVLSFIRPAGFTGISGVGYPLL
VAVVVVVLGVPPLILYALRRPGWDVRSDEEKADDQAILVNPAPKD
>PFR_JS14_2088□PFR_JS14_2088□6-deoxyglucose synthetase (2)□2402083:2402982 Reverse
MRVFVTGGTGFVGSAVVRELLAAGHEVLALARSEASAARLTAAGATPQAGSLEDLDAIRA
GASDADAVIHAAFDNSSVASFLRNSKIERAALQAMGDALSGSRRPLVAAGGFAPVVATGP
VLVETDEASAHTGPAGRNVERTIVDLADRGISASVVRMPAVHGAGDHFTMSRLIELARRQ
RVSGYAGQGANRLPAVYVADAARLFRLAVEHPAASLRYHAVGETGVEFRQIAQAIGRGLG
VPAVGMSALRARWYFKAFAGYAMSDRPASSELTQQLLGWTPTGPGLLDDLAGPDYFSAR
>PFR_JS14_2089□PFR_JS14_2089□MFS transporter□2403295:2404563 Forward
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LGGALVDRISRRTGMVVRGLTGMVLWIGFGVLVWTHLLNLWILIAIFLTAQLLDGLFGMA
DNAALRSIVHDDEQFVQVTGINQGREAAVRIGGGPIGGLLYALGAAVPFLVSGALLGLVI
ASAKAIRADLRPPVVAENRPEQRRGIVRSVARSVAQGISFMWSQRIMRTLAITSLFINAA
FSIVISTAMLGLLGAGYTALQLAYLETVYGVVMMLTAFVAARLVSRLPTGRLLIGAQLFM
MVVAVGAAFWHSYAMLFLWLSLYGLVTPLFATSLSGYTFARTPDHLQGRVRSVAALLELS
ATMVIPAVAGWMVNSGHNTPSYLLGAVLALVGIIVVCVNPGARRLGPTRMWREDATENSL
ST
>PFR_JS14_2090□PFR_JS14_2090□Conserved transmembrane protein□2404630:2406159 Reverse
MAEAGSTQRGRGWRRVVPLNVRGDIVLGLVVVVLTLVGAAHVSPWLDEAATANIVSYPTW
DMTQLWTASRWWFKGVDVALAPYYLVVHQWVRLVGISPLTLRLPSVIAAGVGTAVMAAVG
RRLVGRRGQLAYATCYGLLPRTTAMAIEARPYALSSMFMAAALLFVVMARRKLAWWGWLL
LVMSMVGAVAMQLYAAFPIAGLVVASWFFLKGRARWLVTIAAAFSAAILSPFLWLSYQQI
GQSSWLADQKFSLANRFLVESWATSRVNAAPTVTDLTPGRVALAMAVIAGLLIVLVIVAS
RGRGLARLGIASIPLVLSVGTMWILALTSMPVFASRYLSSAAPFFAMVLAEAVLLARWRA
AKVLVVLLAVGALVLYGFQQRPFSKSPIDDYGLMPSVVRQHGRAGDGYLVDPLDGLIGSY
RAAIVTDPGAYKGMADLAAPERLPLDYPWAHDPPAVDLATLPNLPNRIWVGAWNQGGSLY
GEQLAALGYHVGYSKRGPAQGNTIFLWER
>PFR_JS14_2091□PFR_JS14_2091□Putative oxydoreductase□2406375:2407202 Reverse
MSGRVVVVTGASGGVGAAAARELARQGDDVVVVGRNPRRTQQVANEIKAQHFICDYSDLD
DVRRLAEDLRNNLDHIDVLANNAGGVMPSRELSLDGHEMTLQVNHLAPFLLTNLLVDMLE
RSRASVITTSSVAHRTARLTMRDPELARGWSPWRAYANSKLMNILFTRELHKRYSLKGIS
SACFHPGIVASSFALDLPGPVGVFYRSRVGRSMMVSPEHAAKTLVFLARGRPPRDWISGL
YYNDSEPVRPSRKARNPRLATQLWRMSAAMVGLPE
>PFR_JS14_2092□PFR_JS14_2092□Hypothetical protein□2407619:2408020 Forward
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RRTGTRHLRVWGLTLIPVGVIAILFVTRAPGIVAGVEGLLAFASFAWLVVALRDGADAVA
RQRTDDEGPGAPH
>PFR_JS14_2093□PFR_JS14_2093□Choline transport system ATP-binding protein□2408348:2409238 Forward
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VNRLVTPTSGSVLIDGDDVANTDPVQLRRHIGYVMQDPGLLPHRRVIDNIATVPRLLGRS
REAARAEALHQMDTVGLDRDLAHRYPRQLSGGQRQRVGVARALAANPRVLLMDEPFGAVD
PIVRAELQHDLLELQRTLGKTVLFVTHDVSEAFKLGDHIVLLDTGARIVQQGRPSDFITR
PADEFVSRFIGLGSGAATLHTEYVDGHTLVLNSSEQPVGLLGDQSEDRNSAEGSTP
>PFR_JS14_2094□PFR_JS14_2094□Choline transport system permease protein□2409235:2409882 Forward
MRWLSGNWTTIGAAVIDHLLLALPAIIAALVIAIPVAWLAHHFRWTRFTLVTLGSLLYAI
PSLPLLVVLPLIIGTNVRDRLNVIVALSVYGFALMIRAATDALDAVPVSATTASTAMGFG
WARRFFTVELPLSGPGLLAGLRVVSMSTIALVSVSGIVGVNSLGMLFVDGFQRGILAEVV
AGIVATVAVALAVDFVLVIAGRLLMPWARGEEVRS
>PFR_JS14_2095□PFR_JS14_2095□Choline transport system permease protein□2409879:2410559 Forward
MNWISQAIAWLTDPVHLAGPTGLWALVGQHLAITGWATLIAVVIGVPAGLVIGHTGRGRQ
LVVGLSGAARALPAIGLLTMVALIAGIGLIGPLVALVVLAMPSVIAGAYSGIDSIEPVTR
DAARGVGMSPMQVLWQVELPLALPQLVGGIRAAALQVIATATLAAYVGAGGLGVLLFRGL
KTQDYPQMLAGSIVVVALAFLVDAVFEVLGRLISRCTGVVNLATSR
>PFR_JS14_2096□PFR_JS14_2096□Zn-dependent alcohol dehydrogenase□2410634:2411653 Reverse
MTTMFANELDHTAPITTHPVNWRETAKPSAGPGQILMKVVACGVCRSNLHMIEGDWLPDV
PSISPIVPGHEVTGRVVELGEGVTNFAVGDPVGVTPLWKTCGVCEFCTSGREMLCHHREI
TGETVNGGYAEYMVATADYAYRIPEGLDLIDAAPLFCPGITAFGAVEKLDVGPGDTVAIF
GPGGVGHMAIQFAALTGAEVVAVGRTPEHLKVALEVGATRAVNSTDSDELASLTDAMDAV
ITFADSDVVTAQAFEALKWGGTLVNAVPLHFKEFPFNKGQIIKGTILANHAGMERVLELA
AAGKVHTITQRFPMDQADKALQLLAEGKLASRAVLYNEE
>PFR_JS14_2097□PFR_JS14_2097□Aminotransferase class I and II□2411723:2412913 Reverse
MPQLSARVSTFTDSVIRRMTRINAETPGSINLSQGFPDFPPPTPVLDRLAQVAYEGPHQY
ATTWGAQNFREALADKYSPTIGRTIDPASEIVVTCGGTEAMMAAVMTVCDPGDKVIVFSP
FYENYAADAILSGADPIFVPLDPPDFSFDPVILEAAFARGVKAIIVCNPSNPTGKVFTRE
ELEVIARLATKYDAFVITDEVYEHIIYAPNVHVPVASLPGMFDRTITCNSLSKTYSMTGW
RLGFLIGPARVIEAARKVHDFLTVGAAAPLQEAAVVGLRLGPDYYKQLQATYTHKRDLLC
GGLEKLGFTITWPQGTYFVMIDVADFLALPQFANMTDLEFCEWVIREIGVAAVPGSSFFH
EPVNRYIRLHFAKADEILTESLKRLEKLAALLPANA
>PFR_JS14_2098□PFR_JS14_2098□Hypothetical protein□2413001:2413390 Reverse
MSLWWPVFDDVQSWVTRNGFIARDWGLFDAALNRPLATIGGQEVYPTLWDKAAAFLDSIE
RSHPFVDGNKRVGFLMVALVLTGNGVDISHISDDDWFELIIQAAAGHLEVAEGASRIRGL
VEAEGRPRA
>PFR_JS14_2099□PFR_JS14_2099□Hypothetical protein□2413387:2413659 Reverse
MPDGGGFAPWTSPGWYRGGTFARMGMQLRLSDSDDKFLEQMAAQEGKSKNQLVADLVRQE
WQRRQTRTYTHSILDQLASERADLMRRLAQ
>PFR_JS14_2100□PFR_JS14_2100□Hypothetical protein□2413728:2414510 Forward
MSVRDKFPADVLTTRDRGFQALQSAYDLWVGARYSREGFEALAPRDQEKAALYTLLTRTM
NASFTSFLEDDVATFMGTAAQQALKNIGATDTLAIIEEYRQHLTPFADAQAWPPYSQVPE
ADNDNELVARLHKEFFDYPDDIETLAADYYGNDPEPTDAPKLPSSGEELAMDIDEITYII
EARFIGVFDPPTGDYGTYESWPAIRLLPRQRRQIIEGWRYQIPYGAHATGDDLAEASTFL
YQNNVDLQAAAQEQLKAATN
>PFR_JS14_2101□PFR_JS14_2101□Protein of hypothetical function (DUF1697)□2414525:2415121 Forward
MNSPQPATTRFALFLRGINVGGVKVPMAQLREVLTQMGGSSVRSWLASGNVALDWPGDAP
GLQRAAEAVLGERFGYRARVLVRRVDELAAIIAACPWAPDDGFHRYVVLFDDADDAARAL
AGLASPGGSAGDPGRDGPVVPAGALLAGERVQLHGDLIYWRCPKGRTTDSAFGKQQNRGP
AVRRPTVRNLQTLQRMVG
>PFR_JS14_2102□PFR_JS14_2102□MFS permease (Fragment)□2415278:2416177 Reverse
MCPVGALLPTAAHDLMGTNAAGYSTLLVLLGVGAIIGALLMDKVRQIMSNSTALFISAIV
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FGLGTLAVAKVSLQVMWPIALISGIAWILSLTTLNVAMQLTLPEWVRARGLSVYLLVFMG
SQAIGSFIWGIVADRVGVAWTLVVAGVFLLLAGLSVPLLPLIKVKGKLDRNVVALSTDLP
VLSLDESKSDPVVVRSTYHVKKENIDAFREAMWPVRAARLRTGAASWQLLEQTDAEGSFA
EEFTVPSWEEHILQHTVRWTGHEEDLLTAARALADDAPQVTHYMILGAPPVTNTGQMKS
>PFR_JS14_2103	PFR_JS14_2103	Major Facilitator Superfamily protein	2416132:2416938 Reverse
MGVSDKQTSGRNTEKARPSGGGSLAVLRRPVFLMLFVAQLVSNIGSWMQSVGAQWFLAEQ
AGSPALVAWVQTAGTLPVLLLSLFAGVAADLVNRKRLLLTLSLVSAAIAVALTVVTAAGW
LGPWELLGFTFILGCAAAIMGPAWQAIQPELVPREELPQASSLGSITVNGARAIGPAIAG
IIVVASGPAMVFGINAVSFLAVALALVLWRRGTQQQPAVREQVLPGLLSGMRYVRSAPGI
RRILIRCVLFAFPGCALWGPCCPPLRTT
>PFR_JS14_2104	PFR_JS14_2104	Sn-glycerol-3-phosphate transport membrane protein ABC transporter ugpA	2417215:2418210 Forward
MTAIESHYVAPAPPQVSTPEPLPDQPAGRRLRRHPHRGRASRNGLREKLLFVALIAPNVV
LIAVFVYRPIIMNLYYSLLDWTLGSSTAKFVGLGNYVEFFTSRDAPSVLGTTAVFTIATV
GGSMAIGLMLATVLNRRLIGRNVARATVFAPYVLSGVGVGLVWSFIFGPTIGVLAGVLRK
LNVASPQWFLDPKLSLVMVVLVYVWKNLGYCAVIYLAALQAVPRDVLEAAALDGASRTRT
FWSVIWPLLGPTNFFLLLTTLLGSLQAFDIIRIMTPMGQGTTTLMYSSYLQAFGSYNRAG
YSAAISTVLLVILMILTLVQMRLLERRVHYA
>PFR_JS14_2105	PFR_JS14_2105	Sn-glycerol-3-phosphate transport membrane protein ABC transporter ugpE	2418207:2419187 Forward
MSVTINRPRGDHRETDTAHDDRARRRTLSKLLKRGSLRHDRTDNAPIGVVGPTSRTRTLL
GGYLPLILASLAVLAPLAWMVLGSFKGSSEIVNQNVVWLPHDPNWDAYLTASQRVNFPRL
FANSVLVTAVGATIKLVLAVLSAYALVFIRFPFKRVIFMFILAALMVPAQVSMLPNYILI
SGMGGVNTYWGIILPGLGTAFGTFLLRQHFMSLPGEVLEAAKLDGAGHLSRLLRIVVPIS
TPAIATVALVTIVDEWNSYLWPLVITNDDTRMTLPVGLTLLKNIEGDPSAYPVLMAGAVL
VIVPVIVIFLFLQRYIVAGLTQGAVD
>PFR_JS14_2106	PFR_JS14_2106	ABC sugar transporter, solute-binding component	2419220:2420653 Forward
MNPVSPRNSAPSHSASSQGSAAPHVLSTTLSRRRLLSMAALGAGAVALAACAGPSTSSGA
SSSAADANGPDFSGVTPATTITFWSNHPGSSEDITKQIISDFKNETGITVNLVTAGSSYE
DVAQKFQTAQTGGTLPDIVVFSDVWWFRYYMQDSIIPLTNALKAANVDTSDYRDGLFADY
QYKGSQWAVPWARSTPLFYYNKSHWAAAGLPDRVPATWDEFAQWAPKLKDANSSAQHVYE
HPALADYAGWTLQNILWGYGGGWSAKGSFDVTCDSEASVKALQYVKDSVYQGKWAGVASS
AGTDDLAAGACSATLGSTGSLVGVQKAAAGKFEVGVGNLPGGPSVTTPVCPTGGAGVGIP
KKVPAANQLAAAKFIGFLTNPKNTVAFSQQTGYMPVRKSADTSELLAKNPLIETAIKQLD
VTRTQDYARVFLPGADQEMAKSVAQIVTQNADVASTMKSLRSTLEGIYNGQVKSKTS
>PFR_JS14_2107	PFR_JS14_2107	MFS family major facilitator transporter	2420898:2421893 Forward
MSQDSAAGRSSAGHSSSPTDVGDDGARPHPNRGIVMAAVFIATFMTSVEVTIVTTALPTI
ISELHGLSLQSWIMSAYLLTTAITTPIYGKLADSLGRKRIFQFGVVLFTVGSLLSGLSPS
IGMMIGFRALQGIGAGAVMPLTFTIIADYYSFAERARIIAFNNTAWGLSALIGPLLGGFL
VDALSWHWVFFVNVPLGAAVLVLVAWGYKEKRQPAHGLRPDWAGIWWLTLCLVCLLLAVQ
DLDVRPLVSGALFVVAVVAGLMLVHVERRSADPLIAPAMFARPTFTVQIVTATILSGVLI
GYQTYVPMWLQSLYHRPPTIAGLVVTPSSIM
>PFR_JS14_2108	PFR_JS14_2108	Hypothetical protein	2421936:2422439 Forward
MPKRIAVVFIAVLLVGYGALAVAPAGFPVWAFYVFAAVNGTGMGIVISMNTVLTQHLVDP
SMVGSATGIFTLGRSLGPTLMAGIYGAVLNVAIRVQLRGQQAVGAGVDFGQVNTVISSSG
GAGSSVDRAVVDPILLNSFHALFGVVVVILVVALLINVFDPNKKVIR
>PFR_JS14_2109	PFR_JS14_2109	50S ribosomal protein L9	2422568:2423020 Reverse
MKLILTAPVENLGVAGDVVEVKDGYGRNFLLPKNFAIVYNRGTAKEIEGIQRARNAKTIR
DNEHALQVREQLDGLEVQVPANASDTGKLFGAVTNADIALAVRKAGGPAIDKRSVTANKP
IRTVGRHGVEVKLTDAVKIHLDVEVVPAGK
>PFR_JS14_2110	PFR_JS14_2110	30S ribosomal protein S18	2423032:2423271 Reverse
MAGPQRKSVNKKKVVPVKTTHVDHVDYKDTTLLRRFISERGKIRARRVTGLSVQDQSKVA
MAIKNARELALLPYTTTTR
>PFR_JS14_2111	PFR_JS14_2111	Hypothetical protein	2423373:2423939 Reverse
MAGETPITLVGNLTADPELRFTPSGAAVANFTVASTPRTFDRQANEWKDGEALFLNCAVW
RQAAENVAESLTKGMRVIVQGRLRARSYDDREGNRRTVFEVEVDEVGPALRFATAKVTRA
ASGGSNWQGNNAGGGQSRGNAGGGQPYGGGQQQAPQGNQGMAGGGQQGGNQGPVSDPWAS
AQSDEPPF
>PFR_JS14_2112	PFR_JS14_2112	30S ribosomal protein S6	2424120:2424407 Reverse
MRKYEVMAIISPDVDERQLQPIVDKYTAIITKEGGTVDNVDIWGRRHLAYPIQKKTEGLY
AVIDLTCEPASVSEMNRLMGIDEQVMRTKVMRIDS
>PFR_JS14_2113	PFR_JS14_2113	Hypothetical protein	2425078:2425374 Forward
MSTYRTEVFEDGEPCWWCEREALRAELDTEAGEPDPSVVAALAEAEHHPDLEMKEVIAEA
RNSPADPEDIALAERVFGQGPASEPTGQGDATSGTPTE
>PFR_JS14_2114	PFR_JS14_2114	Inorganic diphosphatase	2425446:2425805 Reverse
MGDKGFNTSFEGPLFRELLSRPVRLDRPKGSRHPRFPSIVYPVDYGYVDLKSVDGEGLDV
FVGTLPEHRVTGVILCLDLMKQELEPKVLISCTSEEIGIVRNFLEQELHMLVWSSSDAA
>PFR_JS14_2115	PFR_JS14_2115	Chlorite O(2)-lyase	2426396:2427076 Reverse
MAHTADEINHMQRYTMWSVFRSEAAAGPGAGEQALEQLQAVAADTDLVIRGWYDVAGLRA
DADLMVWWHAHDYETLQRAYHVLRASTLGNVLTPVWSQLALHRAAEFNKAHVPAFLADEQ
PRDNICVYPFVRSHEWYLLPDEDRAQLLADHGRAASGFADVRANTMASFGLGDYEWILCF
EADEMARIVDLMRVMRTTGARRHVRVETPFYSGRRRDLTEIVNSWG
>PFR_JS14_2116	PFR_JS14_2116	Hypothetical protein	2427301:2427690 Reverse
MSMLWRRKAAKEGPDESGRGISVDDALTLMSKGAVVADVRKRREFERGHLPGSRLVDIKA
IRADPVDAIWGDDPLADTSKPVIVVSSTGLRANGAAALLRQEGRDAFALAGGLAAWVQDG
QVLIPGPQR
>PFR_JS14_2117	PFR_JS14_2117	Isochorismatase hydrolase	2427834:2428550 Forward
MSAITSPSADLDPDDELDDTSELDSGPDATGRAALLVIGMQQGNLDGCWQAEQVTATVSD
LIDRARLASVPVIWVNDLTPPASVTGSGELLSSLTCGAGEYVVLKPYRDGFESTGLADSL
ATLGSGTLFLCGAWSHESVRATMVGALSRGYSTVLVEDAHTAPSRHDGTATVSGESIVSV
VNMIAAAPGAPAQDSSTMPCYDVNFSAFVHTDDTAVGDEALAAQEQAQDEALDPGDDD
>PFR_JS14_2118	PFR_JS14_2118	High-affinity glucose transporter	2428617:2429870 Forward
MTTPGIRQRVVGGLSRDVLVLGLIAFFVAVGFGVLVPVLPTFAASFGATDFLVGMVVSMF
AATRLATSPFCGWILDKIGGRLTLAVGIFIVAASSWLMGEAGDFWWLLGWRAAGGIGSAM
FTVSAMTLLLASVPPDMRGRATGFYQSGFLIGGMAGPALGGLLTRISLVAPFRFYAITLA
IAGLIGLTMLSSATTHADRPAHARATPRPLRQVLADTRFQAACVANFAQGWNSMGVRNSL
IPLVIVATLGLTPTWTGIVFAVSAVVQVIVLHPIGHFVDTVGRRPALLAGGVVMAASIAA
VPLSGSIWIVMALMCVYAVGAAAMSTAPAASVGDATGGVHGGTPVAIFSMSSDVGAIIGP
LAAGAISDVAGRPLAFAVGAVFLALSSLVALRMPGGRPDHSAGSVASADPDALLSED
>PFR_JS14_2119	PFR_JS14_2119	DNA-3-methyladenine glycosylase I	2429962:2430588 Forward
MTETPHSPSSHADPASNPELVRGEDGRVRPRWAATDPLLRDYYDHEWGVPIRTGRGLYER
LSLEAFQSGLSWATILRKRPAFRAAFADFEPDAVAAFGDDDVRRLLADAGIVRNERKIHA
AITNARATVSLRSDGGLVQLVWGFQPAPGPRPQSYAEVPAKVPASEQLAKALKKAGFVFV
GPTTMYALMQAIGMVDDHLVGESGPLAG
>PFR_JS14_2120	PFR_JS14_2120	Protein RtcB	2430970:2432178 Forward
MTELPVPVPGTTSDTLMWADPTTVEPEALDQLRAISRLPWLAKLRVMPDVHLGKGATVGS
VIAMRDAVSPAAVGVDIGCGMVAAPTNLTVDDLPDSLHAIRSRLEELVPVGWKSHTGTAP
VLSRDEQLKGRFTTLFDRFGQLRAPHIDDRETRALSQSGTLGGGNHFLELQADDTGTVWL
MLHSGSRNIGKELADRHITEAKGLDHNLDLPDRDLAVFLAGTPEMDDYLHDLYWAQEYAR
LNRDIMMRTFKGVITEFFPHATFDHDVNCHHNYVSQECYDGVDLIVTRKGAIFAGSGTLG
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LIPGSMATGSYVVRGLGNATGLCSASHGAGRRMSRRAARRTFTVDDLAAQTAGVESRKDE
GVLDEIPGAYKDIDAVIHDQTTGPSPLVEVVARLRTLLCVKG
>PFR_JS14_2121□PFR_JS14_2121□Alpha amylase, catalytic domain protein□2432208:2433476 Reverse
MSDWRRDVIWWTVYPLGFTGAPTHLDEQAPVAHRLPRLENWLDYLIDLGCNGLVLGPIFR
SESHGYDTLDYFAIDPRLGDDADFDALVAACHARGIKLVLDGVFNHVSARYPALRQALAE
GPDGPLADMFHIDFSTTPPTRLNFEGSDDLVRLNHASPQVRKLVTDVMLHWCGRGVDGWR
LDAAYAVDPEFWAPVLATVRERFPELYIYGEVIHGDYAQIVHESGMDAVTEYELWKACWS
SLATENFYELEWTLGRHNEMLDDFRPFTFIGNHDVTRIATKVGADKAILAAVLLGTVGGT
PCVYYGDEQAFRGEKYDRPGGDAEVRQPMPERPDQLAGFGLPTYRAYQAILAIRRRYAWL
PDARTEVESITNPRIVYRAHDPADADHWVRVTLDVTDTPTASVVDNSGELFHWPHRGGRR
GV
>PFR_JS14_2122□PFR_JS14_2122□Mannosyltransferase PIG-V domain protein□2433584:2434738 Reverse
MSTTATRTSPALRSRTVAIVAAWLATRLVMGAALLLAMRQSGLTPARALGNWDVQHYMLI
ATSGYADPKEMAFFPALPMVMRLLDAVGVPMAIGAAAVSQLASLVAAFAMERLGGLNAAI
VWLLAPMAVFTTVGYTEALFCAVAFWAWVLARRGRWGWVAVLASVACLTRISGLFLVGGL
GLLALFGGEPTVAGAEPAKRVGSWSQRLRNLAWLVVPLAVLAAFAVYLYTLSGHWDSWLS
AQRAGWQREWTSPWDSLHNTLAATNEARWPTETTRAWIFRFEIVSMAIGCLTALGCLVRR
AWAQAGYVAVQVFAFSIATWFMSVNRADLLCFPLFIGVGSWLGRRPHGATARTVRTAVVR
VLIAAALLLMFWWARLFYLGHWAS
>PFR_JS14_2123□PFR_JS14_2123□Putative membrane protein□2434735:2436393 Reverse
MSPVSGSVEEPAPEGGPGKTVPKGGSGDAAPQESAPARSNLPTISVRLSHRIGGPLGRHA
RPGGLWFDPAPWALLLSTINWVLLLWRQAPCQQYTFGKPVNPFLRLCYSDIPVFFQNNGI
GSGAGIYSDAASPLPVLVGYLASLDRFIIRLLGAGVGPDASGQAQLDSSYMFFVLAAIGL
FCAFLALVLAHLQMGRDSFSDATRGVRVRSFDALLIAIAPVVFTGGLISWQLLPVALTSL
AVWAWARKLPVVSGVLFGLAVGADAYPVLVVLAVVVLCIRAARMREALRMLVPGIVAWVA
LNLPVVITAPHGWTAYWSTVLGGGSGVGSFWYALQLLGVSGTLLGVVASVFVVIAVLAVV
WLVFTAPRRPRLGQVAFLLVAAVAVFGPHYSPQYALWLLPLLVLARPKVLDWAVWNVAEV
LYWLAIWGYLEGILGAGSGADALYWLAVLLRIGVVLWVASRVIGDMFSPWNDPVRRPFVD
DPVGGVLDHAVDAPWLAEAESDRKKQAADQSGPVDEQGASEQVAATATMPAPATTSDADM
PGPGTRDEESGQ
>PFR_JS14_2124□PFR_JS14_2124□Transglycosylase□2436390:2438525 Reverse
MADRKKSRKPRRALAPSASQRHGPHRTKKKASRARRVVTAIAITLATLMIVGVLGSLIFY
ARVKLPDPNADFNSQTSTVLFRDGSTKLGELAIQNRTMVDYSAMSDNVKAAVVAAEDRSF
WSNKGVSPKGIVRSLFQIARGKDLQSGSTITQQYIKIRYLTSKQTMSRKLTELALAVKMN
REVSKDEILAGYLNTVYFGRNAYGVEKAATTYFGTNAAGLNVPQSAMLSALVNSPSTLDP
ANGDDAKRDLTERYDYVLDGMLEAGKISQADHDANYDKLPDTLPVTQSDLYGGTNGFLLT
MAEQELRKAGFSEEQIDGGGLTITTTFDQKMQDAAVKTATDNVSTAIRKAKTNQDASTLH
AAVASIGVGTGEVYALYGGPDFLKSQINWATTARPAASTFKAWALVAGLRNGFTLNSTLT
GSTFTPNGDNVVVRNDGGVNYGSVTLQKATSYSMNTAFTDLEQRMPNGPADTVKAANDAG
VPTGDGWDLNNRIALGTGQVSPVDNATGFATLANDGQRNTTHVVKEVKDASGKVVYTGDT
SATQTIDASLVHNAQTALESVVTSGTGTEARQLGRQVIAKTGTKDVDDQTVSAWFVGATK
QISTAVMFVAGDGNANLDPYAASGAFESDSYPAYLWEDYMEQASQGMDRLNFNTNAPTQA
ASVRPSVRRTPTPSVTASATPEAPAANEPAVDVPTAPPASPEPAPAGTAGP
>PFR_JS14_2125□PFR_JS14_2125□Hypothetical protein□2438518:2438856 Reverse
MMEADPCDADPRLISSALHHGTPAGRECPVCASDRMAVLRYVFGDQLGQYSGRIRQPAEL
EEMEHQFGEFTVRVVEVCPDCGWNFMIASYVLGDGRKRRAPRHKQTVEDIYG
>PFR_JS14_2126□PFR_JS14_2126□Cassette chromosome recombinase B□2439251:2440954 Reverse
MSSATLDTTTSERAADASVLLAVSYLRVSTREQAERGGTEEGFSIPAQREANARKADELG
TRVVREFIDAGESARTADRDGLQDMLAFIAATRVTFCIVHKLDRLARNRADDVKIHEALI
NAGVTLVSATESIDQTPSGMLVHGIMSSIAEFYSRNLAAEVTKGLTQKVAQGGTPGRAPI
GYLNVRRTDERGREVRTVEVDPERAPLIVCAFEQYATGETSVTALLRDLTARGLLSVPSP
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RHVQHAHHLKGLLHCGTCGSRMLLDFATNPRGTTYAYFVCSGRAAKKTTCTRRAVPVQVA
ERLVESSYGNITISEAEYRHLAAEVDAAFDKRSAGRDQEFADLTANRARLEAESDKLLAA
HFADAIDLATLKRHQDRIRAGLADVNRRLAEHSEHHTGGRAFLHDSLRLLTDAHRAYQYS
GDADRRIANQAFYTRLDITDDEQLRPTLAEPFATIFREAHQGGDEGKEAKREHTTSFDVA
CSRKTLWVEHRGFEPLTYGLQSHRSTN
>PFR_JS14_2127□PFR_JS14_2127□Transcriptional regulator, TetR family□2441356:2441961 Reverse
MVEMRRGPGRPAYDSKQKLVAAACALLAERGFEATSPQMFQQRSGVGHGSMYHHFPGKGK
EGLALDAVSRMRASTIAFLDGSPAPEGSEVEEVRAIIVAALDRLFARKEGQALVRLLADA
VAGAIPSLATATQDWCDDIRAVIVVRLRADEPGADLDVADAAARFLAPEFDALAEELFAA
ALGRGLLHLPKLALPEAAEER
>PFR_JS14_2128□PFR_JS14_2128□DNA polymerase III, gamma and tau subunit□2442162:2443028 Forward
MFNSKLRKRAVESFNEAVERYAASTGRFETAVAGLYSLRVGAAQQVGAVSDHINALANVP
REFKVSLERTTAEIRSFEGKQSEIKKAEAQAKRNAKGSAAGASLGALGVAVATMGPTVAM
GVATTFGVASTGTAIASLSGAAATSAALAWLGGGTLVAGGGGMAAGTALLALAGPVGWTI
AGGAALVSASVGTVAAVKNKKAAEDLNKERLEVEAAIRRFDQTTAEVEALRELTLTQTEQ
VAELSSQVPTADYQSFSDDEKRLAAALVNANLTLAQLINKEIEVDAEA
>PFR_JS14_2129□PFR_JS14_2129□Mu-like prophage FluMu protein gp42□2443015:2444562 Forward
MPRHSTTENAVAQGIAAQVNYLESTRVAEFASTLERILVSETDELTKVASREARAVLHLD
LARINAQGIIDANRGGATGLHGFIAEYAEAGVTNAERAINGIRPLTRVLADNGPADLSSW
GVPVQMKFYANPYNEVLQSAHYRDMKMMFPQNHFEVFDRIMRGETYLEVDGSALSAKKVN
AIREFIEQESTARGEPYTNWMRPSKLEYAEVQRGAIGDTLDEKTAAMRQRADDRRQQVRD
ESDTKRASAAQQAAPSWGEAAKVAGTAAAVQGALSFGVYVYRRHREGTSIWEFSKDDWRE
GGIETAKGGLKGGVSGLAIYGLTQVCRMGAPAAAAVASGTIGLATAAANRRAGKLDDDEF
ADLVFFNAIEATGAAVGAGLGQVLIPIPILGAVVGSIAASMILGQGKKFLSEAENDAIRA
REAEIQAYVDGLDAELQAEYVRILAEHDYYRDLQNRAFDITANVELQLLGSIELARSIGV
HEEQILHTVAEADAYFLGAAPSPVVPSTPEVSVPE
>PFR_JS14_2130□PFR_JS14_2130□Low temperature requirement A□2445200:2446402 Reverse
MDGALPARARGLRHARPHAGEGATTFELFFDLVYVFAVTQVTDLISHEHGAEGVLHGLIL
FGMLWWTWCTFVWLGNQLRADVGLGAVGFGLALVGVFVIALAIPSAWDSAGEGLPGPVVL
VSAYLFVRLVHLVVYTIAARDDAGLRRQIAISRLPLLVQAVLLVIGVVVGGQAQTALFAI
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PAIIRLPALGGLAAVTMVLVVLVVFERLYFAELRRQSRDA
>PFR_JS14_2131□PFR_JS14_2131□Hypothetical protein□2446634:2447005 Forward
MATRYTTAPGAPHATLSDGIAARVPRREGHHPGIPGASIAWHNRRMNDIVANLTAQPILG
VGTVLFVIGLGFAVLFGLSFRIRAVLNKRAWNGPTRPFFFLMLLTLIPGIALIGLQLWLN
QGH
>PFR_JS14_2132□PFR_JS14_2132□Cytochrome P450 109□2447106:2448320 Reverse
MTSDTPSRDNPAPHEPQSYEWDPRAPEVLDNQIAAYDALRARCPVAHSEQMGWSLLRHDD
VLRAATQTRTFSAVVSKHVAVPNGMDPPEHTVYRTIVDRYFTQEVVDAFEPACRAIAADL
IAALPRDKPADIVNDLAEPFALQVQSAYLGWPERLREPLREWTLSNRRATASGDRAATAA
VAEQFDGYITGLLDERRAMGDAAPDDLTTRLMKEQVDGRVLDDGELVSILRNWTVGELST
ISAAAGIVVDHLAEHPDVQSLMRAKAGSPATLDDAVDEILRIHPPLISNRRVVAEPTQIG
GRQFEPGERLTILWASANRDEDVFGDPNEFRLDRPREDNLLYGAGIHACPGAPLARLELR
MLTQELLAATGTITPDRGATSQYASYPASGFAELSVILGSVTEG
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>PFR_JS14_2133□PFR_JS14_2133□Aldo/keto reductase of diketogulonate reductase family□2448653:2449507 Reverse
MILNETFDLSNGEKIPKLGLGTWFIDDDRAAQAVRDAVQIGYRNIDTAQAYGNEQGVGEG
VRTADVARDQLFVSTKLAAEIKDFDQAVAAIDGSLAKLGLDYVDLMMIHSPQPWNDFRGG
NYDEGNREAWRALEKAHHEGKVRSIGISNFLKEDVDNILGSAQVAPQVNQLLVHIGNTPQ
ELIDYCTSKDILVEAYSPMAHGEMMGNERVRDIAEDNHVTVPQLSIRYALQLGTVPLPKT
ANPDHMRANAQVDFVISDDDMATLRGLDQTDYGKYTKFPVYSGK
>PFR_JS14_2134□PFR_JS14_2134□Hypothetical protein□2449715:2450758 Reverse
MTQGTPRDHDPRHRRRDDETDVERTMQLPPVGGRDPSNDDAEPTVYIPAPNEPTVNLPSD
EPTRPFSGPVNGYPADPTVSLPSDEPTRPFSGPVNGYPADPTVSLPSDEPTRPFSGPVNG
QPADPTVPLSAAGYPGDPYRSGYRDDPYSEGYRASSSQGGPEPTKVLPGVEAGAGYGGAQ
YSDRGNYSGRGGYPSGPDYPGPPNYPGTGYQEPTGPEPQGNGGSNKTGRRIVWMLLVILA
LVVGTVVGAVGLGGSSSPSPTVTATTTTTNTVTAPPVTTTTTAPGPTVTVTGGNPIGSAW
SQATSQVGSTKVGGICLDEGSTGTASDGTAVTCRKADGEFLPHWQAQ
>PFR_JS14_2135□PFR_JS14_2135□Alpha amylase catalytic region□2451068:2452855 Reverse
MSMSTPSAGSNGRPTARQSAGKQPVARQSVADPSKAWWRDAVIYQVYPRSFADSDGDGMG
DLGGVREHLGDLEALGVDAVWLSPFFPSPQADAGYDVADYRDVDPLFGTLDDFDALLAGA
HQRGLRVVIDLVPNHTSSKHVWFTAALAAAPGSRERNRYVFRDGRGEHGELSPNNWPSQF
GGPAWTRVDDGTANPQWYLHLFDAGQPDLNWDNPEVIDEFQDILRFWLNRGVDGFRVDVA
HGLVKQQGLPDVASGEHDALSRLDDPRWDQPGVHDIYRGWHRVLEGFGGDRMLVAEAWVA
DATRRALYVRPDEMQQAFSFGYLMAGWDAGAVRHAIDDALGANDAVGATTTWVLSNHDVV
RHASRLGYPVPASDQGAPAPSWTNGIGPDDPKPDDELGLSRARAATLGMLALPGSAYLYQ
GEELGLPEVTDLAPEVRQDPEFLRTAGAVIGRDGARVPLPWDSGAPAFGFSPSGRSWLPQ
PASFADYAANEQRGHPGSTLEMYRAAIDLRRTHRLGTGRMHWNEADPGVLDFTNGEVRVV
VNMSRSPQPLGDHVLGDQASGDQATRDRALLLESSPGSVIDGQLQPDRCVWLLVG
>PFR_JS14_2136□PFR_JS14_2136□Hypothetical protein□2452914:2453519 Reverse
MRKFKARFVWAGVAVAAVVGVSAAWVAGSVGPGTAQSRPVAAGMTAEQLLTLEPASNASG
GDQSVDASGNGQAPVPRAGQDTPSSPAEGQVSAQVRHYFDVDPGTALPPDATISPDPSSW
RKIDDKTAVMRVDVLTPGAAATPYAAVMAEQGGEWKVMGTLNVDETPTPTPTPEENAEPS
APASSPAKGAPASAAVPSPTP
>PFR_JS14_2137□PFR_JS14_2137□Transporter of xanthine/uracil□2454032:2455978 Forward
MSLTATAPAVKDPVDRVPPIPKLTILGLQHVLAFYAGAVIVPLVIAQGLGLDSATTIHLI
NADLFTCGIASIIQSAGLGPKIGVRMPLLQGVTFTAVSPLIAIGLAGGGGVGGLATMYGS
IIVAGLATFFVAPFFAKLLRFFPPVVTGTLLTIMGTTLLSVAANDIVSWGTAAAKAGGSP
ISGTMRGLIYALGTLAVIVLVQWLFKGFMATISVLIGLVAGTVVAIFLGDADFSGVGQAA
AFGVTTPFFFGMPKFSVGAIISMLIVMAITAVETTGDVFATGEVVGKRITSKHVANALRA
DGLATTLGGVLNSFPYTCFAQNVGLVRLTRVKSRWVVTMAGAIMIVLGILPKAGAIVDAI
PTPVIGGASLAMFASVAVVGIQTLGKADMHDNRNAVIVSTSIGLALLVTLKPDLAGMVPS
WLSIFFGSGVTFGSIVAIVLNIAFFHIGPHRSPDVARSKKGRNVSLDQVNRMGKDEFVDT
FGELFSGTTWPVESAWELRPFNSTTELRQAFEDSVLTAEPSCQKDLVRGYFDIADLVSDE
NGDLQAQIDTGSVALDRMDDVQRQEVRAASHAYRDRFDMPMVIAVENLASREQLVKDAWR
RVEHSPELERRIAVAQVVAIADNRFTKLVADANPIRNAWSRKFEQLDE
>PFR_JS14_2138□PFR_JS14_2138□Putative xylan esterase□2456077:2457078 Reverse
MRVTTESLSDTATLTSYLLDDAPTTHAVYPTMPPRPAVLVLPGGAYLEIAEREAEPVAAA
YLAQGFNAFVLRYAVGADVPFEASLADATAALLRIRSGAEEFGINPHRIACAGFSAGGHL
ALALGTIAEEAPDALVLGYPVTMAQMGRPLGQRIPDLVGAITPDTPPIFVFATCGDPMVP
VRNTLDLIAELDSHLVPFESHVYLLGGHGLSLATPASSGGQAHNVEPGAAEWFADSVRFL
HTVFVDVELAGSQPGYDTLLVRRRLGVHMPLRNLVADERAVHVMAAAAPALTLAVQDGEL
SLLVSPAQVAQQSPDLIDRETLDRLQVSLDELN
>PFR_JS14_2139□PFR_JS14_2139□AMP-dependent synthetase/ligase□2457607:2459274 Forward
MNESLDALQPTMFREVFDHHFTWASGFERNIHRYADRPAMTDLPSGRHWTYAELGRDTGR
LVAGLAARGVGKGDLVAYQLYNCPEFAMLYVAAQGLRAVSSPSNFRLAAGELAHVFDQTR
PKVFVYDVRLADQVAHALELADFNPQTLAGVGSGELLPGAIRFDELFADEAPSFHAPDDA
STWDWTSLLFTSGTTGMPKPVPLTSLNEVLTAHDVIMHFPLNAHESSLNMSPWFHRGGNY
CAGPNTMFYLGGEVVIMPKFDADAVLDTIAERGLAYVVGAPTNLERLADAQERRPRDLSS
LSGIVTMGAPLERAAALRYQRVLSPRIANGYGTTEGFWNTYLRPYDLPEGSGTAGHACLD
DDVAVVRLFDDRTAAPDELAAKDNKEVGEVVMRTPKAGYTYLGHDAEAADKFRDGWIYPG
DLATWDETETLTIVGRKDDMVISGGENVHPVQVEEILDADEQVADSLVTGLPDKEWGQVV
VAYVVPEPGAFTDHQQAARHLDQLCRDAATLANYKRPRLYAFVDALPMTATGKKQHYKLH
ERTTADAAKGLFVRP
>PFR_JS14_2140□PFR_JS14_2140□Catalase□2459415:2460863 Reverse
MPIDPKASPTQENGAPAASEEHSLTVGADGPIALHDVHLVETLAHFNRERVPERSPHAKG
SGAFGTFTVTGDVTAYTKADFLQPGRSTPMLARFSTVAGEQGSPDTWRDVRGFALKFYTQ
QGNFDMVGNNTPVFFMRDPMKFPHFIRSQKRLPDSGLRSPNMQWDFWTLSPESAHQVAYL
MGPRGLPATWREMNGYSSHTYSWINAGGELFWVKYHFISAQGVRNMTAAEAAEIAGDNAD
FHRQDLFDAIADGDFPSWDVKVQVMPYDDAREYRFNPFDLTKVWPHGDYPLIDVGRFTLD
RNPDNFFAEIEQAAFSPSNYVPGTGISPDKMLMGRVFAYNDAARNRIGANFEQLPVNRPV
IPTNAYTFDGQMRFDHSGAAPVYAPNSAGRPWAEGGGRAEDSWESDGDLVRASATLHSSD
DDFGQAHALVRDVFSEEDRAQLVNTIVDQIVNTDVVEPVRSRIVEYWTKIDAEVGADIAG
RI
>PFR_JS14_2141□PFR_JS14_2141□Dyp-type peroxidase family protein□2460968:2461885 Reverse
MPTESAPIGAPQPGILAFGTTHHAYLEFDLTVDASTEVLRGVVGALDESLVTGAGSMAVV
GFRPEMWAKLVPEHVLPGLAGFNRPLRGLDDFTMPATQHDVAIWVQGGAQDAVFDLSRTL
INAVSTWATLADETEGWVYHHHRDLTGFVDGTENPHLSQLPGVVQVPDGPAAGGSVLLLQ
RWPHDVQAWEGLPVAEQEKVIGRTKETDAEFDPKPPSSHIARTDQDDLGDILRRNTAFGT
ASAHGTMFVGIGAGSDVMQKMLDQMAGVDGLRDALTFYSHPETGGYYYLPSVEQLDPYRP
DLSEE
>PFR_JS14_2142□PFR_JS14_2142□Hypothetical protein□2462503:2462895 Forward
MPAPLLELLVLALLAVAMAQVAKRIIAGVSFGRRFVASLLVFLLTLPAGTWVVEQTRVVG
PDDTMQVNWFVFLLVMVLCFVWVFAAALTALVALELVLPSGSLPSPIQSVRDIRMALRRR
AATCSSVGSR
>PFR_JS14_2143□PFR_JS14_2143□Hypothetical protein□2462892:2463368 Forward
MSSGLWKALRKGPDSPGFGEALVKMLNRSGVTFIKLGQVLSTRPDVLPGAVMTALTSLWD
TAAPAPEQNIRTMLRSQWGRDPEEVLGSFDDTPFAAASIAQVHRATLKDGTAVVIKVQRP
GAASRWWSIPTSCCASPGLPSSASPGRAQWASTPWDAA
>PFR_JS14_2144□PFR_JS14_2144□ABC1 family protein□2463338:2464453 Forward
MGVDALGRGMTKALKEELDYRREARNTKAIAATLADNPAITTPVVDEELTREKVLVMSPV
NGSSLVSKVDTLDDDTRHELARTLMTATLQGILVHGIFHADLHPGNILLLDDGRIGLLDF
GSVGVIDAETRQLIAALLVAFVADDNSAATTAVTAAFDVGDEVDRMALQRDLGRALTLLT
HTGDESAATLNEFFTVMRDYRITIPGDVAGAFRTLTSLEGTLTALSADYGLLAGAEDAMP
SIITKLAAPKQLAMIAATTTMTSALLARRLPARTEQITDLLARGQYTLNTRMLSDRSDRQ
WLRSRLDDAMSSLFAAVAVVLAVVFIVIPGGPAITSTLTGYDLAGAAIGCVGLVLILRLV
VRLFTRYSGRP
>PFR_JS14_2145□PFR_JS14_2145□Transposase for IS3514a□2464918:2465898 Reverse
MVGEGLDAGPLTIAWHLERDGVRPPAHSTIRRILHQAGLVRPEPDKRPRSSFIRFNADLP
NQTWQSDVTHWQLADGTPADIISWLDDHSRCLLHISAHRAVSVHTVLDTFTATIALHGPP
ASTLTDNGIIYTTRLLGGPNSGPNRFELFLEAMGIVQKNGGPHRPTTQGKIERFHQTLKR
RLNAKPDAHDIADLQTVLEDFQDLYNHRRPHTSLARRTPGDVYRASPKDRPDPTGPRPVR
DSDYRVKHVRVPRAGVITLRHHGAPHALGVGAAHAGISTVITLDATTVTVIDPTTGQILS
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THHIDPDRRYWPNTQRPPGRWPKHDP
>PFR_JS14_2146	PFR_JS14_2146	Hypothetical protein	2465865:2466122 Reverse
MSKNHVAVMSVVSGSMSVAQASREFGISRQHVYRLVARYRAEGPEGLEPRSRAPRSHPNQ
TPAGGVNGSSRCVDSWSARAWTRVR
>PFR_JS14_2147	PFR_JS14_2147	Hypothetical protein	2466262:2467032 Reverse
MLTPLDTNFLDGISVGVFLIILAIPAILWVITLVSIITSRNWTPGMKALWALAALPSGLI
GMICWFVWGRPEGNKLAIEYYGGQLPTAVAPYGQQIPGTYATQPQQAQAPAAPAPAPAPA
QPPADAAPYGTGAFGDGQAAPGAAKYATTQGQRFDAGTAYGATQGFAPGQDSAGQDSAGQ
DGAGQASAQDATGHSAAAQGAADQPTEPIVPTSQGGAAPQTDAAPRADEASDDGDTRPDI
PQVPDNGPDASGKTTN
>PFR_JS14_2148	PFR_JS14_2148	Chloride transporter, chloride channel family protein	2467116:2468372 Reverse
MVVLIVVAGVVAGVIGGLTAEANRLIETLAFGFDFTKSPNGPAGAPWWRRLLVALLGGVA
CGLIWMRIRPRPGGNLVGVKGASTDPTGTKRLPPLATVLDAFAQMLIVGTGISQGREPAP
RQYAAVAAQALARRFRVDVATRGLLIAATAGAGLASVYNVPLAGALYALEEVVRPNLRTR
RGWWQVAVAVIISALSTAVSWLFNHRARTYVMPQVRVDVHAYAWAALIAVVALVVGFAFQ
RALAWIKAHEPDTRRLWWTVPIGAVAVAAIGLWNPQIPGNGQVLVQTVLTGGLLPGALLI
ACVAKFGATLLSFGAGSNGGVLTPSLAVGASLTMALMGWCHVDAAVGVTVAVVGAACVLT
LTQRSPMFSAMFALELTGSGLFTSSAVAWGVGLTWALYLLLPRLARRLRRRGPGPTGA
>PFR_JS14_2149	PFR_JS14_2149	Hypothetical protein	2468775:2469008 Reverse
MNKQTSWQRLVIIAAACIVVFGIGWFATDVQSAIVLAIGTGAALGAVSHFWPKKKVVVTA
DGRTVKTCDDGGACCCH
>PFR_JS14_2150	PFR_JS14_2150	Hypothetical protein	2469235:2469648 Reverse
MDTRTKRVCGLMIAFMAFMFWSIVADLVDMKASWSGPLILALVAALLLVCAGLVLLVRYA
SGSESAGSWIKGFCIVVLFLIWGSGGLLRGGMTAWSQIPLLGLFACVVAILSSLKRPSPN
RTATPVDTPQGLSPMGN
>PFR_JS14_2151	PFR_JS14_2151	Fructose-bisphosphate aldolase class 1	2469811:2470698 Reverse
MNQDQKDRMATGRGFVAALDQSGGSTPKALRTYGIPDDAYDNDDEMFKLVHQMRTRIITS
PSFTEEHILAAILFERTMDNTVDDVPTAQFLWERKRIVPFLKVDKGLGEEAHGVKLMKPI
PDLDKLLDRAVAKGIFGTKMRSVIAHHDEQGIKAIVDQQFELGAQILAKGLVPILEPEAD
ITATDREASEQVLHDQLASHLDDLAEGQQVMFKVSIPLKDDLYADLIDDPRVLRVVALSG
GFSRDEACERLARNHGLIASFSRALSEGLSVDDSPEDFDGKLEASINKIAAASLT
>PFR_JS14_2152	PFR_JS14_2152	YceI family protein	2471083:2471634 Reverse
MSTDLTSLSGDYTIDASHTTLGFVARHAMITKVRGSFTDFSGEAHLDGANPSASSVEVTI
NVDSVDTRSKQRDEHLRTADFFEIEKYPTITFKSTAVKLVDDSHVEITGDLTIKDVTKPV
TIVFEFTGAATDPFGNHRIGFEGSLDVNRKDWGLTWNAALEAGGVLVSEKIKLEFEVSAI
KKA
>PFR_JS14_2153	PFR_JS14_2153	Citrate (Si)-synthase	2472014:2473297 Forward
MEHTAVLSGEGTKAELPIVESSVGSDGYDIRNLLSTTGNVTYDMGFANTASCQSAITYID
GEKGILRYRGYPIEQLADKSTFLETAYLVIYGELPRPAELADFEERIKRKTIIDEGMRKF
FETFPRGSHPMPVLAAGVQALGTFSTTSIGDDAGSIEKATERLIAKMPTLAAYGYKNSRG
EPFLYPDNALSYVQNFERMSFGYPTEPYHFEPEITRALDVLLILHADHEQNCSSSTVRLV
GSSGANIYASISAGINALSGPLHGGANQAVLEMLEAIKASGISVKEYVQQVKDRKAGIKL
MGFGHRIYKNYDPRAAIIKQHADRVLALKSGRRDLLDIAQELEQAALADDYFTERKLYPN
VDFYSGLIYEAMGFPKEMFTVLFAIGRLPGWIAQWREQRADPNSRIGRPRQVYTGVPERD
YVPMDDR
>PFR_JS14_2154	PFR_JS14_2154	L-glyceraldehyde 3-phosphate reductase YghZ	2473467:2474525 Forward
MLTDGVSYQPDPKRYDGRMIYRRVGHWGLQLPAISLGLWKNFGDAQPFETQRAVVRAAFD
AGVTHFDLANNYGPPYGQAEINFGTLLRTDLAPYRDELVISTKAGYDMWPGPYGQGGGSR
KYIRASLDQSLARLGLDYVDIFYSHRFDPETPLEETMMALDRAVRSGKALYAAISNYPAA
ETAQAAQIARELGTPLLIHQARYSIFNRWVEGGGDGAARESLLDRAEAEGMGVMAFSPLQ
QGLLTSRYLQGVPDDSRARHSSDFRQSWLDEDTLAQVRALNDIAAARGQSLAQMALAWLL
RDERVSSVVIGASSVKQLANSLGALKNLYFTAEELAAIDAHGARPGHELWSD
>PFR_JS14_2155	PFR_JS14_2155	Protein of hypothetical function DUF1345	2474668:2475309 Forward
MRRKLGDSLHMRLWISIAVGVAVGVGTLWMGHSPGSLMLGWVVAATLFTVSTWYLVFRMS
DDDTRDHAQENNPSAGVSDTLLMSACMASIVGLALLMFGAKSKGQLVPDSIIGVLGILAS
WSAIHTLFTLRYAYVYFRDGGTGINFNGDDRPCYIDFAYLAFTIGMTYQVSDTNLGTKEL
RRIALHHALISYLFGTVVVASMINMFVQVAAGG
>PFR_JS14_2156	PFR_JS14_2156	Putative RND superfamily drug exporter (Precursor)	2475395:2477899 Reverse
MAKLLYRLGRGAAHRAWAVIICWLIVLAAAGGAYAAFHGTLSTSFSIPNTETQQVADSMK
QALPQASGGSERIVFTSDSGSFSDTQKAQIADLLAQVDKKDGVTGTINPFQTADQRAAQA
GQLADAETQLQAAQQQLDAGRAQFDAAQQKLTSAEDQAKAAGAYDAMATQFQAQQAQLDA
QKSKIDDSANQLSAQQDKATAAKSLIDMSQGLRTVSQDGSSAIATISLEKETMEMDSGQK
QAIRDVIDDTSIPGVQTTYSNGLAFDIGGLGGMEVAGVAVALVVLVLMMRAVLPAITPLI
SSLVGVAVAVAGSLALSGKVTMMNVTPMLGLMIGLAVGIDYSLFILNRHRKQLLAGMDVR
ESIGLAVGTAGNAVVFAGSTVFIALLALNITGIPFLRVMGDVAAAAVLVAVLVAITFTPA
LLSLMGMHALNKKARKSVGTPEQAAPVIRPMRTRNAVLRAVIALAVLVVMAIPAASMQLG
MPTGAQEPTDSVQYKNYKTIDEKFGAGVNGPLMVVATLPQAMSADDEQVVEAKIGQQLAA
QPDVAAVAPAAVSDSRTVVAFQVIPKGGPNDQSTEQLVHDLRGLSPTSDGTTLGVAGQTS
MSIDVSQKLSDALAPYLIVVVGLSLIILMVVFRSILVPIVATGGFVLSLFAALGATTAVY
QWGWLGSLFGVHDPSPLLSFAPTIIMGVLFGLAMDYQLFLVSGMREAYEHGVEARVAVRS
GMRIAAPVVRAAAIIMISVFAGFIFSPMNAVRPLGFGLAFGVLFDAFGVRLFIMPALMHL
MGRTAWWLPKWLDRILPNVDVEGTSLERTHNVLVSDSAHDPAASHGKGANPATQ
>PFR_JS14_2157	PFR_JS14_2157	Transcriptional regulator, TetR family	2478111:2478830 Forward
MDARIVRTRHALQGALLELARDTPLDDITVGDITKRAHVNRSSFYLHYTDKDTLLADALE
MQIDRSTGDEDLRTDSPEHMPTGLTDYLNHVQEYASLYGRVLNDGGSGVVANRLRSHVHD
IVERALNESDADPFPNLPRDIAAAGVAGLAVGIITAWLGRDPMPPVHTAATWIWDMLVPV
AGVAGRPSDAASSRDDGSTENAASSDDGAGPNPATPSGGDSGYLALGLRRPTRKSSIPG
>PFR_JS14_2158	PFR_JS14_2158	NAD-dependent epimerase/dehydratase:3-beta hydroxysteroid dehydrogenase/isomerase:NmrA family protein	2478888:2479544 Forward
MEKKTTTKNVTVLGAHGQIARIVIERLLAETDDHLTLFLRDAARLGSVDAARETVVDGDA
TSTDDLAKAVRGADIVYANLAGKIEAEADAVVAAMRAAGVKRLIWISTLGIYDEVPGAFG
AWNHKMLDGGYLQPYARAAATIEASGLDYTIIRPAWLQDEPTVDYETTQKGEPFKGTEVS
RASVADVVVHLINQPDRGIGHSVGVDKPGTDGDKPSFY
>PFR_JS14_2159	PFR_JS14_2159	DoxX protein	2479621:2480052 Forward
MSHHRQAHATHDASSRTRRHPVRTAARWGLAGALAFTGVGHLSFAREGFAVAVPDWMPSS
KDATVLASGVVELALAAALASGVQRKQVGRATAAFFAAVFPGNVHQYVKHLDASFLNSDQ
RRLVRLYFQPLLVAWALEATRED
>PFR_JS14_2160	PFR_JS14_2160	Respiratory-chain NADH dehydrogenase 24 Kd subunit domain protein	2480105:2480896 Reverse
MAAEERGWQVVLVSMNATSNAAVQAWGEQLPGVASASLEGDGTPLVEVLDELAGVDASPG
AGPEGRASTSRRAPLGSSGVGIRLIGCQPGGGATSVSWLRRVAGHWLRTRRDGAPAVVLQ
VRHERHDGAEPPDVGPLCGPVAVASAPGEFPCDDSPSGARWDPISGEEAPLHSPAWQAPP
PFRRHLLVCCGVRCNAQGSREVVESMVRTAKELGVVHDEVLITRTLCLFPCNQAPVVVSY
PDNQWHGGVTPAQAAEIVRRAVE
>PFR_JS14_2161	PFR_JS14_2161	ABC transporter (Iron.B12.siderophore.hemin) ATP-binding component	2480886:2481617 Reverse
MTRLACRGLGWQVDDRWIVRDITTEVAEGCCTALVGMNGSGKTTLLQLLCGLRKPSRGQV
LVDDRRLTDMSRREIARTMALMEQLPQARVALTARDVVALGRIPHEGRWQLNAHGARVDD
RSWNTLSGGERQRVQLARALAQEPQVLMLDEPTNHLDLHHQIALLRIVTSLRLTTLVVLH
DLDLAAAFADRLIVLDDGHLVAQGPTDEVLTAQLVAERFAVRGQVSRTDRLRFSWQGLVS
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DGG
>PFR_JS14_2162	PFR_JS14_2162	Iron chelate uptake ABC transporter, FeCT family, permease protein	2481614:2482720 Reverse
MTRTAADARADAGGSADAGSRTHAGHARTAHWLWLGVLVVALAVSVVMALGIGSVPLSPG
EVVGVIARRLRLITGADVTPLADQIVWQLRLPRVLASIAAGAVLAVCGAILQTLTGNALA
DPYLLGISSGASVGAVFVLEIGLSVGLSQSVLMMGAAFVGAVLAMLLVLVLATGRGGELP
PARTVLAGVAVAQVCAAITSLLIMVFGGTTAARTAMEWMLGSFAGARWLAAGVLAGVALV
TLVGAMGYSRTLDAFSFGDTSAASLGINVTRVRWGLMIFTALTTAMTVAFVGPIGFVGLT
VPHIMRLLVGPRHAGLLPLTALGGALLLLWSDTAARSITGNTEIPVGVITALLGTPVLAV
LLRRQASQ
>PFR_JS14_2163	PFR_JS14_2163	Iron transport system substrate-binding protein	2482728:2483813 Reverse
MSAYSRPNSPRPNSVRSSSGRSSSARPNVARRLPVRSRLVALGLGLAIAATGCAGAPGSG
SSSASATGGAFPVSVNNCGRTVTVKQQPTRAVALNQGAIEEALALGVQKQMAGTAYLDDK
VADKYKDAYASIPVLADKYPTKEVFAQAKPDFALASYASAFSDKAVGTRDELEQQGIPTY
LDPFACDNKADRAQVSFDNVWSSLGDIAKLFGQPGNATTVIDAQKTELDAVKQAKAGDGQ
KVFWWDSQTDTPFTGGNAGGPALVMQAVGATNAFADVDGAWANVPWEKVVAADPDVIVLA
DASWSTAQSKIDYISNDPALKNLKAVQNKRFITVPFSQTTPGATLVDGAKSVSDQLAALP
R
>PFR_JS14_2164	PFR_JS14_2164	MscS transporter, small conductance mechanosensitive ion channel	2484229:2486004 Forward
MIPLEVSVKFPETVIEIVVTLVLALVCRFALRKVIDRAVARATQRQGEHGLLAMGRSSSV
VATTGGVNTNRSMQRAKTLGSVLKSMTDVVLIIVVVLMVLNSLNINIGPALASAGIVGVA
VGFGAQSLFKDLFSGVFMLAEDQYGVGDIIEVNKLKGTVRSVGFRVTELQDFNGEVWYVR
NGEISTVGNVSQGFTSSLVTIPVSVDESPKLVIRLLARMLKKMDSEPDWHNKMLEEPSML
GLSALDATTASYQISIKCPANSQWDVEREIRSRALSTLSQAGVRMPVTRVATVPPHTADE
TMAMPHSRRRRLGQLAQQRMAERHATDQSATGRTGTEPAGEATQEPSAEQGTPPTGEVIR
RPAEPGQAAADSRPTDAAQAAAGPASDQVVPADDTLPAPKVKAADTGQLRKARAWLDHGA
DRSVRWVAQATPGASEVHDMTADQTVLMSADDVLRRPDQADGTGRTHRSTAASGTTASGT
AASDTAASGSGTDGAKPTGDRPGADPSDPRTGAADSGATKSTAAGSSDAKGDDEASKTRS
LRAIDTGHQPGTDPKQGTGDPAPQSGDRSDPSEPPADQTRRLFGRRGRKRD
>PFR_JS14_2165	PFR_JS14_2165	TRNA adenylyltransferase	2486059:2487549 Forward
MSDSSQALSVAQRHAVDELLRITPVIDELGALFHKAGEELYLVGGSVRDALLGRLGHDLD
FTTSADPDTTERLLHRFSSAVWTVGKEFGTIGASKKSNGHELQIEITTFRADAYEPDSRK
PIVAYGDNVQDDLVRRDFTVNAMAIDVHSKAFVDPHGGIRDLAAKVLRTPTAPEISFSDD
PLRMMRACRFAAQLGFKVDPVTFNAMKAMHERIEIVSPERVRDELSKLLLADAPRPGLNL
LVASGLADIVLPELPAMRLERDEHFRHKDVYEHSLTVLDQAIALEKARDYKDGKPNPHHQ
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IEQHLRFHGYGEASWTDSAVRRYVRDAGDQLEHLHILTRSDCTTRNARKADTLRRAYDEL
EARIDELAATEELKSIRPDLNGDEIMTILGLAPGPQVGRAYQHMLSVRMDQGPLDHDAAV
AELKRWWATQPHPDAG
>PFR_JS14_2166	PFR_JS14_2166	MFS transporter	2487986:2489476 Forward
MDFRNERHLIHVPGTDRVFNRLKVLIVLMIPLAMSLMSISSINVALPTIETSIGASDTSV
QWMLSGYALVFGMLLVPSGRLGDAIGRGTVWITGVSIFSIGSLVCGFASTPGLLNIARVA
QGFGAGVLNPQTIGMIQQYFRGEGRARAYSVFGLVIAASVAAGPLFTGLIIRALGAQNGW
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TQFLGGTSIFVLVALFLQDGMHVSALQAGMIGLPNAVLSAIASLWCGRQALTRGRNLVIV
GLSCILVGVLGSIGMAKLIMEHGVNFWWLAVPLSLIGIGNGCMTGCNQTLSMLEVPPKEG
GVAGGVKSTTERVATAIGNAVITAVFFTLVTKGWAVALTWAYVVIAVIIAVAIGLAIYDR
VTLGRGAPPTAHSVTV
>PFR_JS14_2167	PFR_JS14_2167	Hypothetical protein	2489634:2491730 Forward
MSPRHADDASGDRRRTGPQARLPRWLAGLLCIVLTTLSLGVVHPAVRADDATLDVTFTSM
SPSAVTDEGDLTLTGTITNKGSATVNRPTVHMWRNRAPLTNADALNFLVKNQSSEPMGDV
VTTSAAAQTVASLTPGASANFTVRAAFSGGGDPLALVSPGNAYLVGVRVDNSAGTQVGSS
RTLISYPGTSKYDATTVAELASAPSYVGTDNGKPVFTDDHLAAEISPDGRLGQLVQLAEA
DNVSSVIDPLLVDELTAMASGYEVRSTDGTRVPGRGQDAATSFLRRIQGVAANGRSYRGL
YGMLGVSAAASASRHDLLVSAAQQSAGNQTLKALPLAITATGNALTSNDLEYLASAKPTL
VLAQGIDPASPVRQATVRQGAPTQLTVVSVQTTLGDGGPAPAPDQDLVHRVGRLQSEQLV
RAGAYGTSVHLVTGGDAARAELAAAIGRVRVPLQELLKKQTTPVALQTGNTDEISAPGSL
TGAESTAQTQLGFYKALTGEDAGIDTELLITRVWSGSFADADAAEAYLNTAMATVSAALQ
SGGVEVHMSEKLVVPSKSTSLPISLTNSMSIPVRVRVHFDSDNSSRIDIDDTDVIRLDPG
ESATVRITPHASGSGTVQMDAMVMTAGDQAHQLGDSVRFTVQANNVGNIGWIIIIASGVV
LLGATALRVRQVRHERAQQHTPADDDPDVPFDPSPLDD
>PFR_JS14_2168	PFR_JS14_2168	Hypothetical protein	2492153:2494204 Forward
MSAESQPELPGARPYPRNLIAGDLVANRYQLEAQLNQWDAGVTWRAIDRTLSRRVVVHLF
NPHSPETARALEAARRAAVAVDSRFVRVLDAMDGDQPFIVTEFATGITLRSLLAHGPVTA
LQSAHIVRELADALAPMHAEGLFHRRLNPDTVVVTRTGNVKIMGFLLEAALAGATISSSD
NWARQEAEDVRALGKVLYACLVARWPIDPSLAQTSQWGLPAAPMSAPGPDGPHWAPPTSV
DPRVPPTVNAICIQSFDPRPDSVPLRTADEIVIALGRVLGTAEADEVLGRRIRALPADEA
GENAHIGLHAPGIDELPQRAATPDDDGPATQRMPPVTGHDDPNWPGGDDPNWPFGADDSS
PLGTTDTGTRTPLTGAQAAAAGSAAPRPPAPVGTVQTFITALPEPEDGGAPHPDRRDSDR
GDLDHRHSDLRDFDPDRTDPRLRRLRQSDADAFDDDDDPDDDLTIDVSGKLVGPLPDRDA
EPRRLATDARAYRLARWLIPLGVVLMLVIALTGMVRSCQATSAAKAAQAKVVAPASVVEF
DPTADGGEAAESPGEVSLATDGDPSTAWHTQEYGGSAAFGGVKPGSGLLLDLGRARELSS
VTLTLIGAPTGVQLLVPHDDANPSMSTVKDWTVASRADAAGQSVTLTPDKATSTRHLVVY
LTSLPQLTNGRYQGAIAEISVNS
>PFR_JS14_2169	PFR_JS14_2169	Phosphoglycerate mutase family protein	2494280:2494999 Forward
MKLLLIRHGQSANNALSGANHPVSSQYPDPTLTDLGRQQAETLAHAFTDGLLPRPSVLLS
SPMTRAVQTAAPLADELDMPIELETQAHEVGGIFQSVQGEPGSFQGASRAELADISDRLI
FNEDIHDEGWYRLGSHVETPAEGQGRGKRLYRSILERYGNQDGVVALVCHEWITNYVLRA
ALGLSDPEGEPDPWFSLPNTSSTFIQTGLPLPGPYEGGGTAMIWWVGRFDHLPDEQVSR
>PFR_JS14_2170	PFR_JS14_2170	Extracellular solute-binding protein family 1 (Precursor)	2495128:2496447 Reverse
MRLQRRGLLAWAGAAAAAATLSACGGKSSSSSTLSSACTPSPTPTWQDAKSHGSGRLNML
SALYQDQASQDSYANNMLTGFFAGTGYSLAATYTSLDKLPDKVITSLAAGKLADVLMPGQ
GWVPVLERQNALAEMPADITDGLNLDQRLMTGCYWGDKLFALPYALDLTVIGYRTDVLAD
AGISAPPRTLDELREMAKQLNAPDHGGFDVFGAGVVHLWAMLVGSYGGSLFTPKGGLAFN
DGTGVKALDYIIGLVKDGTADPAKIPTGGAQPLFIQQKTAMSPMSSTLWPALRRSHLDDE
GHLGFFPLPPDQASKDPVVLQTGTQLAVSRQSQFKEVAFQFCQYALQSQPLLSAVSMLPA
VPPRSDVIAGSQLAGNRVMSAGLANVKYATASLGGCPAWLDLEPVIEGQLMAAIRGQQSS
DMTVGNLAKVVSDSLSRAA
>PFR_JS14_2171	PFR_JS14_2171	Thioredoxin-disulfide reductase	2496866:2497843 Forward
MNDEIRDVIIVGSGPAGYTAAIYTGRAGMRPIVLEGSVTAGGALMTTTEVENYPGFPDGV
LGPVLMSDMRAQAEKFDAELIADDATKIELGGDIKKVTDSEGNVYRARAVILAMGSAYRH
LNLPEEEEFSGRGVSWCATCDGFFFRGKEIAVVGGGDSAIEEATFLTRFADKVTLIHRRD
AFRASNIMAKRALDNPKIEIAWNSEVVGMSGDGTLNALRLRDTATGEERELAVAGLFEAI
GNVPRSELVKGQVELNPDGYVKVAGDSTLTDAPGVFACGDLVDHVYQQAITAAGTGCRAA
LDAEHYLSALMDENSDQATEALANA
>PFR_JS14_2172	PFR_JS14_2172	Thioredoxin	2498017:2498340 Forward
MAQPKDVTDATFSDEVLKADKPTVVDYWADWCGPCKQLSPILDQLAEEYGDKINFVKVDA
DANTKVATDQGILGLPTVQIYQNGEVVKQFQGGKPKSVIVKMLQEFV
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>PFR_JS14_2173□PFR_JS14_2173□Putative redox protein, regulator of disulfide bond formation□2498340:2498786 Forward
MSGEQTKTSRVGVNLKRVSPVHYEVTNGRGSTISVGHGDDVFSPVELLLAAVGACSSIDV
DVVTTRRADPEKFDVSIAGDVEKGPEGNRVKDVDLNFSLSFPDTDEGRTAQSLVARLVKL
SHDKDCTVGRTVMLPTELHSAVDGEVVA
>PFR_JS14_2174□PFR_JS14_2174□Chromosome partitioning protein ParB□2499081:2500064 Reverse
MSARPGGLGRGLGELFQRTDIQAAEEPREPASEQMADGSYYAELPVAQITPNPKQPRQVF
DEDDLQELTESIKEVGLLQPIVVRKLDATHYELIMGERRLRAHQEAGIAQIPAIVRATDD
ESMLTDALLENLHRVQLNPLEEAAAYEQLMGDFGITQDELARRLKRSRPHISNTIRLLKL
PITVQRRVAAAVLSAGHARALLALDDPLAQERLAQRIVAEGLSVRATEEIVALGGDEKPR
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AGSGAAPRPSNQADPWDFLIPPHGHTK
>PFR_JS14_2175□PFR_JS14_2175□Putative partitioning protein ParA□2500061:2500900 Reverse
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GNASTALGIPHQEGVRGSYELLLDEVPVADLVVDSPEAKGLKVVPATIDLAGAELELVSK
VAREQRLSRAIRDYEADHDVDFVIFDCPPSLGLLTVNALVAASDILIPIQSEYYALEGVQ
QLMRTISLVKRQLNSDLELWAVLVTMYDARTRLSAQVAEEVMAHFPKETLHTMIPRSVRI
SEAPSYGQSVLNYDPNSVGSNAYRKVAQELSQRAMKEQE
>PFR_JS14_2176□PFR_JS14_2176□Ribosomal RNA small subunit methyltransferase G 1□2502760:2503530 Reverse
MGDPMDDARHAAARRDDGRVERTGGPPEDAPHGVHAARERRVEQARDDDAGREQQAAQGA
RALFGDQFESMSRYVDILVGQGVEWGLLGPREPERIWSRHIMNCAALLEVIGEGVDVLDV
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DVVTCRAVARLPKLLGWTMPLFLPDGELLALKGESIDEELADSADIIARNGLSAQVMQVR
ATPEVDVAHILRVQAG
>PFR_JS14_2177□PFR_JS14_2177□Hypothetical protein□2503553:2504518 Reverse
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>PFR_JS14_2178□PFR_JS14_2178□Membrane protein OxaA□2504570:2505661 Reverse
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KKK
>PFR_JS14_2179□PFR_JS14_2179□Putative membrane protein insertion efficiency factor□2505672:2506022 Reverse
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>PFR_JS14_2180□PFR_JS14_2180□Ribonuclease P protein component□2506019:2506447 Reverse
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>PFR_JS22-1_1□PFR_JS22-1_1□Chromosomal replication initiator protein DnaA□1:1467 Forward
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IKQNSARR
>PFR_JS22-1_2□PFR_JS22-1_2□Drug resistance transporter, EmrB/QacA subfamily□1442:2911 Reverse
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>PFR_JS22-1_5□PFR_JS22-1_5□Sulfolipid (UDP-sulfoquinovose) biosynthesis protein□4962:6209 Reverse
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GASTQAAGPSTVQG
>PFR_JS22-1_7□PFR_JS22-1_7□ABC lipoprotein transporter, permease component□7627:10185 Forward
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>PFR_JS22-1_17□PFR_JS22-1_17□Family 2 glycosyl transferase□23012:24934 Reverse
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>PFR_JS22-1_19□PFR_JS22-1_19□Alpha-1,3-rhamnosyltransferase WapR□26730:27611 Reverse
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>PFR_JS22-1_20□PFR_JS22-1_20□Hypothetical protein□27672:28124 Reverse
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AHDEEAAE
>PFR_JS22-1_22□PFR_JS22-1_22□Glucose-1-phosphate thymidylyltransferase□29031:29900 Forward
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LIYDIFDAELLIWVVRAAHRREVYDR
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>PFR_JS22-1_31□PFR_JS22-1_31□Putative conserved lipoprotein lppS□36962:38161 Forward
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    >PFR_JS22-1_54□PFR_JS22-1_54□DNA gyrase, B subunit□65075:67117 Reverse
    MSEQLNESAVTEKTEDEKRMDALTLTDTEDDSVDGEYGADEIQVLEGLEAVRKRPGMYIG
    STGERGLHHLVREIVDNSVDEALAGYADSIEVTLLNGGGCRVVDNGRGIPVAEHPAEHIS
    TLTLVLTVLHAGGKFGGGGYKVSGGLHGVGSSVVNALSSRFDADVYRDGYHWHQSFTLGD
    PVAPVERLEETERTGTTITFYPSADIFETTDFSYETLATGFREIAFLNKGLRIAITDERT
    DHVDEDGKQLHDVFKFDNGLVDYVTFLNGNRETMTPVIDVEAHAPEVGMGVEVAMQWNTS
    YVTSLHTFANTINTREGGTHEEGFRAALTTTINKWGENWGLIKKREDRVSNDDIREGLTA
    IVSVKLVNPQFEGQTKTRLGNTEARGFVQRAVNERLGDWMEQNPGDGKLIVRKAQAAASA
    RIAARKARDMARNRKGLLGSGGLPGKLADCSSNNPEECEIFIVEGDSAGGSAKGGRNPRI
    QAILPLRGKILNVEKARIDRALQSETIEAIISALGTGVHEEFDINKLRYHKIVLMADADV
    DGAHIRTLLLTLLFRFMPELIDGGYVYLAQPPLFRLRWTNAPHELAYNDGERDSLRDKGL
    EAGKKLPSVNPIQRYKGLGEMDAQDLWTTTMDPDNRILLQVNLDDAARADQTFSILMGED
    VEERRRFIQRNAKDVRFLDV
    >PFR_JS22-1_55□PFR_JS22-1_55□Hypothetical protein□67538:68014 Reverse
    MILFILGGFGLITTLAGASMTRVTVLGVAGPLLLALLMLAVAVYLTVNGKRRRQEEQTGI
    TWMNTELRSIVAAEAAQRVARFGFDPLAVPQGYTGFAWGATFDPSAYADQLMWMIINGPV
    NFPEPDELPALVMPDVLAPNPAFRPEVNAALADFQQQS
    >PFR_JS22-1_56□PFR_JS22-1_56□Uma4 protein□68037:69344 Reverse
    MSHPTFTTPCLTTFCGLDELGLEAVGQRLDPDRAVIECRVVEPDRWCRECGCEGAPRDTV
    IRRLAHEPFGHRPTTLLIRVRRYKCCGCGRVWRQDTTAAAPVRAKISRGGLAWGLAGLVL
    DHLSVTRVAAGLGVSWSAANDAILAEGRRRLIDDPARFEGVTTIGVDEHVWRHTRHGDTY
    VTVIIDLTPVRDKTGPARLLDMVAGRSKAVFKTWLAARPKPWREGIEVVAMDGFTGFKTA
    AAEELPDAAPVMDPFHVIRLAGDALENCRRRVQHDVFGRRGMKGDPLYQARRTLLTGAGL
    LTDKQQARLDALFAEDRHVEVEATWGIYQDMITAYRDKDRGLGRFFLAHTIDKISASVPE
    QLVEIRKLARTLTQRASDVLGYFDRPGTSNGPTEAINGRLEHLRGTALGFRNLSHYIARS
    LLEAGGFRPALHPRS
    >PFR_JS22-1_57□PFR_JS22-1_57□DTDP-rhamnosyl transferase RfbF□69508:70422 Forward
    MKFAAVVVSYNRIELLKRCLDALEHQTRPLDEIIVVDNGSTDGSADYVAAEHPGITLFRT
    GENLGGAGGFAWGVEIALDHGLDGAWLMDDDAEPELDAFQPLADRFESMHPEPSFLASLV
    TAGRDVFNKRNPPVISTDAKRQVEANEDSGIAIDTATFVGVLINLHYSAKTYLPLSDYFI
    WMDDSEYTYRLSRMANALTIPESQVNHPDTETLSNDMAGRLFYMVRNRLWFIRERESSKT
    RDLVDILDVAQISLGQFFVAKDKRLWLDSVGRGLAQGLFKRPKHRKPGSLLATLTPDQRA
    AIGS
    >PFR_JS22-1_58□PFR_JS22-1_58□Polysaccharide biosynthesis protein□70518:71708 Forward
    MVTTLMPAVVGLVAMPVIIRGAGAHAWGVQSSVQSAAVLFGVAVGFGWSVTGAAETARLA
    PVKRPQWFADSLVSRIYLFCLIAPVMVLVMWLINRDYLSLVAVASVAYLVPYVGADWYFV
    GEARPSRLFRLNALPQTIGLAVSVVAMLATNSIVVTVAVQLASNICAVVLSAAVIVRSSS
    EPLHFDWSIPRAFGRLKGQRDPFITAGTSALYVASPMLIINLFQPGALALYAMGDKLFKS
    SLTVFAPVLQVVQGWLPEGGPENLGHRIKQAARLSPLVSIAGAACIFALGPWAARLLSHG
    EIALGLDISLPFAVVFAAVSVTQVFGLAFLVQLGRSAALAKSTVVGAVIGVPMIIVGAVL
    FSAHGVAWAVALSEITVLIYQLAVVIAELRRRRATA
    >PFR_JS22-1_59□PFR_JS22-1_59□Fused dTDP-4-keto-L-rhamnose reductase and dTDP-4-keto-6-deoxyglucose-3,5-epimerase enzyme
involved□71775:73193 Reverse
    MALDYEKKLAATATPIPGFLVFDLTVHGDNRGWFKENWQRAKMTALGLPDFGPVQNNISF
    NDEVGVTRGIHAEPWDKFISVATGRVFGAWVDLREGPSFGTVFTCEIDPGVAVYVPRGVG
    NAYQTLEANTAYSYLVNAHWSPEAKYTFLNLADETVAINWPIPLSEAILSDKDKGHPRLD
    AVTPFPPAAPRVLVTGAHGQLGRALMTQLPEAGFVPVGVDLDELNIADRTSVDAYDWSDV
    DIIVNAAAWTNVDGAETPEGRPQAWAANATGPSNLARVATKHGLTLVHISSEYTFDGTHA
    PHTEDEPPSPLGVYGQSKAGGDAAVESTPRHFLVRTSWVVGAGKNFVATMADLAARGIAP
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AVTPISTEEYFAGKSVAARPADSTLDLSKIEGTGFQPPAMDQRLQEYLATRD
>PFR_JS22-1_60□PFR_JS22-1_60□DTDP-glucose 4,6-dehydratase RmlB□73198:74196 Reverse
MARLLVTGGAGFIGSNFVHHVINHTDDTVVVLDKLTYAGNMGSLEGLPADRYSFVKGDVC
DRELVDKLVAGADAVVHFAAESHNDNSLLDPAPFVQTNLVGTFSLLEAVRAHDVRYHHIS
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>PFR_JS22-1_61□PFR_JS22-1_61□Hypothetical protein□74329:77727 Reverse
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TGTHIVHGGINDTYTSLGSSAFVDLGLATGDETAVTNGWAQQFEKGSIFWSYATGGVVVH
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FAALANAPAALGMPTADEVDLGNGAWMQQFQNGRVYWSSAAGGHAIKGGIGDTFAAMGDS
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LANEVGLGNGAWMQQFQNGRIYWSGAAGGHAIKGGLGDTFAAMGDSAYGLLGLPTSDEIS
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SNSANRYYPAFLTTNDRDFVRAIAAAGYATDPTYANKIISIMDRYNLYQYDV
>PFR_JS22-1_62□PFR_JS22-1_62□UDP-galactopyranose mutase glf□78020:79207 Forward
MQADLVVVGAGLFGLTIAERAANELGLKVVVLDRRDHIGGNAYSEKDEATGIEVHRYGAH
LFHTSNEKVWEYVNQFTDFTGYVHHVYTNHQGEVFPMPINLGTINQFLRSALSPAQARDW
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LDMHMAIGSALSMYENKVRPHFANGEALVSGGVDE
>PFR_JS22-1_63□PFR_JS22-1_63□UDP-galactofuranosyl transferase GlfT2□79204:81240 Forward
MSIDTAKAPMASDFSEVSVSATQSNGFRVATRVIFPLDADLDVMPLYIDPADNESEASLH
PEDVRGRDSVVVRAGARMSLGSYFNAFPASYWRCWTVVRTVRLVVNTSGAGSIVVYKSNA
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LVTNAEGTGIAWYRREPEEMRRMLAESAANQARILTEWPKLRQEYRDALPRLTSFVLWEE
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>PFR_JS22-1_64□PFR_JS22-1_64□Polysaccharide ABC superfamily ATP binding cassette transporter, membrane protein□81212:82129 Forward
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FAQEL
>PFR_JS22-1_65□PFR_JS22-1_65□O-antigen export system ATP-binding protein RfbB□82129:82908 Forward
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EVTFDGGVDGAVDFLRSTE
>PFR_JS22-1_66□PFR_JS22-1_66□Hypothetical protein□83059:85374 Reverse
MRVALLCDIGHSVYHVGNEATAIASAAQLRKRGHEVVMISHDERPEAVDPAAAATTEIIP
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KVTRMLTELQGQLQATEEAAREACAANVARRAVRVARGYVTRAAGRITRRR
>PFR_JS22-1_67□PFR_JS22-1_67□Amylovoran biosynthesis glycosyltransferase AmsE□85519:86376 Reverse
MTAFSVLLPVYAGDEPEHFARALTSISVDQTLRPNEIVIVRDGPVPSALEEVIAQASEGS
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>PFR_JS22-1_68□PFR_JS22-1_68□DTDP-rhamnosyl transferase RfbF□86373:87335 Reverse
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>PFR_JS22-1_69□PFR_JS22-1_69□Thioredoxin□87559:87975 Reverse
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CAPCVATGRLLSGLTAQRDDVNHVEIDGEERLDLVREFGINRTPTVFLLDPDGAIRYRFV
GPSRKAEFVDALAELQAA
>PFR_JS22-1_70□PFR_JS22-1_70□Integral membrane protein□87980:88489 Reverse
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AGAVLGVSRQPYGLFFRSVVRPRIAPASEFEDAAAPRFAQGVGLAFAIAGLAGVVFSLPV
LFYVAVAFALVAAGLNALFGFCLGCEMYLLGKRLFGSSRPSTGNATQTG
>PFR_JS22-1_71□PFR_JS22-1_71□1-acyl-sn-glycerol-3-phosphate acyltransferase (Precursor)□89608:90405 Reverse
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HFDGPLVMLTMPKRLTKNLATGAAADYFFNHWYKAFGTQLLMNAFPVDRGSMHGHRGLAS
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GAKKDIEAEQQKKKHSRDKKHRDDE
>PFR_JS22-1_72□PFR_JS22-1_72□Oxidoreductase, short chain dehydrogenase/reductase family protein□90405:91301 Reverse
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VARDPQRLGSAARAVRNKFGVQVHEFSADLSDHDDIARVEQVFADRPIDLLVNDAGFAAH
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LDQTTAEAVLDVLFATAQRTGTALVVVTHDDQVAARAQTRRELDGGRFVA
>PFR_JS22-1_79□PFR_JS22-1_79□ABC-type antimicrobial peptide transporter, permease component□97941:99089 Forward
MRSFGRELWWDLLGNKTNFWLSCLALFVALFSFIAVVSTGTLAHDSLLAKTLMVDGVPTS
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>PFR_JS22-1_81□PFR_JS22-1_81□Hypothetical protein□103202:104770 Forward
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LSASGGVNLYGDYAYSDSRGFKYDNTYKSESTENWGILNDNQLEGQDNRSYSANVVINGA
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MQAKGIAAGWDDGTYRPLNDTNRDAMAAFIHRAVNQGIITLK
>PFR_JS22-1_82□PFR_JS22-1_82□Hypothetical protein□104873:105592 Forward
MSSEDSTQAGPQRGETPDGGNRKKALIIGAIVVAVVVIAAVVFFAVRGSGNSGSSKSASA
AASTSVAQASGDMGSASASGSYSGVMRSMIDEEKSAGVPSLKQEHVDIPPAENGGTGYCG
RIQDFKKFTDANSQAGTVQTAQELNGRWTEMANAAQKISDEAPDQGAKDAWKKYADATNA
VNNAIGPVSNPDDVAKKLNDQGFATAFNNFNNSWNDLVKNYKDAIAGSCSVTLVGQATA
>PFR_JS22-1_83□PFR_JS22-1_83□Apurinic endonuclease□105823:106626 Forward
MALLIGSHVEQEDPIAGARVRGAEIAQISLGDPRSWKGPVVEFPGGAPALREAAQQANLP
LVVHAPFVINVASTNNRIRIPSRKLLQKHVDAAAEIGALGVVIHGGHVVKDADPADGFAH
WHKAVDGLDAKVPIFIENTAGGQHAMACTLEAIERLWDSISTAAAFAQVGFCLDTCHAHA
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PAVVETPGGAEDQAADIVWLRDRIAQL
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>PFR_JS22-1_84□PFR_JS22-1_84□AMP-dependent synthetase/ligase□106623:108629 Forward
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AALMYSGVEKGDRVGFYSRNRPEWTQVDLACQFIGAVSVPIYATDTVDEVVHIANDCGMV
VAFAGRADEAERMGQASERIPSLRRVISFDSCPRTDVTWLEYFAPSDRPVPEQVVSRINA
RLNKASGDDLFSIIYTSGTTGAPKGVKLAHRAIMSELGALHRSFPISTRDHSLCFLPLSH
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APLRRETELFFGAAGLQILNGYGMTEAAPLISYNTHSAYRVGSMGRVMPGGRIKLGDKHE
ILYQGPNVMDGYWDNEEATREAFLTDDEGTWLRTGDVGRIDRRGFLFVTDRLKDIIVTEG
GKNISPQPIEELLQSDPMFEHVVVLGDNRPFLTLLVQPSMANLQKLAEALHIDYGHVSEL
FNNQNILDEIKKSAEALTKNLPKYQQVRDLRMSSEGFSIANGLLTPTLKVKRREVERRFR
GLIDEMYTKIGLHHDPKSASGRDPKSASGRDSRSASGRDSGTASGGDRGRTHGQAPRSTR
GGDSPTAR
>PFR_JS22-1_85□PFR_JS22-1_85□YdjK□108669:110297 Reverse
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MVIFRFILGLAVGGASATVPVFIGELAPTHIRGPLVARNELTIVTGQLLAYTTNAVIANV
FPGHPHAWRFMLVLCTLPALALFFGTFHLTESPRWLVSKGRRDDAEKVLWQLRHDDDVSE
ELNALEKHVQWTRREASTSFFDDLRVPWMRRITLIGIALAFLSQMTGVNSVMYYAPMILI
DTGLGTNAALVATIGNGVVAVCSVAFGSIVLLPRFRRRPMLLIGQIGVTCALALIGAMFT
VIAPGPTRAYLVLAFMMLFLFFMQGFVAVIFWLMLAEIFPLRIRGKAMGLAVFANWMADF
LVASLFPPLEAALGGNLFFIFAAINFATIFFYLKFIPETKGRSLEQLEEDFAMHGRALPE
SP
>PFR_JS22-1_86□PFR_JS22-1_86□Hydroxypyruvate isomerase□110443:111240 Reverse
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TGYLTGDLVTDTGRHDFLESARASIEVAHTLGVGRLNFHGTGLGDQGLPVAPVEHVTGAM
WTRATLTLQELARLGADASVVFTMENLNLPVDHPGTPFSHPDDTRALVSAIDSPALRMNL
DLYHAQIGDGQLIETCRQCLPWIGEIQVADVPGRCEPGTGEINYPRIAVALQQMGYTGVV
AMEAWASGDPDRALDAFIDAFTPAG
>PFR_JS22-1_87□PFR_JS22-1_87□Transcriptional regulator, LacI family□111732:112754 Forward
MSGSSMGRRPTMRDVARAAGVSQSLVSIVFRGAPGAGAQTRDRVLAAARELGYVRDESAR
SLRASQSTSIGVCFQTRQPFHHVLLDGMYAHTAGTNHPLVLSAVSDARDEATAIRGLLAY
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IAVERASQRIHPSSPPTDPHGTLVPTHLVVRSTTGEAPRR
>PFR_JS22-1_88□PFR_JS22-1_88□Isochorismatase family protein yddQ□112945:113517 Forward
MTDKALLVVDVQNDFVEGGALGCEGGKAAAAAITQLIAGLDPATELVAASRDDHTPGSDN
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SLDQALRDAGVTQLDVCGIATDYCVRASALDAVRLGYQVRLLGALCAAVNPESGARAVDE
MRDAGVTIVA
>PFR_JS22-1_89□PFR_JS22-1_89□Serine/threonine-protein kinase PknD□113898:114917 Forward
MTHVSVTRPRRIGALALAAAAAVALSACGASGMLAQSPPTDADVATGTGPSAGRPAATRS
ASASVKADPALAALVPQEIRDSGELVVDSNPTLPPMSFKADDGTVAGVDADLAKAIAGRL
GLRPQVQPYSLDGSEWHVLGRSLGDADISVSSSVITASSRWNWKNVQYMKTGLRWIVRAG
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TLTSLADDGTYGRILEKWGLSAYASSEFPVDPSTPEVGE
>PFR_JS22-1_90□PFR_JS22-1_90□ABC-type amino acid transport system, secreted component□115053:115964 Forward
MFISRFRRAAAVGLAAVTALSATACSGSSSSSSSSASSALPSVSADSTLVNQVPEKFKTK
GTLQVGTNATFAPIEFMAEDGKTIVGLDADLSKAVASKLGLQVQMQQAEFGTIILGVTSG
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DQLAEKAKACTDAGKAAITQVVEDDQSKTTTDLNSGKSDAMLADSPIVDYAIEQSNGSLE
ALGDMYDAAPYGIVLAKGDTDMANLVSKALASLKQDGTYQKILDKWGNSAGGVDDFAVNP
TVS
>PFR_JS22-1_91□PFR_JS22-1_91□ABC-type amino acid transport system, secreted component□116131:117042 Forward
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TLEVGMDASYAPNEFVAEDGKTIVGLDADIVNAVAARLGLKTERVNADFGTIILGVSSGK
FDLGASSFTINTVREEQVNMVQYMKAGTAWAVLKGNPKKIDVDNVCGQTVAVQKDTTQVD
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LGDMYDAAPYGLLVAKADTDMADLVSRALTSLKDDGTYKAILDKWGNASGSVDDYPVNPS
VGG
>PFR_JS22-1_92□PFR_JS22-1_92□Permease protein of ABC transporter system□117124:118104 Forward
MSEQVSAGTTAQTAEKRPGRIDAVPVRHPWRWVAVAFIAVLVAMVVHSFVTNPRWDWAST
FEFLFRPPIIEGLIKGTILGTVIAMIIGVGLGVLLAVLRLSKNPVLKYASAGFTWFFRAI
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LGLSESAYMAEIARAGIVSVDDGQTEAAEALGMSHRKTMRRIVLPQAMRVIVPPTGNEFI
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FGRGFSNGDDELNPRARRLLQKTGEH
>PFR_JS22-1_93□PFR_JS22-1_93□Phosphate ABC transporter, ATP-binding protein□118106:118933 Forward
MSQGNASRSTGSASSRGEVAAVNAVNVHKFFGRTHVLKGIDMEVAPSEVVCLIGPSGSGK
TTFLRCINQLEEIDGGRIWVNGDLMGYYEKNGRLHVLDDAAKARQRRPIGMVFQRFNLFP
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LAMHPKLMLFDEPTSALDPELVGDVLKVMRDLAEEGMTMVVVTHEMAFARDVADRVVFMD
AGKVVEEGTPDQVINHPSQERTQQFLSRMVADPHV
>PFR_JS22-1_94□PFR_JS22-1_94□Hypothetical protein□119810:120691 Forward
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>PFR_JS22-1_95□PFR_JS22-1_95□Glutamine-dependent NAD( ) synthetase nadE□120904:123018 Reverse
MNFSSLYDQGFARVAAATSNTAIADPATNATRVIEHARRIAATGASVIAFPELCLTGYAI
DDLLLQDTVLDAALDALHTVADATRDLAALIIVGAPLRNGSRLFNCAVVLHHGDVLGVVP
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DHLVVPFGPDLIFRADDLPDLAVHVEVCEDVWVPVPPSSLAALGGATVLVNISSSPITVG
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LIRWVIASGQFDDRVGRVLQSILDTEISPELIPVAEGAKPQSTQDTIGPYALHDFALYYW
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RTAIPNGPKVMAGGSLSPRGDWRSPSDGNARAWLADLDKVPDQH
>PFR_JS22-1_96□PFR_JS22-1_96□Bifunctional PLP-dependent enzyme with beta-cystathionase and maltose regulon repressor
activities□123186:124391 Forward
MGSQMDLQDFVEQYAVERKGTDSLKWDALGQRFGNAGLLPMWVADMEFKAPEAVIEALRT
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RVSHGAFGYTYVDDAYFEAFDDWAARHNEARVQRDWVRFSTGVVSSFYWMVNAFTQPGDA
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>PFR_JS22-1_97□PFR_JS22-1_97□Ribose-5-phosphate isomerase B□124494:124940 Forward
MRIAMGSDHAGFELKEHLKGYLQGKGHDVIDVGTHSTESVDYPVYGAGAARKVAAGEADR
AIVVCGTGLGIGMAAGKVPGIRCAIVSEVYSAQMSRLHNDANALALGARVIGTGVAEEIV
DVWTTTDFLGGRHGRRVDMIEDPPALDA
>PFR_JS22-1_98□PFR_JS22-1_98□Pyridoxal phosphate biosynthesis protein□125233:126243 Forward
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>PFR_JS22-1_100□PFR_JS22-1_100□L-ribulose-5-phosphate 3-epimerase ulaE□127637:128617 Forward
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TEQYGGDWLGVGAENADYIRQVIRSA
>PFR_JS22-1_101□PFR_JS22-1_101□Major facilitator superfamily transporter ACS family protein□128844:130133 Forward
MSPTTKKASRARLKVFGVLWVIILLNYIDRATLSIAIPFISQDLHITPEAKGWIMGTFFW
TYLIFQIPGGWLLDKFGPRRIITICAALWGLAQAAIGLARGGMSMGILRLGLGAFEAPAA
PAGSKLNANWLPASERARGATFVDMAGSFGTAVGGVLVTAVIGLFGSWRWAFVATGLLTL
VVAVFYFFYVRDVPEDHSGVNEAELAHIRGEVATEEVADSTGPLPTVFDYARSMSFWGLW
LGRLGWALVWWGIISWSPSYLRDVMHFDLATLGWSTFLIYGMGVVGQLVAGALADKGRAL
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PRRQVGTVGGAMNIASSLGGAIAPVVMGYFIAWTGGYTGSFVFLGCCAALYLAGSLVINF
KKPLAVARP
>PFR_JS22-1_102□PFR_JS22-1_102□Hypothetical protein□130152:130517 Forward
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VGTVTMETEWDEDDQLGEMVYMQRMQDEFGLPNACVAHAVLDDPAVGELLERYSGSSQST
V
>PFR_JS22-1_103□PFR_JS22-1_103□Uma4 protein□130577:131923 Forward
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HRCGQHGVLRDTVVRRLAHEPLGWRPTLLEVLVRRYRCADCAHVWRQDTSRAAEAKTRLS
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>PFR_JS22-1_104□PFR_JS22-1_104□Hypothetical protein□131862:132341 Forward
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DYAKISWLTASLATVGGALGAGLEDDDVVRAAAYTRPST
>PFR_JS22-1_105□PFR_JS22-1_105□Hypothetical protein□132301:132933 Forward
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>PFR_JS22-1_106□PFR_JS22-1_106□Min□132965:133546 Reverse
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RRALARAQSTPSS
>PFR_JS22-1_107□PFR_JS22-1_107□Nucleotidyl transferase, PF08843 family□133543:134322 Reverse
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>PFR_JS22-1_112	PFR_JS22-1_112	Uma4 protein	138567:139913 Reverse
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HRCGQHGVLRDTVVRRLAHEPLGWRPTLLEVLVRRYRCADCAHVWRQDTSRAAEAKTRLS
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YSARRTLHTGASLLTDKQKTRLDALFADEAHTELEVTWAAYQRMVTAYRDPDPARGRDLM
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LGFRNLTHYVARSLLETGGFRPQLHRGL
>PFR_JS22-1_113	PFR_JS22-1_113	Hypothetical protein	140560:140988 Reverse
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TGRRTNPSARLVGALAQVFGVDVDYFFNDLRAHQIQKQFLALQQLRESGVKIEGIAARGE
GLNPDLVMEAIRALRRDSDDRR
>PFR_JS22-1_114	PFR_JS22-1_114	Glycogen debranching enzyme GlgX	141058:143190 Reverse
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PSVGPGQRYGYRVHGPYDPARGQRSNSAKLLLDPYAKAVEGPVDWDESLFGYRFGRPWER
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LMSDHEWTAGHARALTVFLNGEGIPEPDRRGRPVRDDSFLLMVNPTPAPLSFTVPGIEYG
TTWTDYLDTADHTTGITVAAGAIPASAPRYGPRDVITLEPHSLRLLICTH
>PFR_JS22-1_115	PFR_JS22-1_115	Hypothetical protein	143144:143671 Reverse
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WVLIERSGPREEPTLLVSGLFTGPHPIVWERLVHHGGGLLLAVHDSAPEGQMPSLWVGVV
RAHVGRATDMTPPGPPVYSGAPGFGGTPSATRAGRMTGGVRGSLAGHTVPVGGDL
>PFR_JS22-1_116	PFR_JS22-1_116	Hypothetical protein	143668:143931 Reverse
MPDLGGLVVVLILAVCLVSMLLLAPLVEAWLWRAIGHENHTGDNWPAAEDESPSLAGRAR
PSPSVSPASVEAASLSHRRSTGGAPVS
>PFR_JS22-1_117	PFR_JS22-1_117	PF13834 domain protein	143935:144237 Reverse
MARDYDAPRETDEDLTETPVAEMPGREPSVATIDDDEDLLLAETFELPGADLSGEELTVQ
VVPKQKDEFTCTRCFLVHHHSQLVSTVGSEPAVCAECATE
>PFR_JS22-1_118	PFR_JS22-1_118	XerD	144821:145762 Forward
MVVHRDQRRADVRDVLDEFERWLLQERSAQECTAAAYTARVAAFVEWLPAPVEESLRKLT
AAMLIEWVDLEAARGLKASTLGKQLVMLRSFLQYAHRSGRMGQDLSGVVPHAAAWRLSSI
PDPVPAGTIDALFDTLDLRSPKGLRDRAILLLLTGLGLRACEIAGLRLDDIGWRTGSLRI
RGKGDRVDELPLPDEVGHALEDYVLHGRGGRVQGEEVFWTVIDPVQPLSANGVCGTIRQI
CIKAGVEKFGPHRLRHTFATGMLATGATLQEVQGLLRHAHLRTTALYAKVDKNRLTALAP
EWPAAASLGRCPR
>PFR_JS22-1_119	PFR_JS22-1_119	Hypothetical protein	145759:146106 Forward
MSGLRDLMDGYLATRRALGFKLVAPGKTLDAFVGWMEDAGEPTIRRDLATAWAAQFSRGT
VLERLNYVRQFAEHVAWFDPATEVPVLDGRPYGAHRPRPRIFTDQQIDTLLVAAG
>PFR_JS22-1_120	PFR_JS22-1_120	Site-specific recombinase, phage integrase family	146157:146690 Forward
MTGMRISEARNLNDDDITIDDDAGDGSGWVRVTDTKFGKSRLVPLRPTTMTAIRRYRRLR
DRTFPVPKTTAVFVARRGTRIARSTAGNTFREIREAAGLAGGPTEPAARLHDFRHSFATN
TLIGHIRTGGDVDAMMPVLSAFLGHVGPEATYWYLSNTPELAAALAERIQARGGGDE
>PFR_JS22-1_121	PFR_JS22-1_121	Integrase family protein	146683:147252 Forward
MSDLAPLLQRFFTDKLDRHLDASPHTKAAYADTFRLLLTYAERATGIAPSALTLADLDAD
LIGGFLQHLETERGNSVATRNARRAALRSFFTYASYRAPDAIATISQVLAIPAKRTKTTL
VSFLTAPKQRRSSLPRTPGPGSVAATGSCCTWASKPDSASANSSTCASVTFSSDHTANSN
ASGRAASNA
>PFR_JS22-1_122	PFR_JS22-1_122	Putative integrase/recombinase y4rC	147249:147674 Forward
MIPLQKNTVRLLTAWLAELPPAREGPLFPTNSGTPLTRAAVGKLVTRHAATAAERCPSLT
GKNVTPHTLRHTCAMSLLHAGIDTASIALWLGHASIQTTQIYLHADLELKQRTLERVPAL
DERPPARYKASDALIAFLKNR
>PFR_JS22-1_123	PFR_JS22-1_123	Hypothetical protein	147801:147968 Reverse
MMTSLSEVANDERTARMVLSMLIEPNDPVTGRILSRLGAVETLWRLIANESVGAV
>PFR_JS22-1_124	PFR_JS22-1_124	Hypothetical protein	148042:148326 Reverse
MDALVGDYLAGMSVKALAERYGIHRATVFSHLRRRNVPSRRPRLGIDEKAEAVRLTRAGV
SMRAIGRRMGVDRKAVRAALVEAGLIVDEASDDS
>PFR_JS22-1_125	PFR_JS22-1_125	Hypothetical protein	148615:148791 Forward
MPKKFSPELRDRAVRMVYERQAREGGPRAESIRAIAPQLGVGLVNRPGSGGGSESTGG
>PFR_JS22-1_126	PFR_JS22-1_126	Hypothetical protein	148797:149105 Forward
MAAPRKYPDELRERATRMAVQSRRDPSTRSGTFRRVGEQLGINPETLRNWVVQAEVDEGH
RPGTTTSESQRLVELEKEVRELRRANSMADSSDGRKELCELL
>PFR_JS22-1_127	PFR_JS22-1_127	Transposase, ISlxx5	149067:150224 Reverse
MQGRHGHLSREQKQLALRLHGKGWRLVDIAKEIGCSAPMVGIMARTGRHLDARPFGWEPR
QGCLTIDEREQILLGINRGDTFTAIAEQLGRAVSTVSREVKRGGGRCGYSAWRGHERARE
QARRPKPFKLASGRLLEEVASRLEQLWSPEEIAARLRLDHADDPEMRVSHETIYQSLFVQ
GRGELRRELARCLRSGRSARKPRRTTDGRGRIPGMVMLSERPAEADDRAVPGHWEGDLIL
GEGSRSAIGTLVERSTRMTLLLHLPDGKSAEQVEAAMRAAISKLPSSLIRTITWDQGAEM
SKHAAFSIATGIPIYFCDPHSPWQRGSNENTNGLLRQYLPKGTDLSVVSREELDAIQDSL
NGRPRKTLGYLTPSEKLAEFLAPIA
>PFR_JS22-1_128	PFR_JS22-1_128	Putative membrane protein	150620:151099 Reverse
MSHPSPLPPTASAHYQVLRTVPSYDEAQRLVDRLSDAGFPVEHVRLVGTDLRLVEQVTGR
MTYGKAALYGAASGAWLGLLIGLLLGLFTVVGWLSVILWAVLLGAVWGLIFGLLGHAATG
GRRDFSSVQGLEASSYEILVEAEYFEAATAKLDASRPTT
>PFR_JS22-1_129	PFR_JS22-1_129	Hypothetical protein	152025:152372 Forward
MTAERCRSTADPAEPLSDAELLIGLVVSPSLNAVLGPEVTTSVRKILVQRYPGVRWQLKM
AEDRLVDPPTETLDLLEAARNRVLEENWDLAVVLTEIPLKTGRRPVLTQLSPVHG
>PFR_JS22-1_130	PFR_JS22-1_130	Hypothetical protein	152408:152746 Forward
MRQKVQETTVHVVGQLLGYDAEDPNAQRDLARRAHQLSTDLDERPDDNVVQFTARVLSGN
VRLLLGMIRANQPWAFVARLSRALVVAAATDILTLVAADLWGLITIHGVVGV
>PFR_JS22-1_131	PFR_JS22-1_131	Uma4 protein	152795:154141 Forward
MGVLTPTHREDLDVPDATFATPDLTTFCRLDELGLVAVGQRLEPGRAVIACQVVEPDDWC
HRCGQHGVLRDTVVRRLAHEPLGWRPTLLEVLVRRYRCADCAHVWRQDTSRAAEAKTRLS
RRGLRWALEGIVVRHLTVARIAEGLDISWNTANDAVLAEGKRVLINNPHRFDKVTTIGVD
EHVWRHTRRGEKYVTVIIDLTPARTNSGPVRLLDMVEGRSKSVFKQWLSERDQAWRDRVE
VVAMDGFTGFKTATTEELPDAVAVMDPFHVVRLAGDALDRCRRRIQQDLHGHRGRAGDPL
YSARRTLHTGASLLTDKQKTRLDALFADEAHTELEVTWAAYQRMVTAYRDPDPARGRDLM
NKLIASLASGVPAALVELRTLGRTLKQRAVDVLAYFDRPGTSNGPTEAINGRLEHLRGSA
LGFRNLTHYVARSLLETGGFRPQLHRGL
>PFR_JS22-1_132	PFR_JS22-1_132	Putative TIM-barrel fold metal-dependent hydrolase	154141:154782 Forward
MSRYSQMPIVRSVRHKPGQAASPAEAASHPSKMMDPQWRQGYRLVAENGLLFDLQVAWWH
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MREAVDLARSYPQQTIIVNHAALPSDRSPEMMQGWSRAVHELAACQNTVMKISGIGLPSV
PWRAENNRLIVETLFEAFGSQRIMFASNFPVDSLCGSYDDIFGGFLEISRDWSPDEQSDA
FIGTAVRTYGLEESLLSRVAAPARAYGTETSRP
>PFR_JS22-1_133	PFR_JS22-1_133	Cyclase family protein	154922:155578 Forward
MNTSNAQELPRAVDLSMLIEPHWRFGPEFGEKELEKPHFTFHSTLLRMAAHAFSHCDAPF
HVSPDMETIDEMGLDRFFGPARMVDVSGHGDRAALGEKELREGGAAALQPGEIALIRSDH
ELRHPTTTPQYWVDSPWITAGGARFLLDCGIKAVGFDFPQDRGIREDYDPDFVPSTDPVE
DWACHSVLLTQGVVQIEYLCNLRNVHAENFDGSSRSGV
>PFR_JS22-1_134	PFR_JS22-1_134	Uma4 protein	155676:156983 Forward
MSHATFAAPDLTTFARLDDLGLVVVGQRVLPDRCEVACRVVDDDRWCRECGCEGIPRDTV
VRRLAHEPSGWRPVTLVVRVRRYRCSGCGRVWRQDTTGAAQPRSKLSRGGLRWALEGIVV
QHLTVARVAEGLGVSWDCANTSVLEEGRRVLINDEHRFEGVTTIGVDEHVWRHTRRGDKF
VTVIIDLTPLREGRGPARLLDMVEGRSEKAFKEWLSQQDPAWRDRIEVVAMDGFTGFKTA
AKEELPDAVEVMDPFHVVQLAGDALDHCRQRVQQDTTGHRGRSGDPLYGVRKTLHTGMDL
LTDKQRTRLEGVFAQDAHVGVEATWGIYQKIVAAYRDPDPKAGRAQLAHVIEVISRGVPA
ALAEIITLGRTLKRRATDVLAYFERPHTSNGPTEALNGRLEHLRGSALGFRNLTNYIARS
LLEAGGFRPQLHPQS
>PFR_JS22-1_135	PFR_JS22-1_135	MFS transporter	157080:158372 Forward
MSNDKMELTDRARAGSTNRRWTRLIPVILVIYIIAYIDRVNIGFGMGQIRESLHMDAAQG
GFAAGIFFIGYLVLQVPGGYLAQKWSARKVVFCLMLGWGLCAILAGFVANYGQLLTARFM
LGVFEGGVQPALMVLINRWFPKSEKGRAFSLFIMHNPIATVITAPLAGLILMHGSWRELF
VIQGLLPLLIGVGLWLWVAADDPAEARWLSAQEAQEIATLKAADGDDSAASNWRAAVKSP
YVWLLALMGMLVWLGFYGLQLWLPTLLKTVFKGELTVGLVAAIPPICAAAAIWINGRGAD
RDGRYNVRVAVPLIVGGVILATSTLITANQPWLVVLALAAATACQLSFFGPYWTMNSTLV
RPEAVGAGFGIINGIGNLGGLLGPYVGGWIQDTTGSLALASVFFGCSVILAGIMALALRG
AVRRRVSADS
>PFR_JS22-1_136	PFR_JS22-1_136	Propionate catabolism operon transcriptional regulator of GntR family	158411:159241 Reverse
MRACGVDQPRAGTISLPIRMPREVTIIQRSQTASLATVDSQSARIDQLTPLRSRALVDDV
YDLLLDKLTSGELAPDTALGIDPLARQLRISPTPIREALARLEHTGLVHRAANRGYRVAP
PLSLEQMLELLDTRLVLEDGAIERAMRHAEDLLPDLDAAYEEHARAARALEGSGALHDQH
RIHEYYAADWAFHQTILDHSHNRYISRAVNSLSFSFHRMRQTNAMGTTDAPVALAEHAAI
LNAVRTLDAAAAREALDVHLASLTKRATDAAGNPTD
>PFR_JS22-1_137	PFR_JS22-1_137	DAK1 domain protein	159389:161107 Forward
MTYLVNDPKQFAADSLTGMVAANEDYLTEVHGGVTRATDSPQGEVAVIVGGGSGHYPAFA
GWVGPGMAHGAVCGNIFASPSASQVESVVRASDHGGGAVLLFGNYAGDRLQFGAAQSPLG
ADGIDTRIVTISDDIASDTPQNWKDRRGIAGDLFVVKAACAAAAAGRDLDAVEAAANKAN
EATRSMGVAFTGCTLPGADEPLFTVPEGEYALGLGIHGEPGISSHKMDTAEGIATLLVER
VLAEEPARTAGGYDGHVAVLVNGLGATKYEELFVLYGTVKKLLTEHGLTIVHPIVGEQVT
SLDMAGVSLSLMYLDPDLEELWLAPGDSPAYKTGSVTAGQRREVVAHDEKVAIRAGSPES
AAQAEELLPLLQALADMSSANEASLGKLDSIAGDGDHGQGMVLGSTAALKAAKQAVAAHA
GTSTLFDVAGAAWSEGAGGTSGALWGAALRELGTMLSDDQAATEDRLGRAAIAAARRFAQ
LGEARPGDKTMVDATAPFADELTARLDAGDDLATAWAAAARAATKGAESTADMVARKGRA
RTHGTASLGHQDPGAVSFALLMSGLADRLANS
>PFR_JS22-1_138	PFR_JS22-1_138	Triosephosphate isomerase 2	161182:161934 Forward
MLWVGTSWKMNGTRASSRTYVEALKQADHSAWDGVQAFIIPPATVLAEVSELLGPDSDVL
LGAQNAHWADAGAWTGEVSVPQVADAGAQLVEVGHSERRANFGDTDEVVNKKVRAIIGHG
LRPVLCVGESQEVFDAGDSVKFITDQADSALQGVDPSSVVLAYEPIWAIGEHGREPQRDD
LLRAFDALQSRYGDAVTAVIYGGSANPGNARELLGIPGVEGLFIGRAAWTGPGYVQMLGI
AGEVARAHQG
>PFR_JS22-1_139	PFR_JS22-1_139	Transcriptional regulator	162096:162926 Forward
MSVSSSHNGVEKRHLEGQKERQLAIAEMVIKQGTISVEDLAALTGVSSMTIYRDVASLEE
SGVLQRHRGQVVAVASGLHEADAEFRVEQSSQEKQWVAAKAGQLVTPGSSIMLDDSSSAV
WLLRSLADLSSVSVVTNSLLVANEVAENRSTKLFVTGGEYQAWAHALMGPTVVQNVRAMH
ADICFLSASGISDLACFHPYQEVVEVKRAMLESAEVRVLLLDHTKFHRRALFKFADLTEF
DHVVLDSGTPQAQIDELTDAGVQLMIADDPRSESSL
>PFR_JS22-1_140	PFR_JS22-1_140	Oxidoreductase, short chain dehydrogenase/reductase family protein	163135:163818 Reverse
MTERRSVLITGATRGIGRAIAEELAEGWHILVGGTHADTVNELVASLPSAEPFVVDLTDD
AAMADATVRVGQLDALVHSAGGIVVSPIAEMDPQAWRDLFEINVVAVAALTSKLLPQLRA
SHGQVIAINSGSGFHTRANQSAYSATKHALVAVTNGLREEERGQVRVTSIHPGPVDTDMQ
VTMQELLGGTYQPEKYLHAADVARTVALALEMRPGANVDYLSVRPAG
>PFR_JS22-1_141	PFR_JS22-1_141	Putative ribose 5-phosphate isomerase	164637:165125 Forward
MGFKVAVAADAAGVDYKEAIKADLEADPRVDEVIDVGIAPGETTPYPRKGIAGARVIAEG
DADRGIFVCGTGMGMAISANKVPGIRACTAHDSFSVERLVMSNNAQVLCLGERVIGLELA
RRLAHEFLDYTFDPTSHSKANVDLIVEYEKETGADDNSVTSC
>PFR_JS22-1_142	PFR_JS22-1_142	Putative membrane protein	165670:166749 Forward
MFTASLGVFLFGLLAAIAGGAVGAAIGGNYAFVLTGFAVIASWGIFAATGNTFGLDYLAF
GPFMGPHIAFAGGVAAAIYARYRGYFEDGKDVNSPLAGLGKPDIVYVGSLFGIFGYLCQI
GVSHIPWFGTHTDSVALSVLLSGLLARVVFGGLPGKGLMRGSLHNAEAFHPDATTFPQKI
KPGPNGRWLEWQEKPSQLLTIGSLFGILAGGASLFLAGNVGAYLTERGFANTLAAANANS
FTFGISAIVILFLITNRNMPVQHHVTNIAGLAAIQFFPILMGKTFSTYTWTATSTWDSHT
WLMAFLALIIAAVFGVFTALLGEFCARLWYDRGTSHIDPPAASIWLGNTVVVSLAMLFS
>PFR_JS22-1_143	PFR_JS22-1_143	HAD-superfamily hydrolase, subfamily IIA	166809:167681 Forward
MSSDTSTADIINVPTDFAQAYVFDLDGTIYLGDQLLPGAKRMIEELRRRRIPVRFLSNNP
TKDPEQYVEKLAKLGLPTDIEDICNTVVTTTRWLKENHPDAKLFPVAEEPLKRALRKAGF
TLTDDPSEIDIVIASYDRTFDYHKLQVAFDAMWFYKRAFLIQTNPDHFCPFPGGRGEPDC
AAVVAAIEACTQMKSQVNLGKPSPIMLAEALQGLDVEVSRCVMVGDRLQTDIQMALDTGM
GSACVLTGEATPDDIRGLDDAHHPTYVLDRVDQLIPASAWRELGWTEDND
>PFR_JS22-1_144	PFR_JS22-1_144	FGGY-family pentulose kinase	167713:169287 Forward
MIGNTNGSGPYVMGIDYGTESCRVAICDLRGRPIAIASTAYETTHPRPGWAEQNPEDWWK
ALQASTHKVLANAGIPASAIAGISYDATTLTLVAMDEKGEELRPAIMWMDVRATEQAARA
ADSDSVAKLYNGGGHSPAIAEWFPFKAAWLKEHEPDIYARAAHLVDAPDWVTYKLTGEWT
TNINSAALRMYYNRAQGGWPTDFYETIGVGDVFEKISDRVLDLGQPVGQLGLIPAQLLGL
RPGIPVAQGPADAWAGQIGLGVLSPGSMALITGSSHVLTGQTDTEIHGKGFFGGYSDGVM
PGQFTVEGGQVSTGSVLKWFKDNFAADVVSAAEKVGLNPYDVLNEKARGIRPGSDGLIIN
EYFQGNRTPYSDSKARGIIWGLSLAHTPAHMYHAIQEAVCYGTAHNLRAMKAGGFDVERI
VACGGATKSRDWMQMHADVTGVPITLTEVGDAVVLGTCMLAAVGAGLYKDLPEASENMVH
EIDVIEPNQAVHDEYQFYVDKYCDTYPQLQSMIHDMVDHEAAQK
>PFR_JS22-1_145	PFR_JS22-1_145	Arabinose operon protein AraM	169300:170676 Forward
MSDLIAKALADADDTDVVVMGQNVLPDTGKVFKQLFGNAHAIVVADGITWGVAGEAVTKS
LTDAGITLDEPFVFPGHPTLYASYENVEKVRDHLKATDAIACSIGSGTLNDLVKRASDEL
GRRYMNVCTAASMDGYAAFGASITENGFKHTMSCRAPQGLVADLGIMAAAPQRCTATGLG
DLIEKVPAGADWILADELGIEPIDKGTWDLVQGPLRGAISNPQALADGNPEAFDGLAEGL
IMSGLAMQKYRISSRPASGAGHQFSHVWEMEHLGFDDDPPLTHGLKVGLGTISVLALWDK
ILDIDFSALDIDAAVAKWPTADEQEAIVRKSFTGAMLEPSVKQTMAKYIDADALRARLAI
VKEKWPEIQQRCRSQVMPAVDVESILKQVGAVYHPGQIGLTEQRFHDTYYRARLIRSRYT
LLDFLFETGVLHDEVEKLFAPGGFWAERPWGGQKYWNE
>PFR_JS22-1_146	PFR_JS22-1_146	Ribulokinase	170914:172662 Forward
MSDQFVIGLDFGTLSGRAAVVRVSDGKMMGTAVHEYPHGVMSRTLSAADGQMLPPDFALE
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APDDYLEALYASVQGALAEAGIDPALVIGIGVDVTSATVLACKADGTPLCDLPEFANNPH
AWIKLWKHHGAYEQANRIVELAQARGEAWLERYGGMLSSELALPKVLETLEAAPGVYAAT
EVFCDAVDWLTWYLTGQLAYAAGDSGYKRMFQDGSYPSREFLAELNPGLADVYAEKMNAP
VLPLGARAGGLRADVAQRMGLPAGIAVATGNIDAHVTAPAAKAVENGQMTAIVGTSACYV
VSGPQMVLVPGIFGVVEGGIVDGSWGYEAGQTAVGDIFAWFIDNCVPASYHQEADQLGIP
VHELLTRKAELQQVGAHGLIGLDWHNGNRSILADAQLTGLMLGQTLATTPEDQYRALLES
SAFGARRIIQAFRDAGVAVDELVMAGGLVKNRLFMQIMADVTKMPLSLCTAPQPGALGSA
IFATVAAGAYPDVRTASAAMGSKAENVNTPDPERSRDYDLLYAEYSRLHDYFGRGANPVM
HRLKEIRRDALARTQRIDNAELVAGAEPLAGDGQLANDGQAM
>PFR_JS22-1_147	PFR_JS22-1_147	Transketolase	172781:174847 Forward
MSDLKWTDEDREAVNIARTLAADAVEAAGSGHPGTAISLAPLAYLLYQKVMNVDPDDEHW
IGRDRFLLSAGHASVLQYSQLYLGGLGLELEDLKYLRQAGSRTPGHPEYGHTKFIEATTG
PLGAGISMAVGMAMAARRERGLYDPDNTGASVFDRYVYSIAGDGCMQEGVQSEAASLAGV
QELGNLIVFYDDNRITIEGKTRIAFDEDVEARYAAYSWDVQHIDWTNGGDHYEENVQALF
DAIEAAKKVTDKPSLIRLTTVIGWPLPHMAGSAHVHGAAIGEDEINAMKKVIGFPTEPFT
FNQDIVADTRKALAERGRSARAAWDERFAAWQGSHAEQAALLDRVLARKLPDDLQVPSFE
AGAVSTRKASGKVISALAEQLPELWGGSADLAGSNNTTIEGAESFLPADRATDEWPGNPY
GRVLHFGIREHAMGGALNGINLSGLTRAFGGTFFVFADYMRPPVRLAALMGAPSVFVWTH
DSVGVGEDGPTHQPVEHLASYRAIPGLDIVRPADANETAAAWVEILSHHDRPAGIVLTRQ
NVRTVDRTSGEFASTDGVAKGAYVLREARNGKPEVILIATGSEVEPALDAQDILETQGIA
TRVVSMPCQEWFDAQPAEYREEVLPSSIDARVSVEAGLSLGWSKYVGFKGASVSLEHYGA
SAKGSLLMEEFGFTGEHVAEVAKGVLGK
>PFR_JS22-1_148	PFR_JS22-1_148	CHY zinc finger	175128:175439 Reverse
MSIAFHGIGLDAEGRCTHYHQASDVVALKCAQCGRYYACYQCHDALEHHRFVATGPDEPV
PTLCCACNTALSHEQYSQGACPVCGHEFNPLCALHKDIYFTGR
>PFR_JS22-1_149	PFR_JS22-1_149	Putative excinuclease ABC, A subunit	175616:177904 Forward
MDQFPQGFIGVHDAQQNNLRHVSVTIPKYRVTAFVGLSGSGKSSLVFDTIAASSRRELNE
TFPSFTQQYLPKFGQPHVGAIDHLPVAIVIEQQRMHTSVRSTLATYTGIYSLLRLLFSRA
GKPFVGYSDTFSFNLPQGMCPRCQGLGYVDDIDESKLIDPDKSLNQGAITFVSFGPNTWR
WKRYANSGLFDNDKPVRDYTPDEYDTLMNAPRHRLTDAPAAWPKSALYEGVIPRIRRSII
GKKEAAHHLEALAAIVTRRPCPACGGTRLRPGALTSRINQLNIADVSRMDLVHARDFLDS
VTEPLVAEVVRQLHTKVQSLIDIGLGYLTLDRITSTLSGGETQRIKIAKFLTSELVDLVY
ILDEPSVGLHPHDIALINKALRKLKARGNTVLIVEHNPEVIAMADHVIEIGPGAGSAGGT
VTFTGSYGELMASDTLTARMLHQPLRYRAPRPATGSLALRHVGLHNLHDVSVDVPLGVET
VISGVAGAGKSSLIEALREQLHGDYVDLRQSAITVNIRSTPATYLEVLDVIRKLFAAANH
VATSWFSYNGRGACPRCKGKGVTITNMAFMDPVVQECEQCHGQRYNDRALGYLYRGKNIA
EVLTMAINDALEFFAPVPEVHAKLDNVARVGLGYLTLGQSMTTLSGGELQRLKLAGELNR
VGSIYLLDEPTAGLHLSDVAGLITLFDELVAQGNTLILVEHNLQVISQADRLIDVGPGAG
VYGGHILYSGTPEGSLGVSESVTGQALANYDSVVRAGSGPTQ
>PFR_JS22-1_150	PFR_JS22-1_150	Aldose 1-epimerase family protein	177972:178868 Reverse
MQDITLPEGLRLNEESPTNDQSGAGFATIDVSTRLCTGRIHLHGAQVTAWQPRGASEPVF
WQSAQAKLASDKAIRGGVPISFPWFADGRSHNQKPAHGLARLADWKLVDASSTPGGEVTV
RLRLDDETLAKSKFAPDAEVTLVVTMGVAVQMSLVVRAGSAACHFEDAMHNYFHVGDVTR
ASVKGLDAARYLDKVSGRDGQLQEGPVTFSGETDRVYQSVASTSIVDPVLNRTIRIEKSG
SESTVVWNPWSKRSEKDFGMAPGEWQQMVCVETANALADEVYLEAGEKHVLSQVISLG
>PFR_JS22-1_151	PFR_JS22-1_151	DNA polymerase beta domain protein region	178983:179816 Forward
MLVEEDLLMALVGAIMEAVGERVVGIYLGGGLADTDFSPSQATVNLLVVTDVDPDRAMLD
TVRDIHAGVEDEFSGWGDRIDIEYVGLPGLAGFRTGQHVGLRSEAGETLHLEPLTELNVL
SWESIRERSVDLVGDPADTVLPEFSRDEFLRAVRQHAVGWPQWTRSHTRMDQQVYAVLTM
CRAWYSARLLRQASKREAALFTAAEFPRWEPLITWADEWWYAVEEPTPRGPAERTLIERV
QDLVDELSERVLMAGTPAQGAGIEPPRPPVDAPDARG
>PFR_JS22-1_152	PFR_JS22-1_152	Hypothetical protein	179809:180894 Forward
MAEASSLRPPRSPLLPAVLVLVVLVAIAAVLPGMRARMREEIPRDDVAASQDFIDWAVGS
TLQRSGAVGVTALRLTDFALDVTVRTGDGAEQRWRALPQKPVELVANQPLTPTNGVVSGD
GFAPSALMAAWTDLRGQDDQCEASDAQVDATVSWGGAIRYTSRCNSPEAGASTNLIKGFS
SPNRIGVANVYELDSFAAGTSLEIVLRQLRQLAPGGQVSQLTVLADAGTAAAGLGITGGS
CGVEALWRQAEPDGTNTWLRQSRLCSAADGTMLPTTTLDAPADAAQLEAHRFDLSAVDVA
SLVGHLQTTGLPAQQGSASVVQIAWSDRFDEVVARVSSGTGSDARTGWYSLTGEQLAMDA
G
>PFR_JS22-1_153	PFR_JS22-1_153	Hypothetical protein	180895:181752 Reverse
MTFRLRARPVIAALSVLALAACAQPPSARHTETGDGPTSPASSASSSATEAQAIRGFDFV
HADWYDANGNATVRNGASASPEASDKSWAKVDEANAGNATQFGDLNGDGFADAVAWITVG
NGSSYWHYAYVWLWDDAQHTAVQLHQPVTDDKQCGNVTKTLTISDAKITVDRLIRAGEAC
SDQPAHPVANTIAIEGGFPVRETPVRASTMPALAASSDAMQPGAQLKKPLKLAPAADAPE
LDLGQVSFIVLGGQRGTLDNGFHQVLFRASGDPVTWYTAYTDEIQ
>PFR_JS22-1_154	PFR_JS22-1_154	D-inositol-3-phosphate glycosyltransferase 2	181925:183154 Forward
MGEGLRIGFVSLHTSPIASPGSADAGGMNVVELNAALALAAAGHQVDLITRRDHPGEPAV
EQLAEGVRLLNLDAGPPHPMAKSASEELIEPFRAAMARLPGNYDVIHSHHWFSGVAALPL
ARQWRLPHVQSFHSVAAPSGSTSLADGEPAESPGRVAGEALSARESDLVIAVSHAERRAV
ELRYHRFDGIDVVHPGVDTEQFHPLRAGQRHWAWDDTGGCYFLFAARLQPLKGPDLAIRM
MAEIPEYDRPQLIVAGEASADFADYEASLHALVGELGLTDKVTFLGSQSRDELASMLRGA
CALINPSYSETFGIICLEAEASGVPPIAARTGGIPEAVLDGKTGILLDDRDPASWAAAAQ
SVRNDGVLRQRLTSAAREFACQHTWTVMAQGLEDSYRRVIAAFNEGNRA
>PFR_JS22-1_155	PFR_JS22-1_155	1D-myo-inositol 2-acetamido-2-deoxy-alpha-D-glucopyranoside deacetylase 2	183151:183969 Forward
MSTAAEIIDQIMNQPAGLSLLVVHAHPDDETLETGPLIAGLTDSGARVDLLTCTRGERGE
VVPGVLPAGITQDQLVVQRERELEAACDLLGVRKQYFLGEAPFRAPAQQGRHYLDSGMVW
VTPTQAGPAPDASPISLTKSPKKEEIEDLITGLRQREWSAVVSYDDAGSYGHPDHLRTHQ
VVSAAAKNVGIPCIQILSDPTADVPGAAWFAPDDVRSRDVVVEALRAYRTQLQVLGTTAD
GTESADEKNDLHIRHVGGQRQEIPTRVGLIAS
>PFR_JS22-1_156	PFR_JS22-1_156	Integral membrane protein	184140:184751 Forward
MTDQSHLSGWDVFRLNAPDLTRRAITTVRASFALLGVLALGLGIALLAWPGKTITALAVI
LGAYLLVEGVIRIVMALVTPLIHAGSRLLSILFGVLFILGGVVMMRNPGLSGETLLVVVA
IIIGVAWIMEGVLALLESGSAQSRGWAIAFGIISLLAGIIVLVTPAWSAVMLMVFTGASL
VVMGIVSLVRAFTFGREVLRAQH
>PFR_JS22-1_157	PFR_JS22-1_157	Ribose-phosphate diphosphokinase	184869:185849 Reverse
MKDIIVFSGSAHEPFAEQVCQHLGVRLSPVNISRFSNDCLQAQLLTNVRQRDVYIVQPLV
PPTQDHLMELLLMVQAARGASADQITAVIPHYSYARSDKKDASRISVGGRLVADMLSTAG
VDRVLTMQLHAPQVQSFFSVPVDQLTAMGVLARYFQEHCENSVVVSPDFGNAKSASTFAR
LLGVPVAAGSKRRLGDNRVVIDTIVGDVVGKHCIVMDDEIATGGSILELVRKLKDQGAVD
ASVTCTHGLFAGNALEKLSGEKFITEIVSTDTVPEPAEHWPELHVLSVAPLFAEAIDRIH
NGKSVSKMFEGIDPVYAPPKGQEGLF
>PFR_JS22-1_158	PFR_JS22-1_158	Glutamine amidotransferase class-I	185933:186622 Reverse
MPTAVVLQHVAFEDLGLFAPRLRARGYGLQVLQAGVDAPEPLVDADLAVVLGGPLGARPD
AEFPWMATELEALTRRVQARRPTLGICLGAQLMAAALGASVEPMGVKEIGYAPLTLTREG
ADSPLSVLGSAPVLHWHGDRFGLPDGAELLASTPTCDHQAFRLGPNLLGLQFHPEADPAQ
IERWLIAYDDELNAAGIAPHALRDRARTDGVATARVAPGLVDAWLDQLA
>PFR_JS22-1_159	PFR_JS22-1_159	Multidrug resistance protein	186648:187895 Reverse
MGSGRRLDLHTDVNVCVTAVKRIPVLSFAVMFLVATDTFLVAPLLPDLTRRFGNSPRIAG
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WMVSAYAIGYCLTAVFSGPISDRFNRRNVLFAGTIAFCVATFACGLAWSFPAMLALRFAT
GVAAAVGSPQIWAAIPQLVAPSRVVATMAAPTAGLTIAQLAGVPVGSFLAAVSTSTPFFV
VGAVAALVAIAVGIWFPSVPPTGHSGGIIAQYAGLLRTPHAPTRFAAYLVFQLGNFAVLS
FAATWFARGFGLSVSGIGVAMIVLGAGNTLGAVVGPRIVRRVGQGRTLAVAMACYLVGYL
ALPFSAGIVAAAAILSGTFFLGGTIFPVFMGLLQSLTTTARGTVSALANMFMYLGSTIAG
IIGGPLLAALPGFWGISLLAMVAMAASLGLWAASGSLRRMPASAARGSRTEPATG
>PFR_JS22-1_160□PFR_JS22-1_160□Transcriptional regulator, MerR□187933:188277 Forward
MRIGEFAEVAGLSTRQVRYYTDMGLLAARRLSNGYRDYDAGDVARARRVHALFAIGLTSE
QLKRLSPCLADEATTFCDATRQALVRQLSQIDERIGHLQEAREAVARQLETADL
>PFR_JS22-1_161□PFR_JS22-1_161□Hypothetical protein□188360:188914 Forward
MADEPQHLKIDLHPVLVQADGEVAVREGDEVTPVAADFAELARESDPVGRAQGLLMLPIV
VGLQKGTKPVKSMLVEVTRDGVLNEPEDRNAYATAIRQGSAYEGSYRHDVTLTRVGVVVG
EMNQKLPDTLWVPLFVLKESDGRLVPLDAKYFNAVQRRNHGGQEPGTQGAPQASADEESG
PDKG
>PFR_JS22-1_162□PFR_JS22-1_162□Hypothetical acetyltransferase YafP□188985:189530 Reverse
MWLPSFFSRTFGRAGNNGRMASAPGHVRVRPYMDSDAGITRSIFLQSVTLTAAEDYTKQQ
IDAWASPQDRPLDEWNRDRQESGTLVAVVAGVVMGFTDIRETGYIDMLFVSPKFVRRGIG
SALLREAENRARIAKAPLLYSNVSITARPFFAHHGFVEVAEQHPIIHGVQVKNYRMNKHL
F
>PFR_JS22-1_163□PFR_JS22-1_163□Transcriptional regulator□189662:190009 Forward
MIHETREQALARVGHALADPTRCRLLLAIVDGVVYPAQMAEHLELSRANVSNHLACLRDC
GLVSATYEGRRVRYAIADAHLSAALVQLAQVALDVTPTDSCLNEADQPIELEARA
>PFR_JS22-1_164□PFR_JS22-1_164□Metal cation transporting P-type ATPase ctpG□190006:192120 Forward
MSSATQCCDHDAPAGADDHDELAWWRDREVIFPIGSGVLLAAGFVSALAQANTASLVLYW
AGLLLGASTFVPGALRALLKGRLGISLLMMISAIGAVILGAVAEAAALAFLYSISEALED
KAMDRARSGLRALLELTPKTATVLVDGKPTDVEASQLQVGDLLLVRPGERVATDGVVRDG
ASSLDTSAITGESIPVQVGSRDAVSAGCINISGPLQVSATAPGSDNSLTTIVTLVEQAQA
KKGRRARLADRIAAPLVPGVLILAVAVGVLGSLLGSPEVWIGRALVVLVAASPCALAIAV
PVTVVSAIGAASRFGLVIKSGAAFEEFGAVRHVAFDKTGTLTQGSPCVGRVLTASTVDGG
SMEDSVRTSDAASTTDPASTTSTASTADARPAGVSEQQVVDAAAALERGSNHPLATAIVA
AATNAPGATDVTELPGRGIRGRVQGHEITVGSPRWLAPGALAAGVEQLETDGMTVVLVHR
DGQPLGAIGIRDELRPEAAETIRALGEQRIGVTMLTGDNERTAQALARQAGIDDVRAGLR
PEQKASAVSELSRRTPTAMIGDGINDAPALSAASLGIAMGARGGQGSAGGSDVAIESADV
AFTGSDLRLLPGAFAFTRRGRRIMNQNIALSLLIIATLLPLAITGVLGLATVVLIHEGAE
VIVIANGIRAARVARARGGAPAAQGPVPPSVEGPAAPRMVAHSA
>PFR_JS22-1_165□PFR_JS22-1_165□Hypothetical protein□192172:192663 Forward
MSVSTPGTGLEVFSVVVDTDGSIAQMEDDDQYHTIAPDFAVLFDDLDQQFTQRGVTKIPV
VTGFGDGMAAPRPRPIMVATTGALVSPDDPDAFMDAFGANEAYDGEYHDVTLAQVGTLVN
DLNLAEASHAADQRVHWVPGFILITPDRKLVDLAYALHKGWIK
>PFR_JS22-1_166□PFR_JS22-1_166□Hypothetical protein□192782:193387 Forward
MSRSTGPKGPQRGKAPRQVQGYRVSVNPDGTLLTNRPDGELEEVAKDFRELTARLSLRGE
QQGLLILPVVTEFSKLMQRPSLWPVVLGAGGRLRRPTGRQSFINAIQTGSPYEGEFVDTT
LVEVGKDVTEMSASNPMLQWVPVFLILTPDGQLADLGETIMEGRRMLYPQEAANTAPDAP
DEPGAPDASREPGAAEEPSAG
>PFR_JS22-1_167□PFR_JS22-1_167□ABC-type Fe3-siderophores transport systems□193443:194252 Forward
MSDELMGGDLLADDLGAPVRISRPVERVVSLVPSLTEALAESARELIYGATDFCVRPENL
DEVAGHPVTRVRGPKNPDRTVIEQLHPDLVVANQEENRAFDVEHLRADGVPVWVTSIDTV
DSAITSLTRLFTEALGRERPDWLTRAEQNWAEPDPTVTASAVVCIWRDPWMVVGPNTYVA
DVLHRSGVGLAPLPVDDWKNARYPKVDLYALQASGADRVLLMDQPYAFSPTDGPEAFEGM
DVRIMPERPMAWYGPGMTDARAEVRKLIF
>PFR_JS22-1_168□PFR_JS22-1_168□Hypothetical protein□194325:194549 Reverse
MMHSRRRLVYKWVTITVLMLGLAVAIDVMIGDRRSDIEYLMWSVTAAAIGYAGSFGHDWW
VRAGFSGRHHPLAG
>PFR_JS22-1_169□PFR_JS22-1_169□Transcriptional Regulator, TetR family□194695:195303 Reverse
MPEQSRSVRSHQAIIDATADLIRTRGVAGTSIADIITASGTSAGSIYHHFPNKQAIVVEV
AHQTMRWPLTAIEAYLNRPAPPADLFGYALDALRVAPELSDLLVQLGSGSLSDDELGRQL
RAEFSQLRDALDETLAVWATRNGLTDDRVAGLGQMLVGLVLGYAAQRVLIDQFDEEAYVS
HGKAMLDAAVCRPGNDQLPDGR
>PFR_JS22-1_170□PFR_JS22-1_170□YghA protein□195483:196172 Forward
MPIGAGTLPIMGEAFLVIDLIGVLANAILGGITAKRLRFDLVGFTVLALATGLGGGILRD
VLLGRGTPVALTNPIYIPLAAVGALVAFVVPIRKVFQERLFPLMDALALGAWAYTGTHKG
LVFGLGPVQAVLLGVVSATGGGMLRDLLGRKMPVIFGDNTLYATSALVSSVLVVIFYKLG
DSAWGAVIAMAVGSLLTIVSAWRGWTLPRSISNPFKGKDFRRYIRIRRR
>PFR_JS22-1_171□PFR_JS22-1_171□SAF domain protein□196716:197426 Forward
MGFIYVSHARVPPARAERDLSMVAFPRKSLSELTRRAVPSLRARRSPRLIIIGVLCACLG
GLGCAVAWHQATDARQVVVMARAVPRGATIDGADLGTTSIGSAPGVATIGAEQLSTLIGT
TALVELQQGMLVPASALGEETVRPGRHHVGVHLVAGRVPGDLVAGSAVIISAAPGPTDDA
SFRAEQLSVPATIVGTPSRQSDGSWNFDLDVPAGASLRIATLAAAGRLVVVHGTAA
>PFR_JS22-1_172□PFR_JS22-1_172□Hypothetical protein□197426:198463 Forward
MAIVLLTCATGSPGVTTSALALTLCWPRDVLLVDSDRDVSQTVQAGWLGARPLATRGLVE
LAQAHREMRPVAPLLWDRTVSLLDDAPAGSAGVPDQAMGRFDATGQPIADQRPGAPAVAE
SRPVARQFLPGFSHPGSVAVFDPVWPEVAEALAGLAGSGVDVIVDAGRVGHQGLPSALLG
AADVVLMVVRSSLRSLAAARLHLPPLRERTAALAPAAKLGLLVVGPSRPYSDGDVEAQFG
VPVVADMAWQPQEAAVLSEGGDEPRRFRERSFMRSASAAASAVSARVIATPNSSRDLATG
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>PFR_JS22-1_173□PFR_JS22-1_173□Hypothetical protein□198460:199365 Forward
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TTPANVSASASPLGTQPVDLPQRGVPQESESAPTSAGAAHRVRTPGTVPAGRPVGTPMQA
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RSLIRRAVHDYADELNRAGRALWPIALEQRYVKAVEDAIFGYGRMQPIFEVSEAENIEIH
GYDCVFAQFGDGRRTRLDPVADSDDELVAAVRFLGENADPPRPFDDAHPTITVGGSRNPL
D
>PFR_JS22-1_174□PFR_JS22-1_174□Hypothetical protein□199362:200483 Reverse
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LAPPGTATVALHSRAVEGGSKRYQRAPSGADMQLALLLPSGRTISLLLQAKRLYPKVRAN
PRYEEWSARQNKDLECWAWNHGQQPGMILYNDLVPPFTAMRNPKASSDFTCAAFGACQGA
NHLQLHSHAEMMQRRWDLFDGTPGGVSLCINSTELRRSSPDAAQITTHHFPLEHLAHVAA
PGRTPGGGGPGGDNGPDDVSGPTPTTPGSGPHAPESPVEVGIELFADVPVWASNLLELAN
RESAWDDPEADEAADMGDDSDFWIASSVVLDFRQLPELLRLPTPQALSAATGNARGKLIG
AQGNPLAAQRSIT
>PFR_JS22-1_175□PFR_JS22-1_175□Hypothetical protein□200623:201744 Reverse
MGKKGRARLRLDAVSYLEPVALAPLDGELSACLVAAKSSSPICCEVQARSDLSFTEEIVS
TLTEVDLDSLTAQQGAFQLLANPSTALRKVRKGGVATMRQALLVEHPTEELCVRLSISVE
VEPGLPPKITTTSCDARLVAMSSEDEQAELVAELEEWSQEFTEPQVGPAPPQLSRWAILG
DPTQAGFTDLPDNWNTRLTKLGAVYGQDPILARSLSAFKQAHVEQLAKFGFILPKVPWTK
DLGGVVDDFLRVPSSDHSFEQLLIEMRTHILQQAGEQAASSRQRALAPGEVVYHRKVGDS
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VDASRGKANRQAS
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>PFR_JS22-1_176 PFR_JS22-1_176 Hypothetical protein 201759:202682 Reverse
MTSPFQEPLDIDAPREAALKLAVEVVSAWRRDGRVTTTAGLSSALKQSGIEPKSLGFPAF
KDFWQFAEERKMIFRHRAPSGHWLIMLPGEDAPDPDAIPTRVASPRTLDPAKVRLKAVVW
RAFVVWDEAYARFWDRETAEAFMVPSAWVPSQVDDTRYLRFEPITQATQIAWMREFAETH
DGVNKQELLEALEDNAPLGAFRKALSASGSLRDWHATLTLRVAKTVLLWCQQSGVPETEL
VEPTRRKTSQPVPSSVSDPYDVAPSERTHDARSNLEAELRAAVHRAVDQMSLDELAALPV
RACHLVH
>PFR_JS22-1_177 PFR_JS22-1_177 Hypothetical protein 202970:203521 Reverse
MRLADFEALSITHRENHGSGLQGFLHEPAVVSLGWPADVVEQWLYDHAGYPPFQRDYGHI
VLEGLAWRLETVPTATFLTMKTGDSEHGLLDHFASMHEHSVRVRDQSGSHVHAGVQRWWD
ERGTWKRPPLLLDRGLLLPNGTGLQVVEGRTRVGVLHGRHRDGLSVATEHVAWIATKRTH
NPS
>PFR_JS22-1_178 PFR_JS22-1_178 Hypothetical protein 203531:204571 Reverse
MSQFEQDSLQLTDRPVNLYRDRSTRCAACGHEQRFDPEWFVRWECQGEVCPGCGVDCTEE
KATRVICEPDDPALDDSLVPKLSWWHTSTYEDWPSPDFNPAARLTDLARQRMGEPMIARW
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GDVPLTKVCPSELDVFRYENQHEDKGSISLALGRGAIQSVQQLALPVEDVERPAWWTDAV
DRMSVASQTLPAPGTPVGPLAQLRRPGWAVSSPVAEVQNDLRMELTSHLPGTLRGAAEAA
IRIDATLTPTEWCSLAAAVLQPLNDPAAVMQAARASAPRTVSTESL
>PFR_JS22-1_179 PFR_JS22-1_179 Tetratricopeptide repeat protein 204601:206400 Reverse
MSHPLSPGIMLATSMQAQPGVYALLLGSGVSTGAGIPTGWGVVKNLIRRVAVLEDKDTLK
QAESDPEGWWTAHHDEPLGYSTLLEALAPTPSARQAVLAEFFEPTDEERQEGIKRPSKAH
LAIAELVKRGAVKVIVTTNFDRLMEQALDSVGVAPQVISRPEAVQGMKPLAHAPATVIKL
HGDYLDLGSRNTPSELESYPQEWNDLVSQVLDQYGLVISGWSADWDTALVALMEAAPNRR
YPLFWDQRSSRGTVAQRLLAARAGLVVPAAGADELFTELASNLDTLDKLAEPPLTTAMAV
GRLKRYLPNPVHRIDLHDLVMAAVDRAGEATQAQPLLIPGLDEQGWGDLYQSHREAVMPL
LHLLATGVWHDTTDEHADLWVEALQRLVDLSATQAPSGQQYRPDLWKVRLYPAILAHYVI
GVAAIARRRDHLMLRVLGEVQGVSDAAHDQRLAAHQLLDPSQLPQLNELPRWNGQRLMFL
ASHLLRQDNRAAFDSLVPDDDLYLRLTHDWEYRLGLVQTKESGYFVFYGDSAGELQWGSR
SQGVPSCETRFLDRQMHDPRWPWTDYLGGAQEQQAIQDTHRGNMRDASHQARLGLSRAH
>PFR_JS22-1_180 PFR_JS22-1_180 Hypothetical protein 206603:206950 Reverse
MNGWPWEGTVQQVFADRLATEGWVIERLADTAKRQHGIDVLASHGSRHLGAEVKGYPSDR
YTDPNKTGVKKPSTSPAKRGTGTPKGCSQPSCSEKPNPTSNRCWSCPTTLAIASS
>PFR_JS22-1_181 PFR_JS22-1_181 Hypothetical protein 206947:207423 Reverse
MARPGLGTDGGQRGNRQRIAAFADPDGRERNLALLRAALEAAAVGDPRAAYSTLIRPGRA
AIRGLGPAFFTKVLYFASEGTSGTRCLILDARVAGNLYAAGWTSLPHRGNNFTYNWFTTT
YGAYCELLQRWAGEATQKRNTAIWPDEIERALFEGPAA
>PFR_JS22-1_182 PFR_JS22-1_182 Hypothetical protein 207751:208965 Forward
MDREPNPNQLDVLRWLVDHPEEPEPPGNWKASAVALKNRGLVTIRRKGGQYQVTPTEVGR
YFCKHGTLPPAPVRTPGPKRSKATSRAAQASTPVQEPAPVEPHPKPVAAASEPTTSEPEQ
VSLEDRLGPRPHPAVRSLWKHPAALPEDPEVRERAILAAHELVQSAKEAGLKIEGHTQPR
KRSHAYGLYLGELLVTLDAGDSPVRVKIGEVMKRVPHELTAEEQAKKRRNEYVWAPTYDH
VGTGVSCFRVYTDKPTGGGTRYAETKSRTLASFVPAIIQAVQRASEAKREREEQQRRWQE
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>PFR_JS22-1_183 PFR_JS22-1_183 Hypothetical protein 208976:210499 Reverse
MLARKVSAICGSIEPKTIGPEKGRSQNMRFSEQHQITRDNSEDWFDANVEMDSPLYVDPF
LIFEDESVEWAPAHEELIAFFDATLDMLALAEGDKRSMHWEKAERFLLFPEPKEFALGLS
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>PFR_JS22-1_184 PFR_JS22-1_184 Hypothetical protein 210529:210996 Forward
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TADGWLQARPLLQEGLTSAGAVLLAYGKQAPSGSARQHFRDQVAWMDEQIALAGLPVWWV
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>PFR_JS22-1_185 PFR_JS22-1_185 Hypothetical protein 210968:212761 Reverse
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TFVDQFQRLKIILRWDDSGPSMSMSTSSLEGLPADQVKELSTAILAMRQGGNSFTIAPQF
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AARALLMGEVLEVGVESGQALTEHDAELAVTEQTIWSLSPWTVQVPEAEIELGPVITSFE
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>PFR_JS22-1_186 PFR_JS22-1_186 Type III restriction enzyme, res subunit 212776:215349 Reverse
MRYTLKDYQDTAVRQVLNQLRRARGNYHSYDSLSQFALAATTGAGKTVMAAAVIEALFFG
SDEFDTEADPGATVLWFSDDPSLNAQSRIRIQAAASELDSRLQIIESNFSQTTLAPGMVY
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WSVLESIPSLTVPKTHVKPIKRLDALAVALSKDGLIENAVAQAEAHLCAVLDGRAVQYKA
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ADVVDPHGHHLSDALPKLRGLADFAEQYGSEFRRIESVAETGGKLRVLDLTRANVRNAVR
GATDAKALYESDTAGDY
>PFR_JS22-1_187 PFR_JS22-1_187 Putative type III restriction-modification system methyltransferase 215346:217475 Reverse
MSRLTDLLRQARATDPQLGKDLEAEFAALMKRRTFGLVFEKHQPEAVDLAGRPIRVGDKV
RVLPPRRELTKGDQRLWKVKRIERVDGSRVAHLEEIDADTPEHRVVLLEDLVVVAEFRDR
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NNDYVEGDDDYRHSKWLAFMERRLEIAKELLNPEDSVLIVTIDEKEYARLALLLEQVFPE
ADIQMVSSVINTSGAVRAAGFARVDEYLFFVFLGAARVQRNQMDMLTPDVTTKTPTLWRN
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SGQEGYWQLGQDTFETYREKGYVRVGQVRGDRISLNYLRGGDVKRVESGQIATRGTDPSG
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KDKRDAVILDFFSGSGTTAHAVMRLNKQDGGRRQCISVTNNEVGAEEQKNLRQEGLRPGD
PEWEQWGICDYITKPRVTAAITGKTPEGDPIKGDYKFTDEFPMAEGFEENAAFFTLTYEA
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VETVETVFIVTDSDAAFQAACRDLPSRVTAVRLYESYLHNFTINRRAGA
>PFR_JS22-1_188□PFR_JS22-1_188□Hypothetical protein□217631:217852 Reverse
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CWADVGASDRQSL
>PFR_JS22-1_189□PFR_JS22-1_189□Hypothetical protein□217849:218454 Reverse
MVDVRSAAGWIGFGGVAWAAGQAIEGRAFMQAAAKMNAQIGNDINYLARHGRLPDTPPAL
PLHGGLVASKPRIMAKCFAGGAGIAFLSAALLSFPVLASHQPTSGSPMAQAIFGALVTGF
GSAILLGWLIGAVLWIVFGAKENARRSANVVLQHFQDYWREREQARLALTQGADFLLVGA
KLRSYHIADKPDDDLFGSELA
>PFR_JS22-1_190□PFR_JS22-1_190□Hypothetical protein□218627:218794 Reverse
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>PFR_JS22-1_191□PFR_JS22-1_191□Hypothetical protein□219363:219812 Forward
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GRLKRRGEVESLGYGLYRATDSLRGPSRP
>PFR_JS22-1_192□PFR_JS22-1_192□Hypothetical protein□219809:219946 Forward
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>PFR_JS22-1_193□PFR_JS22-1_193□Putative phage integrase□219936:221165 Forward
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FGFGVHVHPQQATTLVLTAIPFGQPVGRPAGGDGDEPGTPEPDPLALELRRGMVERALEL
TACDDVVARYLPGPGMEAELVLTRTTGQHDSQSPEQSEKPMTHIRYFAAAAEAAGTDSEQ
IGLDEIGAQEISVDKHPTTLGELVDHLAGRHAGLAKVLRVSSFLVNERPADRDAPLPAGA
VVDVLPPFAGG
>PFR_JS22-1_229□PFR_JS22-1_229□Respiratory nitrate reductase, gamma subunit□258960:259679 Reverse
MSLVEMLLWVALPYVSIVLLVTGLVWRYRTDQFGWTSRSSEWNESALLRWSSPMFHLGIL
CVAAGHVVGLAIPESWTGALGVSEQMYHLGATVLGSLAALATLIGLGGLLYRRIVVKSVR
LATTRMDIVTYVLMCIPIILGTIATVSTQVLGDPGYNYRETISVWFRSIPTFNPQPELMA
TVPLAFQLHIVAGMLLFCVWPFTRLVHVLSAPIGYPTRPYVVYRSRKGEVAATPKPRGW
>PFR_JS22-1_230□PFR_JS22-1_230□Nitrate reductase molybdenum cofactor assembly chaperone□259685:260479 Reverse
MGEFVGLPSVPVADTVTLDDAPRRIARMACSLLLDYPDEALATTLGAVRAEVGALPAPVR
EEIDAFCAAAEQLGVRALQEHYVEVFDQRRRCALSLTYFTHGDTRGRGQALLAFREAMRR
AGFSQVREELPDYLPIVLELCALDDTGTGEALLAANREGLEVIRTALRSAHSPYAHLLEA
IVRTLPAASDETMAAYRRLIAQGPPTELVGVGRPTLHEPLEPNTREPGPHEHGPHEPGPH
EPNTHEPGLHASNPHAPSPHGRGK
>PFR_JS22-1_231□PFR_JS22-1_231□Nitrate reductase, beta subunit□260479:261990 Reverse
MKVMAQIAMIMNLDKCIGCHTCSVTCKQVWTNREGMEYAWFNNVETRPGVGYPRTWEDQD
RWKGGWRRTKSGALVPRQGGRARTLANIFANPTLPDVNDYYEPWTYEYDKLLTAPAGERN
IPVARATSSTDGRHIDTIEWGPNWDDDLGGSMETLDSDPVLKAMNLQVAKTIEDSFMFYL
PRICEHCLNPTCVSACPSGAMYKRAEDGIVLVDQDRCRGWRMCVSGCPYKKVYFNHKTGK
AEKCTLCYPRLEAGMPTVCSETCVGRLRYLGVLLYDADRVSWAASQADEHDLYRAQREIL
LDPHDPEVVARAQADGVPHSWIDAAQASPVWDLISTYGVALPLHPEFRTMPMVWYVPPLS
PVVDAVTASGSDGEDHKVLLSAISQMRIPLDYLAGLFTAGDPAPVELSLRRLAAMRSYMR
DVFMDNPPDESIAAAVGMSGEQVQAMYRLLSIAKYDDRFVIPTTHPEMPPGITELEGCPV
GYDARAFPGGHTPGGPTLPLEVI
>PFR_JS22-1_232□PFR_JS22-1_232□Nitrate reductase, alpha subunit□261990:265808 Reverse
MSTSQRQHDPHEQNAQPAHEHDHATDGGDSGSPLLRMGSWLRRGKASRDTRQLFLAGGRD
ADAFYRQRWSYDKVVRSTHGVNCTGSCSWKVYVKDGIISWETQETDYPTTGPDLPEYEPR
GCPRGAAFSWYEYSPNRVKHPYVRSALLDPYREARERLGDPVLAWASITDDPAISRSYKS
ARGHGGMVRVSWEEATEIIAASYVHTIKAYGPDRIAGFSVIPAMSMISYAAGSRFHELLG
APMLSFYDWYADLPPASPQVFGDQTDVPESGDWFNAQYLIMWGSNVPLTRTPDAHFMTEA
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QPGQASLGGGTVRRGVPARRINGRLVTTVFDLLLAQYAVGREGLPGQWPTGYDDASTPGT
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RADAMANPLGGASFAGKTTADCLVESAQRGWMPSYPTFDRSPLELGRQAHEAGMAPGDYV
SGELRAGRLHFAAEDPDAPENMPRVLANWRTNLLGSSAKGTEFFLRHMLGADNDVQASEL
DADHRPASMTWRDEAPAGKLDLMWAADFRNTSTTLHSDVVLPAATWYEKHDLSSTDMHPF
VHSFNAAVDPPWEARTDFQTFQELAHLISRMAATHLGTQTDALAVALTHDSPDELATPGG
VVDAERGWVPGVTMPRIVAVERDYTQIGNKFDTLGPLLASAGMTTKTVAFHPDRELDELG
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AADEDKRISFADTAVQPRSVITSPEWSGSEHGGRRYSAFVQNVERNKPWHTLTGRPQFYL
DHDWMIDLGEALPIFRPPLDMAHIYGGQALGEARSTATGETQVAVRYLTPHNKWAIHSQY
YDNPYMLTLGRGGQTIWMSPADAERIGVRDNEWVEAHNRNGVVSARAIVSHRIPAGTVFM
HHAQERTMNTPLNESTGKRGGIHNSLTRIMIKPTHLIGGYAQLSYSFNYYGPTGNQRDEV
TLIRRRGQEVQF
>PFR_JS22-1_233	PFR_JS22-1_233	Transporter, major facilitator family protein	265842:267200 Reverse
MATTPAGAPSSPGAALHTSGRVLTNWNPEDAATWSPRIAWRTLAISTYSMILAFCVWFLV
SAIAPKLNSIGFGLTTGQLYWLAAMPGLSCGLIRLVYMFLPPIMGTRKLVGWSSLLYLIP
MFGWFFAVQNPHTSFWVLMVLAFTCGIGGGTFSGYMPSTGYFFPKRLQGTALGLQAGIGN
LGMSIIQLVGPILMGFSLFGITWLAPEHTASGNLWVHNAAIFFVPWTIVAAILAFTLLKD
VPVKASFRQQIDIFSNPDTWLMTLMYVMTFGLFSGFSAQFGLLINSTYGETSRFAGMAAL
PQGVTYAFLGPLIGSLVRAGWGPLCDRFGGAIWTFISGVGLVITLGWAALFLNPSDPGQF
PGFLWAMLIMFFFAGIGNAGTFKQMPMIMPKRQAGGAIGFTAAIGSFGPFFIGIALSAMN
AAVWFWICAAFCALCSVICWIRYARPRAPFPG
>PFR_JS22-1_234	PFR_JS22-1_234	Molybdenum cofactor biosynthesis protein A	267344:268519 Reverse
MPATPLPSADGALRDRHGRTAHDLRVSLTDRCNLRCSYCMPPEGLAWLPTDQMLTDAEVT
RLCTLAVTHLGIHKIRFTGGEPLLRKGLESIVAACAGLRTDRGSSPELALTTNALGLAHR
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INAPDLPELFDFCLDNSLQLRVIEQMPIGPEGSWDRASMVSRAEILELLATRHQLAELSS
PPTTGTLPDGALPDGMPPSTVQPEHSAPSTSAPHTAEPTVAEPTTAPLDPHAPAQLWQVD
GRADTTVGIIASVSAPFCQACDRTRLTSDGQVRSCLFSTTETDLRALLRSGATDAQLADA
WRTAMWAKPRAHGLDEPWFAVPSRTMSRIGG
>PFR_JS22-1_235	PFR_JS22-1_235	MobA-like NTP transferase domain protein	268618:269292 Forward
MPGMFGRVMRDDRAMAATPSGARPDAGRRGRVGAVILAGGGGQRLGGVSKADLRLGQRRL
LDIVLSGLVPAVDGDAVVVAPRDVEVPPGVRRTLEDPPDGGPVAGMAAGLAALAGSHALV
LVTAVDSPGIVDLAPLLVAALSARPDADGVVARGGEPAPFRQYLQAVYRAGPLRRLLADA
GQVRNRGVARTLRVLNLVEMPSPADLCRDIDTPDDLDWWRGRLV
>PFR_JS22-1_236	PFR_JS22-1_236	Molybdenum cofactor synthesis domain protein	269665:270171 Reverse
MPHSDYDLAGIRAAIITTNNRVLAGERPDRGGQLAVEQLAAAGLQTSEPVVIPEEHHAVA
EQLRDSLDEGNRLVIVLGGTGFGIRHESPEVVREAIEVEIPGIAEQIRAHGLTNTPLSPL
SREVVGVTARDKTGALVVASPSSKGGVADTLSVLIPLLKDIFGQLDEI
>PFR_JS22-1_237	PFR_JS22-1_237	Molybdate ABC transporter, periplasmic molybdate-binding protein	270391:271167 Forward
MRTRPFALVTACLLSLTLAACGSSKGSGGASSSQNATLTVYAAASLTESYDELGKQFEAS
HPGVKVTFSYAGSQTLVDQLDNGAPADVLATANTSTMAKASDKKLVGQPTTFASNVLTLI
TPAGNPAHVTGLDSSLDSAKLVICAPAVPCGAATTQLTGLLGVTLHPVSEEDKVTDVRAK
VSTGQADAGIVYRTDAMASGDAVDTIPIADADKVVNDYPIATVTASRQQDLAGRFVALVT
SPAGRQVLDAHGFSTPGQ
>PFR_JS22-1_238	PFR_JS22-1_238	Molybdate ABC transporter, permease protein	271164:273284 Forward
MNDARPRRRAPRVSPAPWWLVALAGVALAYLVVPLLFMGAKVPWASFGRVITSDSARDAL
WLSVRTCAAAIVIDLVLGVPAAVALSRRWRGVRVARVLVALPLSLPPVVAGLALLVTFGR
KGVLGAGLEAAGVHIAFSTIAVVMAQVFVSLPFLVITLEAALRSRTQGLEQTAAGLGAGP
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GTALTLGVVLIVAAAVIVALTEWSGRRRRPAAEDEPASPTPTDVPDPAGQQRAAAVPVHV
DGAVTARDWQVSLDIPAGRVVAVMGRNGAGKSTLAQVLAGALALDSGTASIGPQVHDTAT
TFTPARRRGVAMVRQDPQVFAHLSVLANVAYPLRARGVPRAAARRAAHAQLAAVGADQLA
FRRGDELSGGQAARVSLARALVFDPRLLILDEPTSALDVQARARVTQVLADRLAHRGTTT
VLITHDVVEAVRLASWLVVLEHGRVAEQGEPARLLAAPTTDFTARLAGLNIVSGALIVGA
DALPGIAIGSRRLAAARIDPDSLFPGTLSPGELFPGALPPDALAPDTPLSDSMPPDSMPS
ASTAPGAGFPAPGSPVSLVFAPEAVSLFRVPQQGSPRSLLPGVVQAVDAASGLVTVRVAL
DDGPVISARITPAAWAELQLAVGQRLWCSVKATQVRLVPAPAPVGP
>PFR_JS22-1_239	PFR_JS22-1_239	Putative CoA-substrate-specific enzyme activase	273477:277853 Forward
MSDDALRLGLDVGSTTVKAVVMDGGRIVFNDYRRHNADVRGEMKRLLLDIRNRFPDDVLK
VAMTGSGGLGVARMMGVDFQQEVIAATAAIERLNPEADVVIELGGEDAKITYLHPTPEQR
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TPDDAQLYVAIGAAFLAGGPTLSLPHLAAELDSANEVSVASKTMRPLLLDDAERAEFIER
HSRATVPQGEMADAKGHLYLGIDAGSTTIKSVVIDDEGTIVHSSYGSNQGDPVAAAVGIA
RTVLGALPAGANLARACVTGYGEDLVKTAIHADEGEIETMAHFRAAKVVCPEVTSVIDIG
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LTDAKATRGEIGIPRALGMYEDYPLWFTVLTELGFKVMLSGRSNHDLFEAGMESIASENV
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PQMAPIHFRVLAPLFKRHGYTMELLEHASREDMECGLKYVNNDACFPAIMVIGQLINKFI
DGGGDPEKSVVAITQTGGMCRATNYVGMLRRGLAAAGFSQVPVLAISAQGLESNPGFKMT
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KLSFKWLCRQMVHEFDELPLLDIPRKPRVGVVGEILVKFQPDANNNLVDVIEDEGCEAVL
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TLRERYPMANITSIDYDPGASEVNQLNRIKLMIATAYKNAEDSGLAGWSNDFDTDSPLDL
PSVLGATRGDGNAVNARA
>PFR_JS22-1_240	PFR_JS22-1_240	L-aspartate oxidase (Quinolinate synthetase B)	277904:279493 Reverse
MSTSTRLGRQLEAPAPTWNKSAAVVVVGGGAAGLSAALPLAAARIPVVLVCRSTLLDTAT
ARSTSRGIGWRNPPTSEQLASAGDGLADPTAAGRLIEQAPELLDWLDALAHQISSVEQDP
RQPLGMTMQRTLASVARVQELLPAGTLAIDTHSRAVDVLTDEDGHVAGLRVSRGDGTIGD
YRAGTVVLATGGAARLWTHTTAPALANGDGLAMALRAGAALRDLEFVSFAPTALNAPPEE
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ARPESRGWHRRIDHAGASDKWAKHVVVSLADDGTLQVTTAALDKPVTTR
>PFR_JS22-1_241	PFR_JS22-1_241	Mebrane associated protein	280104:280901 Forward
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MRRLWRRRIVTRDERITYVDAVRPSKPAGRNRPDKHDDGSEEASPERLNWLRAGVLGAND
GVVSTAGLVLGVAGASADNRAILVAGVAGLVSGSMSMAAGEYVSVSTQRDAQRSGLAKER
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AAAFASMLSFAIGAVVPLLLITLVAPSARVLATVLASALALAVTGVVSAKLGGSPTRAAT
VRNIGGGMVAICITYVIGALLGSHL
>PFR_JS22-1_242□PFR_JS22-1_242□Methylase involved in ubiquinone/menaquinone biosynthesis□280912:281592 Forward
MADQHPFARHWNHNSHYYPRIAELLDGHRVVLDVGCGEGTLARYLATGDTVPVGERRDGL
KQPQPAPESFDDKDLRHEVVGIDADAKVLAPDAPGVHFMLADAQQLPFPDASFDAVVSVG
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TLTAEPDLNWTQSRELIEGNLPGAHWWRVPLWRWVAVWDAPAARRA
>PFR_JS22-1_243□PFR_JS22-1_243□Ribose-5-phosphate isomerase B□281927:282409 Forward
MRIAMGSDHAGFDLKEHLKEYLQGKGHEVIDVGTHSTESVDYPIYGAAAARKVADGEAAT
AIVVCGTGVGIGISANKVHGIRCAITSDVYAARMSRAHNDANALALGGRVVADGLAEEIV
DVWLATDFEGGRHARRVGEITALEDGQDITADDLDEHDQL
>PFR_JS22-1_244□PFR_JS22-1_244□Sulfate adenylyltransferase subunit 1□282742:284091 Reverse
MSTLTDTTVNPEAALTQRTLLHLATAGSVDDGKSTLVGRLMYDSKAVLADQLEAVERVSH
DKGLGTVDLALLTDGLRAEREQGITIDVAYRYFSSAERSYILADCPGHVQYTRNTVTGSS
TADVLVLLVDVRKGVLQQTRRHLAVGALLRVPHVIVAVNKIDLVDFDEAAYAPVEKQIRE
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LVLRPQGGALDPQYVEYRAYAGEISAGRVHVGDPVVVLPSGLRSTVAGIDLAGEQLDEAV
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QSGWTLAAGMVRGHEVFGDSLEPEPDWQI
>PFR_JS22-1_245□PFR_JS22-1_245□Sulfate adenylyltransferase subunit 2□284094:285161 Reverse
MNNPPLESSLVDTATTDSFIPSGTGASIFGQPTSSRENPRGATSAGQPAGHQASHDTSGA
LSHLAALEAESIHIFRETVGELEHPVLLFSGGKDSVVMLHLAAKAFWPGRVPFPLLHVDT
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>PFR_JS22-1_246□PFR_JS22-1_246□Phosphoadenosine phosphosulfate reductase□285188:285937 Reverse
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AKTECGLHL
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GQEPLNANEVVKAADDGLHVRPRIIDIYSKTGFDSIPEDDLQTRFRWWGLYTQRKPGLDG
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R
>PFR_JS22-1_248□PFR_JS22-1_248□SubI□288527:289633 Forward
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VLAGFGFRPLAGAVPAQVMGANDPSDPYPTPGRLLTIDKDFGGWSKVNKKFFADGGLVTK
LLSKVASS
>PFR_JS22-1_249□PFR_JS22-1_249□Sulfate-transport membrane protein ABC transporter cysT□289630:290694 Forward
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IVAGIAVVINLVFGVGISLLLVRYRFPGRRILSLLVDLPMSVSPVVVGLALTLVYAKDAA
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MEAPQHKDGRATRRPGRHKDRHKDHDRGPGAAELAGRPGDFRKRLWITFAITATIVVAQA
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ECVAEHFPVAVHHATIQIEPGGPSACAHGICEPLAVGHADRS
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LGLSQSTVSKHLIVLRDAGVVAVRPQGRASVYSLAHPETLVELLSAAERFLGLTGGAVTL
CPLHGPGVVADH
>PFR_JS22-1_254□PFR_JS22-1_254□ABC-transporter transmembrane component□294845:295675 Reverse
MTTLVENPTVTTSPVATGLHNRADLAQTVRNSLTMAYRGLLKIRHNPEQLVDVLVQPILF
TLMFAYLFGGAIAGNVASYLPALIPGILVQTVITTSMVTGTQLREDMDKGVFDRFRSLPI
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ALLGVVARTAASVQGFGMIVLFPLTFLSNAYVPVDTLPAALKWFANVNPLSHLITAVREL
INQSTISGEFWLTLLGAAVIVAIFAPLTVRAYMRRA
>PFR_JS22-1_255□PFR_JS22-1_255□Daunorubicin resistance ABC transporter ATPase subunit□295672:296742 Reverse
MTETLAVEAHGLVKQFGSNRAVDGVDLAIDQGAIYGVLGPNGAGKTTTISMLATLLRPDA
GSATIFGHDVERQAGIVRQLIGVTGQYASVDETLTATENLMIFGRLLGLSRRQARAKATE
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GPQLH
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>PFR_JS22-1_289	PFR_JS22-1_289	Hypothetical protein	337042:337878 Reverse
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>PFR_JS22-1_291	PFR_JS22-1_291	Divalent metal cation transporter MntH	338954:340369 Reverse
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>PFR_JS22-1_292	PFR_JS22-1_292	Transcriptional repressor sirR	340591:341268 Forward
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>PFR_JS22-1_295	PFR_JS22-1_295	Toxin secretion/phage lysis holin	344095:345774 Reverse
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AKVPDLPDYDDWKQRGIFRKDMGPVIALADFRADPVAHALETPSGKIEIYSQRLARMSEK
WEYGVFRDKLPGDSLHPLPEFVDTWEGALAARASREYPFQVIGHHYKARTHSTYGNVDWM
KEAHRQQAWINILDARNRGIADGDQVFLYNDRGTIRLEAKVTERIMPGVISVPQGAWYAP
KSADEVKPPPGANPERPVDTAGSVNSLTSLHPSPLARGNAVHTTIANVVKA
>PFR_JS22-1_325□PFR_JS22-1_325□Dimethylsulfoxide reductase, chain B□377773:378417 Forward
MADDLTRPGADYGFFFDQTLCTGCKACQVACKDKHDLPVGVTWRRVVEYSGGSWQTNEAD
```

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HTVTPNVFTYYTSISCNHCEDPLCVQVCPTTAMTQRDDGTVFVDQSKCVGCRYCEWACAY
GAPQFNAEAGHMTKCDLCYDYRQSGQDPACVAACPSRALEWGPIDALRAAHGDEAGIAPL
PDPAITHPRLVIKPHRDAQKWDQADGHIANPKEI
>PFR_JS22-1_326□PFR_JS22-1_326□Anaerobic dimethyl sulfoxide reductase chain C□378417:379421 Forward
MDVHHLPLVLFTVIGQMCVGTFLCLGVMQLVVSARHGRAVAQRIIEPVVYAIGPVMVLGL
VASMFHMHDITHTLNVIRHWRTSWLSREIIFGIGFAGLGFAYALLEWFEVAGFRLRQVVA
ALTALFGIALVWSMAQIYYSVPTIPAWHNWAVPFQFFGTTAVLGPLAVGCALMATAALRA
RHAAHDVATPAANPAHGGPTARIRGRIRAINAPATAGEWAISTSVVRWLALVAAVAAAAV
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WGLAALMATCLAGAFVAEVIGRFFHYAAMYRVGI
>PFR_JS22-1_327□PFR_JS22-1_327□DEAD/DEAH box helicase□379418:381880 Reverse
MAIPQWLAGDPCVLHVDHRDALPGTTAEWPEWLSADCVATIRAAGVPLPWRHQREAAELA
HAGRHVALSTPTASGKTLAYLLPLMAATAPGAAAEGFEWADAAQGDRRGPSTNRGLAAAL
VADHGLSADRLDPGLSGGGLAGAGLSGEAMVGSRARATTVSRARSALGLKQGATALYLAP
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RWARLLSGLRYVVIDEAHRYRGVFGAQVGGVIRRLRRLCHAYGSDPVFILASATASHAGE
SGAALIGEPEPIAEVNDDASPHPARDVVLWRPESSAYDDAKILAGLVDQGRQTIAFVAS
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HPERREALVNRRRPGYFTQPRTIIEARILHEDAHKPLGRTTVCTGDIDLTTQVTGYLRRD
EVTTQVWDENPLELPVQRMGTKAVWWTVPEDVAAEVGLSAIKLANAAHAMEHTAIGLLPG
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DATDAQADLIRLFPLQQIVPRSRLAAFLDVPALIEAGVLGAIGREGIHADIDVRPYGFTD
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QSLHLARHADTVTLTDINPRALDMARLTLALNGLDLDVRAGSFYEPVAHDSFDLIVTNPP
YVMSPPTDAADRLVYREGGFAGDGLVRHVVREGASHLADGGLLQVLANWADTREASWEDR
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GLGWIMVRKSGSAEPSVHMESWPYTIAQPVGAALSAGWTARDVAGLDDDELLARTFTVDP
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DQPVDELEAAILPRLREAIEQGFIA
>PFR_JS22-1_329□PFR_JS22-1_329□DNA topoisomerase□384055:386841 Forward
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VNVDDDFAPIYVVSADKKSTIKQLKAELKNADELYLATDGDREGEAIAWHLLQELKPKIP
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GRVQSVATRLIVDRERDRMAFRAASYWDIEAILDAGASATPRQFPARLVSLDGQRIAQGS
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RKLGFTTDRTMRVAQELYEDGYITYMRTDSVTLSGQAITAARDAITQLYGADYVPERPRI
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ELTVEAARELLAHTGGDERELGLDPTTHLAIVVKAGRFGPYVTEVLPDDDDAPAAKKSKV
KPRTASLFRTMDPATVTLDDALKLLSLPRVVGGEGEEQVTAQNGRYGPYLKKGSDTRSLP
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DALEAATRTPPLTVDGATAARAVLGERLGGDRLRLIGHVDALIRGDLVGGDLMGRDQARG
GGSQSITRKEWMRALTVGEQALQLTEVAGVLFGRRKHMVRLLGKVVAALSAARPPEGPLS
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R
>PFR_JS22-1_331□PFR_JS22-1_331□DTMP kinase□388327:388965 Forward
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>PFR_JS22-1_332□PFR_JS22-1_332□DNA polymerase III, delta' subunit□389223:390605 Forward
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DALLKSLEEPPARTVWVLCAPTPDDVIVTIRSRTRQVALRTPPNSDVVRLLVERDHIDRA
MAEYAAKAAQGHIGRARALARDEKVRNARHAVLLVPSRLTSVGACLTVADDLVKAADAEA
DRITGRLDEADRARLSEALGFGTKGARPRHAAAALRDLEDQQKARAKRVRRDALDRSLTE
LTTWYRDVLAVQTGAVDPSGLHSASGVVEGALDEPPTHTVGLINAEMRADVARAAVATTP
EQTLHSIDAILECRQALETNVNPLLAMEALLLQLGTATQS
>PFR_JS22-1_333□PFR_JS22-1_333□Hypothetical protein□390753:392441 Forward
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GVPDFSAPDAGPRPGFMTAAELAARDGAPGSAAATGQGAASGEAAVPAGSATSSFLRTTS
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>PFR_JS22-1_334□PFR_JS22-1_334□PSP1 domain protein□392571:393620 Forward
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GAATPADLARDEANRQVRADAAEVARLLIERHGLAMKLLAVDFLDQSSDYDRLTVFYYQS
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VDGTGAGKTSGTGGPTGSADASGTGGPAGSDDGAGPSRPTAASDAGTAQ
>PFR_JS22-1_335□PFR_JS22-1_335□ABC transporter□393975:394817 Reverse
MYTLTDVTKTYAGKHPVTALDRVTITIPDGQMVAIEGPTGGGKSTMLQMLGALDVPTSGT
VTLDDVELSDAGERRLQEVRAERVGIVFQNFNLIATLSALENVQTALVPLGVGAEERLER
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ALLHSSWHAMGLTVIMVTHDSRVAASAQRRLRIAHGRLSEIGDGRRAGADEPDGARGDAG
GARRSPAPAQDHPDDALEDATPGASHQPTAPGTYEERPLG
>PFR_JS22-1_336	PFR_JS22-1_336	Integral membrane protein	394817:396331 Reverse
MLMTFARRELGRRRRQTIIVALGLAIAVALLMVVHSVSSGVSRAQSEVLSSVYGVGTDIT
VTQKSTQQPGQGFDMAPGAQDANGNTSVSSTTVRTTRGTEAFDASQLATVQGVQGVAGAT
AVLNLEQTTFDGQIGSSGSASSSSSGSSSSASASPSASASSGTSRGAMGGGRMNLNQTTI
TGVEPGATLGPLSTLSVSSGRALATSDDGNDVALVSSDYASQHNVAVGGTISVANKDVSV
VGIVTSSSSSSISEVYLPLKTAQALSDNTDKISEILVQASDSNQVSTVASALTKALPSAT
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LLAGVIGGWRAGGMRPAEALRSVE
>PFR_JS22-1_337	PFR_JS22-1_337	Amino acid permease	396596:398047 Forward
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MLVYLIIGVMLYFVMRAMGELLLSNLNYKSFQDFAADLLGPWAGFFAGWTYWLCWVVTGM
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IVLAVVLVVIGFTAPDGVKASLANLWNDGGVFPKGMNGFLAGFQIAVFAYVGIELVGTTA
AETKNPLKTLPKAINAVPVRVLMFYVVALAAIMCVTPWSQVNPAVSPFVNLFGLVGFGAA
ATVMNFVVLTSAASSANSGIYSTSRMLYGLSHKGMAPNAFGRLTRHGVPASGLFVTVVLV
SSSLLLTMSNSVIEAFTLVTTVSSVLFIFVWGLILVSYLRYRAKRPDLHASTTYAMPGGR
VMCWVVLAFFAFVIWVLTQQPDTLKALVVTPIWFVILAIGWFAVRGRAHLDDTITQELRA
EKG
>PFR_JS22-1_338	PFR_JS22-1_338	FAD dependent oxidoreductase	398223:399578 Forward
MLDCLIVGAGFGGLTVATQLVRRGHDVMVLEARDRIGGRVDNARFSSGELVEQGGQWVFP
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RRLAERTVSDPAWAGANTAWLDQPMERWLTANLRTPSAQRDLRGALRAVVHGPLSDTTLG
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DALVTVFGEQAATPLEYLDHDWGADPFTKGSHGAHFAPGLWSVTGQQLGARFGRVHFAGA
EYASKFNGYMEGAVRSGTDTAAQVVMQLHGQ
>PFR_JS22-1_339	PFR_JS22-1_339	Transposase of ISAar20, ISL3 family	399978:401054 Reverse
MRRYRCADCGHVWRQDTSAAAEPRAKLSRTGLRWALEGIVVAHLTVARVAEGLGVAWDTA
NNAVLAEGKRLLINDPTRFEGVKVIGVDEHVWRHTRRGDKYVTVIIDLTPVRDGAGPARL
LDMVEGRSKAAFKTWLADRDDAFRDAVEVVAMDGFTGFKTAAAEEIPDAVTVMDPFHVVR
LAGDALDRCRRRVQLAIHGHRGFRDDPLYKSRRTLHTGADLLTDKQSDRLRALFVDDAHV
EVEATWGVYQRMIAAYRHEDRQRGRELMEKLITDLSAGVPKVLTELTTLGRTLKKRAADV
LAYFERPGTSNGPTEALNGRLEHLRGSALGFRNLTNYIARSLLETGGFRPQLLHPRLG
>PFR_JS22-1_340	PFR_JS22-1_340	Nitrogen regulatory protein P-II glnB	401837:402175 Reverse
MKLITAIIQPDVLEDVEIALAQAGASGMTVSEVSGYGRQRGHTEVYRGAEYTIDFIAKVR
IEILAAEAEVEGIISIICESARTGNVGDGKVWSSTVEDVVRIRTGERGAEAL
>PFR_JS22-1_341	PFR_JS22-1_341	Ammonium-transport integral membrane protein Amt	402172:403533 Reverse
MIALEISAGDTAWVLISAALVLFMTPMLAFFYGGMVRAKGVLNMMMMSIIAMGIVGVLWV
LFGFSEAFGNSWHGLIGNPFQYAGLKGLATAQFGTIPAFAFVGFQAAFAILAVALISGAV
ADRMKFGAWCLFAAFWSVLVYFPAAHWVFAFDGYAADKGGWIANSLKVFDFAGGTAIHIN
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AGVGCCYAVGLKYKLGYDDSLDVVGVHLVGGIIGTLAVGLFCKADLTNGINGLFYGGGFE
QLGRQALGAVAMFAFSFIVSSLIALVIKKTIGIRVSNEVEYGGMDISQHAEIGYDLSIIG
YSSTKSVRRTIIVPPDASSLTDKPARTQEEASA
>PFR_JS22-1_342	PFR_JS22-1_342	Hypothetical protein	403695:404759 Reverse
MADSARHDARRRAREQRRRKLRHDLHGLVSSSPIAGRTRASAGLLWRAPVWLITLLMAVV
LVGVITFGSFRSTGRPAQPAITVSPSASPTPSVSQTPVVAPQTMAPTGEDLADLQAQVAA
IENRYGVRVGLAVSGIAPVGAQLDATWTAGSATSGPALGTIDLPIALAVLNLNPVPSNIT
YLLAKSISGSSLSGDEALYSFLGNGEEAATRTNAVLRAYGDQNTTVATSTARQDVPAFSQ
TDWPVAPQAQMAGQLWCSSDAWYAVSRMHYFDDDHAYGFGSVVGSYLRTSDGVDDNGNPV
VRQMAIIPNANGDRIGVGLVVNGARDKLDDVKAAADAVAGRVYFGAVGFDGGHC
>PFR_JS22-1_343	PFR_JS22-1_343	Magnesium transporter, CorA family	404916:405818 Reverse
MKTVFGEGQFRWYATATSDTGGLKRLASQFNIDQEILTYAQDPHERAHVEYDADTGTFLL
IFNVAHREKIENHYDASPMTFIVKDHELFTINDEHTSYVNDLIAGFVKAHPEVTPIELLF
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IRQIKVQQPYHRLSDSAREQLDDAEIEANQLVEMTEMSSQIIGQLSDTYNNVLNNNLNDI
MRFMTVWSLLLAIPTIVAGFFGMNVALPLENAPHAWLIVTGIAAVLWLAMGLMLRHSMRK
>PFR_JS22-1_344	PFR_JS22-1_344	Phosphoglycerate mutase family protein	405822:406364 Reverse
MTSKLYLMRHAQAESFGPSGDMSRGLTDLGRDQAHHAGELLAAAGIQLAMVSAAQRARET
FAAMALSDPEGRPVRAEYMKALYDASPATLLQRIGETPDEVSALLVLAHAPGIPSLAANL
TWAASHREADLMQCAFPAATLVAFDVDGPWSQLTDFDPYDYTDAAHPRVSPVRPADLPTG
>PFR_JS22-1_345	PFR_JS22-1_345	Putative DNA modification methylase	406366:407634 Reverse
MTSGHRDKMCDVSAYLMLLAPSANHVYAAETATLAAAELAVTSPDLGAAVERRVAGVDYL
AFEADDLDPRKIAAQSSVLALFERASAPAELPGRASEQAALFGSEPAADVPTTSPSEVLL
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TTVRRDGRMMGQRLDATARPGEQTRGHRAVPDAPQLAMTMFTGDTRDAAVLFGKRKFDAI
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AGGALGLSWNTYGLSREDLAAICTDAGLEVRDDGPWLQFAHRVDSSIKRDLMVAVKPARL
VS
>PFR_JS22-1_346	PFR_JS22-1_346	Inorganic diphosphatase	407784:408341 Reverse
MTDEFRIATGLPQYDLTFDMTVEIPRGTKNKYEMDHNTGRIRLDRTLFTSTQYPYDYGFI
EGTLGEDGDPLDSMVILTEPTFPGCLVRCRAIAMFRMRDEAGPDDKVLCIPTADVRRDYM
DDIDDVPQMVMLEIEHFFTVYKDLEPGKSVEGASWTGRTDAEAEIRASFERAKGTSYEHL
KVDLQ
>PFR_JS22-1_347	PFR_JS22-1_347	D-alanyl-D-alanine carboxypeptidase, serine-type, PBP4 family	408403:409773 Forward
MKSATRRPLTRWIVAFGVVLVLVIAGSVGLHASGALVSGGASTVPAGVFATPATNLNGNG
VIGDAPVPASYAALSADKVAAALNRVGVRNGYSVVARDLSNGQVLDATRGDDAVIPASSM
KLMTTSSVIDKLGPTHTFSTRVMRQPDGSITLVGGGDVLLASTPTSYAYGSPQPATTQDL
AQRTADALKAAGTTSVTLGYDDSLFSGATRHPDWEPGDMAYVNDISALMVDEGGGSTTPA
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DGGMVAFALVGNGVGAEVRPYLDQMAGALSGCACAA
>PFR_JS22-1_348	PFR_JS22-1_348	Coenzyme F420 biosynthesis-associated protein	409935:411026 Forward
MGVQSTPEEPPQSGAALPWVDWDTTLRVATSSAPIGPPVSLAERRQAVEQLRASAERAPQ
IVADASHLQPPARGEALIVDRAGFARANTDMMRQIWQGIGVEVRPRGPGLIPGIVRGGAV
GKMIGLLSGHVLGQFNPLGSPPRLLLVAPSIMSTERRLGVDPGDFRLWVALHEQTHRAQF
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AAAVLEQVSGVMSLLEGHADVMMDRAGPEVIASLATIRARFDARRGRGGPQMIMLRALGM
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VHR
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>PFR_JS22-1_349	PFR_JS22-1_349	Cell cycle protein mesJ	411026:412015 Forward
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EALVVDHQLQPGSHEVAHTAVDAVRGLGLAARTVAVRVPHSGEGPEAAARRARYEALAAP
DAPGGRRPDLVLLGHTLDDQAETVLLGLARGSGTRSLAGMPAHFGSAPQFWRPLLGVRRA
DTERACVEWGLSPWHDPQNRDDRFTRSRLRHRVLPVLTAELGEGVIEALARTATLATQDA
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VTRWRGQKGVDLPGGHRVVRRAGVLFLDH
>PFR_JS22-1_350	PFR_JS22-1_350	Hypoxanthine phosphoribosyltransferase	412181:412732 Forward
MYATDISNDLEHVLIPADKLAARVEELAAQIDADHAGQDLLLVGVLNGAMMVMSDLSRAM
KSLVTVDWMAISSYGAGTQSSGVVRILKDLSTDIHDRDVLIVEDIIDTGLTLSYLVQNLT
SRGPRSLEIAAMFRKPEAVDAPVDVKYVGFDLPNEFVVGYGLDYNGLYRNLRDVATLATH
VYR
>PFR_JS22-1_351	PFR_JS22-1_351	PIF1 helicase	412804:415263 Forward
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SNERTVVVAAPTGIAALNVDGYTIHRLFSFNTATTTEQVASGDYYPGRFARTLKSLDTLI
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LVLARRGTGREFPEGSGPRTAAPTTDPWADIETFSRAGAADGGPVRHGDGAEQPAVLLVR
DGAQRSFVVDAPDMASEADRAAFLAARLRAAASRTVVDDGALAELEQLERQWGVTVITDA
MRRPADSAEQVFVPGARVCFTGSVIDARGTTISRSDMEQLAAEHELVAVPSVTRTRCDVL
VAADTASRSGKARKALDLGKPVISAAEFLAWANPAGPGR
>PFR_JS22-1_352	PFR_JS22-1_352	GTP cyclohydrolase 1	415290:415991 Forward
MPSRKGDPLSESTRAGRSDETRETDATDHAIDNSAYEQPGLELPPGFDGKRIEAAMREVL
IGIGEDPDREGLVETPARIARAYGEIFSGLGKEPDKVLARTFDISHDEMVLVRDIDVHSM
CEHHLLPFHGRAHVCYIPAKDGRVTGLSKLARLVDLYARRPQVQERLTTQMANALVDQLG
ARGVLVVLECEHQCMTMRGVRKPGSTTVTSAVRGVLRDPATRSEAMSLIVRNR
>PFR_JS22-1_353	PFR_JS22-1_353	Transcriptional regulator, GntR family	416002:416469 Forward
MPSAAREPGDGPDHAERPDGAPRRTAPQDASGRGGRPTGPLVHIDAASPTPVFEQIIEQL
RRGAVQGSLPAGTRLPAVRALAGELGVAVNTVAKAYRQLEAEGTVVTGGRNGTTIAGLAD
AEPTRVAEAARTLIARARDAGLSRDQALGLVARLW
>PFR_JS22-1_354	PFR_JS22-1_354	Dihydropteroate synthase 1 FolP1	416606:417439 Forward
MADRADRPGDGHTRVMGIVNVTPDSFSDGGLYLHADAAIAHGVELVRQGAELLDIGGEST
RPGATRVSEDEELSRVIPVVGGLAADPRTRDIPLSVDTMRASVARASVEAGAAIINDVSG
GLADDAMFATVAGLDVDYICQHWRGFGQEMNQRARYHDVVTEVRDELAARLALAEQAGIS
HDHLIADPGLGFAKMGEQDWQLLRHLDVFVALGHRVLVGASRKRFLGVLLNGREARDRDA
ATAAVSAWCAQRGVWGVRTHEVLSQADAIAVTEHLML
>PFR_JS22-1_355	PFR_JS22-1_355	Dihydroneopterin aldolase	417586:417960 Forward
MSVEPEMGFVVVSLSGITAMGHHGVLESERREGQPFSVDLRLVAPEPGTDELSEAVNYAE
VAELVSDLIRSQAVNLIETLAARIADAVVELPRVREVDVTVHKPHAPIPVPFNDVTVTVN
RRTP
>PFR_JS22-1_356	PFR_JS22-1_356	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	417957:418502 Forward
MNAFIDSDTLGDLKPLNRVVFSLGSNQGDSLDILQGAVDMLAATPQLIMVDVAPVYLTKP
VGNTNQPDFYNTVVLAESTMEPRDLLDRANVIEQAYARHRDPDNPHGPRTLDVDLIVVGK
RTSATQRLELPHPRAHERAFVLVPWLDIDPKATLPQGPIADLVARMDVGGVHKLDAGLLK
P
>PFR_JS22-1_357	PFR_JS22-1_357	Hypothetical protein	419076:419432 Forward
MLLILGLRKGFDMARNVKVVLIDDVDGGDADQTINFGLDGVNYEIDLSNANAQKMRDELA
VWVGHGRRVTGRRGAAARKQGPSDAAKIREWAKSTGRQVPLRGRIPNAIRAEYEEATK
>PFR_JS22-1_358	PFR_JS22-1_358	Negative regulator of genetic competence ClpC/MecB	420281:422857 Forward
MFERFTDRARRVIVLAQDEAKMLNHNYIGTEHILLGLIHEGEGVAAKALEQMGISLEAVR
EQVIEIIGQGSTPPTGHIPFTPRAKKVLEYSLREALQMNHSYIGTEHILLGLIREGEGVA
AQVLIKLGADLNRVRTTVLQLLSGYQEEGGGQPATAGAPEMGPGTSTNNGALDQFGRNLT
QAARDNKLDPVIGRQKEVERVMTVLSRRTKNNPVLIGEPGVGKTAVVEGLAQAIVRGDVP
ETLRDKQIYTLDLGALVAGSRYRGDFEERFKKVLKEIKTRGDVMLFIDELHTLVGAGAAE
GAIDAASILKPMLARGELQTIGATTLDEYRKHIEKDAALERRFQPIQVDEPSVQLTIEIL
KGLRDRYEAHHRVTITDEALSAGANLADRYIQDRFLPDKAIDLIDEAGARMRIARMTAPP
DLREFDDKIAANRAEKEAAIDHQDFEAAAKLRDDERKLTAARAEKETAWREGESDTPAVV
GEEEIAEVLSSSTGVPVARLTEEESQRLLNMEDEIHKRYIGQDEAVKAISRSIRRTRAGL
KDPNRPSGSFIFAGPSGVGKTELTKALTEFLFGDEDALITLDMSEYSEKHTASRMFGSPP
GYVGYEEGGQLTEKVRRKPFSVILFDEIEKAHPDIFNSLLQILDEGRLTDAQGRVVDFKN
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FHQLSQDDILHIVDLMVGQIENRLGDRDMGIELTPAARELVGKRGFDPVLGARPLRRAIQ
RDIEDPISEKILYGDLKAGSIVLVDVAEGATEKSTEAFTFKGMPKHDEVTDSEFAQLTGA
GSTGGDAGPAEPQAPSAS
>PFR_JS22-1_359	PFR_JS22-1_359	Hypothetical protein	423008:423694 Reverse
MSIPTPPQGWRSQARLLTMLLWLNMAVQLLAGAMCLLLATRVDTPTDSVDDPGLRMFDAW
QLLTTATGLVFMLTAIVWLVWQRGTARMALRWAPELSQPAWQLFNWVIPLINLWRPLVDL
RALHRVFTIVRKDEMAADGIRGSIELAQVRLDDFRAATTRWWACWITFATAQLVAAWIVA
GASGTTGARAGFIASGIADLLALPAAFLATRVVSELTRRVADAAGLRA
>PFR_JS22-1_360	PFR_JS22-1_360	3-dehydroquinate dehydratase 2	423691:424446 Reverse
MAVLELAGLTLGGPHTAIIVPLTGADPGAVQAQAEVASQPAVDLVEWRVDAFAPGADDAL
LADTARHIRTTTGKPLLATVRTGSEGGHFTGSPEDYARLVATLAGLDDVDAVDVEYRHPA
APETIASAHRASTAVIGSFHDFAGTPSLDAMVAHLEAMEQAGAQLCKLAVMPHNPEDTAR
LLLATATRSRDAHTPLLTIAMGRLGLASRLCGRDFGSCASFAALDEHGSAPGQLPLDDLA
QALSIVRHAER
>PFR_JS22-1_361	PFR_JS22-1_361	Para-aminobenzoate synthase, subunit I (Precursor)	424592:425173 Reverse
MATDMTLPDDLDRLVDRLVRDARGRRPVMVLDGGSGAGKTRLATRLVGALGERGMHGVQL
VSMDSFYPGWDGLQAASTMLPEVLRVHDPGYWRWDWQAGRRTDRVGLDGDAPILVEGCGA
LTAFSAGVGTTAMWFVMDAARRKQRALGRDGELYAPHWDRWAAQERQHWRRDRPRELADV
ILHDAGQVDAGAV
>PFR_JS22-1_362	PFR_JS22-1_362	Cobalt transport protein CbiQ	425184:426011 Reverse
MTALPHAPLTGTDQSGASGADWSGALARLNPVTRLLLTVLVAIPVLISLDWLSATVIFVG
ELVVFLACGVRARMLARRMIPLLIVAPLAAISMALYGKPGGDVYFQWWLVVISQRSLTMA
IAVVLRIFALGLAALVLMGGLDLTATADGLAQICHLPARFVLGTLAGMRMINLFAADWRT
MAQARRARGLGDTGRLRRFATMAFALLVFAIRRGTKLATAMEARGFDASTAAHRTWARPS
RMGRADAVGWLVAVVMVALALAVSIRLGTFTPVTR
>PFR_JS22-1_363	PFR_JS22-1_363	ABC transporter	426008:427678 Reverse
MPTPSTDLAPGVVASDWGWRYAGRQRWAARHLDFTIEPGERVLLLGASGAGKSTLLGALT
GVLGGDDEGEEAGSLLVGGKHPTRMRGHVGLVMQDPTSQMILQRIGDDAAFGCENLAVPR
EQIWPRVRAALDAVDLRLPLDRSTTALSGGQQQRLAIAGALAMMGGPGAPGMLCLDEPTA
NLDPEGVTTVHDAIASVVTDRHTTLVVVEHRVDIWTDLVDRVIVVSADAGLLADGAPREV
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GLSTTIVGPNGAGKTTLALTLAGLLEPLAGSVEAAPSLRPTSARFLTRAMHRHFDPARPI
TWASRDLLTRIGTVFQNPEHQFVTGSVREELAVGLKALGRGARDIDSRVDALLARLHLES
LADANPFTLSGGEKRRLSVGTVLAAEPRVIVLDEPTFGQDRATWIDLVQLVQDVLEQGRT
VISVTHDRDYLEVLGENELRLDIASPHPASASSPAGGRPAGHAPGERRPKDRQPSADQPS
GERPSADQPSDHRMAP
>PFR_JS22-1_364□PFR_JS22-1_364□HMP/thiamine permease protein ykoE□427704:428339 Reverse
MSPSKTTPATSDQTRPLEVGTRHWRVVDIVVAAVLGVACGLIFWIWNSIGYAWYSAMGAL
LPGLGGIAAGIWYLGGTLGAQVIRKPGAAIFVELVAAIVSALIGNAWGIETLTSGLFQGI
GAEIIFLIFRYRAWSLPVTLLAGAFAGFGAWANELFIGSTPNIAKSFGYNAVYLVSNLVS
GAVLAGLLAWLLTKALARTGVLSRFASGREA
>PFR_JS22-1_365□PFR_JS22-1_365□Adenine glycosylase□428571:429449 Reverse
MEPGQRRAVVRTVNQWYAHAARDLPWRRVGTSPWAIMVSEFMAQQTPVARVVGPWREWLD
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GDYTAGAIASFAFGARALVLDTNVRRVLTRLDAARQFPANSTTAAERRLAMDWLPDDAPT
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>PFR_JS22-1_366□PFR_JS22-1_366□DNA integrity scanning protein DisA□429515:430585 Reverse
MASIGDAKGRVAEQFRQYRSLLAPGTPLREGLERIVNGRTGALVVLGDNAIVQQISTGGF
VINTDFTPTALRELSKMDGGIVLSSGLDRILRAGVHFVPSGSIETIETGTRHRTADRIAQ
QAHVPVATVSASMSTIALFLEGMRFPIEPSHQIMGRADQALATLSRYRDRLTDDTRYLTG
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LENDYSIEERPGKPSLEELEELPTGDLLDPESVSSAIGFGAMPLDTHLRPKGFRLVHQAA
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>PFR_JS22-1_367□PFR_JS22-1_367□DNA repair protein radA□430623:432017 Reverse
MAKKQQDSYQCTECGWTGVRWVGRCPQCQAWGSVVERGASVSTSTAVRTSAPTTRALPIA
QVSAQASDRHLTGIGELDRVLGGGLVPGVVVLLAGEPGVGKSTLLLEVAAQWARAGHRTL
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RRPLLAEVQGLVAPVPNETPARRVTNGVDFSRVAMILAVLQRKARLPMSRRDVYVSTVGG
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LAIVPTNSRDNSRGAPTLHNLKVVEVPSVADALGVLDLRRAERR
>PFR_JS22-1_368□PFR_JS22-1_368□Hypothetical protein□432133:432771 Reverse
MHVDHLTFAAGPEGLEVAAKHLGELLGEEFKDGGFHPRFGTRNNILPLLKDRYLEVAEVL
DHPVAEKAVYGQAVRARSEQGGGWLGWVISVDDLAPFEERLDRGAVPGSRHFPDGRELKW
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FDGVNIEFTSPNAHPGINAAIFSTPEKGLVRI
>PFR_JS22-1_369□PFR_JS22-1_369□AP endonuclease, family 2□433028:433897 Forward
MFYRGGVVSKPLPDASGSKRLSVSLSTSSCYPEHTAEAFDIAAEAGYDGVEVMVGLDAAS
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LRWQREYAAGFVAGVRDISEHTGVTIAVENMYPWRTPGRAFQAYLPSWDPTDLDYDALTL
DVSHAATSQLDALELARTWGPRLRHVHLTDGVGLRRDEHLFPGEGTQNVWGLLQYLNDSP
FDGRIVLEVNTRKADNHAERVRELREVADNTRLHLGQLDAARPGASPTS
>PFR_JS22-1_370□PFR_JS22-1_370□CAAX amino terminal protease family protein□433971:434780 Forward
MPLSGESAPLLGDGARPARRRVRLGLETFGLLSLCLGKSAVYSVLSLVTSLTVGPKLNEQ
TTTINGAVTPDRPWLDVAYKLADDFFLIVPVVMAIYLLASVRRPGPSVWRAIGLDGLRVR
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IVMIGYLLTRWRQAGWNAWAAIVTSALIRGSYHLYQGFAGFIGNVVMGLAFGWYWQRTRR
LWPLIVAHTLLDVFSFVGYALLKNVWTWL
>PFR_JS22-1_371□PFR_JS22-1_371□Hypothetical membrane protein, DUF1211 family□434941:435648 Forward
MRAERVQAFSDGVFAILLTILVLEFVVPDYQEGHLFEAILGQWPIMFAYVLTFTYMGVVW
LFHHDLFASVKTTSIWLNILNLVLIFVCSLLNYATSLLSTAIATGNGTDMAAAFGIYDVN
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ALLIGGVIFHALAYAGSAHSYRRSRRKVLREARRQALKDAPGPESEPGPQSGPPA
>PFR_JS22-1_372□PFR_JS22-1_372□Aspartate-semialdehyde dehydrogenase asd□435740:436774 Forward
MRVGVFGATGQVGGVMRTLLAERNFPVDEIRYFASSRSAGRHLPWGDKQIAVEDMATADF
SGLDLAIFSAGKTASKEYAPKVAAAGAVVVDNSSGWRMDPDVPLVVSEVNPEDTKNLPKG
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>PFR_JS22-1_373□PFR_JS22-1_373□ProC protein□436778:437638 Forward
MALRTPAASVDRVHRLAFLGAGTMGGTIVAGLVRAGRDAAGIAVTTHTPAHREKLAAELG
VQAFADNRQAAAWASTIVIGVKPADALALLDEISPELGPDNVMISLCAGLSTDLLSAHLP
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ISGSGPAYVFAFVEALIEAGVTQGLPRGLATELATQTLLGSARLLDEGNDSVTQLREAVT
SPGGTTAAALRELDDHGLRSAVQDAVEACARRSAELAAAAEQADAR
>PFR_JS22-1_374□PFR_JS22-1_374□Uroporphyrin-III C-methyltransferase hemD□438127:439743 Forward
MSQRVDVEAPDNAGPDDVAGRLCHGRVVFVGSGLSSADQLTRAGLRALSSATMLVTTPEL
REMLDEAGVEVPDKDATRFVGDLPDVARFVVEAAGDDQSVARFVRGDPLLEGNIADEVSA
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KASHRPEGMNWYESKPLFGWQVLVPLTRDRNEELIERLSLHGAHCTEVPTIDVEPPRNAA
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>PFR_JS22-1_375□PFR_JS22-1_375□Phosphoglycerate mutase family protein□439798:440457 Forward
MGDQQTIVHVMRHGEVHNPQAVLYERLPGYHLSDNGSRMAQVVAAEFADVSLTHLRTSPL
LRARETMAPVAAEHPGLQVHYDPNLIEAGNKFAGMKFGRYKTALVDPRNWKLLRNPFTPS
WGESYEHIAQRMRTAIIDSARAAGPGGQAFVVSHQSPIWIARLSFEGRRLFHFPWTRTST
LASVTSFHFLGDECIDITYSEPAAHLLGSDGNAAFSSGN
>PFR_JS22-1_376□PFR_JS22-1_376□Mycothione reductase□440573:442093 Forward
MATESSGGTGLSGAGRHSGGGASDHFDLCIIGSGSGNTIVNHEFNDWSVAIVDQGVGEGE
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ALISLDRAMRHDGDDDSEHRRRTGEG
>PFR_JS22-1_377□PFR_JS22-1_377□Glycosyl hydrolase family 3 protein□442147:443376 Forward
MVTPRNPHRSHRPRLRRASRLAVFGMALALVTACSASPGGAGGSTSARDSTSGTTSPSAS
AASGASSLPPRACLDAARAMDPQARVELLYMGSVTATTPAAGAGQLANQPVGSVILMGDP
GSLQATSQLTDALGAARPGLLIATDQEGGQVQRLTGPGLDQMPSARQQSTLATDALTQRW
TSWGAQLRRGGVHYNLAPSADLVPRANRGANAPIGQLDRGYGATRADVATNVTAVLAGMH
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IDPAGPAAFSSRVVSGLLREQLGYSRVVISDDLGAAAALADYPVAQRGTLFLRAGGDLAL
DVDPASVAAMVADTRAAVAADPDFAEQTVAKAARVLQLRAGAGLGQCGA
>PFR_JS22-1_378	PFR_JS22-1_378	Arsenical pump-driving ATPase	443397:445172 Reverse
MTHLLEEMPRFLFLTGKGGVGKTSVACASAVALASAGRKVLLVSTDPASNVAQVFGQEIG
NHITAISALPGLDALEIDPQAAAEEYRARALAPVRDFLSAKDLASATEQLSGSCTTEIAA
FNEFTDLLTAHGPGAGYDHVVFDTAPTGHTVRLLKLPGEWSQFLSDGLGDPSCLGPMSGL
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>PFR_JS22-1_379	PFR_JS22-1_379	Putative arsenic resistance operon repressor ArsD	445169:445636 Reverse
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AFMQVAGADGLPLVVVDGVAVSTNRYPSREELAVFAGLASAAGCCSGDAAGANAPGCCGS
NNDSTGPSTEGSSCCGGSAPQALPLENTSGSAVQL
>PFR_JS22-1_380	PFR_JS22-1_380	Toxin-antitoxin system, antitoxin component, ArsR family	445733:446107 Forward
MATELTATGTPRSTSEALSAERADRVAEVFKALSDPVRVRLMHHISANCCSSVCVCHMPA
DLGITQPTLSYHLTRLLKAGLISREMRGKWAHYTATAHGLDVVRAFMDGLGAVGPGTCDA
TDCC
>PFR_JS22-1_381	PFR_JS22-1_381	Putative heavy metal reductase	446107:446559 Forward
MSATGARRVPSIMFVCVHNAGRSQMAAALTRCLAGDRAEVRSAGTAPASEINSQVVAAMD
EIGIDLLGTRPKVLTADAVQESDVVVTMGCGDSCPYYPGTRYVDWALDDPAGLSLAEVRP
IRDEIRKRVIALLDELGLHPDRPGISRSDR
>PFR_JS22-1_382	PFR_JS22-1_382	Phosphate ABC transport system ATP-binding protein	446540:447319 Reverse
MAKRIELKKLSIFYGDFKAVEDVDMMIEPRSVTAFIGPSGCGKSTVLRSLDRMLDVTPGA
KVEGEVLLDGVDLYGKHIDPVRVRRQVGMVFQQPNPFPTMTIRGNVLAGLALNKRRLSKS
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IFSNPDEAQTEDYITGRFG
>PFR_JS22-1_383	PFR_JS22-1_383	Phosphate ABC transporter, inner membrane subunit PstA	447324:448484 Reverse
MSADQLIESDPTHEGAGDEFARRPGARRASSQRESDAVQFSDSLTAGHLPPFTAIGLLVV
CVVGVFLVSQLAHSFSILSWVVISVIAYLALHYVVSRSVEGRRRAFDRFARDLVTLAFLL
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LILIVMVLNLLGRLIAARFAPHISRK
>PFR_JS22-1_384	PFR_JS22-1_384	Phosphate ABC transporter, permease protein PstC	448481:449461 Reverse
MSTTTSLRQAPGERPVPADELAALTTRGRRGGDTVFSGLSKGAGLVIVVILASVAIFLIW
QALPAFTGKALPFGNTLKYVGPFLFGTIYSSVLALIFAVPLGIGIALFIAHYAPRQLASG
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FVITFAVNAISRWVIHRRADFSGANG
>PFR_JS22-1_385	PFR_JS22-1_385	Phosphate-binding transport protein of ABC transporter system	449458:450561 Reverse
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QTTWRSAFTKKQAGIKVSYNGGGSGKGASDFTSGAVAFAGSDDALSLDAMKAGSFAGCAE
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GSIDSIK
>PFR_JS22-1_386	PFR_JS22-1_386	Hydrolase, NUDIX family	450754:451644 Reverse
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QSPEDPLVVCGHRPVLGAMQAGLHIPIQHLTTAQSLVLHIGDEAEPVAVESYPSPL
>PFR_JS22-1_387	PFR_JS22-1_387	Polyphosphate kinase	451641:453830 Reverse
MSNAPGPGDRDATSADQSADEQLPPDRYSERELSWLAFNERVLDQARDRLRVPLLERAKF
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LLHHPYDSFATSVQRLVEQAAADPHVLAIKQTLYRTSGDSPIIDALIEAAEAGKQVLALV
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NPKTARQYEDMGLLTCNPIVADDVARLFNHLSGMTQETHYRRLLVAPQGVRSGLIAAIDR
EIANKKAGLPARIRIKVNSIVDERIIDALYRASRAGVEVDLWVRGICGVRPGVPGLSENI
RLISILGRFLEHSRLFWFENAGNPSVGIGSADLMHRNLDRRVEAIVLITHANHIAEIGQL
FDLAFDPGTVNWKLDDRSWHADTTNAAGEPKLDLQEHLIDVVSHRRHAPSDGPSRRTLFF
QRPGVLPRP
>PFR_JS22-1_388	PFR_JS22-1_388	Mycothiol acetyltransferase	453827:454765 Reverse
MNPVVTGPIIRLSADDRDHIADLVRACTEHDGVSPLNESGWFGLQGLTASHTHWIARDGK
QVVGYAQADAREHTVQLMVAPPARRQGIATTLAKAAWQLHPAMWWSFGDCPGARELATQL
GLREVRKLLKMSLPMPADQPHDAHLPEGLRLDHFRDDDLDQLVAVNHAAFAHHPEQGAMT
AEDARNRMAQDWFDPAGLLVARDEAGTLVGFHWTKVADEDGRPRGEVYVLGVDPDFEGKG
VGRALLDTGILHMRELGVEAIDLYVEGANERVVHMYERAGFSVVSTDVGYAPAKPARHQD
HGRQSSPQERDA
>PFR_JS22-1_389	PFR_JS22-1_389	UDP-glucose 4-epimerase (UDP-galactose 4-epimerase) (Galactowaldenase)	454977:456005 Forward
MKILITGGAGYIGSSVAACCADNDITPVILDDYSKGLREFAAPYLNYEGDIADVPLIRRI
LSEHPDIDAVIHCAAKIVVPESVSAPLDYYENDVSKTLVLLRELCGHGVRRFILSSTASM
YEGGDGHLVDESSAVVPHSPYSASKWMLERMLRDLAATGAMEVVALRYFNPIGADPKMRS
GLQDERPTHALGKMIEAYQGGGTFTVTGTDWPTRDGSGLRDYVHVWDLARAHIAALECFD
SVMLQAQVPGFDVINLGSGRGTTVFELVDAFGDAMGVRLDMGTAPARLGDVVGCATLTGK
AERLLGWNAELSISDGVRHSLEWAARLPAVLERERARAAGQA
>PFR_JS22-1_390	PFR_JS22-1_390	Carboxymuconolactone decarboxylase family protein	456037:456762 Reverse
MAHKQTAGRDNLGELAPTFAALNDDVLFGQVWSREGQMPARQRSLITCASLMSQGLFPQL
EAHLRIAKANGVAKQELVETFTQLAFYAGWPKAWSAFGLLKDIYADVPDDTPDAGLFPLG
SPADGPNFTGHAWLHMLTGPDNPLSAGNVTFAAGCYNRWHTHPAGQLLLVTAGHGWEQQQ
GKPARELHAGDVVECPAGVQHWHGAARDSTLTHVAVTPVSAGQAAVEWLEFPSRSDYEQL
D
>PFR_JS22-1_391	PFR_JS22-1_391	Putative oxidoreductase GLYR1 isoform 1	456941:457741 Reverse
MIPHLVETDFEIVAYDKLPERLQLAKDAGAKVAGSVAEAATGADVVIQLTMSDDIPDVLI
GEQGALAVVKPGAIVVVTSTTTPQMLNRVIEAAPAGVEVVDAPIVGGVRYAREKSVTFLL
GGSEQVASKLDPVLSVMGIIRYVGKSGNGVAYKLITNVAIMAAEAGLREALDLADELDMD
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YELSLDLMSVGPMAAVVSRALDTSNPRPLRRSAEDDDTLLSAVSDPERVLPISVAGRGRL
WEAVHAKEGFDPDFVDLTRKTTARNN
>PFR_JS22-1_392□PFR_JS22-1_392□Inositol 1-phosphate synthase□458167:459246 Reverse
MSSIRVAVVGIGNCASSLIQGVTFYHDARADETVPGLMHVQFGSYHVSDIEFVAAFDVDA
AKVGLDLADAIDASDNCTIKISDVAPTGVTVSRGVTLDGLGKYYRETIEESAEEPVDVVR
TLKDVHADVLVSYLPVGSEEADKYYAQCALDAGCAFVNCLPVFIASDPQWAQKFVDAGLP
IVGDDVKSQIGATITHRVMARLFEERGIQIDRTYQLNVGGNMDFKNMLERERLMSKKISK
TQAVTSNVEHHFEERDIHVGPSDYVDWLDDRKWAFVRLEGRNFGGAPVSLEYKLEVWDSP
NSAGVVIDAIRAAKIGLDRGIGGPLLSPSSFFMKSPPEQRHDEAALDSVEAFIRGELAP
>PFR_JS22-1_393□PFR_JS22-1_393□Transcriptional regulatory protein GlnR□459618:460277 Reverse
MSDALFVSPTTDPKPLPGALTLLPHTIDQVQGGDKAILQIPDTDAVIIDGRGDLGATRVT
TRLIVNSGAAKPTLLLIPLQGLSVLTAEWGVTDFIVEDAEPAEWEARLQLMLTAQGHATI
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RTVDVHIRRLRAKLGPEYDSYIGTVRNVGYRFNPQQRKD
>PFR_JS22-1_394□PFR_JS22-1_394□D-tyrosyl-tRNA(Tyr) deacylase 1□460442:460873 Reverse
MRVVLQRASRAQVSIDGQVVGQLPAPGLVALVGVTHGDDAATADKLAAKTWNLRILEDEK
SASDVNAPILAISQFTLYADTHKGRRPSWGAAAPGPVSEPIVDAYVAALRKLGAHVETGH
FGADMQVELVNDGPVTIILDSEH
>PFR_JS22-1_395□PFR_JS22-1_395□UPF0678 fatty acid-binding protein-like protein□461186:461689 Forward
MPFEIPTDLNPALMPLAWLIGRWQGNGHGTWPDSGDFEFGQQIEFSTNGQPYLHYFSQTY
VADKNGNPVSPISMETGFWRPINDKSVDVVMCHPNGWSEVWTGKIDGAKIELVTDVVART
KNSELEYTGGERLYGNVEGDLLWTFDRAAKDVPLQPYMWGRLARKSL
>PFR_JS22-1_396□PFR_JS22-1_396□Folate-binding protein YgfZ□461829:462878 Forward
MSGVVLVPEGPDAGLLWHRGDPFAEERAIAAGQAIVALTNRQVLTVTGDDRLGWLHSLST
GRFDGLPPGQGLNALILSPTGQVRYGLQAVDDGERLWVITDPASSASPDDPAEPAPATGV
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PIALGLVRRAVPVEATLSVDDIAANQEPIVDPDIGLHVKPEPGLRRRLI
>PFR_JS22-1_397□PFR_JS22-1_397□GTP-binding translation elongation factor typA□462968:464851 Reverse
MTVKRRKDLRNLAIVAHVDHGKTTLVDAMLWQSGAFRAGSDVETRVMDSMDLEREKGITI
LAKNTAVKHTMTDGRTLTLNIMDTPGHADFGGEVERALEMVDGVLLLVDASEGPLPQTRF
VLRKAMAKKLPIVVVINKVDRPDARIDEVINETYELFMDLLDDADGNGLDFPILYASAKA
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GENARPDDMDVNPTKEKHLTNVRSATGDELERLIPPRRMSLEHSLEYCAGDECLEVTPDV
VRVRKVVLDARDRAKVRTKEKSADANV
>PFR_JS22-1_398□PFR_JS22-1_398□Surface-anchored fimbrial subunit□465966:468554 Forward
MPGPAATDVPTASPAPAAETRAAGAFDCTPGYVYTAAEDGTIKQVSSTNAVTTPVTAPGS
GAGDSRTWTSDTRKWGTGLLTKTWGMGPFGIGAGGTKAYSLERGNAATADTNYGIPSLQG
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VGGAMSFRLSSYKPGGLNGAWRTIGTIPLPDFASDATTGNPESDYFAGSRGLEGDIAFDA
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GAPTDPTAWTLRAISRQAFMANPNAAWTDFTSGQTRSLGAQTYLLDEAPQPGYELTGITC
TPLGGTAQTLRREPVDPARPELGEAYQWSLAAGQQVTCQLHNSVQPGTLTWTKTSQSSDL
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RPGGLVPGVVVNPTAGVGRFDVTGLPTGNFWLVETRSLPGHALLPAAVPFTVVSGTTALP
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RSRLSHPAAASPGDPLSDKEMR
>PFR_JS22-1_399□PFR_JS22-1_399□Type-2 fimbrial major subunit□468551:469690 Forward
MRMTTTLTRRTRWWRRFGAGVVAMVMASLAMFGASRASAADVGNPATIDPGATGTLNVNK
RVNPTGTPTPGNGLEQANVTGDPLGGIEFVVKQIPGIDLTTQAGWDALAAMTVDQARTAT
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STKVAGDIGDGIILNDARLFPSMSVDPGDPQSGVSVADPPVTKWGNIEITKKDAGPTMLA
GAQFRVYPTPPTPRPAPTG
>PFR_JS22-1_400□PFR_JS22-1_400□Hypothetical protein□469783:470055 Forward
MASGEPGYNEYWLGEIKAPDGYELQAEPVQVVVDQLTNQVSVTNVKHNVGFQLPMTGGTG
TLVFIIVGLAIIGVATVVLVRSHRRSRQLA
>PFR_JS22-1_401□PFR_JS22-1_401□Hypothetical protein□471056:471358 Forward
MAEDNHSNARRNGIRPTVAERSSWRTAQGPLASVVPIGVGGWPRPIRGNSHELGVAANSS
VPASASGSQSAPDATGPVVIPATRRVPGDDAGGMATTTPC
>PFR_JS22-1_402□PFR_JS22-1_402□Putative fimbrial associated sortase-like protein□471555:472481 Forward
MNAARQARRPTTRPAGWDRVLIAGLVLLGVLVMCYPSAASWFSARAERDAMHSYAEAVGR
MSPEQRAALLKSAEDYNASLPGGLIIDPFTNTAGVEPMVLDEPARLYLAQLNAEADGVMS
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ASPRPGMM
>PFR_JS22-1_403□PFR_JS22-1_403□Uracil phosphoribosyltransferase□472424:473065 Reverse
MELRVVNHPLVAHKLTHLREASTPSPTFRLLVAELVTLLAYEATRDVLLTDVEVDTPVAR
AKGSALAKPKPLVVPILRAGLGMLEGMTRLVPTAEVGFVGMARDETTLQPTTYAERLPHD
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TLVVAAVDDHLNEHGYIIPGLGDAGDRLYGLAE
>PFR_JS22-1_404□PFR_JS22-1_404□Putative tRNA adenosine deaminase-associated protein□473254:473982 Forward
MTGDKKNDKDIDVTDVDHADVDDTSADRAGTADDLDSLDDDDNELDASVVTDDYDDDLDD
DSDDDDDDDDSDDDDDDDDDYDDATSDEIDFVVALYREGGEPTVTELPDICANDLDELVA
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DPDDDSEPVGDLDILADQGVSDFEMESIAEDFDEDSGELVGRVVEDMKFTEPFDKALGDD
GP
>PFR_JS22-1_405□PFR_JS22-1_405□Cytidine and deoxycytidylate deaminase zinc-binding region□474054:474485 Forward
MSRALALARGAGAAGDVPVGAVVLDGNGVLLGEGGNRREQDGDATAHAEVLAIRAACARR
GAWRLDDCTLVVTLEPCTMCAGALVNARIRRLVFGAFDPKAGAIASLWDVVRDPRLNHRV
EVVGGIMADDCQRVLTDFFATRR
>PFR_JS22-1_406□PFR_JS22-1_406□Hypothetical protein□474960:476816 Forward
MFGRKSRKKAAAQATPDAEVRADDAVSPAVSEGGADQPAKGPGNAAGNPDHIAAGDPDHS
AAGSMPDADVSPATDSAAATSDIPDGNHGDDATGEATAGDDGSRAVIAQAISEDANHSQP
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DQPAPDKTVGVLDPETAAWLAGFDDPDEGGEHYVPRYARPKARHTEGVPMADWPTEPMRA
LTPEYLAQIKAQLDDKSK
>PFR_JS22-1_407	PFR_JS22-1_407	Na /H and K /H antiporter	476832:478412 Forward
MSAFDLTLLLGSAVALVAVAAARLGSRAGVPALLLFLFVGIGLGSSGLGIDFSDATMAHN
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LTDLGRGGRLAMWHRGGRRWTRAQRRAHAQARRLQAQADKQAGTAQ
>PFR_JS22-1_408	PFR_JS22-1_408	Hypothetical protein	478494:479093 Reverse
MIDDSRTRPTPVRLSPPPLSRKRYPVHKWRTPLILTVVTCIVVLGGWWGWRAFMHPEANV
PPCVSQSASQLSTSQVQLRVINAGTVRGRANEVAGIMRAQGFVIASTGNASPSPSSQATP
APGVTVPVTIVGTSTEDPEVQLVAGFFPGATVTADGRPDHRVDVIVSDTSAMPLQSAERT
VPIPNGVICLPAGAASTGN
>PFR_JS22-1_409	PFR_JS22-1_409	Ferrous iron transport protein A	479457:479816 Forward
MSARVVPDEFTAETTQAVASFETVGSKIVPLSNLHAGDVGVICRLDEEADESITHRLQLL
GFDCGREVCLIRQAPLSGPMVFRVCDAQMCLREAQADMIYVRIPDDAAQVVADAEAIVA
>PFR_JS22-1_410	PFR_JS22-1_410	Ferrous iron transport protein B	479995:481959 Forward
MSSVVDASRHSTPGAPAPSGTAQIALIGSPNGGKTSVFNRLTGLHAKTGNYPGVTVSRTR
GVMKVHDHTYNIEDLPGSYSLTPISPDEQVVSDMLNGKLEGVGEPDALLVVADSTALRRS
LLLLSEVLPRHKPTALAVTMTDELRRRGGVLDIEGLSKALGIPVVAVVANRGIGIPELRK
TLTEWQDWSRPPIDPPADPAELAGWVDSILASAGYEGPNPDSRTEKIDKVLLHPVWGTII
FFAVMFLFFQALFTWAAPLQDAIDTFFGYLGGLVDEHISNPVLGGLLGDGILGGVGSVLT
FVPQILLMYLILALLDAVGYMSRAAFLMDKVMSKAGLEGRAFVAVLSSFACAIPGVMATR
TIPSSKDRIATMLGVPLATCSARLPVYLLLVGMLVPSEAKLGPVSWQGITMFLLYLLGGV
AAMTAAWVVKKITDRSGAVLPFYMEMPPYRVPTPRSVGIAMWEPTKAFLRKAGTIIMAAT
IVIWALTTFPMRSDEQLSAAGVDPGDAVAVSAYTMENSVAGHVGRFVEPVFEPLGFDWRI
DVALMGSLAAREVAVSSLGQMAASSDPEATDDVASQLEGWTYTQGPSEGQKVFTPATTVA
LILFFAFALQCLSTVAIMKRESGGWKWPSIAFGYMFVLAWVMAFIGHTITLLVT
>PFR_JS22-1_411	PFR_JS22-1_411	NifU domain protein	482086:482733 Forward
MARAGQSPAPRPDAGSRQAGPAGGRMDCPPLRDPSSATPPGVIALHPEATDDPATLRWVV
SHHILPFAGTLASAPGLDDLLADRVSRVVVGPDTLLVTLAPGSDWAELGPVVRRALMRAL
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ACRGCPAAVITMHQRLEHQLRRRVPGLVDVRSING
>PFR_JS22-1_412	PFR_JS22-1_412	Galactokinase	482923:484071 Forward
MAEIFPQHFNARPTGVWSAPGRFNLMGEHTDYNRGFCLPVPLDARTFLAARARDDERIRL
VSLNIEGDVDVELSAVDAERPGGWGAYAAGVLWALRQAGHPVRGVDMVIGSTLLIGAGLS
SSAALECSVAAAASDLFGLGLLADDAGRKQLAVACQTAENEIALAPTGGVDQTSALRGSR
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RAGYATPQGFVGEAGSPAARDL
>PFR_JS22-1_413	PFR_JS22-1_413	Hypothetical protein	484288:486060 Reverse
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AASGTTAGQPRPTEPSTTGPAAASPGAGGPVTSGKGADDTGTDDIAHETPIATLQDGRYR
LVERVGAGSIGQVWRAYDATLQREVAVKTVNLAMSADPATGARFRREAVATAGLDHPNVV
QIYDSGVDGHTAFIVMEFLHGPNLQTVVNQEGPIPYAVAVPLLAQVAAGLGAAHAIGVTH
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>PFR_JS22-1_414	PFR_JS22-1_414	Protein kinase family protein with PASTA domain	486184:487974 Reverse
MTDSPIVLGDRYELRSVIGRGGMAEVWQARDLRLGREVAVKRLRADLATDPTFQTRFQRE
AQSAAGLNHPNIVSVYDTGSQEDSATGVMRPYIVMELVSGHTLREILHEGRTIVPAKALE
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GTAQYLSPEQARGETVDSRSDIYSAGCLLYELLTGRPPFIGDSPVAVAYQHVREQPVPPS
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TTSTVDQDGCRAGIICGQTPPAGTPYLRSAPVNIQVGRAVSPSPSPSPTPSPSRSS
>PFR_JS22-1_415	PFR_JS22-1_415	Penicillin binding protein transpeptidase domain protein	488066:489490 Reverse
MNKSLRGVSLIAAIMFLALLVNATFNYGFRSKGLNDDPSNRRVTDSQFNTDRGSILASNT
PIAQSVAVSGNRFSTQRTYSNGALYAPVTGFYSYIYGRTGLEQSYNSQLSGQDDSQFFSR
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QLSSVDLPATQTAWQNLVGDPSNPMSDRATQQIYPPGSTFKLVVASAALENGKSAASTVS
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>PFR_JS22-1_416	PFR_JS22-1_416	Cell cycle protein, FtsW/RodA/SpoVE family	489487:490875 Reverse
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NWVIVAALMQISHAGRRPAAAASNPDPDMESAPTAMIGRVEP
>PFR_JS22-1_417	PFR_JS22-1_417	Putative SERINE/THREONINE PHOSPHATASE PPP	490872:492407 Reverse
MTDPAHRPPATAHPQDSAHSTATPDPGAASGGLSLDYRAHSETGPVRRNNQDSAYVSPTM
LVVADGMGGAAAGDLASSVAIAELKRSDAPRPPDEMLEVLAGAMNRANDRLADLIAWDHQ
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LQSTNGTYVNGVRIVQPTLVGAKDVIRIGRTQLKLER
>PFR_JS22-1_419□PFR_JS22-1_419□FHA domain protein□492886:493602 Reverse
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HLSTHDYDRLAPYSRTLNAEIVPDLREHASARGYVFDGPIHIEYVLDDSLPTGRFEVTSA
SVATVAENGGAASSTMIRRAPLVLEVNGVRHPLMPPGFTIGRGTEADLRINDPGVSRKHA
RINVSENADGELLISIDDLGSTNGVIVNGQRVTHSPLEDGSRIEMGSTRMLVHSPVGT
>PFR_JS22-1_420□PFR_JS22-1_420□Thioredoxin□493773:494201 Reverse
MATLTVTEQNFTETIEGNQIVLLDFWASWCGPCMQFGPIYDQVSEDHPDIVFGKIDTEDQ
QSLAGAANITSIPTLMALKDQTIVFSQAGALPRAALEELIEQIEKLDVKAALEAERAQRE
ASGDSTGDDNPQPDIEANSTRE
>PFR_JS22-1_421□PFR_JS22-1_421□Glycoside hydrolase family 2 multidomain protein□494339:496246 Reverse
MATPRGSRPPGDSIRGSRPPADPIRGSRPPADPIRGSRPPADPIRGSRPPADHPRPTMVR
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DDQKVSVDMNQAGDGVEVKGEAPVSA
>PFR_JS22-1_457	PFR_JS22-1_457	Oligopeptide transporter, OPT family	536206:538197 Reverse
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TTS
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>PFR_JS22-1_522□PFR_JS22-1_522□L-serine dehydratase 1□612442:613833 Reverse
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GHQG
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>PFR_JS22-1_531□PFR_JS22-1_531□60 kDa chaperonin 1□624433:626055 Forward
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DAQRSQ
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>PFR_JS22-1_554□PFR_JS22-1_554□Hypothetical protein□656157:656567 Forward
MTSPAPSDDSTVDGSAPDLAQCASFALTGHYLGGARPEVSEPGQLLAVLRDHGWTPQRLA
ALRDQRHHDGQGWPMALPIGVPAPGGFARFHAWVSEVVVALNLDSRDAGVRDASQPLDAE
TRRLMADLPPHYGSAG
>PFR_JS22-1_555□PFR_JS22-1_555□Large conductance mechanosensitive channel protein□656621:657064 Reverse
MKGFKNFIMRGSLIDTAVAFIIGAAFGAVVTSFTQIVLDLLGKLGGTPNFSSWAPGGVHV
GTFLTALISFLILAAVVYFAIVVPINKMRELRHPDAEKTQTEAEILTEIRDLLARNEAQG
IERVNDLAASNSPSLEGRTQARRSSDG
>PFR_JS22-1_556□PFR_JS22-1_556□Hypothetical protein□657157:657798 Reverse
MGVTPPAWLNSLVRAVRWHRRGLGLIAAAICVVAVLTALDPSASSSHTVVIASRPLAAGV
AVGADDVTTLQVPAEVATSATLADPGAAIGQVVAVPRPAGTVLTSSDFVGKGLVADSDGL
TLVPFRIEDKGVAGVLGVGNQISVVGANPGADTRVIASRVRIAALPSPGSSGALDDSSSS
SGALVIVAADSHTARELAAAASEYTLSVVLESD
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>PFR_JS22-1_557	PFR_JS22-1_557	Type I antifreeze protein	657898:658305 Reverse
MPTYEYTCTDCGHDLEVFQKFSDDPLTVCPDCNGHLRKVFSPVGVVFKGSGFYATDNRTS
GASTAPGSSLHDTESAHGADSSQASESATHTSGDASTGSSTASGATTSGSTSTSGSTTPT
ASTAAAGSGTQAKVA
>PFR_JS22-1_558	PFR_JS22-1_558	Hypothetical protein	658461:659174 Reverse
MHVWAQHRGTHRARCRRAEHAPAAGGPSAPPTEGGQNTKAQLRRLARRRRADRTADERRE
ATRELTGRVLDLARGRIPNDAVIASYLSLPDEPDTHPLVDSFLEAGYRVMVPYMTGGPAA
DDIDWAWYTTGSELSPGVLGIDRPRGEPLGAPALSRASVVILPGLAGGRDGSRLGMGAGW
YDRALAHTRPGTLLWLLLFDDEVTDTLPQEPHDHAVGVIITPHHTIVTADNGNRPAV
>PFR_JS22-1_559	PFR_JS22-1_559	Molybdopterin molybdenumtransferase	659189:660475 Forward
MALFGRKQAPVAAEPEPEPDPTLPGAPAPQANGLRSVSAHRDFLLSKVQPLMPFGMRLLD
AWGLSLCEDLVADGDLPPLPEAESDGYAVIALDVRDAAVGTRVQLSVRGDVQKVGSAVPV
YAGQPMPPGADAVLPLAQVRREGQELSLLAPVVTGEHVRPTGIDAAMGEVLIHAGKQLDA
RAIGLLAGAGFDKVFCRPRPRIVVLAVGEQLADDAPASMAERRRDAASHMVAAAAKADGA
QVWRESVAGTTPDDVAEVVSDQLIRADLMVICGGTAGGRDSLVGRSLKSLGQTDFAEVAM
EPGGLQGFGIIGQDEVPVVMLPADPLAAYVAFELFAHPLIRTLMGARDMALSSVDCRLTM
DVSGEAGLMQVVAGVITRDAQQWSVTPLDFAQGSLTTLVDADALIVLPAELGTIAAGAVV
TCWLLDRD
>PFR_JS22-1_560	PFR_JS22-1_560	Acetytransferase	660479:661189 Forward
MVDLDLPRAHRWPLTLRFGPLALRPIERRDAAELRQLRARNREWTGPWDTTVPPQGVPRS
LTFGRMVAEQRARGRAATQLSWLLTLDPGAAGGGEARRRRRAPIVGQLTVADIVYGAGRF
ASIGYWIDEGHAGRGLVPLAAAIATDYCFEVLELHRLEICIRPENQRSLRVVDKLGYRRE
GLRPRYLHIDGDWRDHLVFVMTSEECPAGGLVRALVEQRVQDAATNPAKAAGDAVD
>PFR_JS22-1_561	PFR_JS22-1_561	Hypothetical protein	661264:662067 Forward
MTGLIWLAIVAGWLAYLVPRFLLHKEVSISPTLSAARDALASPMHLVRRGGQDDFAEPTD
PSLQISTPLQRDSVLFQTRRAAQIAMRRRRTGFLGSLLVMVAGVVVSVITPAPWWLALVG
VGVLAVFVVLSRISVHTVNAMIADQLEAADQDWAEDTVTVCEVDLTHVHDENTEISIPLN
LPVDSTIGDLWEPIAVTPPTYVSKPLVPRSVRTIDLTMTADPPAQPKMPVTAERPEDVDD
TTDIRAAQDGRHDHGGDEGDLPRAVGE
>PFR_JS22-1_562	PFR_JS22-1_562	Low similarity to site-specific recombinase	662115:663617 Reverse
MIQYVKANKVAYCIVHKVDRLARNRADDVSIHLALQQCGVMLVSASENIDETPSGMLLHG
IMSTIAEFYSRNLATEVAKGMTQKAIGGGTNGRAPIGYLNVRKRDELGREVRTIELDPER
APMIEWAFKAYASGNWSVSQLHDELTSRGLRSLPTPKRPAKPLAVSTIHRLLTNPYYKGD
VIYRGTRYKGNHPALVPAEVWYQVQSVLTAHQCAVEATQVHGHYLKGTVHCGQCGSRLIV
SNAKNRHGNVYCYFVCSGRHSKRTDCTRQAMLIEDVEKLVEDYYTRVQITPAQQDALAGM
LHHEFDRLMAAETEALERLTTNRDRLEGEQDRLMQAHYADAIPLSVLKREQDRIVAELDQ
VTRRIDAHHGDYADARAHLDDALGLLANCADIYTRCDDTNRRLCNQAFFTKVYIDEDNEL
RVEHNRPFEMLLDPQVNANALTWAADVNKARTSANVSIGKGSSLVRAVELGGFEPPTFSL
RTRRATNCAIAPDHRAQRAL
>PFR_JS22-1_563	PFR_JS22-1_563	Hypothetical protein	663623:663868 Reverse
MTTIADDPAVSLIDPPKTMAAAVSYLRVSTREQAEKGGTDEGFSIPAQREATRRKAEQLG
AGIVEEFVEREPQPSRPTGPS
>PFR_JS22-1_564	PFR_JS22-1_564	Thioredoxin	664229:664654 Forward
MNSRISACPGCGARNRVPAVAAGLPRCAKCRASLPWIVEAEDTDFGRISDSSRLPVLVDL
WAPWCGPCKQLSPILEKLAVQYAGRLKLVKVNVDQSPAAQAEFGVQSIPTLVLLRDGQVV
AQQAGAMPLGALQRWIEPYLA
>PFR_JS22-1_565	PFR_JS22-1_565	Hypothetical protein	664758:665492 Forward
MASRPDSKTTATPERSHASWSLPQRLLLVGVSSVPLAFASALEWFKGSDGIGTVSFVALS
AIGYLLAMYGRMPDEFNVAGHSAKFTTEQRLEVQAVLDEMSAQQLEEMACDGSDEMRELA
SDALDFRDRARAYLEEAASLEGFSLSKTGHGSLDGGSGLGAVRAIQGLVLTHRDQVVAVD
LGEFEDSHLELAARGVTHILEIQRTEVTVRRVADDRELFVSERVICVDQLRRALRAVAAD
STGG
>PFR_JS22-1_566	PFR_JS22-1_566	ATP-dependent chaperone protein ClpB	665561:668287 Reverse
MPTIEVRQVFLLGLPVQPLTARREPWRHSLAAARPARAQTSPDPKEKHMDTEKLTTMSRD
AVSAAVRNALAAGNPSVEPAHLLHALLMVPENSVGPLLESVGVDPAQIDQRAQAAISKLP
SSQGSSVAQPQLSGSFARVLADAEIRADKLGDSYVSTEHLLIALTSIPSEAQTILVGAGA
TTEKLEEAFAGARGDRRVTSPEAEGGESALSKYSVDLTERAREGKLDPVIGRDQEIRRVM
QVLARRTKNNPVLIGEPGVGKTAVVEGLAQRVIAGDVPDSLRGRRVVSLDLSSMVAGAKY
RGEFEERLKAVLKEIKEAEGQIITFIDELHTVVGAGASGEGAMDAGNMLKPMLARGELRM
IGATTLDEYRERIEKDPALERRFQQVYVGEPSVEDTIAILRGLRERYEAHHKVRITDGAL
VAAASLSHRYITNRRLPDKAIDLIDEAASRLRMEIDSSPEEIDALRRQVDRLKMEQFAIK
KETDAASKARLARLEQELADAEEKLRLLESRWAQEKAALNRIGELKTQIDQLRIEAEKAQ
RVGDLATAAEIAYGRIPALERELEQAKQAENEEKASRMVADEVTTEDIAEVVSAWTGIPV
GKMLQGESDKLLHMEEHIGKRLIGQKRAVKAVADAVRRSRAGISDPNRPTGSFLFLGPTG
VGKTELAKSLADFLFDDETAMIRIDMSEYSEKHSVSRLVGAPPGYVGYEEGGQLTEAVRR
RPYSVVLLDEVEKAHPDLFNILLQVLDDGRLTDGQGRTVDFRNTILIMTSNLGSQFLADT
SLDTKAKHEAVMGVVRSAFRPEFLNRLDEIVMFDPLTLEDLTHIVDANLRKINARLAERR
IVIDVTDRGKEWLARNGFDPVYGARPLRRLVQSTIENQLAIKLLAGEIIDGAVVTFDVDP
DTDQLRIG
>PFR_JS22-1_567	PFR_JS22-1_567	Hypothetical protein	668510:669277 Forward
MDFTDHVVVGVDGSSTSIAAAVWARDIARAGHWPLGIVYTQGMAPDVREMLGEGGTLMCV
ESTLAPALVQASRTAAMVVMASRGQGSTVLPIVDAAAEAVLQEAAGPVVVLPYTTWNTLD
RPLVLGLDAERPSPASIRFAVSVAGRTGARLKVIVDDKGQGPDRARLQTVQVLTRVLGSD
LPETFDVEVSAHELTDALLAKASEASLTVVGSQHARRSTERERSENRLLLRLSTSPVAVV
ANTVEAGQADGSATR
>PFR_JS22-1_568	PFR_JS22-1_568	Sensor kinase	669401:670324 Forward
MGVGAFVVMTTILIATPITMSYPPTPGQIAWVITGVIVLSLISWRIIKHGLSPLIRVAQD
VEATTNLDAGRRIETAPGLPELDGIVLAHNALVERLRAQRRATVSALIEGQELERARLSR
ELHDDVGQTLTYALLLLQSAQDDPHSQQKIAMAQDAVRTSLQTVRQLAAHLRPSVLADIG
LVSALTSLATAHAEATGMAVRREINPVPDLGWAAQLVVYRVAQEALTNCAKHSGASVVTL
SLTHRENLVQLVVTDNGKGLGEAIPGTGMAGMRDRARSINANLNVADNPDGGTRIELRIN
LDTLPKE
>PFR_JS22-1_569	PFR_JS22-1_569	Two-component system response regulator	670327:670986 Forward
MHTPTTRISRVLLADDHTLLRQGMKMMLDPQPDFTVVAEAADGAQALDRINHGDIDLAIL
DITMPRMTGLQVAREVSQRKLPTPMLILSMHDNEQYLFEALKAGAAGYVHKSMADRDLLH
ACRAAVRGEPFLYPGAMSTIIREYVQRGQANEGDRLLTPREEEILKLIAEGHSGKEIAEM
LFISPKTVERHRANLLEKLGMKDRLELTRYAIRVGLIEP
>PFR_JS22-1_570	PFR_JS22-1_570	Hypothetical protein	671209:671730 Forward
MSKTFRTLALIELFGAALLILLGFMLIWWPGLTLQSLVMFCGAFLLVESISAMIGAWRCY
GVLRWLRGGVGALGVALALLIVLLPGLTLSFIAAAVGLWTIMCGLGLMTEKTARRRWLYV
LAGVLLVLAGIWFIFNHAAAIITIGLWAGMSLLVLGMSQVAAAIAVWRAAKNS
>PFR_JS22-1_571	PFR_JS22-1_571	Trypsin	671793:672884 Forward
MMRNSLPARTVAAAIAMTALIPLTSCSATAPKTPAPVASNSPLTSPTSGNSSVTSCSIDD
PSWTTLAEKVSPSVVSVEVSSGGHPVGEGSGVAVDEHHIVTNAHVVGDATDSDVSVTLSD
NSVQPVTIAGRDPITDLAVLTLLDTKLTPIPIANSAQVRTGQPVMAVGNPLGLSGTVTTG
IVSALNRPVTASEQGTGPSVATVTNAIQTSAPINPGNSGGALVNGCGELIGINSSIATLG
PGSGSIGIGFAIPSDEVSMVAQQLIRDGRAHHAQLGISVADGIAARGTQQIRSAMVASVV
VGSPAHKSGLQVGDHIISIDGVATTSALSLVGHVRGLPVGKSVNLLVVRDGRELTVSATL
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ASD
>PFR_JS22-1_572□PFR_JS22-1_572□Chaperone protein DnaK□673264:675093 Forward
MARSVGIDLGTTNSCVAVLEGSEPTVIPNAEGSRTTPSVVAFAKGGEVLVGEVAKRQAVT
NVDRTIRSVKRHMGTDWSVNIDGKKYTPQEISARVLQKLKRDAEAYLGEPVTNAVITVPA
YFNDAQRQATKEAGEIAGLTVDRIINEPTAAALAYGLDKGDKEQSVLVFDLGGGTFDVSL
LDISDGVFEVKATNGDNRLGGDDWDQRIVDWLVTQFKNANGIDLSADKMAMQRLQEAAER
AKIELSSAQETQINLPYITAGAAGPLHLDAKLTRAEFQRMTKDLLDRCKTPFQAVIKDAH
TSLDKIDEVILVGGSTRMPAVVDLVKELSGKEPHKGVNPDEVVAMGAALQAGVLKGEVKD
VLLLDVTPLSLGIETKGGVMTKIIERNTTIPTKRSEIFTTAEDNQPSVMVQVYQGEREFA
RDNKPLGNFELTGLMPAPRGVPQVEVTFDIDANGIVHVSAKDKATGKEQSMTVTGGSALG
KDDIDRMVKDAEAHAEEDKKRREAVEMRNQADALAFRTEQLLADNAATIGDDVKAPVVEA
LDKLKEALKGTGNDDQVKALMEELNEKTSVMGQAVYAASQAQAQGPASPSEQETSSDDDV
VDAEIVDDK
>PFR_JS22-1_573□PFR_JS22-1_573□Protein GrpE□675254:675823 Forward
MSTDDVTTTPTPQPAADEVLAPEAQLEALRDQVAQLESRLAERTEDLQRLQAEYINYKRR
VDRDRDLARRAGKEQILTDLLPALDAIQLADQHGELDGPFKMLADQISAVAARHGLSSYG
QVGDQFDPTLHEALMQLPMSGATKTCVSQVMQPGHRIHDKVLRPARVAVSEPDTQQPATE
SSTHGDEER
>PFR_JS22-1_574□PFR_JS22-1_574□Chaperone protein DnaJ 1□675820:676917 Forward
MSAQDWVDKDFYKVLGVSKDATAKDIKKAFRKLARQNHPDQHPGDAAAEARFKEISEANS
VLSNPDSRREYDEIREMVANGGFRYGRGAGFPGAGGQYAYGNPAGGPYTYSYSTGGSAED
LFGQGAGYEDILGGLFGQGGAGFSGARRPSGPRKGADIEGEVTIGFLEAVKGTTVSMQLV
SEVACTACGGAGITSGNPPQVCGSCHGTGRVRQAKTMKVRIPAGVDDGQTIRIKGKGSAG
LNGGPAGDLLVRVHVTPHPLFGRKGRDLTLSVPVTVDELILGADIEVPTLEGGRVKVRIP
ECTPNRRTLRVRGKGVTTKAGTGDLLVTVEVVMPTSLNDRARQAMRDFARAVGQTNPRAS
ILGRN
>PFR_JS22-1_575□PFR_JS22-1_575□Heat shock protein transcriptional repressor HspR1 (Hspr1 protein)□676919:677338 Forward
MTTTDNSVHDGVVFTTSQVVLLTGLHRRTLEAFERAGIVSPRRSAAGQASYDQHDLVRLR
QARNLVQRAGMDLDEVRQLFALQDQIEQTRQRLDQMVTELWEVLDRTVPTPSGRVFTTGS
DGRAWPGRQTMTGRRRLQR
>PFR_JS22-1_576□PFR_JS22-1_576□Hypothetical protein□678239:678790 Reverse
MTDEGVPARRGDPFICFSLVDLRREFENPCPHLKTLSLRRSRGFYDHDHRSSEPTVSDSR
GRVVRSLGMAQTLLRPEQVDDLVAQYREGATLVELASVFGVNRRTVATHLTRREVTIRRG
RFDPSRIHEAADLYLSGLTLVEVGMRVGAGPQAIRQALASHGVVIRPGGRRGSRITALAA
VGG
>PFR_JS22-1_577□PFR_JS22-1_577□Hypothetical protein□678837:679400 Reverse
MTVQNAPATDEYTAYEYATVRVPHTFEPLFRDTYPGFGWTVENPRATTSVASVPLGGTQR
SETVTLQLKRDRNLKNRDMVRALQEEADTALTTIISLERSKTSRAMVVAVTIGIVGSAFL
AGSVFAMNAGLAVLSVALGALGLFGWVGGGISYRQVKRRRARHVDPLIENALDTLHEASR
RAAHLLR
>PFR_JS22-1_578□PFR_JS22-1_578□Integral membrane sensor signal transduction histidine kinase□679551:680738 Forward
MTSTARPAIATTGPRWRALPRVAQITVQVILMVAVGVEVVTVAVSRAPVIQYVPAVAMTA
GILLGRFGRSWGYVGLGLVALAPMIAVLVDRQATGIWSMACLAAFWFVLRGLSAWVVGVV
IGVANFVAVGWEAGTIDVRYDTSSSVSAFAAAVCAAIASALRGNYRYRVEAEARMREAEQ
GRQAAVERGVAQERLRIARDLHDGVGHQIAVVNMHLGAAEVHLSDPRALRGDLVAARAAV
QAVLRETQQILAVLRVDDAGERPQATPSHAVVGDLVESYRQAGMVVNANLGSFGIALSGQ
SSVAVYRVVQEALTNAHKHGVGPVSLEISQNGEGLVSIEVANMRRSTSSPGPGGGNGLIG
MRERVESVGGSLRTRADDRLFWIVATIPADGREAR
>PFR_JS22-1_579□PFR_JS22-1_579□Two-component system response regulator□680735:681394 Forward
MTTVMLVDDQEMIRKGLRVIIDAYPGLDVVAEAGDGFTAVRRLDSVQVDVILMDLNMPGM
DGVEAVRRIREARGPEGPRILVLTTFDQDENVLAAMRAGANGFLGKGAGPDELAEGIRRV
AAGAHALSDNAIGALVSHVSDPHAVPPDPDKAKLFEGLTPRELEVVRLVVEGLDNAEIGR
RVFISPFTAKTHVNRAMAKVGARDRAQLVSLAVQAGIRP
>PFR_JS22-1_580□PFR_JS22-1_580□Hypothetical protein□681557:682336 Forward
MQSEDPPSNLPVRDGLAKIRRGMGDANLRYLYFSVLAVPGHLAMAGAKGVVLFTGFSAFM
AANVLFTLGLAAMKVVVIRAAWGAGSASACVLPRAYQVIGVLVIVFSAAFAVSCLPLALG
SSSSGNYSRVQAIAIATITFTELAMAVHGLLSSGRRRNPLMEAIKLSNLAASLVLLVITQ
TALLSFAGEGGDPSRYNGWFGIGMGLSAVSVGVYMVVRHARLSKRDLLGPDSQPANFVPN
APRVRRRPRTIGGSGSPAA
>PFR_JS22-1_581□PFR_JS22-1_581□Hypothetical protein□682384:682593 Forward
MDRDMQTDQGKRGPIRPDLGMMPGMNSSPTGPPFRDGGTRQPGSSGLVVSVTIVILLLLV
AVVCLMAIG
>PFR_JS22-1_582□PFR_JS22-1_582□SEFIR domain protein□683690:684643 Reverse
MSYSHDDKEHRDWVLALATRLRADGVDVCLDRWDVTLGGNLAHFMEKAANASYRVVAVIS
ASYARKADERKGGTGVEAQMLSTRLYESMHSDQVIPIIRNNPTAPPLLPAFLGGRLWLDF
RDDQAMEAAYERLIRDIHNAPVDIVPTLGPNPFEGKSDIEARLEIRNSPLRWHSPGLTGD
VEFIYSQNSGMYTIGTGSCQFTLELSPRGTSSVYAYRDPLDIKHVAMIEKGESRRPLLTD
VSQFDTSSRAVGAGIDDAIVLHNKNDYWAIVIITAIFERQKLNPEKVIQFRYTIQSNRTA
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>PFR_JS22-1_583□PFR_JS22-1_583□Hypothetical protein□685023:685286 Forward
MIRIGGDGPFVLIAHLQQGSLTVSAGDMVHRGEPIASCGNSGNSSQPHVHVQATDTVQWD
RAVGLPIAFDAAGNPVLPGESQIIRAG
>PFR_JS22-1_584□PFR_JS22-1_584□Lactoylglutathione lyase and lyase□685336:685704 Reverse
MTVTGPDFIALQVRDLDRSARFYETQLGLHRAPVSPPGAVVFATSPIPFALREPLPGVDL
NQPSRPGLGVALWLLGDDVQALHDALADAGVKILQPPTAGPFGLTFTFADPDGYAVTVHD
KH
>PFR_JS22-1_585□PFR_JS22-1_585□Putative HTH-type transcriptional regulator MarR□685783:686202 Forward
MGIGRQIGCQLKEVQAVLRARMDEVLRPLGLTTPQYACLTALEQTRGASNSELARRAFVT
RQTMNVLLRGLEARGLVARAEEAPHGRARPVSLTGEGSALLIQAAEAVGVVVMRMVGSLD
DAQRTDLHDALNSCIEALR
>PFR_JS22-1_586□PFR_JS22-1_586□Transcriptional regulator□686279:686590 Forward
MTVELMGGSSSTDMEDEARVKVFKALSDPIRLQIIRYLNQVHRGVTCGEIGGVVDISKSA
GSYHFKVLREARLTITRKESREKYVSLNYETLDKYLTRFFDTL
>PFR_JS22-1_587□PFR_JS22-1_587□Drug resistance transporter, EmrB/QacA subfamily□686630:688096 Forward
MPLYSSKEVEQLNWKGVVRGDDRTTTGRVPPTSGQRWVLALTSLGFFMAMMDSMIVTTAS
TAIRADFGATVGQLQWMLNAYNVAVAAFLLIGVALGARLGYRRMYVVGLIVFVVGSVVAA
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LSESVTHASMVPPTVVGALGILLAVAFIVHQHRESTPMVPLGLFRSSAFSGGAVATFLLY
AAMYGVVFLLPQYLQAVTGASALRAGLELLPWTGTLVVFSPLAGRIVDRLGERLVALVSL
LLQAVGYLWLALSLSPGARYSTMVAPLVLSGMGISMAGPALQKAVLGAVDRTQTGIASGV
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RHRPLPTS
>PFR_JS22-1_588□PFR_JS22-1_588□Proline/glycine betaine transporter□688235:689674 Forward
MTHHGSAPDPSATSDAPAATTVEPLLVHPRTIRKAITGTAVGNFMEWFGFGIYGYLAVTM
TTVFTSGVERSAGLLITLFGFAVSFVVRPIGGLILGPLGDRIGRKSVLFLTMALMAIATT
LIGVLPTSQQIGLWAIVPLYLLRLVQGFSTGGEYAGATTYVSEFSPDKKRGFYSAWLDVG
SYIGFAAGAGVVGLVTVIVNHLSGPDAMLDYGWRIPFLSALPLGAAAIYFRMRIPETPVF
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EEESDELDAELSVAAADDPMARHGVLGIIRHHWRPILVCMALVSATQCSAYALTSYMPTY
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LICQWLIQLTGNPYMPAFYIMFFAVIAGIALVPMKETAGQPLMGSAPVVEAPEDSPIPA
>PFR_JS22-1_589□PFR_JS22-1_589□Regulatory protein TetR□689750:690343 Reverse
MPTRVRDRSREMFRERLAEALSEVFVARGFDDVTVAEAARAVGISRATFFRYFSSKEDAA
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LRARLSFRRLQLEPSLTAALVGHGVPADRAHTAAMAGLAALEVAWERWALHESPSLARAL
DEAFADLTAADKPISAG
>PFR_JS22-1_590□PFR_JS22-1_590□Probable multidrug resistance transporter, MFS superfamily□690456:691943 Forward
MTELESTRSTVAGHGARHPGVIVAVLASAGLVASFMQTILIPIQSSLPERLATTRDNTAW
VITITLLVSAICTPISGKLGDMFGKRRIALILLSLLVAGSVVAAVSPSVGPLIVGRGLQG
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AAMGAIVVALIAWLVPDAGVRTGGRVDAVGLIGLALGLGGVLLAVSRGNEWGWISGTTLG
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AVVASVLASMSSTVGGQSIPSADGFHMALILGLVAAAVCAAIAAFIPTRRKGNEVADQAA
RVLAQHDGELAGARA
>PFR_JS22-1_591□PFR_JS22-1_591□Glutamate dehydrogenase□692098:693462 Forward
MANLDIDRLAETLRPQYKAVVARNPGESEFLQAVYEVLLGVGPLAGKIPAYAQWSVMQRI
CEPERQIIFRVPWIDDKGVVQVNRGFRVEFNSALGPYKGGLRFHPSVNLSIIKFLGFEQT
FKNSLTGMPIGGAKGGSDFDPKGKSENEIMRFCQSFMTELQRHIGATTDVPAGDIGVGGR
EIGYLFGQFKRIRNQYESGALTGKGLTWGGSQVRTEATGYGLVFFVEEMLKAHGQALDGK
RVVVSGSGNVALYAIQKAQQLGGNVISCSDSSGYVVEESGIDFDLLREIKEVRRGRVSDY
ATERGASATYVAGGSIWDVPCDLALPCATQNELDETGAKALIKNGVQLVAEGANMPTTPE
GTDLLRDAGILFAPGKASNAGGVATSALEMQQNASRDTWTFEYTEKRLEDIMVGIHHRCL
GTAEEYGVPGDYVAGANLAGYIKVANAMVAMGVI
>PFR_JS22-1_592□PFR_JS22-1_592□Transcriptional regulatory protein PadR□693582:694055 Reverse
MSTSLSISFTPAPPDSALGHHLLGLYFAELQTSLPGGFDPSGQESYGPDEYYVAALHDGQ
AIGYCGYRPLGPTDAEIKKLWVSPDFRGMDVANRLMAHVEQQAARDGFTRALLDTSDLLT
HAVGLYEHRGYHRIDRYNDNPYATLFFAKALGTAPGR
>PFR_JS22-1_593□PFR_JS22-1_593□CrcB-like protein□694115:694501 Reverse
MNITAPLLWLGVFVAGGVGAWCRFRLDGLIARHWSRSVPAGTFTINVLGSFGLGLLTGLA
AAYASLAPLTVVLGTGMMGGFTTFSTANVEVVRLMLSGRPGAGIGLDVATLVVAGAAAVL
GLFLGGLW
>PFR_JS22-1_594□PFR_JS22-1_594□CrcB-like protein□694498:694914 Reverse
MSWPGGLLVAVGGGLGATIRFALSTVAPDHAGSFPTTILAINLVGALALGWLSRFLVLTG
PDEGWRRRVRLGVGTGVIGGFTTYSTFIVQTLSLMQLGRVWMALGYLFASLLGGIACVWL
GIVVADRMARTAGETVRP
>PFR_JS22-1_595□PFR_JS22-1_595□UspA domain protein□694911:695444 Reverse
MAKQVPQPSVERIVAPASHPLVVGVEPGTSELVVRTALSWAASLGAELYIGYADPTRITV
AEYPDGTVRHTELDSDLPDDSWHDREKALTAELARVCHGSGVTWHFRYLAGRTDRALTHL
ARAVDASAFLIGAKGRGRRRDPLEFLRSSVGTQLAHHQHRPVILVPVSVVDWKEPLL
>PFR_JS22-1_596□PFR_JS22-1_596□Galactokinase□695601:696797 Reverse
MSQLAHTAAQRFEQIFGHAPTGVWAAPGRVNLIGEHTDYNGGLCLPIALPQRTYAAAGPR
DDDIVRVASLDFDEQAEVSLDDVAPGVPGGWLGYVAGTIWALRERGFAVHGLDLATTSDV
PIGAGLSSSAAIEGAAGGAASGLFNLGLLDSDASRVTLVDACRRAENHIVGAPTGGLDQT
ASLRCLPRHALLIDFGHDARVRQIPFDVAAHGLRLLVIDTRAKHALVDGQYAARRANCEQ
AARELGVDLLGRITPEQLPDALSRLSDQTLRRRVRHVVTEIARTRQCCDALEHGDFQQVG
ELFNQSHASLRDDYEVSSPELDLAVAAARGAGALGARMTGGGFGGSAIALVPVAALDAVK
RAVADAYLAREWTPAHVFAVHAAGPADTVAVHEAQLVE
>PFR_JS22-1_597□PFR_JS22-1_597□Twin-arginine translocation pathway signal and cupin region containing protein (Precursor)□697061:697582
Forward
MSETPSENGPVEPARHLLADNGVVPNSALPALVYKQAAPQRSDLDDWFRTTFAENRWVGA
RDEMLSDTDHYHSTAFAVFGVVSGSGEVALGGSGGVEIALNARDVVVLPAGVSCRRVSGD
LRVISAFFEEPHPDTLTVEPVEHDAAAERINNVSPPDVDPIYGDNGPLDRIYG
>PFR_JS22-1_598□PFR_JS22-1_598□Uracyl permease□697613:699163 Reverse
MIWKLHNGGVLKPGEVVAPDERLSWGKTIGLGAQHVVAMFGATFVFPLLMGLNPQLAVMM
SGISTIIFIIVTKHEVPSYLGSSAAFPGVATAIYAAGGKPNDVSGALFVVGLTLFMCGLI
IHFAGSRVIHKVLPPVVTGAVVMLIGFNLAPVVAKNYWPQDQWTAFITMIVVVALSVGPR
GFLSRIAIFLSMVIGYLISWLQDVVFGPMHKVVDGQATDVLRVDWSGVAKADWFGLPPKT
DLATWTYSMDANGVAHFPASNVVGFHLPSFHLAFILLALPVVIALIAENTGHVKAVAEMT
GKNLDHQMGRAIAADGATSMLATLAGAGPTTTYSENIGVMAATRVYSTAAYVVAAIVAIL
FGLSPKFGAVISAMPGGVLGGICVVLYGMIGLLGAKIWKENRVDFANPVNLVPVAAGIII
GVGDVSLKFSDSFTLGGIALGTLVTVVVFHLAYWLAPKRLSDAALDGSGVLFDAPGSYSA
RPLIPPATRPGRAPRPATAPHPQADGPAGTDPDPTR
>PFR_JS22-1_599□PFR_JS22-1_599□Integral membrane protein with DUF218 domain protein□699285:700349 Reverse
MSDGLWVLFVTAAVFTVASLIALWVTARRDPRRLRCAVLLLIAAFWLLVTLVTASPMFGE
RGQAIFLVIAGVLLVAWLAAMGMLPLLLVIDGLIVLRREGIRSRTGLLVLAAGIALLLLP
GVTASLARNDRWWSMALFTLVTFIGTYLGTFLVVMLAQFVVRALFGGRRRVPDPDVLIVL
GSGLINGKVPPLLASRLDRALQVSAEEALQGRRPMFVVSGGRGSDEPRAGAEAMAEYLTS
RGVPDERIIVEDRSRSTRENLVNSTRLLRERGIGGPMLAVTSSYHTTRTDVLAADLRLDD
VFVTGAHTAWYYAPGAYLREYIGVLTYRLPLNIGVGIFCVVAAVAMAWATSRVG
>PFR_JS22-1_600□PFR_JS22-1_600□Dolichyl-phosphate-mannose-protein mannosyltransferase□700399:701958 Reverse
MSTIDKLDDATILQRDRWRSWILTAAFVVVGFLIRLVNLGRPNRLEFDETYYAKDAWSLL
HFGYERAWPSTADARIATGSTDLWQSNASFIVHPQLGKWLIAAGEKLFGMNSFGWRFAAL
VFGALFIGIVIRMARRLSRSTLIGCLAGLFITVDGLSFVMSRIALLDIFEAFFTVAAVSA
WLVDRDHFRHRLAEHLRANNLLNLGGSYGPLLLFRPWLIASGVLFGLACGCKWNAMYVLA
VFGILTVIYDRSARRTAGAGRRAWHAVWRDGLAAFVQLVVVAVPVYVLTWISWLVTQGGY
DRQWGASHPDDPLVKLIGKPLASLWQYHKEIYAFHTGDWIASQTHTYQAHPFGWPVIGRV
IGIDAVNDIQPGDDGCKAVGDTCLRVVSGAGTPMLWWMAALAVIIALFIWIGARDWRFGV
PIIAAATTWLGWFPNADRPTFYFYAIMMIPFTATVLAMVLGKVLGPSDAPPRRRRNGAII
VTAATVIIIANFMFIYPILTDELMTRRQWLLRMWFRSWI
>PFR_JS22-1_601□PFR_JS22-1_601□Glycoside hydrolase family 95□702245:704632 Forward
MDRYRIEVARPAASPADAFLLGNGNLGVAVHGAPGTETLDLGLDSLWSGGPLDATPRRAP
GLVEALRAAIVAGNSPRTEQLARTMQHPVPPTPALQQDGRRDSPQPLGSLRWGYAPDVAD
APHGYSRVLDLSRAIATTRFGTGRRGTGQLDCFISAPDHVLVADWMGAAHELVAPEFDCP
HPCERQLRRRGGRIWLTVAGRAPVEAPADPSYARRATAVHYGTDAPDGEGRVPAGMAFAL
VVAVEATASGSRLVAAARDGFLGWQTNPIGDPGPLVRAAGQQVDAALAMDSELLARRHVA
DHAALFDRVDLDLGAGDGAARDELAFHLGRSLLIASTRRTSSMPTSGSLWATTRSADPGD
ALERSGGGLAPLGLDVVGLGELMDPVDQAAGELVTAGRATAANSYGFAGACVHGTPDIWR
HGAPGEGPTDQANWPSALLGLIAPLYRHAAHGGDRGAALEAHRAAVEFVLDQLINGPDGA
LLPCPSTLPGSLCLGPDGRLAGVGAGSSFDLSLVRQSLEHYVELVGARPGSADAALVVRA
HAALAGLAPLPVRAGRLRDWPRGRRPADGGAGLLRSLHGVFPGEGISRRRDPELFDAARR
TFIARTGAHGDGARGEGLVRRLGLAARLRLPDEAAAVLDELVGGGSSASLLALRDAGADS
DAGAGSDAGAGPRRLLPAAMALPWAMVELLVQVADGVVALLPTLPARWPDGRVAGVRVPG
DHSIALSWRGGALREATVAARRDDVLALDLPRGEFAVRDAAGTAVDATRVGGSDPGRMLV
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SFPASRGQTYTVSAL
>PFR_JS22-1_602	PFR_JS22-1_602	Ribosomal RNA small subunit methyltransferase I	704646:705596 Forward
MAGAGSSGRALISRLSDDADSLTAVTTSDEGLLILAGTPIGGSNQASDQLRETLRDADVI
AAEDTRLFRTLLARIDVTTRAHIVSYFEGNESERTPGLLDDLEAGKTVVVATDAGMPSIS
DPGFRLVNAAIKAGIRVTAVPGPSAVTTALAVSGLPSDRFCFEGFLPRSGGPRRHRLAEL
ATEPRTMVLFEAPHRLADFLSDAAEALGHERAAVLCRELTKPWEDVVRGTLDELHAWAVE
HARGETTIVIAGHTVSAEQGLAQALVQVNARVAAGERLSGAVAEVADQTGVRRKLLYQAA
LDEKAHNATGRADQRP
>PFR_JS22-1_603	PFR_JS22-1_603	Hydrolase, TatD family	705729:706757 Forward
MLTKKHVDKENKLTTRNGTVHTSNMDITTREGIMADVKRAEIESQLSKAKLPALPEPLPA
LVTDNHTHADATVEFSGLDPELNLSSAAVVGVHRIVEVGCDQPSSEWAVDFAATHEQVVA
AVALHPNDGARMVARQGPEAVNDVMRRIEQLATAHERVRAVGETGLDYFRIQDPAGQAFQ
RELFARHIEIAQRTGRALVIHDRDAHADVAAVLDEYGWPPRTILHCFSGDAEFAATCLEH
DAWLSFAGSVTFKANGAVRDALRSTPADKVLVETDAPYLTPVPMRGRPNAPYLVPHTVRF
LAAARGIETSDEQALAAWCRQLDANTSRAYGSNPQAIVTGTW
>PFR_JS22-1_604	PFR_JS22-1_604	Ribosomal RNA small subunit methyltransferase A	706754:707623 Forward
MSGVAEFLDPTSVRRHANAINLRPTKTLGQNFVVDANTVRRIVSLADVGPEDEVLEVGPG
LGSLTLGLLASAAGVTAVEIDPVLAAQLPLTVAEHQPDRAGRLRVVTDDALRVESLPGPA
PTRLVANLPYNVAVPVLLHMLERFASWRAGLIMVQLEVADRLVAAPGSRTYGVPSAKLAW
YAEAHKAGTVPPSVFWPVPNVESGLVAIQRREPPATSASREQVFAVIDAAFAQRRKMLRS
ALARIVGSSAAASAAIEAAGIDPTVRGEALDIAAFAAIAEQLPHATPSR
>PFR_JS22-1_605	PFR_JS22-1_605	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase ispE	707700:708677 Forward
MSETEFPASGARGLGAVDLRVRVRVPAKVNLALRVAARGDDGYHQLATVFQAVALFDELT
AERRRDDAITVTTRGLHAHRVDDDPTNLAVRAAVALRHHFGTADLGVHLSIDKSIPVAGG
MAGGSADAAASLLACSVMWDLDTTPDDLVQLAADIGSDVPFELVGGTALGRGRGGDVMPA
LARGNYHWVLALSDRGLSTPSVYACFDEQVDAGKVVPLRPDDPDACTALLDALASGDAAR
VAPLLGNDLQEAACQLRPELREVLAAGTAAGALAGIVSGSGPTCAFLCASQPDAYLVQTV
LRSLEQVDETLCVTSPAPGAQLVVS
>PFR_JS22-1_606	PFR_JS22-1_606	Transcriptional regulator, TetR family	708712:709494 Reverse
MTSAERREQLIVVARSLFAERGFDGTSVEEVAARAQVSKPVVYEHFGGKEGLYAVVVDRE
VTTLDNAIMAAIAVPATSYREVIERGTLALLDYIDASPDGFRIISRDSPVGSASGSFASI
LNDIVTRVEDLLAPPLIRRGYDATIAGVYSQALVGLVASAGLAWLDTRKPDKRRVAAELV
NLAWNGLASIEHKPTLITDRGAVPGKRRHTNNKRRHTNKLRPTRTASKGATAAARKRAAK
SSHASSEDDSGPVDRADGQD
>PFR_JS22-1_607	PFR_JS22-1_607	Aspartate carbomyltransferase	709637:710683 Reverse
MSSDDATVPVSSLPPFGPGQHLLSVSQLDRAALTSLFGLAESLRPVGQGTQVCRILEGAM
LGSLFFEPSTRTRLSFESAFQRLGGAVVSTTGFTFSSMAKGESIHDTARVVSGYSDALVV
RHPDTGSVAEFADASVVPVINAGDGSGEHPSQSLLDLFTMRQELEARGKSIDGATIAVLG
DLRYGRTVHSLLRILGLYSKVTFRVFGPPALALPAEFFEVVSASGNRIVECDSVGEAIGP
ADVIYCTRVQKERLSEQDEESVHLKGDLLNMAILTQYGRPDAIIMHPLPRDSRHNSFDLS
PDVDDFPGLAIFRQTDNGLLIRMAIFSIALGVADHVTDDLRPAAWQRR
>PFR_JS22-1_608	PFR_JS22-1_608	Bifunctional protein GlmU	711110:712657 Forward
MSTHSERTAPQRSSDATAVPRVAAVIVLAAGEGTRMKSRTSKILHEVAGESMISSALRAA
AALEPQRLVVVVGHQRAQVEEHLAEVAPEATIAVQEQQNGTGDAVRVGLDALPADLSGDV
VVTYGDVPMLSGATLQALVDTHNTQHNAATVLTANVDDPTGYGRVVRENHQVLRIVEHKD
ADPDELFITEINSGIYVFDADLLRRGLASLRTNNSQGELYLTDVIEYANRHHHAVGAYQT
EDTWQTEGVNDRVQLARMNAEVNRRICEHWMLQGVTIADPATTWIQRDVTLEQDVTLLPG
TQLLGATSIAAGATIGPDTTLKDVEVGEDAQVIRTHGELAVIGPRTNVGPWARLRPGTEL
AMGGKIGTFVETKNAKIGENSKVPHLTYCGDAIIGEDVNVGAGTVFANYDGKHKSTTHLG
DDVFIGSNSVLVAPVDVADGAFVAAGSAIIDDVPAGALAVARGREHVSDSWVAARHPGSK
ADEAARNSTGDIHPAVQASRQALAADAAKNSSQDN
>PFR_JS22-1_609	PFR_JS22-1_609	Ribose-phosphate diphosphokinase	712691:713686 Forward
MTGVKRNSKQHLMLFSGRAYPELAQRVSDLMDVELVPSRLITYANSEIYVRFEESVRGCD
AFVIQSHPAPVNEWLMEQLIMVDALKRASAKRITVVAPCFPYARQDKKHLGREPISARLV
SDLFRTAGADRIMSVDLHAAQIQGFFNGPLDHLSGLPVLADYVEKKYGGDDMVVVSPDAG
RVRLADNWSDRLTVPLAIIHKRHDPTKANQVKVHEVVGDVEGRTCLLVDDMIDTGGTICQ
AANALLDRGAAKVIACATHPILSGPAQERLNETPFEEIIFTSTLPIPEGIDIPKMTVLSI
APLLARAIREVFEDGSVTSLFTNKSHSGPQG
>PFR_JS22-1_610	PFR_JS22-1_610	50S ribosomal protein L25	714064:714723 Forward
MAEIELNAEPRNEFGKGAARRIRREDKIPAVLYGHGTDPVHLTLPGHQTLLALRTANALL
NIHVEGDEDLLALPKQVQRDPIKGFIKHVDLLRVRRGEKVTVEVPLEFVGVASPEAIINE
ERTQLAIQAEITAIPNRIEASIDGMEVGDQLLAGQITLPAGAELEDDPETLILSAVAQIS
EEALEAELGETEAEEPEVPVAGEEGAEGAEAAEGADSES
>PFR_JS22-1_611	PFR_JS22-1_611	Peptidyl-tRNA hydrolase (Precursor)	714931:715521 Forward
MSWLVVGLGNPGPQYANTRHNIGFLTVDELARRAGERFSASRGMHAETASTRIGPQGIGG
PAPEKLVLAKPRTFMNESGRAVRKLSDFLDIEPDHIIVVHDELDLDPGRLRIKLGGGDNG
HNGLKSIRAHLGTGDFYRVRLGIGRPQGHRAGADYVLGRFSKAEREELAIEVDDGAEAVI
SLINAGLGPTQNRFNN
>PFR_JS22-1_612	PFR_JS22-1_612	Hypothetical protein	715589:715954 Forward
MAHDGAIDGIHDRLRIALKDAMRARNRTRMSTLRAALSVLDNATAVGVDVMPAAGAIEAS
ATGLGAAEAGRRVLSEPEQQELILREADELAVSAAMFTDAEQAAAQRAEADALRGLVEQV
D
>PFR_JS22-1_613	PFR_JS22-1_613	Transcription-repair coupling factor	716033:719728 Forward
MLQGLIDTVCNDPAIADAIEQARAGVPALDIAGPPATRAFITSGLVRRAGRPLLVVTSTF
REAESLVDELSSLLGDEEVAYYPAWETLPHERLSPNSDTVGHRLEVLRRIAGKDDLPAPS
VVVAPIRSVLQPQVRGLADLPVVKLRTAEDYDPSRLEADLVAAAYSRVDLVERRGEFAVR
GGIVDIFAPTYSHPVRVDFFGDTIEDLRFFTVGDQRSTDETVDEFVAAPCRELLITPEVQ
QRAAALVDAHPELSEMLEKISQGQSVEGMEALIPALADGVELLVDVMAPETLTLVCDPEL
VRTRAADLVRTSQEFLHASWAAAAAGGKAPIDLAASSYQELADVRQHSLDIGQGWWSLSA
FAAAPDSAPQGEDPTGESASAGESVSAADAAFAGGIPEMILDMEPLPGWRGDAEKAIATM
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RAPDLKLTLVAAGDITNQPNADRSSRKMPTKRRNQVVPLELKPGDPLVHEQHGVGRFVEM
TQRTVAGATREYMVIEYAASKRGQPGDRLYVPMDQLDQVTRYVGGEAPALDKMGGAEWKH
RKSRARKAVRQVAAGLIKLYAARQASRGHAFSPDTPWQHEMEDAFRYEETPDQLACITDV
KHDMEQIVPMDRLICGDVGYGKTEIAVRAAFKAVQDGKQVAVLVPTTLLVQQHYQTFAER
YSGFPVTVAQLSRFQTEKEVATTLEEMAQGKVDVVIGTHRLLSSKVHYKDLGLVIIDEEQ
RFGVEHKEALKKLRVNVDVLSMSATPIPRTLEMAVTGIREMSTITTPPEERHPVLTFAGP
YDEGQVVAAIRREMAREGQVFLVHNRVASIDRVAARIREMVPEARVVTAHGQMSEKTLEK
VMVDFWERRADVLVCTTIVEAGLDIPTANTLIVDRADHMGLSQMHQLRGRVGRSRERGYA
YFLYPGDRTLTTTAHDRLAALAANNELGAGMAIAMKDLEIRGAGNLLGDEQSGHIADVGF
DLYLRLVGEAVAEFKGDGPGEEEKPMRIELPVNAHLPEDYVESERLRLEMYKRIAEVTST
DDIEALRGELQDRYGPVPEQAESLLTVAAFRLLCRQAGLTEVMSQGRSIRFAPIAGRRAP
DGTELSLPDSRRVRLDRLYPGTLVKNAANLALVPAPRTAKVGGQPIIGDELIAWASGFVR
DILLPDAPRRQGTAGNTAGDTVGATAGAAAG
>PFR_JS22-1_614	PFR_JS22-1_614	Hypothetical protein	719850:720383 Forward
MSRRSLLVRIGVPAAALAMFAGCSPSPATAIELDGARVSESTITRYADGCSKMLDAGGGA
GQYTPGDIRRVVVSYVGEGMIADQLAREYGVTLSDSDMDQAKQALGNARGLLADNDCAQA
VDGQLRLTALVLSAKGKNVQKDAASLAPVVNPRYGAWSPTDFAVAGTGSLSKLSTDR
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>PFR_JS22-1_615□PFR_JS22-1_615□MazG family protein□720383:721054 Forward
MNQRPDDVGSLPAAAQRAGEEFARLVAVNQTLRIECPWDARQTHLSLVKHLIEETAEVVD
AIEVGTADDQREELGDLLMQVVFHASIASDEGEYDIAEVVRGITDKLIARHPYVYGDAEV
PDDLDASWERRKKAAKHRDSSLDGIADALPTLARAAKVAQRVHDVGPDMGPAQDEDLSIS
DREAGEKILSLVRRAQRVGVDADQATRAALRRWEAEIRAAEQS
>PFR_JS22-1_616□PFR_JS22-1_616□Phosphopyruvate hydratase□721169:722458 Forward
MASIEFIEAREILDSRGNPTVEVEVVLDDGSSARAGVPSGASTGQFEAVELRDGDENRYG
GKGVQKAVGNVVETIGEEVLGMEASRQRELDEAMIELDGTDNKAKLGANAILGVSLAAAK
ASAESAELQLYQYIGGPTANELPVPMMNILNGGAHADSNVDIQEFMIAPIGAKSFAEAMR
IGAEVYHTLKGVLKERGLGTGLGDEGGFAPNLDNNREALDLIEDAIKAAGYKPGKDVALA
LDLAASEFYNDGRYEFEGKSRSTAEMIEYLEKLVNDYPLVSIEDPLDEEDWDGWSTLTER
IGDKVQIVGDDLFVTNVERLQKGINEKAANALLVKVNQIGTLTETIDAVTLAHRNGFHTM
MSHRSGETEDTTIADLAVALGCGQIKSGAPARGERVAKYNQLIRIEEDLDEAATYAGAGA
FPKFDSTKW
>PFR_JS22-1_617□PFR_JS22-1_617□Hypothetical protein□722723:723364 Forward
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ARTGARMTRRLAAVLAIVAVLIISLITSLRVYVDQRQQISQAKAAIASSQEHISQLDNEQ
QRWNDPDYVRAQARSRLGWVMPGETGYQVVDANGDPYGGGAKIDRTGVGAQQAEAWWQRA
WDSNKSADKPTETPTPSRIERVVGPSAAPTSGG
>PFR_JS22-1_618□PFR_JS22-1_618□PF04417 family protein□723444:723959 Forward
MRQIEPLSPADEQIVAEQLGREPRAVVGVAWRCPCGRPGVIATEPRLPNGSPFPTTYYLT
CPRAVAACSRLEANGVMAEMTRRLENDPELAERYRSAHESYLADRASLGEVPELNGISAG
GMPTRVKCLHALLGHALAVEPGVNPLGDETVRAVGEFWKHSCVPRPEGSKR
>PFR_JS22-1_619□PFR_JS22-1_619□Exopolyphosphatase□723956:724912 Forward
MRVAAIDCGTNTMRLFVASLNPDGSLHEYDRRLLFVGLGQGVDATGLFAPDALNRAFDAC
EQFNEIIADLDCERGRFVATSATRDAQNRDELFRGVRARLGINAEVVSGQDEAHLSFRGA
LSGIRSKADPVLVMDSGGGSTELVRGVGAGAELAHIDASVSLNVGSRRLRERILRSDPPT
ADEIARARQLVRSELDSSGVELSDIRTFIGVAGTVTTMSALAQHLRRYDRSRVHGSVLSQ
AAVHEVADRLLGATVSEVVSWGPVQPQRAEVLCAGALIVEEVASRVGAPELVVSESDILD
GIALSMLVDGKGQAISAD
>PFR_JS22-1_620□PFR_JS22-1_620□Actinorhodin transporter□725178:726605 Reverse
MTQTLTAVEPTTSSRLGRRLWAILAVVLIADAIDLMDSTIMNIAAPTIQREIGGEEGLIK
WLGASYALALGILLVVGGRLGDRFGRRRLFLIGIAGFGVASVLCAVAIDPAFLIAARLLQ
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SLYFQIHLGLSPVGAALAMMPMMVGIIIASFGARPLIPKLGRNLVVAGLATTLAGIVALI
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SAIGSAVVTTIYFQTSATADANRPFIASLIVVGAITVVCLIAAPLLPKRAPQDAH
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DLAATDMDASRADLDAIMARLEAGWSEFAQRA
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FGGLGVLAAVDHVTHEIADAIVGRRFESVGELDESLLALDGTPNKSRLGANAILGVSMAF
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AGYRQFMSHRSGETPDAFIADLAVATGCGHIKSGAPARGERVAKYNRLLEIAADHPELAY
GLG
>PFR_JS22-1_623□PFR_JS22-1_623□Cationic amino acid transporter□728928:730391 Reverse
MNTSDRTASPHANPPAPSDDGKASPALKQVMGPGLLLLFVVGDILGTGVYALTGQVAGEV
GGAAWLPFLIAFVIAMMTALSYLELVTKYPQAAGAALYVHKAFGVHFITFMVMFTVMCSG
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AVNMAEETKEPTRIFPRILLSGLTVTGVIYVVIAIISVALVPVGNLAASEAPLVLVVENA
APGFPINQLLPWISMFAVANSALINMLMASRLIYGMAQQDVLPGVLARVLPVRRTPWTAV
LFTTAIAAGLILYVSLARGSAVVGLLGGTTSLLLLAVFAVVNLAVVVLKRDRVGHKHFRT
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DIPPEVI
>PFR_JS22-1_624□PFR_JS22-1_624□Similar to Nucleoside-diphosphate-sugar epimerases□730608:731381 Reverse
MSKRPHTILVVGATGSVGRFVVAEALKQGYATRALVRNLDKAKTLPEGALAVVGDLTDAA
TLDRALAGTDAVVFTHGSNSTEEQAEAVDYGAVRSVLTALGDRSVRVALMTAIGMTKRDS
IYNKENHGRDWKRRGERLLRASGLEYTIVRPAAFDYNAPDAHKLVMRQGEHPSNGGVARE
QIARVLVDALSNDAARHKTFELLDTTGEEQADLTPLFAALQPDEPAAADAPGDSENLPLS
DEPQRVLDDLKRLTDYE
>PFR_JS22-1_625□PFR_JS22-1_625□Methyltransferase type 11□731684:732433 Forward
MRPFAELVAEAQSADITGWGFGFLDGRATEERPPWGYARLLAGRLARAHAALDIDTGGGE
VVNEAPQLPPTMVVTESWPPNAERARKLLGPRGVRVVQTTGDDPLPFDDASFDLVTSRHP
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HIESLLTATLRIEYFDIGAIVWILRKCPWWVPDFSPDKYHDQLVCLDAQLRAGRSFVDHS
SRHLIDARR
>PFR_JS22-1_626□PFR_JS22-1_626□Putative CONSERVED TRANSMEMBRANE PROTEIN□732570:733382 Forward
MRSSNPVLTRPDAFVPAGQAGQQYVDAAYQEASYPPGGYPGPSRPAARMTMNDVIAKTAT
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ILIGAFSQVMESIYPGIVGQAVLGTFAAAAVTLFAYRTFGARISGRMQKIFIFSIIGYAV
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>PFR_JS22-1_628□PFR_JS22-1_628□Hypothetical protein□734310:735260 Reverse
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VMEPGMTQAMFETVHLLTRACATLRERCVDGITANVERSREFVMNSIGIVTYLNDVIGHH
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ARLRALDER
>PFR_JS22-1_702 PFR_JS22-1_702 Hypothetical protein 810214:810660 Reverse
MVDHDEIRRQQESLWQTQLKHPDIDIMGKMGGWLAGPPSPDPPAGPVWQWGPEDMHKRFL
IIYPDGTDSTGSIHEYVSLLARLPPFGPDRRFSYDESIELCRLMHTMGAWSWDEPRHCLV
WSSKRTHELEARAIDAWLRWLHSRGGHD
>PFR_JS22-1_703 PFR_JS22-1_703 Fumarate hydratase class II 810824:812248 Reverse
MADNTSAKTRTESDSMGTVEVPANHHWGAQTERSLHNFDIGRPTFVWGRPMIKALGILKK
AAAQANGELGELPKDISELIVKAADDVIAGKLDDDFPLVVFQTGSGTQSNMNANEVISNR
AIEIAGGEMGTKTPVHPNDHVNRGQSSNDTFPTAMHIAVVTELQEMYPRVMKLRDTLDAK
AKEYDDVVMVGRTHLQDATPIRLGQVISGWVAQIDFALKCIKFSDEQARELAIGGTAVGT
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VRWYASGPRNGIGELLIPENEPGSSIMPGKVNPTQCEAMTMVATKVFGNDATVGFAGSQG
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HIGYDKASKIAKNAHHKGIGLRDSALELGFLTPEEFDKWVVPADMTHPSAADDD
>PFR_JS22-1_704 PFR_JS22-1_704 Putative glyoxylate reductase 812412:813380 Reverse
MARICITDGVPAEGIEALRTAGNEVITWDGQEPPTREQLLAHVKGADAVLTVLSDGVDEE
FIAAAGPQLKVVANIAAGFNNIDLDACRAHGIVATVTPGTLFDAVADLAFGLMLSVTRRM
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ACVDEKALVAALQSGHLGGAGLDVYEHEPAIEPELLTMENVALLPHLGSANIETRTAMTA
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>PFR_JS22-1_705 PFR_JS22-1_705 Putative FERREDOXIN FDXC 813616:813936 Forward
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>PFR_JS22-1_706□PFR_JS22-1_706□Succinyldiaminopimelate transaminase□813933:815024 Forward
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LTS
>PFR_JS22-1_707□PFR_JS22-1_707□Conserved hypothetical secreted protein□815052:815897 Reverse
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DR
>PFR_JS22-1_710□PFR_JS22-1_710□Rossmann fold nucleotide-binding protein□818192:819028 Forward
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>PFR_JS22-1_715□PFR_JS22-1_715□Glucose-1-phosphate adenylyltransferase 2□822761:823951 Forward
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>PFR_JS22-1_720□PFR_JS22-1_720□PF06210 family protein□827806:828369 Reverse
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RADMDFLAREIASLRASVGEMATRDFVRSELRDQIRELIAELEDSDDEADDAAPQESSHT
DASPDGS
>PFR_JS22-1_721□PFR_JS22-1_721□CBS domain pair protein□828366:829643 Reverse
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DAGLYQVSRYFATYNLVIAPVVNARGQLVGAVTVDDVLDHMLPDDWRGVQMDGIHPDDQS
READE
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VVRK
>PFR_JS22-1_725	PFR_JS22-1_725	Zn-ribbon protein, possibly nucleic acid-binding	833461:834204 Forward
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RTSQSGV
>PFR_JS22-1_726	PFR_JS22-1_726	Hypothetical protein	834015:834737 Reverse
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>PFR_JS22-1_728	PFR_JS22-1_728	Methionyl aminopeptidase	835593:836501 Reverse
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IH
>PFR_JS22-1_729	PFR_JS22-1_729	Hypothetical protein	836581:837528 Reverse
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PVIKH
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LIFDGMAAALPHDG
>PFR_JS22-1_736□PFR_JS22-1_736□Hypothetical protein□845543:846133 Reverse
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>PFR_JS22-1_738□PFR_JS22-1_738□Oleandomycin resistance ATPase□847993:849804 Reverse
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QTE
>PFR_JS22-1_739□PFR_JS22-1_739□Integral membrane protein□849837:850607 Reverse
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Reverse
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>PFR_JS22-1_743□PFR_JS22-1_743□Hypothetical protein□854236:854451 Reverse
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QLAYSMSLEEA
>PFR_JS22-1_744□PFR_JS22-1_744□Integral membrane protein□854451:855005 Reverse
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RKRDEQYKKVEEMPERVLLRNNIDSHWSVAEFAWPVVFLLLACVLATQILPVLSLVGTLG
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GEAY
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DDLRDSDLIIPGPDSSLQDVATMLASDDRPDGLFPG
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CGGFARSWIW
>PFR_JS22-1_748□PFR_JS22-1_748□Iron-sulfur cluster assembly accessory protein□857480:857830 Forward
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   PLPVSWA
   >PFR_JS22-1_750□PFR_JS22-1_750□Response regulator□859645:860169 Forward
   MSSVASSDSTNGATPLKVIVYSDDRTVRQQVRLALGRKIARDLPEIAVTEFATQDALFEA
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   >PFR_JS22-1_751□PFR_JS22-1_751□Anthranilate phosphoribosyltransferase□860169:861218 Forward
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   >PFR_JS22-1_752□PFR_JS22-1_752□Hypothetical protein□861259:861684 Reverse
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   >PFR_JS22-1_753□PFR_JS22-1_753□Hypothetical protein□861824:862507 Reverse
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   >PFR_JS22-1_754□PFR_JS22-1_754□Hypothetical protein□862533:863201 Reverse
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   >PFR_JS22-1_755□PFR_JS22-1_755□Acetyltransferase, GNAT family□863293:864390 Reverse
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   LRRDSLPLRMSLIAEEFGELFEAVYGTTARRIVDEANATAMDNDEEHRDVVATADALADL
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   RSMKS
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   >PFR_JS22-1_757□PFR_JS22-1_757□Peptidylprolyl isomerase□865922:866434 Forward
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   IIDGFMIQGGDRTGTGRGGPGYEFADEFYPDLTFAKPYLLAMANAGPNTNGSQFFITVAP
   TPHLNMRHSIFGEVADDASRKVVDEIAKVPTARGDRPVDDVVINSVEIAQ
   >PFR_JS22-1_758□PFR_JS22-1_758□Transcriptional regulator, AsnC family□866565:866834 Reverse
   MITAIVFVHADNDRISEVAEQIAGLEHVTEVYSVTGDIDLVVMVRVAGYEEIAPAITDQL
   KKVPGVIDTDTHLAFRAYSEHDLEAAFSL
   >PFR_JS22-1_759□PFR_JS22-1_759□Peptidase M23B family / metalloendopeptidase□867094:868215 Forward
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   >PFR_JS22-1_761□PFR_JS22-1_761□1-acyl-sn-glycerol-3-phosphate acyltransferase (Precursor)□869170:870111 Forward
   MSDTDRPDAPAVRDAPNHPQLPESRPPTLRGSLRAAARAAGFTRGLFRGTREALTAHVEG
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   RYADGGAGERPRR
   >PFR_JS22-1_762□PFR_JS22-1_762□3-deoxy-7-phosphoheptulonate synthase (Phospho-2-dehydro-3-deoxyheptonate aldolase) (DAHP
synthetase class II)□870260:871606 Forward
   MPQVQQPHYADASAEKRVVDKLRSLPPLVFAGECDDLRDKLAQVANGKAFLLQGGDCAET
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   >PFR_JS22-1_763□PFR_JS22-1_763□Zn-dependent hydrolase of the beta-lactamase fold-like protein□871637:872380 Forward
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   VTRGITL
   >PFR_JS22-1_764□PFR_JS22-1_764□Membrane spanning protein DUF6□872393:873316 Reverse
   MSSAPEHPAARRPSSLPAASALLLIAMLWGSSYFMNKALVGMMPPGDITAVRFTMSAIVL
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   PPPTAVS
   >PFR_JS22-1_765□PFR_JS22-1_765□Hypothetical protein□873359:875626 Reverse
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ALPEGWWA
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A
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>PFR_JS22-1_810PFR_JS22-1_810Two-component system response regulator929473:930126 Reverse
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GQPA
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>PFR_JS22-1_815□PFR_JS22-1_815□Putative sporulation transcription regulator WhiA□935644:936627 Forward
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ANIASNT
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>PFR_JS22-1_821□PFR_JS22-1_821□Triosephosphate isomerase 1□941288:942076 Forward
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>PFR_JS22-1_829□PFR_JS22-1_829□Glutamine amidotransferase subunit PdxT□949062:949682 Forward
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VISTHLIHDLEPVIDTVVFLHQGRLRLQGDADELRAANKTDLEGLFRKVYLP
>PFR_JS22-1_832	PFR_JS22-1_832	Transcriptional regulator, GntR family	951341:951715 Reverse
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KEEK
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NHRATDNNREATSA
>PFR_JS22-1_834	PFR_JS22-1_834	FeS assembly protein SufB	952745:954202 Forward
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EGSVG
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>PFR_JS22-1_836	PFR_JS22-1_836	Putative ferredoxin subunit of phenylpropionate dioxygenase	955416:955763 Forward
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DEATCSLECYLHGSHFDVRTGAALNPPAIQPVPVYPVRVEDDQILVDVENPLKEN
>PFR_JS22-1_837	PFR_JS22-1_837	FeS assembly ATPase SufC	955768:956517 Forward
MATLVIKDLHVDVDTENGPKEILKGVDLTVNDGEVHAIMGPNGSGKSTLAYAVAGHPKYH
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DALKVVAGGIDAFSKKPGKAVLLITHYTRILRYVHPDRVHVFVDGRVSVTGGSELADNLE
ERGYEQYVK
>PFR_JS22-1_838	PFR_JS22-1_838	Cysteine desulfurase, SufS family protein	956507:957763 Forward
MSSDFDVETVRRDFPILSRQINGHPLVYLDSSNTSQKPRTVIDTVAEHYAKHNANVARAM
HTLGAEATAAFEGARARIADFIAAAEPEEVVFTKNASESLNLAANTLGSRLGPGDEVVIS
VLEHHSNLVPWQMVCERTGATLRWFDVTEEGRLDLDKAEREHLINEHTKVVSIAWVSNVL
GTINPVARIAEMAHAVDAVMVIDGSQGVPHLPTDVTALGGDLLAFTGHKMLGPTGIGVLW
GRRELLDELPPFLGGGEMIGVVTMEKSTWAEVPHKFEAGTPPIAQAVGLGAAVDYLDTLD
MDAIAAHDHEITSYALGLLGDLDFVRILGPKQAVDRGSAISFTVDGVHPHDLMQLLDSRG
VAVRGGHHCAAPLHQRFCVQSSTRASSYLYTTREEIDALRDGLVWAHDFFTGKVKARQ
>PFR_JS22-1_839	PFR_JS22-1_839	SUF system FeS assembly protein, NifU family	957760:958212 Forward
MNVEEMYQDIILDHYREKHHTGLRDPYEAEVHHVNPSCGDELTLRVDLDGDTIADVSYAG
EGCSISQASTSVMTDLVIGHSVAHAMELFDEFRTMMESQGRIEPNEDHLEDGIAFAGVSE
FPARVKCAMLSWSALRDALARAGASIEEEK
>PFR_JS22-1_840	PFR_JS22-1_840	Metal-sulfur cluster biosynthetic protein	958209:958658 Forward
MSVPDSDQMSPTPAQTEQSTAAAARPSDLVRDELPEVSTTPTDPNLKPPTEEQVLEALRE
VVDPELMVNIVDLGLVYGVDIDEHANVLLDMTLTSPTCPLTDQLEWGAQAALDGIANEVT
INWVWLPPWSLDRITDDGREQLRYIGFNV
>PFR_JS22-1_841	PFR_JS22-1_841	ABC transporter related protein	958932:960530 Forward
MIQAKELEVRAGARLLLNPVSFQVIPGDKIGVVGRNGAGKTTTMRILAGEGLPAAGAVKR
AGQVGYLPQDPRESDLSITASKRILSARGLDRIMERLTKFTEEMSTASGAAREKAMAGYD
RAEAQLTAAGGYGAEAEAARIAANLGLPDRVLAQPLHELSGGQRRRVELSRILFSNADTL
LLDEPTNHLDADSIMWLREFLKTYPGGVMMISHATELLEETVNKVFYLDANRATLDIYSM
GWKLYLEQRQADEKRRRRERLNAERKAAQLMAQSDKLHAKATKAVAAQNMARRAERLLAS
VEPERVSDKVAKITFPEPAPCGKTPLMAKDLSKSYGSLEVFTGVDLAIDRGSRVVVLGLN
GAGKTTLLKILDGIEKPDTGEVLDGYGLKLGYFAQEHDMLDMSATVLENMQAAAPELNDT
DARKVLGAFLFTGDDDQKPAHVLSGGEKTRLALATLVVSAANVLLLDEPTNNLDPASREQ
VLGAIRSYKGAIVLVTHDEGAVEALEPDRVLLLPDGDEDLWDHEYTELVSLA
>PFR_JS22-1_842	PFR_JS22-1_842	Mycinamicin-resistance protein MyrA	960681:961514 Reverse
MTDFSALDAACPLLECPVCRGRGAAEVPLVRHDRQLACPNGHGFDIARQGYVNLAGGAPP
ANADTAPMIDARQRFLDSGVYEPIRQAVSHASDAAHWLVEVGAGTGWYLDGVLTHRRDAV
GLATDVSVAAAKRAARSGLASVVADTWAGLPIRSASVDAVLCVFAPRSAAEFARVLAPGG
RAVVAWPTPRHLAALRERLGLLNVATDKDEQLVTQFGEAGLNPADRELVEFSAECTAQQV
ADLVGMGPNAFHDHAPAQGPTTIDVSVEVGTFLRAGA
>PFR_JS22-1_843	PFR_JS22-1_843	Short-chain dehydrogenase/reductase SDR (Precursor)	961522:962268 Reverse
MDLGLASKVFIVTAASGGLGLASARALVAEGARVVLVARRAEALAAAAAELGAQNAVVLP
ADLSAPETADAAAQLALDTWQRLDGAFVSVGGPPKGHVVENTDEQWQAAFSSVFLAALRV
SRAVVGANPAARLGFVLSSSAKSPLADMAISNGLRPGLAMLVKQLANEIAPDGGRAFALL
PGRIATQRMVDLLGHDPTPQDAVDSGIPMRRMGDPDEFGRVAAFMLSDAASYVTGVMLPV
DGGLLQVL
>PFR_JS22-1_844	PFR_JS22-1_844	3-oxoacyl-[acyl-carrier protein] reductase fabG1	962338:963072 Forward
MTATDPTTIPAGRVALVTGASRGIGAEIATELLAAGYRVAGTSRSGRAPDGVLGVSADIT
DPEQVEAAFARVEEELGGVEVLVANAGITRDMLLMRMSDDDWDGVLATNLTGTFRMVRRA
TRRMMRARFGRIVLMSSVSAYVGSPGQVNYSASKAGLIGMARSVARELGGRGITCNVVAP
GFISTDMTDELSDEVKDDYLARIPAKRFGETRDVAHAVRFLCSDAAGYVTGAVLPVDGGL
GMGR
>PFR_JS22-1_845	PFR_JS22-1_845	Enoyl-(Acyl carrier protein) reductase	963162:963935 Forward
MGILDGKNILVTGVTMNTSIAYKVAEVAEQQGATVIVTAFGRALRLATKVVQKLDPVPQV
IELDASNADELAALPGKLRELGFDHVDGVLHSIAFANPERALGGAFLKTGWDDVAVSLHT
STYSYVSLAMAVRELMSAGSSVVGLTFDASVSWPSYDWMGVAKAGLESANRYLARYLGPD
QISSNLVAAGPIDSIAKTAIPGANSFNDIWTERAPLGWDAKDATPVANAVCALFSDLFTA
TTGEIIHVDGGLASTGA
>PFR_JS22-1_846	PFR_JS22-1_846	Hypothetical protein	964011:964760 Reverse
MSDSLIEGLRLVSVLNAMTGDGLDAARAEDALRVADNGDPNRAHHVFDPAGVLGLEPQVA
TPVRIALGRVANQLPGEHWALLLPQPGRLAGLRGPIATNAAALETGVIVVNHGGGLGWLP
RPVGPAMQWELVPAERPLLPATPGEAAQALNEQILAAGRELGRLDAPAGNRPDDAASIHL
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GAAYSHVNQKLLDRALLWREASRAGIEASPQLLHSHGVLVRDKQLRELDDICRDAISAAA
SWPRAPHGL
>PFR_JS22-1_847□PFR_JS22-1_847□ABC-type molybdenum transport system, ATPase component/photorepair protein PhrA□964913:965707
Forward
MVEVAKLSGVGVRRGKAKLLDDVNLTINEGDRWVVMGPNGAGKTTLLSLLSAQNHPSEGT
VELLGERMGRVDVFELRPRIGLSSSSLAERIPRNETVENVVVSASYAVVGRWREQYDELD
FQRAHELMRLFAVEGLAQRTFGTLSEGERKRVEIARALMTDPELLLLDEPGAGLDLGGRE
HLVATLSMLCQDPDSPAIVLVAHHVEQVPVGITHALLLDHGHVVAQGPINQVFTDEIMSA
TFGLPLQINQLPDGRWAARARLNY
>PFR_JS22-1_848□PFR_JS22-1_848□Sodium Bile acid symporter family protein□965789:966832 Reverse
MSRHEQRGPGKPWFRRIRIDWFVTAICISAIMASIFPVRGGGSVVLDGATKVLIFILFYL
YGVRLEPREAMAGLKHWRLHLLILAFTFAVFPLVVFAIHPILTHVLTPALVAGVLWLSIL
PSTVQSSINFTSIARGNVAGAIVSASASNILGVILTPLLAMFVMSTGGLVIHAQSILDLC
VQLLLPFVLGQLTRRWTAGFVLGHPRLKYVDQLSIITVVYNAFSDGMNEGIWHTVALADI
GRLLPILFAILAFMLWFTWWLPGRLGFNRKDQIAIQFCGTKKSLATGVPMASVLFAPSIV
PLLVLPLMIFHMVQLIACGVIAGRYARKDEAWHEAPGRGVGPEPAED
>PFR_JS22-1_849□PFR_JS22-1_849□RNA methyltransferase, TrmH family□966973:967866 Forward
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APRWIDGLRDVLDATDAPVYVVSEDLAEQITGFHVHRGALASFKRIIAWSMHDLLAMDRL
VVCEDIVDHTNVCGPKLAHPEPAAEPRRRSRIAVLEGLVDHTNVGSAFRNAAALGLDAVL
VSPTCADPLYRRSVRVSMGTVFQVPWTRIPDWTKGIAELKAAGYVLAGMTLGEGAITLDE
LVAEDHEKLALVFGTEGHGITRETDALLDRRVTIPMMGGVDSLNVTAAAAVAFYATR
>PFR_JS22-1_850□PFR_JS22-1_850□Type I restriction-modification system, M subunit□967962:969533 Forward
MAPTTKEAQRAELHKTIWRIANDLRGSVDGWDFKSYVLGMLFYRFISENLTAYLNKNEHD
AGDVSFDYRLTADSDAEFARDEVVAEKGFYILPSDLFANVRERAARDENLNETLERVFKN
IEASALGTDSEDDIKGLFDDLDVNSNKLGSTVAKRNQKLVKLLDAIGDLPLGRWEDNSID
LFGDAYEYLMQMYAANAGKSGGEYYTPQEVSELLARITVVGKTQVNKVYDPAVGSGSLLL
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FEAIVSNPPYSIKWEGDANPLLINDERFAPAGVLAPKSKADLAFTMHMLSWLAVNGTAAI
VEFPGVLYRGGAERKIRQYLVDNNYIDTVIQLPPDLFFGTTIATCILVLKKSKKTSDVLF
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AEDTREEVDIVELNAEIARIVARQAELRTAIDEIVVDLEGARS
>PFR_JS22-1_851□PFR_JS22-1_851□Restriction system protein mrr□969530:970456 Forward
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GWGVSFLTNVGALRRPKRGHYQITDAGKQLIELFPNGAKERDIKALGADPSSPIREYVAT
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LSMGYGGTTGAGSVTQLSNDGGIDGVIDQDILGLNRVVIQAKRYQDGNTVGRPDLQAFVG
ALSGKADSGVFITTSRFSDGARTYAENVPTRIILIDGERLTTLMIRYGVGVQVKETYKVV
EIDEDFFA
>PFR_JS22-1_852□PFR_JS22-1_852□Type I restriction modification DNA specificity domain protein□970453:971655 Forward
MSRIDDLIQELCPDGVPTMSLGELLDYEQPGRYLVASTDYRDEYATPVLTAGQTFILGYT
DEVEGVYSANRESPVLIFDDFTTAFKWVDFPFKAKSSAMKMLTLRAGVPALIRYIYFAMQ
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QYEHYRNSLLAFSNDVERVALGDLGDLFGGLTGKSKVDFTGGNARFIAYTNVFHNIAVRT
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DVEWLDPEFAKHLFRSHSLRSQIVKTANGVTRFNVSKTRLRKIQVPLPSRAEQARIARVL
DNFEELTNDLTIGLPAELAARRKQYEHYRDRLLTFKELAS
>PFR_JS22-1_853□PFR_JS22-1_853□Type I site-specific deoxyribonuclease, HsdR family□971652:974777 Forward
MSDALARTYDPIAVSSESTVVAEYVHDPSQADAYQSESALEQEMIRLLQGQAYDFLPITA
EAELVANLRLQLEKVNKMTFSDAEWEQFFTTKIAGANDGIVDKTVRVQEDHVQILRRDDG
TTKNIALIDKTNIHNNRLQVINQYEIARGEGDAGEGGAKYANRYDVTVLVNGLPMVHIEL
KRRGVDIREAFNQINRYQRDSFWAGSGLFEYVQLFVISNGTLTKYYSNSTRNRHLAEQKK
SGGAGKGNKSSNSFEFTSWWADANNKPITELTAFVKTFFAKHSLLNVLTKYCVLTADRDL
LVMRPYQIVATERILQRIQISTNYKTLGTLDAGGYVWHTTGSGKTLTSFKAARLASKMPS
VDKVLFVVDRKDLDYQTMREYDRFEKGAANSNTSTAVLKKQLEDRGARIIITTIQKLSTF
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TASIDAARRYYNQFQLQMEELPPDKRLKVGLIFSYGANEAEADGILDDEAFDTDALDLDS
RSFLEDAIQDYNDMFGTSYDTRADRFQNYYKDLSQRTKNREIDLVIVVNMFLTGFDATTL
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LTERQRQDYASIYLRLRDEFTRDRDGDREVINDDVVFEIELVKQVEINVDYILMLVEKLR
AEKGDGDDKEVRAEITRAVDASPTLRSKRDLVEDFVESVSLQGAVDEQWQAYMAAKREAE
LQELIETHKLKLEQTRSFVDAAFRDGQLRTAGTEITRILPPVSRFNRESNHGDKKKRVIE
ALSRFFERFRGLATGGGEPAD
>PFR_JS22-1_854□PFR_JS22-1_854□Hypothetical protein□974884:975189 Reverse
MISSPFNTSASNFGNAAMQTADVPWDTPVKMRLGADGPGETGAYIEVSTTRGFAKRISID
EARLSECRQEQDGAAGIALCQQLVDDLAARIKTAVAEAVRG
>PFR_JS22-1_855□PFR_JS22-1_855□RNA methyltransferase, TrmH family (Fragment)□975484:975933 Forward
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RDGLATLQRAGFTVAALALRDDAVGLDEFAARMRARPGKLAILMGTEGAGLSGHWISQAD
AAVRIPMAHGIDSLNVAAAAAVACYALRP
>PFR_JS22-1_856□PFR_JS22-1_856□Peptide deformylase□975967:976587 Reverse
MKSPAEWAVNGKVLRITRWDESIMRSQTRPVTTFDDTLAQLIADMFKTMAAADGVGLAAP
QVDSDLALFVFNCPDIHDKLVYGVMCNPVVTLPEGKDRHLVSAQEGCLSWPGAYQSLARP
DFAVCEGQDETGAPVRVEGTGLLARCLQHETDHLHGTVFGDRLSKRARRRLDQEKEELAP
LYPADWPVHPKIAPSQVPTEPVTPTE
>PFR_JS22-1_857□PFR_JS22-1_857□Tyrosine recombinase XerC 1□976736:977662 Forward
MDDAGRMPTGWVRDAGLFADYLRLQRRRSANTERAYLTDLRELALFLQGRGVHDPDHVRL
TDLRRWLASQQASEAPATVARRAGTARVFFGWARETGRLGTDPAAGLRSPKLGRRLPQTL
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YEQAFPRA
>PFR_JS22-1_858□PFR_JS22-1_858□Peptidase, M23 family□977706:978890 Reverse
MDHSSADRRSADYRSLDELSTEHHEGRHRPGRHRDPAGRGGPSTRTVEQARALRITGMRR
RACAGHPLGAPRAAVRTLLVCLLTCLALMCPVGAWAQQVDGELRQLLPLDGPVSRDFRAP
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QVIGLVGTTGLSTGCHLHFSTYTAGRAVDPRPFL
>PFR_JS22-1_859□PFR_JS22-1_859□30S ribosomal protein S2□979184:980161 Forward
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VAKGGQVLFVGTKKQAQEAVVEQASRVGMPYVDQRWLGGMLTNFQTISKRIARLKELEAM
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>PFR_JS22-1_860□PFR_JS22-1_860□Translation elongation factor Ts□980200:981012 Forward
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>PFR_JS22-1_861□PFR_JS22-1_861□UMP kinase□981185:981898 Forward
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>PFR_JS22-1_862□PFR_JS22-1_862□Ribosome recycling factor□981971:982528 Forward
MTSDIIKSAEKKMQGAIDFAKEDFSGVRTGRANPAMFEKLEAEYYGVPTPIQQLASFSSP
DPRTMLITPYDKGALGAIEKAVRDSDLGVNPASDGNAIRAVLPELTEERRKEYIKIVRTK
AEDAKIAIRGHRRRGMDAIKAQEKDKEIGEDDARVSEKQLDAVTKKYTELVDELLKAKEA
ELLAV
>PFR_JS22-1_863□PFR_JS22-1_863□Phosphatidate cytidylyltransferase□982537:983382 Forward
MSAAKRSPGRNLPAAITTGVILGAVVVATLLWWNWGFALFVALALALGVWEVCNALEKLD
MHPARWPILVGTPIVMIGSYAVGQGSGEPESALGFIVGGLALMVIVALFWRIPRGTQDFV
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RDAGIKDMSHVLPGHGGVMDRLDSLLAAAPAAWLVMYVLIV
>PFR_JS22-1_864□PFR_JS22-1_864□Ribosomal RNA large subunit methyltransferase N□983379:984515 Forward
MSTVQSARTIDEIMSTGPGRRPPKHWMDLGVDERIEAVRALGLPAFRAKQISTHWFSRCE
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>PFR_JS22-1_865□PFR_JS22-1_865□1-deoxy-D-xylulose 5-phosphate reductoisomerase (Precursor)□984586:985779 Forward
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DAIVETLIEEANKIAADFPEQGTPQVLV
>PFR_JS22-1_867□PFR_JS22-1_867□Acetyltransferase, GNAT family□987158:988000 Forward
MSGVVRVLGPQDLPRARALLDRNPLENLFVNARLDMGGLERNRPGTRVWGWESDGELTAL
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>PFR_JS22-1_868□PFR_JS22-1_868□Prolyl-tRNA synthetase ProS□988085:989905 Forward
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VLDQLN
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RSAMAGIDAQCLVPGQHGVGLAWWPGWV
>PFR_JS22-1_870□PFR_JS22-1_870□Ribosome maturation factor RimP□991220:991693 Forward
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ISHALDEAEAPSNSPYTLEVSSRGVSAPLTRPAHWRRNATRLVEVTPLEGEKYTGRITSA
DEDGAELEIDGQPRHVDFGQVRRAVVQIEMNRKSRED
>PFR_JS22-1_871□PFR_JS22-1_871□Transcription termination factor NusA□991695:992753 Forward
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EVNDEGESVGEYDDTPTDFGRVAASTARQVIFQRLREAEDEQKYGKFSAVEGDVVMGVVQ
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LVKKLFELEVPEIEQGVVEVKAIARESGHRTKIAVVSHNPDVSAKGACIGPMGQRVRAVM
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>PFR_JS22-1_872□PFR_JS22-1_872□Hypothetical protein□992900:993097 Forward
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PPPGW
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R
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>PFR_JS22-1_911□PFR_JS22-1_911□Protein often found in Actinomycetes clustered with signal peptidase and/or RNaseHII□1032716:1033030
Forward
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FETASGRVESCPLAA
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>PFR_JS22-1_982□PFR_JS22-1_982□Branched-chain-amino-acid transaminase□1108059:1109144 Forward
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V
>PFR_JS22-1_983□PFR_JS22-1_983□Putative alpha-isopropylmalate/homocitrate synthase family transferase□1109176:1110774 Forward
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DTPS
>PFR_JS22-1_986□PFR_JS22-1_986□Transcriptional regulator, IclR family protein□1113183:1113911 Reverse
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QG
>PFR_JS22-1_987□PFR_JS22-1_987□3-isopropylmalate dehydratase large subunit□1113955:1115364 Forward
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QLIALALSRPATVLR
>PFR_JS22-1_991□PFR_JS22-1_991□Conserved hypothetical membrane spanning protein□1118149:1119144 Reverse
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LPAFQQVVAQNRGPREVAGPVAHPQPATARS
>PFR_JS22-1_992□PFR_JS22-1_992□Putative dihydroxyacetone kinase regulator□1119254:1119988 Forward
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PRAG
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KELQRRDGHVWLMPHNQAYEPINGDQATLVGKVVAVLRRM
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MARSAAGAPMAVPAG
>PFR_JS22-1_1012□PFR_JS22-1_1012□Transcriptional repressor NrdR□1145769:1146266 Forward
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>PFR_JS22-1_1013□PFR_JS22-1_1013□Vitamin B12-dependent ribonucleotide reductase□1146452:1149343 Forward
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AR
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>PFR_JS22-1_1018□PFR_JS22-1_1018□Sugar-binding family transcriptional regulator□1154991:1155959 Reverse
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>PFR_JS22-1_1037PFR_JS22-1_1037PF13834 domain protein1182274:1182648 Forward
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VDCV
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>PFR_JS22-1_1038□PFR_JS22-1_1038□Hypothetical protein□1182760:1183080 Reverse
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>PFR_JS22-1_1039□PFR_JS22-1_1039□PF12502 family protein□1183370:1184191 Forward
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DKPMVPGDPIAMALPDAMRAQLDGQAGAPQGQQ
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SYELLG
>PFR_JS22-1_1041□PFR_JS22-1_1041□TrkB□1184575:1185243 Reverse
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RIMSALVEEAVSVGAVVRLMTFKKGSANLVELTLPEDSPAVGKRVRDLSFPGDGVLVAIV
RDGRSRAPEQDAAVEVGDELLFTISEEHERELSHYLVPVTKG
>PFR_JS22-1_1042□PFR_JS22-1_1042□Trk system potassium uptake protein TrkA□1185257:1185919 Reverse
MHIIIMGCGRVGSSLARALEKRGHSLAVIDVNVEAFRRLGPDFAGKTVKGVGFDRDVLVR
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WAAGQVMNRLLSDSVTPVWRDPSGMTALFQVPFDNAWAGTSVGQLEERLRVRVPFLTRIG
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>PFR_JS22-1_1043□PFR_JS22-1_1043□Conserved alanine, valine and leucine rich membrane protein□1186092:1188086 Forward
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GFAFSLPIGIAVGAVLLVVVMSYRQTVHAYPSGGGDYEVVTTNLGPTSGLVVASALLVDY
VLTVAVSVSSGVQNAKAMMPFIQGHEGLIAAVVIIVLMVINLRGVRDSGGIFAVPTYLFM
FGIGVMVIWGLLQIFVFGHPLRAATADYTVVGVSRYEPLVGLGMVTLLARTFSSGCAALT
GVEAISNGVPNFRKPKSKNAATTLLLLGCIAVSMLLGILALANLTGVKMSDVNSGSYFVT
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VVFILMRAIHSHYAEVAAETTITDPAEWVLPSRVHAVVMVNAVNKPTVKAIQFARATQPG
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RPRR
>PFR_JS22-1_1044□PFR_JS22-1_1044□Putative 23S rRNA (Uracil-5-)-methyltransferase RumA□1188083:1189261 Forward
MTTVATAVGEIIGPLSVGPIAHGGHCIARHEGRVIFVRHTIPGETVMVRITDDSHERYWR
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VMSDPDLLEIYREKRREAHRADHPEG
>PFR_JS22-1_1046□PFR_JS22-1_1046□Glutathione S-transferase domain protein□1189553:1190626 Reverse
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AGDPSYTGRGTVPALVDTKTGKVVMNDYHVMSLELETAWSQFHKAGAPDLYPEALRGQID
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>PFR_JS22-1_1047□PFR_JS22-1_1047□GCN5 N-acetyltransferase□1190623:1191273 Reverse
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DSDRPPLESDGPSPALAVNEAPSHDNAIHQDQGEIR
>PFR_JS22-1_1048□PFR_JS22-1_1048□Cysteine synthase□1191270:1191977 Reverse
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GISSGAAVAAARILAARPETAGQVIVTIIADTAERYYSTDLFDHHTAATPEGTAQ
>PFR_JS22-1_1049□PFR_JS22-1_1049□Hypothetical protein□1191959:1192243 Reverse
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ERDARLAKGGTIVEATSGNTGISLAWLGGCSATA
>PFR_JS22-1_1050□PFR_JS22-1_1050□Glutathione S-transferase domain protein□1192735:1193763 Forward
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RLIVARICPWAHRQLITREVLGLTDAISVGVTAPVRTDNGWRFSLDPGDKDPVLGIEYLN
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>PFR_JS22-1_1051□PFR_JS22-1_1051□Alpha-ketoglutarate transporter, MFS super□1193871:1195301 Forward
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>PFR_JS22-1_1052□PFR_JS22-1_1052□Aconitate hydratase 1□1195555:1198227 Forward
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>PFR_JS22-1_1054□PFR_JS22-1_1054□Hypothetical protein□1198791:1199321 Forward
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SGWPESVSAPGTQRMESDAVGFLLDCCPPDYRAYPLLRREPVVLARFAADQVEGQLRSTR
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>PFR_JS22-1_1055□PFR_JS22-1_1055□1-deoxy-D-xylulose 5-phosphate synthase dxs1□1199372:1201387 Forward
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A
>PFR_JS22-1_1057□PFR_JS22-1_1057□Outer membrane receptor protein□1202773:1203372 Reverse
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>PFR_JS22-1_1058□PFR_JS22-1_1058□Conserved hypothetical protein□1203458:1203982 Reverse
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RTLFADAWVDLYGPTGEERHA
>PFR_JS22-1_1064□PFR_JS22-1_1064□Putative CDP-diacylglycerol--inositol 3-phosphatidyltransferase□1210810:1211439 Forward
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AKPA
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YAAVAGE
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GSLNGTYVNRTLVDGSAVLRPGEEVQIGKFRMVFFVSEHGLH
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DGVSVYECTSEDEVYDLLRGGQGMFAIALDGVVRDIEGTLIELPSEHVNDEAPLARGDDE
LSLARRRRRTS
>PFR_JS22-1_1076□PFR_JS22-1_1076□Glycine dehydrogenase□1219362:1222277 Forward
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SLQLPPARSEQATTARLSELAALNNPRRAMIGMGYYGTVTPSVIRRHVVENAGWYTAYTP
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DAGLLPQSLAVVQTRMGALDIKIVETDDLATSPALDEAFAVIVQTPTTDGRMQSTGELTE
LADAAHAKGVMVIAAADLLALTMAVPPGQWGADVVVGTTQRFGVPLYYGGPHAGYISVRK
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HGPSGLRRIAHDIHQRTRLLAGALSAGGVKARHESFFDTLTVAAPGKAADVVARARELGV
HLRLVDANTVGISVGEDATDEDLNHVVAAFGINPDTQADPWGGFGATLRTDSYLGHRVFN
SYHSETQLMRYLRTLEDRDFALDRGMIPLGSCTMKLNPATAMEPISYPGFANLHPFAPAE
DARGYRILIDELSDWLVQVSGYAACSLQPNSGASGEFTGLLAIRAYHESRADHDRKVCLI
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KATQMALLNANYIADRLSDYYPVLYTGANDLVAHECILDLRELSASTGVSVDDVAKRLID
YGFHAPTMSFPVPGTLMVEPTESEDLGELDRFCDAMIAIRAEMDKVASGAWPVDDNPLVN
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APTDELLAQQQ
>PFR_JS22-1_1077□PFR_JS22-1_1077□Inner membrane protein yhjD□1222295:1223743 Forward
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NQFAGGITYFSVLASVPVLMFAFSGLGLTLTVIRPALLDDVKGIVVANLYPGPMRDTVLQ
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LLLLGLIVLVGVLLAANTVFTGWGSELLGLAHLGELRISAGLLRLISLSASLLGGWALFI
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LNLFARLLLYVAAWIATANQPAVARRWSDFDQLLRERDDTIAVPDHWAAADQDHAERSAE
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AKDSVLVSAGRSLRRPESTRASWGAWLLGVVTGLGAGAGLVRRGLRRTGRDGRGQRGRTE
KA
>PFR_JS22-1_1078□PFR_JS22-1_1078□Phage infection protein□1223716:1225923 Reverse
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TSTSTADYAFSVRPR
>PFR_JS22-1_1079□PFR_JS22-1_1079□ABC transporter related protein□1225928:1226740 Reverse
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VAAMEETVGFRIEKHVELESLTPIEKAISSVALAMIRPSRVVVIDDADMTVPHSQQSLLF
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LTARGRPAGAAMGDDQVAAPSPTQTPNPDK
>PFR_JS22-1_1080□PFR_JS22-1_1080□Transcriptional regulator, TetR family□1226737:1227351 Reverse
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FSTICIENINRLSPPVIAELDAMFANGARDASAIDRIADSFAQIVIESGPWQVALGEFRQ
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>PFR_JS22-1_1081□PFR_JS22-1_1081□Adenosylcobinamide-GDP ribazoletransferase□1227445:1228266 Reverse
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HILARLGGLTGDTFGSLVEMSGLAYLLTLALFA
>PFR_JS22-1_1082□PFR_JS22-1_1082□Bifunctional cobalamin biosynthesis protein cobU□1228226:1228897 Reverse
MTRIVVDVPDSPESRRLLDQLSGLGARQRPARTLVTGGARSGKSSYAEALLGSFDHVDYI
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ATSQRNPDDPEWMARIAAHVARRPKSWNTVETLDVAQVLSDDGSPALVDCLGVWLTRELD
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LNASVADACDEVLLCVAGRALSLPPRPGGPHGAGTDPQPKDAI
>PFR_JS22-1_1083□PFR_JS22-1_1083□Cobyrinic acid a,c-diamide synthase□1228894:1231479 Reverse
MVTATALPRVLIAAPASSQGKTTVAIGLMAALRASGRSVAGFKVGPDYIDPGYHALACGR
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R
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YLGWDGRALLPS
>PFR_JS22-1_1088□PFR_JS22-1_1088□Alpha, alpha-trehalose-phosphate synthase otsA□1235386:1236867 Reverse
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>PFR_JS22-1_1091□PFR_JS22-1_1091□ADP-ribosyl-(Dinitrogen reductase) hydrolase□1238970:1239926 Reverse
MEFSPQVMDRAAGVLVGQAVGDALGVPYEFAAPIRAGDARMVGGGLGPYEPGEWSDDTQM
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SESLGRAKFGASHFFSWGWLPMLRSLDAKPGDVLRISIDPAAARAEVQLGGPELWGP
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>PFR_JS22-1_1094□PFR_JS22-1_1094□Transcriptional activator, TenA family□1242104:1242799 Reverse
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ALYLHDYARILAAAGEVSPTPAEQEFWTHGAQSSVAMELELHKSWIPADAMAHLAPSPVT
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>PFR_JS22-1_1097	PFR_JS22-1_1097	Hypothetical protein	1245844:1246410 Forward
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PTSDAGQSGRGTWQVIGWENIQNGDWDNATKTLSWLLLDGTVGQIAVTTTDRLPGVFRER
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ELRDEYEL
>PFR_JS22-1_1098	PFR_JS22-1_1098	Phosphofructokinase (Precursor)	1246741:1247955 Reverse
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VGSDSAATGRLNGLDARQEAMRAAREHVGTQPGMACTVGIDANDRVHVEVSTRADTAFLS
IVGINHLNARGAATAELRPV
>PFR_JS22-1_1100	PFR_JS22-1_1100	Translation factor SUA5	1248670:1249287 Forward
MARYYPVHPENPQARSIHQVADLLREGAVIAYPTDSGFALGTLFGNKEGIDTMRRIRDLD
ERHHLSVVVSEFAQLGRYVDMDNREFRAIKASTPGPFTFILRATREVPRSMQHPNKTVGV
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>PFR_JS22-1_1103	PFR_JS22-1_1103	Proteasome assembly chaperones 2	1251341:1252378 Reverse
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>PFR_JS22-1_1104	PFR_JS22-1_1104	ABC-type uncharacterized transport system, ATPase component	1252544:1253335 Reverse
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VADLLAQFEHIKGAQLSDRSLLT
>PFR_JS22-1_1105	PFR_JS22-1_1105	ABC transporter, permease protein	1253337:1254290 Reverse
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GPLEDRDQASGLVGPGA
>PFR_JS22-1_1106	PFR_JS22-1_1106	ABC transporter permease protein	1254297:1255277 Reverse
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GETGAEVMARMGETLTHLDRVTEPGPILVCSHGTAIRLGVAALVGWDYPEIWKLASMGNC
CYTEVIREFDAWRVERFNVPPQWNFSG
>PFR_JS22-1_1108	PFR_JS22-1_1108	Glutamine--tRNA ligase (Precursor)	1256111:1257823 Forward
MAKPADNIAASDFIADAITKDNEVGTYAQRVQTRFPPEPNGYLHIGHAKAITVDFGTAEE
FGGLCNVRLDDTNPVAENPEYVESILADIAWLGYQPHTVVHASDYFEQLYQWAEYLVEQG
LAYVDDQDTETISAQRGGFGKPGIESPCRDRTVEENLDLLHRMRAGEFDDGACVLRAKID
MQSDNMVMRDPVMYRIRHATHHQTGNDWPIFPTYDWAHGQSDAIEGVTHSLCTLEFDSHR
PLYNWFLEHLPLPGDQPRQIEFARLELTYTVTSKRRLAKLVADGVVSGWDDPRMPTLRGL
RRRGYPAAAVRDFCRDIGTTRTNSRHNIEELESFVRRELNKTAQRRMVVTRPLRLVIDNW
PTDEHGAPEVDWFDVTNNPENPADGTRRVPFSGELFIERDDFAEVPPPKFFRLSIGREVR
LRGAYFVTATSVVTNEAGEVTEVHATYDPATRGGDAPDGRKVKSTMHWVSAAHAVDVKVA
LYNRLFTTPAPGERTGEPLDDLNPDSVELLTDAKGEGVINEVEPGQVVQFERLGYFCADL
DEPRLFHRTVGLRDEWAAQQRRAAKQAKKG
>PFR_JS22-1_1109	PFR_JS22-1_1109	TIGR03085 family protein	1257868:1258614 Reverse
MSTPDGGRWTSRPAYSDYVAIHPRYDAAHVFRLALADALTQAGPDARTLCTGWTTADLAA
HLYVRENDPLSLPGIAGLPGPAGPAAQRMTIRSMERALTRHGYQGVVDLFRAGPRPWSVW
RAPQLDRIGNALEYFVHLHDVTDAVPHDGNDPLGSDRGLSQRLRDELWHRMPPLATMLLR
GSPAGVQLERLDAPHPSRIIARRGLPIVTARGSAPQLALWMFGRHARVELVGDVEPLAAV
STLVASGV
>PFR_JS22-1_1110	PFR_JS22-1_1110	Phosphoribosyl-AMP cyclohydrolase (Precursor)	1258630:1259082 Forward
MGNNGGMSTNSARSTRLDVSAPTQADTGVPTLDPSIAQRLKRNEAGLVPAIAQEATSGRV
LMMAWMNDDALARTLATRKATYWSRSRQELWVKGETSGHTQAVRDVWLDCDGDTVLLSVD
QVGAACHTGADTCFDAGGPLPLAGESVIAS
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>PFR_JS22-1_1111	PFR_JS22-1_1111	Anthranilate synthase component I	1259079:1260611 Forward
MSRQLRIEPSLEGFREQAVDRRVVGVRTRLRADDLTPIALYEQLTGEAEGSFIFESVEQG
TWSRWSFIGVRCPSMLVGRGNTSEWLGRPLEGIPRHGPCLDVLAATLRALHTPADPELPP
FSSGLVGYLGWDVKRQVEPSLGEPNPDDIGVPDSVMMLATDMAVLDHHRGEVWLIANAIN
FNDTAEGVDEAYRDAVERVHRMATRLTSPRPALLASIEPDARPQVTEQRAPGEFEAMVEK
AKEYVMAGDIFQVVPGQRFDVDVTASGFDIYRELRVANPSPYLFLLKLPGFDLIGSSPEA
LVTVKDGVATTHPIAGTRPRGDTEAEDRRLEDELLADEKERAEHLMLVDLGRNDLGRVCI
PGTVTVTQFMHVGRYSYVMHLEAAVTGSVEPGLSALDVVMACFPAGTLSGAPKLRAMQII
DELESTARGPYGGVVGYFDFAGNADTAICIRTALVKDGVAHVSAGAGIVADSVPANENAE
SHNKAAAVLVALARANASHRITPQTLLEQS
>PFR_JS22-1_1112	PFR_JS22-1_1112	Indole-3-glycerol phosphate synthase 1	1260608:1261468 Forward
MTTVLDDIITGVRADMAARMAVVAPSQLKERIRWMGPTLDPRPGFGGDTISVISEVKRSS
PSKGALATIEDPATIASAYEAGGAAAISVLTERHRFNGTLDDLRAVREAVGIPVLRKDFV
VDPYQVLEARAFGADLVLLIVAALDDKQLAGLYDLALSLGLLPLIEVHTAEEMRRAALLK
PELVGVNNRNLKTLDVDLAQFERLAPLAPHDAIVVAESGIRDAADVQRVRAAGADVVLVG
EALVTSGNPREAVQTMIEATRPGRGPAGSPGRATVMNDDRQGESNE
>PFR_JS22-1_1113	PFR_JS22-1_1113	Tryptophan synthase beta chain	1261461:1262714 Forward
MSSTARELPDELGHFDFFGGQFVPEALKAALEELTAAFRDAQDDPSFAEELKDLQVNYAG
RPSPITEARNFGDKYCGGARILLKREDLNHTGSHKINNVLGQGLLTRRMGKKRVIAETGA
GQHGVATATIAALMGFQCRIYMGKVDTDRQALNVARMQLLGAEVVAVEAGSATLKDAMNE
ALRDWVTNVATTHYLIGTASGPHPFPMMVREFQRIISTESRAQMLQRFSQLPDAICACVG
GGSNAIGSFADYIPDENVALYGFEAGGEGVETGRHAASINGGSLGVLHGTRTFVLQDDDG
QTIESHSISAGLDYPGVGPEHAYLSRTGRAHYEPVNDDEAMEALDHLTRCEGIMPAIESA
HAVAGAERVAKRMLAENPDHRPTLLVTISGRGDKDVDTAMKYFGVRGTVDATTGSMS
>PFR_JS22-1_1114	PFR_JS22-1_1114	Tryptophan synthase alpha chain	1262711:1263607 Forward
MSTTDLTKPFPDENRLGISGKMVAACREQGRPALVGYLPVGYPDVPGSIEAMQALTSGSQ
GQGVDAVEIGMPYSDPMMDGLAIQHATTKALARGVRTRDVFTAVEAVAHTGATPMVMIYW
NLVEHYGSHGRTTHPEESVRGFARDLANAGGAGLITPDLTPDDAAMWAAASDEFGLDRVY
LVAPSSTERRLKMTTDACRGWVYATSVMGVTGARASTSSAAPQLVERVRRAAPDLPVGIG
LGVSNGEQAAEIGSFADLVIVGSALVKRLLDAEDAGTRDLGPLRATVDDLAAGVRKAR
>PFR_JS22-1_1115	PFR_JS22-1_1115	Prolipoprotein diacylglyceryl transferase	1263604:1264575 Forward
MSPLFIPSPPISSFSLGPLTIHFYALCILAGIVVAVVLGNRRLARQGATREQFESMLLWV
VVIGIIGARAYHVITDHELYFGPGRHPIDALKIWNGGLGIWGGVAAGALTAWVWCRRNGM
RFGVVADALAPAVIFAQALGRLGNWFNQELFGRPTTLPWGLLIDPEHRPVGYEQFATFHP
TFLYELIWDVLGGFLLLWLGRRFAMGRGKLFTCYVMYYCLGRFFIEALRIDPANTIGGFR
INNYTSAIVFVLATILFIWQLRFRPGNAPDVWRASPDTAVPTGDHPAGPAPIADDAPTQV
SPGPDASGIGTHVPNAPRGESFN
>PFR_JS22-1_1116	PFR_JS22-1_1116	Class II glutamine amidotransferase	1264719:1269227 Forward
MALPEKQGLYDPAYEHDSCGVAFVAKLDGHPSHATVEQGLEALVNLDHRGATGADPAAGD
GAGILVQMPDAFFRGAVDFMLPPTGQYAAGMAFLPTDEEEREMAMISIEKIAIEERLKVL
GWRTVPVATSTLSPISLGVMPHMAQLFVSARDGSAGIDLDRKVYMVRRRAEHETNTYFAS
LSARTIVYKGMLTTTQLTEIYPELHDPVFASALALVHSRFSTNTFPSWKLAHPYRMIAHN
GEFNTVKGNRNWMRAREALLHCDVIPGDLERAFPICTPGGSDSASFDEVLELLHLAGRSL
PHAVMMMIPEAWQHNDAMPPSHRDFYSYHASLMEPWDGPACVAFTDGTLIGATLDRNGLR
PARYWITDDRVIFASEAGVLPVEPGDIRQKGRLQPGRMLLIDLAKHQVIDDQQVKDELAR
QELYGSWLRDGLVSINDLPERTHIVHSHSSVTRRQEVFGYTHELLRRIVAPMANLGRDVI
GSMGNDAPLAVLSDRPKSLFDFFTQQFAQVTNPPLDAIREQMVTSLESRIGPEDNLLDPT
GDSSRQLVIPYPIIDSEQLAKIVHLGEAPDHTGGQTRTIHGLYEVRGGADALAARLDEIR
REVDQAIADDIRVIVLSDRHGNAELAPIPSLLLTSMMHQYLVEKRQRARIGLVVEAGDVR
EVHHAALLFAYGAAVINPYLLFESAEDLARHELYVNVSPEQAIENVSQALGKGLLTIMSK
MGVSTLASYRGAQLFEAVGLNHELIDNYFAGTSSRVEGIGLPELAEEIRFHHERAYPENG
NSLPHRTLEVGGELQWRREGEQHLFDPESIFRLQQATRRGDYEQFKRYTERINDNSSRLM
TLRSLLKFSHDRPAVPLDEVEPASEIIKRFSTGAMSYGSIGQEAHETMAIAMNRLHARSN
TGEGGEDPERLHDIERCSAIKQVASGRFGVTSEYLSYASDLQIKMAQGAKPGEGGHLPGE
KVYPWIARTRHATPGVGLISPPPHHDIYSIEDIKQLIHDLKCANPSARIHVKLVSEVGVG
TVAAGVSKAKADVVLISGHDGGTGAAPLTSIKHAGGPWELGLAEAQQTLLLNGLRDRIVV
QCDGQLKTGRDVVIAALLGAEEFGFATTALVSMGCVMMRVCHLDTCPQGIATQNPELRKV
FDGKPEYVINFMEFMAEQTREILAELGFRSIQEAVGHVEALDTAPAVDHWKARGIDLAAV
LHRVDVPEGTSLYRTTMQDHELAGTVDEQLVELARPALERGEHVHAELAVRNVNRTVGTV
LGHEVTMATDGKGLPDDTIDLDFHGTAGQSFGAFLPRGITMTLVGDANDYLAKGLSGGRI
IVRAPAESTFDQSTQIIAGNVIAYGATSGEIFLRGLVGERFCVRNSGATAVVEGVGDHGC
EYMTGGEALVIGPTGRNFAAGMSGGVVWVLDLAPEHFNASLADAVAVNELDMARIRELLA
RHVELTGSDVAAALLEDPRLAERMTKIVPRDYARVLAARQDAEKRGASEEEVTDAMMEAA
RG
>PFR_JS22-1_1117	PFR_JS22-1_1117	Glutamate synthase subunit beta	1269220:1270689 Forward
MADFKGFMKYPREVAVRRPADERVDDWDEVYPGTPGEAVLPLITTQAARCMDCGVPFCHN
GCPLGNLIPEWNDLIWRGEWQVALDRLHATNNFPEFTGRLCPAPCETACVEGIHRDPVTI
KNVEVATVDKGWDDLRVTPQMPNWHTLKTVAVVGSGPSGLAVAQQLTRAGHSVVVYERAD
APGGLLRYGIPNFKLEKSVVDRRLKQMRLEGTTFKTGVTIGEDITGEQLLERFDAIVLAI
GSTTPRELPIPGRELRGVHQAMEFLPQATKALSGEVPDQIMATGKDVVVIGGGDTSNDCL
GTALRQGARSVLQLEIMPHPPTTRPDSQPWPTYPMIYRVSSANEEGGERLYSASSSEFLG
DDQGNVRAVRLSEVRREANGRFAPVPGTEREIDAQLVLLAMGFVGPEKSGLVSELDLELD
RRGNIVRDEDFQTTVPGVFACGDAGRGQSLVVWAIAEGRSCAHGVDAFLNGHPSPLPRPI
GPQVRQLML
>PFR_JS22-1_1118	PFR_JS22-1_1118	Hypothetical protein	1270709:1271380 Reverse
MNLSDALTESLRTLGLLPLISGILAVVFAAVALFWPGGTVTSIVVILSLYLLLSGAGTVV
TSLRLRSLPGSGLMTAVGVLGVVLSLVMLWHPGMSTRILVSFMGACLVMFGIFVVAISLA
VRRATGRWAWSLPAGAVAGVLGLVFLARPGFGADALGMLLGIGVLVFGLALIAAGVQLRR
FAAGVRRAARDAGFGGPTVVEGSVVPDEGPDAGGPANPPITRA
>PFR_JS22-1_1119	PFR_JS22-1_1119	DNA polymerase III, alpha subunit	1271606:1275178 Forward
MASKNFAHLHVHTEYSMLDGAASNDKLFAEVARQGMPAVAMTDHGNMFGAYEFYQTAKKY
DGEQNPLVKPIIGIEAYVAPSTRLSRSQEFWGNRRDTGSPDTEGGKDVSGGGRYTHMTML
AANATGLHNLFKLSSLASYEGYYMKPRMDRELIAKYSEGIIGSTGCPSGEVQTRLRLGQF
EEACEAAAAYQDILGKENYYCELMDHGVDIEHQVRADLLRLAKRLKLPLLATNDSHYVTE
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ESYEEVFSYVDRMPQFDVPAGETQESWLRKKVKIGLKKHYGDHPSDAVMERVETELKVIE
PLGFSSYFLVVSDICDAARKMGVPVGPGRGSAAGSIIAYLTDIIAIDPLEHGLLFERFLN
PERVNPPDIDLDFDDRQRDKVIDYVTHKYGEEYTSQVNTFNKIKAKAAVKDANRILGYPF
SLGDRITKAMPPDVMGKGVPLNKLFDESNGRYSEGQEFRNLYNSDPDVKRVVDTGMGIEG
LIRGSGVHACAFILSSEKLLNLVPMHKRDKDGMIIAGFAYPQLEEMGLMKMDFLGLRNLG
IMDHCVKNIKRNRGEDVDLQKLPLDDAATYELMARGDTLGVFQLDGGAMRSLLRQMGPTC
FDDIIAVLALYRPGPMGANAHIEYADRKNGRRPIVPIHPELKDDLDEILAPTYHLIVYQE
QIMAIARKLAGYTLGGADLLRRAMGKKKKYILDENFKPFQKGMRDNGYSDESIQALWDVM
VPFAGYAFNKSHATGYALVSYWTAYLKANYPAEYGAALLTSVGDDKDKMALYLSDMRAQR
IKVLAPDVNASEKEFTAVGEDIRFGLGAIRNVGDSVVGGIVEARTDHGPAHEFFEFLDNV
PLSVCNKRCIESLIKAGAFDSMGHSRRALMDVFETAVDGVIDLKRNQANGQDDLFGDLGG
GDAESDPAMNHTVPDIPDWDKRTKLAFEREMLGLYVSDHPLRGLEHVLSAERTIGLGQIA
EQGAEADGHVEVICGMITQVQRKQTKKGAFWAIIDVEDLDASMQVLIFPKVYETCLTQLS
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PDTIVRIRGRVVNKDESLEMQADELTLPDIRQSSGGPVTIRLPLVRCTPPIVAELRQVLT
AHPGSTEVRVQLVGPQSDTVLRVGDGLRVTNEQPLVADLKALLGPASVAV
>PFR_JS22-1_1120□PFR_JS22-1_1120□Hypothetical protein□1275251:1275976 Forward
MSESVGTAPEAPGPAARDAGGPPPGAGPSRGRAWLASRRRELRFLALFVVICAVAGAVCA
VIWKLTAPVPTITVSNDGSAAVSNQALSEFFGADADFMIIGMFGGVALGTLAWHWFKGWG
WPVAMVAIVGSALAALITWRLGTLLGPHDFAGRLAGAPGGATIPIDLTLRSATAWLLWPF
GATVPVLLYSALGRDEEKDEHQAADHDQDAVGAREAPGPKPATGLTRSGHRLIRFPAFGR
H
>PFR_JS22-1_1121□PFR_JS22-1_1121□Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase ybaK□1276013:1276531 Reverse
MSKSANKSTGTPATVALARTGLPHTLHPYVHDPRSRYFGEEAAAALHVDPARVFKTLVVE
LTSGPEPLVTAVIPADNHLDLKQIAALSKAKRAALADPAVAQRVTGFVRGGISPLGQKRQ
TPVIIDQSVAAAPTIFVSGGRRGLSVEMAPDDLVRATHGRLGTISRPGLHWS
>PFR_JS22-1_1122□PFR_JS22-1_1122□Uncharacterized membrane protein, possible Na channel or pump (Precursor)□1276577:1277377
Reverse
MAPGCHWWWNTCVIPAQLFLGAGTVINALCIVVGAAVGTLFGEHLPSRVRDAVTPVLGLV
VVTIGGLSIPSLLDASVPRAVGQAGVVIVLLALVIGTMLGAWWRLEQRIEQLGEWARSTF
NRGRPAGTTLTSRSVEGFVTATLVFCIGPMGILGSLQDGLGQGNDQLIVKAILDGFTALA
LSASFGFAVAGGAAVVLVYQGLLTVLGWWLGGLLPPAELNVLDATGGIILMALGLRLAGI
ARLAVAEMVPALVLAPVGVVIVGLVT
>PFR_JS22-1_1123□PFR_JS22-1_1123□Histidinol dehydrogenase□1277455:1278768 Forward
MLRMIDVTGQRLDDYTAVLPRGHFDVEHAVAAVEPICRAVAEEGETALRRFAEQFDHVVP
EQLRVPEEALDRALDDLEPGLRAAIEESIRRRREVARGIETEEAFREIEVAPGARVANRL
VPVGRVGLYVPGGLAPLASTVLMNVVPAQVAGVQSIAVATPPQAEFGGLPHPTILAVCRL
LGVTEVYAVGGAQAVAMFAYGVPGLCRRADMVTGPGNIYVVAAKRLLRGRIGIDAEAGPT
EILVLADDRANPAYVAADLISQAEHDPMAGAVLVTDSSALLTRVEEELADQVERLATRDR
LKVSLTGEQSGVVLVADMDQGIDVVNDYAPEHLEIQTVDAAALAQRVRSAGAVFVGSHSP
VPLGDYSAGSTHVLPTGGAAHFSSGLTTRSFLKAMHIIDYSAQALGAIGDAVEQFAHAEH
LPGHAEAIAVRTGREVE
>PFR_JS22-1_1124□PFR_JS22-1_1124□Histidinol-phosphate aminotransferase 2□1278768:1279988 Forward
MSAAPRDPRTTQLQASAVPGPEISLAELPLRPELVGEEPYGAPQLDVPVALNTNENPYSP
SVLVRAQMAAAIERVARTLNRYPDREALELRADLAKYLGFGLHARNIWVANGSNEVMTHV
LSAFGGPGRTVLTFTPTYSMYPEYARNTHTNYVTVPRKPDFTLDSELVLQAVAEHHPDVI
LITTPNNPTGTLTPVKVVEEILERTDALVVVDEAYQEFTEFPEDSALALLPRFGRLIVSR
TMSKAFALAGGRVGYLAAAPAVVDACRIVRLPYHLSAQTQAIARVALANKSELLAQVDEL
RQACQDLQDWLRRTGLDVVPSQANFCLFGRFVDRHAVWQALLDEGVLVRETGPEGFLRVS
AGTPEEMAAFRAALGPIIIHQGVLAPGLMARVKPEGPAKLPKGMKK
>PFR_JS22-1_1125□PFR_JS22-1_1125□Imidazoleglycerol-phosphate dehydratase (Precursor)□1279985:1280593 Forward
MSRSAAIHRVTSESDVSVELDLDGTGSSQISTGVGFYDHMLTSFSKHSLIDLTVRTTGDI
QIDGHHSIEDTAIAIGQALGEALGDKRGIRRFGDAIVPLDEALAQAVVDVAGRPYVVCSG
EPDSQITVRIGGTEPLYPGSMTYHVIESLASNAGLCVHLKLLAGREPHHIVEAEFKALAR
ALRMAVEPDPRVSGVPSTKGLL
>PFR_JS22-1_1126□PFR_JS22-1_1126□Imidazole glycerol phosphate synthase subunit HisH□1280590:1281267 Forward
MTGPTLAPGALREPGALAASPSVGVLDYGSGNLHSAVRALAAAGARVTLSSSRAELEACE
RLVVPGVGAFAACMEQLRSVGGVELVRDWAASGRPLLGICVGHQVFFRHGVEKGISSEGI
GIYHGTVEMLDAVRLPHMGWNTVEPPADSRLFAGVGDKRFYFVHSYASHAVEQPGAMVTW
CEHGGDRFVAGVEWRNVCSTQFHPEKSGAAGARLLANWLAMSPAA
>PFR_JS22-1_1127□PFR_JS22-1_1127□Phosphoribosyl isomerase A□1281336:1282061 Forward
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RGSNAELLAEVIAGVDLNVELSGGIRDDASLERALSTGCKRVNIGTAALENPQWCRKVIA
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R
>PFR_JS22-1_1128□PFR_JS22-1_1128□Acetyltransferase, GNAT family□1282058:1283095 Forward
MTPEWAEAFVDDVLEWSFMGFDDLEEVAELRAAIEYFDDPVQTISYADFVAAWNRPGAHA
SHHAVVGRERSGSIVAYGWNHPGLPTDANPSVWFDIGVHPAWRHQGIRHRLTMWLIGRAQ
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>PFR_JS22-1_1129□PFR_JS22-1_1129□Probable transcriptional regulatory protein yebC□1283259:1284059 Forward
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VPNDNIDRAVKRGSGEGADAVSYEDIMYEAYGPDGVAILIDCLTDNRNRAIADVRTTITR
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LDDVQEVYTNAEYSEAVEKGLEEADD
>PFR_JS22-1_1130□PFR_JS22-1_1130□Crossover junction endodeoxyribonuclease RuvC□1284311:1284922 Forward
MGVDPGLTRCGVGIVDGTPGARPQFVAVGVIRTDPHTEHAYRLLAIEEGLGEWFDHYQPQ
AISIERVFAQHNLSTVTGIGQVAGIAMMLGARHGIDVALHTPSEVKSAVTGSGRADKAQV
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IARAARSRTERQASSTRGTRGSS
>PFR_JS22-1_1131□PFR_JS22-1_1131□Holliday junction ATP-dependent DNA helicase RuvA□1284919:1285530 Forward
MIAQLHGKVAAIGANWLVIDVAGVGFQVSTTPNTTSALRTGQTATVFTSLVVREDAMKLY
GFGGTDERDCFELCRTASGVGPKLALAIVSVLTPEEFATAVRTEDLPRLCTVPGIGRKGA
QKIVIELKDRVDALFVAPTNGSASVAPVTPAWQEQVMAGLESLGWSSRDAEAACETVAPL
AEEDPEATVAALMKAALASLARV
>PFR_JS22-1_1132□PFR_JS22-1_1132□Holliday junction ATP-dependent DNA helicase RuvB□1285594:1286619 Forward
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SVTDAPAAGQAAPSDTSHDDASTADPGNPSSDHEPGTDNKSADAEQK
>PFR_JS22-1_1134□PFR_JS22-1_1134□Protein translocase subunit SecD□1287261:1288979 Forward
MAASNRNKHTHPGRRLIVFALVIVFLYGLMGLTKTWTPRLGLDLRGGTTITLTARNNSDG
SAPSKDNLETARSIIQKRVDALGVGESSVTVQGDRQIEVAVPNVSSDELVSLVGTTAQLG
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GRRTSGSSRTGSDTDAPGDDEGDKPASGSKES
>PFR_JS22-1_1135□PFR_JS22-1_1135□Protein translocase subunit SecF□1288979:1290226 Forward
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RVQVRSLSTDEVTQMRDALASTVNTTPDKVGYSLIGPSWGGQITMKAFQALIVFLVLVAL
MIWAFFREWRMAISALVGLIHDLIVTVGLYALIGFTVTPSTLIGVLTILGYSLYDNVVVF
DKVRENTVDITKQDRTFSEAANAAVNQVLVRSINTTVIGVLPVIALLIAGVGFLGGDGPL
ADLGLALLIGMVAGAYSSIFIATPLLTQLREREPDMKKHVAALAKRRARAAAEPQIRVSA
TTVPGGATVSSVEGTADHDVSASAHEGGGPTARQMRDVGDGRAQPVRTPRSKRKK
>PFR_JS22-1_1136□PFR_JS22-1_1136□Adenine phosphoribosyltransferase□1290229:1290768 Forward
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>PFR_JS22-1_1137□PFR_JS22-1_1137□GTP diphosphokinase□1290831:1293182 Forward
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DPLFSVVRATHPKADLSMVERAYRTAEHYHSGQTRISGDPYITHPLAVATILAELGMTEP
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IKQ
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AMTHAMMFTGVDLLDDAPRRWRVENSWGDDHADKGFFTMNDSWFDQYVFEVAVPKASLDQ
SLRDTLATEPKVLPLWDPMGALA
>PFR_JS22-1_1166□PFR_JS22-1_1166□Proteasome assembly chaperones 2□1328636:1329445 Reverse
MRDPVVIAAFEGWNDAADAASEVVNHLTDTYPTDLIWELDSEDYYDFQTTRPKVEMVNGR
STLRWPTIRMSVVHMPHRDLVAISGPEPNLRWRSFCRILVSTFRACNPTMVIILGAMLTD
SPHSRPLPVNASSSDNRIIAGLGIEPSQYEGPTGIVSALADECRKQRLECVSLWASVPHY
VSGSPNPKATLALLGRVEDLLDEAIDLGDLPELTRAWQRGVDELADEDPDVAEYIQGLEE
QQDAEQLPGSTGDALAADFQRYLRHRRTR
>PFR_JS22-1_1167□PFR_JS22-1_1167□5-methyltetrahydrofolate-homocysteine methyltransferase metH□1329618:1333085 Forward
MLGHEVILGDGAMGTMLQAAVLGPDDFEGHDGCNEILNVTRPDVILDIHRAYLAAGSDVI
ETNTFGANAAALGEYGITDRLAELAGAGARLARQAADEAGPGHWVFGSIGPGTKLPTLGH
IDFVTLRDAYYTQVSAMIDGGVDAVQIETCQDLLQAKAAVIGARRAARDAHVDLPIIVDI
TVETTGTMLLGSETGAALTSLAPLGVDVIGLNCATGPTEMSEHLRYLSAHADCAVMAMPN
AGLPELTADGAVYPLGPDEFARAQLDYVERYGLAIVAGCCGTTPEHIARLRAALGAHRPV
EHRDPELVNTVSSLYSEVELRQETSYLAVGERTNANGSKAFREAMLAGDLETCIDLAKAQ
SREGAHCLDLCVDYVGRDGVDDMAELSQRFSTAVTLPVMLDSTEPEVIRSGLEHLAGRCI
INSVNFEDGDQPGSRFARLMPIIAEHGAAVVALTIDEEGQARTAERKVAIAERLVDQLVG
TWGMDEGDILVDCLTFPIATGQEETRRDGLETLNAISEFKRRHPRAGTTLGVSNISFGLN
AAARVVLNSVFLHEAVEAGLDSAIVRAAKIMPMERIDPEQRQVALDLIYDRRTPDYDPLT
RMLDMFAGVSSADVRAEHAAELAALPLNERLRQRIIDGDTNGLTDDLDEALRTRGALDIL
NSDLLEGMKTVGELFGSGQMQLPFVLQSAETMKRAVAHLEPHMDSTDEAGKGTLVLATVK
GDVHDIGKNLVDIIVSNNGYTVVNLGIKQPISAIVEAAKQNHADAIGMSGLLVKSTMVMK
DNLAELDRLGVGKDFPVMLGGAALTRTFVEDDLQRDFSGQVRYAKDAFEGLSLMDSVMAI
KHGDPDAALPEPRKHRVVARPRATVEPADGGPVRSDVARPVPGSLDVPRAPWFGNRMAKG
IGLAEITEWLDERALFTGRWGLRGPRKTDGTRDLIEQEGRPRLRGWLDRIAAEGLAVPGV
VYGYFPCYSQGNTLILLDPTTPEALDSEASRFDFPRQAAGRRLCIADFFRDRREAEEFGP
DTVALQLVTMGERFSQVTAELFAANAYRDYLELHGLSVQLAEALAELWHHRIRTELGIAG
EDGEMTAMLQKQAYRGGRYSFGYGACPDLDQRSLIEDLLQPDRIGVHLSEEFQLHPEQST
DAIVVTHPEAKYFNT
>PFR_JS22-1_1168□PFR_JS22-1_1168□Signal peptide peptidase SppA□1333447:1334703 Reverse
MSIPQPPDDAATRGAQPPPDRPPEGAAEQPPPPFQPAPPFFPHVVGGYPPAAPPAGLKRG
FGQGMGVALGIGAVLCALSLISAIAMVALVGVARIGRANTSAETSVTKTLWGSSSAKNTL
RAISVSGTIQASGGSSSGMFSSATYGYDVAKLIDSLTADSAAGLVLLMDTPGGSINGSRA
IADAVDRYEQRTGKKSFAFVEGMSASGGMYAMAGVNRIYADQGTMVGSIGVIMGPFARYR
DVTAVDGGLLGNGVTASGGIDQFYLTQGEAKDFGNAFRDMTQKERDVYTAGLSREYDAFV
NWVSTSRGIAPETIRNDLGAYMFDAQTAKDKHLVDDVLGREEAFRQIARDAGVDPDQTKL
VTDAEPGFLSSLMGSRKQAFGHGEALQAGEGVKASSSLCTGAPAVLAWTGDMNAMCGR
>PFR_JS22-1_1169□PFR_JS22-1_1169□HAD-superfamily hydrolase, subfamily IA, variant 3□1334887:1335621 Forward
MTSVSPRLPAAVLWDFDGTILDTEPAWMASEIAYVASHSAVWTLDDARGYIGASWRTLGN
ALGQRIAEETGTTGLDPWDIYQSVSAGVVDQVRAGQAPLRPGALELLDALGAAVVPCALV
SSSPESLLRAGVAALGIPDPFEALIAGPMVEHGKPAPDCYLLAAATLQVPIGQCVVLEDS
PTGCEAGQRSGALVIGIPSVAPLPSVAGQLRRDSLVGLTVADLAAMVRAHGAHSAHSAHK
EDSQ
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>PFR_JS22-1_1170□PFR_JS22-1_1170□TRNA (Adenine-58-N(1)-) methyltransferase□1335618:1336688 Forward
MSQLDPAALSGVHTGPLRAGERVTLTDIKGRRHTLVLEVGKDFHTTKGAVNHDEMIGRPE
GGVVTTAGGAQFTVFRPLLYEYTVGMPREAAVIYPKDAAQILMWTDIFPGARVLEAGVGS
GALSLSLLRAIGPTGTLHSYERRQEFADVAELNVTSFLGGTHPGWTITVGDLVDEIADEP
IDRAVLDMLSPWDCIDAVAERLVPGGLLCCYVATTTQLGRVADQLRYHGGFTEPSLTETD
VREWHAEGLAIRPGHGGHGHTGFLVISRRMAPGVDAPMKKRRPAPAAYGADYAGPVPRNV
LPEQLAANRQRSLDDSDQIAPAVKRALRRHVDAQRSIHPADGAQRAQPAPGDGHDE
>PFR_JS22-1_1171□PFR_JS22-1_1171□Proteasome subunit beta□1336681:1337547 Forward
MSSLDRMNETQWSRPHARPGLDDALMSASTSSFVDLLHAVHPELLATAGVGTDGVQPTRA
TTIVAVKYRDGVVMAGDRRATRGHEIAQRDIEKVFAADEATLIGVAGAAGMAIDLARLYR
LELSHYEKLEGASLSFEGKANRLATMIREQLTMALQGFVVVPLLAGWDPHRREGRVVSYD
ATGGHYEGSEFASIGSGSAFARGSLKKLHHPDLERDEAALVCIQALFDAADDDSATGGPD
LIRAIYPVVMSASEQGVHGFSDDAVAGLTNTMMSGRHGRPNGPGAASS
>PFR_JS22-1_1172□PFR_JS22-1_1172□Proteasome subunit alpha□1337544:1338269 Forward
MSMPFYISPDQMMKDRAEFARKGIARGRSAITARYHDGIVFLAGNPSHTLHKVSEIHDRI
GFAAVGRYHEFENLRVAGIRYADLRGYAYDRADVSARALANSYAQLLGTAFSAGAEKPYE
VELVVAEVGDADPDTAVAQGGDHADRLYRINFDGSVSDEGPFAVIGGHPGAVQDVLRTRL
DPTAPLAMVVSTAMDALRRGGSPELGPADVEVAVLDRTRIPSRKFVRLDVAQVAGLLGKE
S
>PFR_JS22-1_1173□PFR_JS22-1_1173□Prephenate dehydrogenase□1338271:1339365 Forward
MARSTSTADDEESQPLSPVVIMGTGLVGASIGCALTAVGEDVRLRDRYRSHAVVAAGLGA
GSVEHPIPTSVHLVVVAVPPQAVPEVVDWALSHYRNAVVTDVASVKAPVLADLRARGRDL
SRYVGSHPMAGSQYSGPLTATATLFVDRTWVVARGTGNEASQRMVERLAVMCGAHVVHLD
ADEHDRAVAEISHMPQLMSSLTAARLRDVPASDLLLAGQGVRDVTRIAGSDPALWRQIIT
ANSTEIGTQLRAIRGDLDRLIDQLDDPDAIADLVERGREGVAALPGKHGRKIGDMSAVVV
EIPDTPGALARLFTDIQAQGINIEDLSIEHGLSREVGYLSVAVDAERAPDLRAAMVRAGW
DLRS
>PFR_JS22-1_1174□PFR_JS22-1_1174□Putative cytidylate kinase□1339405:1340076 Forward
MADKPALVIAIDGPSGAGKSSTARGVACRLSMAYLDTGAMYRAISWACLTDGVDPTSHSA
LFARAETADLQMGLDPRHPTIIVDGHDVTREIRDPRISDAVSAVATTPEIRTLLTSHMRQ
IINRNPRIVAEGRDVTTQVWPQARVRVLLVADAETRIARREAQLLGKVDRHRVSSSIVDR
DRKDSTMSEFDKPAPGVTLIDSTYLDLGQVIDQVVGLVPTELR
>PFR_JS22-1_1175□PFR_JS22-1_1175□GTPase Der□1340191:1341540 Forward
MTIAETAQAQSTRPVVAVVGRPNVGKSTLVNRILGRREAVVQDTPGVTRDRVSYDANWAG
REFVLVDTGGWIAKAEGMSAHIAEQAEMAIQLADAVLFVVDAKVGLTDEDEAVVKVLRRS
GKPVVLAANKVDDERVEAEASSLWQLGLGEPYPVSALHGRGSGDLLDALVKVLPKTSAVE
PDEVGGPHRVAIVGKPNVGKSSLLNRLASAQRSVVSDVSGTTVDPVDELVTIAGEPFRLI
DTAGIRKRVKEASGSEYYAWLRTQAAIERSEVCVVVIDASEPISDQDLKILSSVEEAGRA
MVVAFNKWDLTDEERHRYLGREIEQDLQTWKWAPTVNISALTGRNVDKIAKAVNKSLAGW
ETRVSTGKLNAFLGRIVAANPHPVRGGKQPRILFGTQAQNRPPTFILFTSGLMDAGYVRF
VERKLREEFGFEGSPVHIQVRARAKRKDR
>PFR_JS22-1_1176□PFR_JS22-1_1176□Protein of hypothetical function DUF1706□1341575:1342084 Reverse
MAVPRTKDELLVAIADNYAKLSIDLGRVPASRAREASMPGHVAGTVMSPADLVSYLVGWN
EQVLEWFTERQRGVEPDFPARGLGWNQLGELTQRFYADHGELTWPQLLDRLARAEQGLIE
LVSAHDDTELYGRPWYRTHTAGRMIQFNSSSPYANARRRIRAWLRDQGL
>PFR_JS22-1_1177□PFR_JS22-1_1177□Putative methyl viologen resistance protein□1342208:1343242 Forward
MSLTKRQRWTLLATVSIGLLLITLDNSILYTALPLLTEELGANGSQTLWIINAYPVVIVG
LLLGAGTLGDRVGHRRMFLIGLVIFGVASAAAAFSPSPAWLIASRAVIAVGAAAMMPATL
ALIRLSFDVERERNFAIAVWGTVSVVGSAIGPIVGGLLLEHFWWGSVFLIGIPFVVIALI
ATVVVAPPNDPDPSKHWDAISSLQAMVGLVGAVFLLKELANVPPNWTVVVLGAVAAGLGL
TSFVRRQQRSNDPLLDFAIFRNRAFSAGVLAAAISMFAVSGAQLMTTQRFQLVEGFTPLE
AGLLVTVVAIGSLPTSLLGACTWIGWDCCRSSPEGWRSVRSALR
>PFR_JS22-1_1178□PFR_JS22-1_1178□Permease of the major facilitator family protein (Fragment)□1343182:1343709 Forward
MGLLPLIAGGLAVSAIGTAVMIFGIEDHLFWLMVAGLLISGIGLGAVMSVASTAIVGNVS
ARRAGMASSVEEVSYEFGSLIAVAVLGSMLNFIYSATVRLPPGTPAVARSSLTEAIGVAQ
GDQAIVGAANAAFDNGFLVTMIVLTVVLALGAAATARLLRHYGPGSRSQEFSDNH
>PFR_JS22-1_1179□PFR_JS22-1_1179□Transcriptional regulator, TetR family□1343735:1344313 Forward
MRPSKRDAILGAALGVVGRGGVSAVTFESVATAAGVTKAGVVYHFPTREALLLALQEYLA
HQWQLDLEAQLGTPVESASQGDKLAAYARDSSHSSSRAELLLMLETVDDPQAYAPWHAVM
SRWTPALDTDQPMGDAELDHAVARLAADGLWLYESLSTHALSPGVRQQIVSRLSALAHRP
DGPAAPGGPGRH
>PFR_JS22-1_1180□PFR_JS22-1_1180□PecM protein□1345410:1346285 Reverse
MSPALPARSTLFGPSLVVTGLFCQETGASIAVMLFPAVGPAGIVALRLVFSAIILCAVAR
PSLRGRRPIAWYTAIAFGLVLTGMNLFFYLALDRLPLGTTVTIELLGPLTLSVVAGRRWM
NLVWAGSALVGVVLLGGSATHLDPLGVAFTLVAAAFWAGYILLSKATGRHFAGIQGLAVA
MVAGSVVTVPIALATTGSRLFGPHVLIAGLGIALLSSVAPYALEMTALRRTPAATFAILL
ALAPAVAAAAGFFILGQTMTIHDVFGIVAVICASIGAVCTPPGKPGGRQKA
>PFR_JS22-1_1181□PFR_JS22-1_1181□Hypothetical protein□1346456:1346977 Forward
MESESGGAGNFHGAKGPHAEGSAGDGHRDEAAATLDALSADRHRLADRLAVPWALMAAFG
ALAAWWVGSAVTTTPGSGYEPPLAGWMTLPVALVIAHLVRRGTGIRFRALGARANGAMLA
VLVACLLLFSVSLGAVSLGMAWLVGVMSLVAFGVTTWLSGVAYRSAVERVRRG
>PFR_JS22-1_1182□PFR_JS22-1_1182□Transcriptional regulator□1346970:1347275 Forward
MVEARFDAVIHAPLRLRICGLLRPVDGLDFALLRDSLEVSDATLSKHVKTLTAAGYVTSR
KAASTERSDGRRIMWLSLTGPGRLAFDGHVRALREIVGTGS
>PFR_JS22-1_1183□PFR_JS22-1_1183□Hypothetical protein□1347615:1349804 Reverse
MTSARLRFALEQLTSGDWQLFERFCSEFLVPEFPGFRTTATPSGDRGRDGEVFTLDSVAH
TGFQFSVTSDWRTKIRSTFRTLIDNGIVYQRLIYCTSQQIGSLADGLKGELWDEQSILLD
VRDREWFCERELTSPEREVSSAELVERVVTPIVNSRGIAKVAGSPLSSGEAKVALVHLAL
NAEDRAGDRNLTKTSFDALVQSVLVDTSQENLLTEAEIIDRVRALAPHGADSQVAALTKS
ALDRLSRKHGPVKHHSSHGGYHLSYEATEAWKEDAAAYILEQQSLEEDLAAAAYGYVEIL
DSDAEQLKAESKTLRIALEAVMFRSGESFAAAVEGGDPARVSVDEMVEQVTALGLPLKLH
PTQAVRAILEVISNPAEATRRHLTRVLDAYTLLAFLQQTPDVQKAMSRVFDNAKVWLDTS
AVLPLVAETLIDDPSERLQTTLLNSATSSGLSLFVTDGVVEEIHYHLERCISYLRQGNGR
YGPPPFLYAAYMLSGRDERQFPKWAEDIRGEIDPDRDIEEYLAEKFNIRLNDLAEFAEKA
DQTLRAATMELFSKRRSRSYDGQADRTQKVIDRLAIHDMESVVGIIELRRNAKPALGHEV
WWLTLDKTAFRLSSWLRQQMGREAPDTPALSPDYLSQLLRLGPLRRNLDSDEVRRLPLII
DVTRLETVPPKLIEIARSTRESMEGLDERRIRREVRDALHKARTELRRSHDYGQAAESSV
AERLRVQRS
>PFR_JS22-1_1184□PFR_JS22-1_1184□Hypothetical protein□1349886:1351385 Reverse
MSPNSTPEAALDLTRAPRGELAAARLIATAAASGDLAERHYLELKGPPDLSSKVNKAKIA
KFILGAANRMPERAAEAFEGYGVMIIGIAKNAIEGVPPIEMLSLSQVIQPFLGATGPHWD
IVRVPIENSPNQVIVVLVDPPQTGQPPFICRANGEGLQNGRIYYRGDGETREPTADELDL
LMARGSAQPTAPVELGVSVVGTVVPLAVDEERTLNEYIAKTRKRLLDALPAPKPSTPASR
QPGQLGAAGVTSGLSSLHSLGTGLSEAMSRIISEQASGALGTAGILGAEVPEQRSEEDYK
DEIEAWASQFREAWPDALEAFAVRLMPANEVGVVNKTLTFLHDVEIKLHIAGAVEALERE
WYEDSLSLNDVGLPYPPRKWGPTKRNFGLDTGYSASLAASIAAQSVQASRSYVPPDASWR
TTGSVDVDVNVGNLRPEGAFQTEDDDSILIVRGEAPENIRATWAATAQGYNEVFKGDFTV
PVAEPTCLTELIRECLGLR
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>PFR_JS22-1_1185	PFR_JS22-1_1185	Peptidase, S8A	1351438:1353828 Reverse
MFDLAGSVKDFQNAINRIDGLEFLSELLGDKSDSDDDFHMTEREKGRTEKQVQHSLYLVM
SNAKAIDELLHLFDKWQKDPTAKFDHGLGKFKAAFQQLTAIRRWGPEDRIRETGLRERWQ
ETLDVIGQSVSTVKVEVELWYRRDPAQRAAAESHVEQIVTVSGGRIMDRCQIGDISYHAL
LAELPIQQVHTVLNDGAAAIRLLTTDEVMFVSPFTPMSVSPATLDPVTEVRLPSGERVEG
LPRVALLDGLPFQNHDALAGRLLIDDPDGLGDNYPTSARNHGTAMASLIIHGDLSAPGES
LDRPLYVRPIMRPHEFVTTHEQIMPDRLLTDLLHRAIRRIQEGDGGREATAPSVRIVNLS
IGAEARALTRRISPVARLLDWLAQTYNLLFIVSAGNHTDPITIPATAANNADSARSAATL
AVYEKGILRGILPPGDAFNALTIGATHDDGLGDVDLPDTVWDITSPGAPAYYGATGPGVD
RSIKPDLHHTGGRALYVRPVAVPGEDNVALELAHTALTGPGLQVAAPGRGGATNNTAFTF
GTSNATALVTREASRLFDILESGTEDPEDSPLPDPQYHPLLVRALLSHASSWGEWEPRLR
RELGLSGQDARRKLSAVLGYGKLDTTRLGTAATNRAVLIAGGLIGRDQRHTYELPLPPSL
RTRAEWHRFTITLAYVAPTVGQLTRYRGAKVYFDTPDTVLAAGDRVEGEHFSVRRGSLQH
ELIQGTRAMVFGDGDTFPIHIDCMDDAQHLHAGKYVRYALVVSVETTEEVSTTIHDEVRA
RLREQARERAREQVQS
>PFR_JS22-1_1186	PFR_JS22-1_1186	AAA ATPase central domain protein	1354047:1355003 Reverse
MARADLLLDLVEAERRGDRDRFRVLVEAVIAEERANQHHLVADRLSELITTTGQSHVRDD
RAAAIRDLVQEIVPSRRLNDLELAPVPHRVITELVEEQKRAELLRSYGIEPRNRLLLSGP
PGNGKTSVAEAIAAELMLPFYVIRYEGVVSSFLGETASRLDNAFEFARTRRCVLFFDELD
TIAKERSDEHETGEIKRVVSTLLLQIDRLPAHVIFVGATNHSELLDRAAWRRFQIRAELD
PPSRAQATRFLERLAARFGGDLGFAPRTLADKLAGASYAELEEFAQDVRRRAILELPDSN
LRQIVQERLEHRQGQAAG
>PFR_JS22-1_1187	PFR_JS22-1_1187	Sulfate permease	1355100:1355423 Reverse
MLRLLWAASVYTRYFLRRSMPTNILLDAIRTRRGLKWGIPATLLAAPYLLAASICTNLIG
GGGPGWLNLLVLLFCWNFLKILIMGPVSLILLIRVRIQEAIARPAEA
>PFR_JS22-1_1188	PFR_JS22-1_1188	TrwC relaxase	1355575:1358589 Reverse
MEREVAATRTGATGRDGAVAQVDVAGLIATAFDHYDSRAGDPHLHTHVVVSNKVQTVLDG
KWRSLDGRPLHAATVALSELHEAVFADHLTRMFGVSWEARDMGRDRNPAWAITAVPEELV
TEFSSRSRHIEVEKNRLIAEYVTQHGRQPSTATIIKLRAQATLSTRPEKNVRSLADLTAE
WRSRAGRILGSDATSWARTVTAAKEEPLLLGADDVPLDVIAAIGQSVVEVVGEKRSTWRR
WNLTAEAARQTMGYRFASTEDREAIVGLVVDAAEAASLRLTPPELASSPTVFRRPDGTSV
FRPKHSTVFSSTVLLAAEDRLLDRARTTTGPTVPLAAVERIAAKPDRKGLVLGPDQAEAL
GKIALSGRVIDVLVGPAGAGKTTAMSALRRAWENEHGHGSVIGLAPSAVAAQVLADDLGI
QTENTAKWWELHERTGATFHAGQLVIVDEASLAGTLSLDRITVAAAEAGAKVLLVGDHAQ
LQSVTAGGAFSLLVHDRDDAPELVDVHRFVNPWEKTASLGLRHGHTDVIDTYLEHGRIQG
GETEAMIDAAYAAWRADTLAGRASVLITDSTESVTALNVRARTDLILDGTVHGTREVELH
DGTRAATGDTVITRRNDRRLRAGRSWVRNGDRWTVTQVRDDGSLTLRRAGRTWGGSVVLP
ADYATEDLDLGYTVTAYRAQGITVDSSHVLADVSMTRENFYVAMTRGREENVAYVAVDKP
DDAHDGPHPGENTEATARSVLFGVLQHVGAELSAHETVTAEQEAWGSIAQLAAEYETLAA
AAQHDRWAALIRTSGLTDDQANDAIASPAFGALTAELRRAEANQHDVETLLPRLVRARGF
GDADDIAAVLHYRVAKATERPADSGRVRKAPRLIAGLIPEATGTMTPELRQALSERRDLI
ETRATVLLDTALHDSQPWVAALGPEPKDAKAAATWRRLAVVVATYRDRYNITDPTPLGAP
AESDAQKIDAARARAALDRARELSRGPNPVSARPAGRESVGRTL
>PFR_JS22-1_1189	PFR_JS22-1_1189	Hypothetical protein	1358645:1359259 Forward
MPASATAHSTDADFGIENVKSNPATARRIAARSPGARLDPPLLLALDEVGNLAPLPSLPT
LMAEGGGTGITTMPVLQSLAQAREKWSENAAGAIWDASIVKIILGGASNSRDLHDLTTLI
GERDEITDSTTIGDHGTRSAQRSIRRVPIMPPDTIRTLPFGTALVLLRSAAPIVTRMRLW
TTRTDAAQLRADRSSIEHMLRHRP
>PFR_JS22-1_1190	PFR_JS22-1_1190	Hypothetical protein	1359331:1359813 Forward
MAGIRTYESFSGFIASTPNTEPTAKGKPRFYAQAGQNQYRKESDGSYTKTGTEYLPIVAY
DKPAAELTSRFVRGDSFVAEGYTRPYSYEKDGQAVEGEEFVIWKVGHDAARTRYEVDRAP
RQTQSAKADRVAATAAQSHEVPTEFEAPATHHPADSGLAL
>PFR_JS22-1_1191	PFR_JS22-1_1191	Hypothetical protein	1359824:1360405 Forward
MNDIDLPEGEMPEPASMADPDDGLAGTVLPGPPHPVNWNLLTAEEAGPEWAELDHWVAWL
RRTYGLPAGVIPPFWHRHPELVWELSALHLHWLCAYDPEQNGSAPLGWHRDFADARQRLR
DWVAASGTRLDRDRATRQTAWPGEEPAAPVEDVVIADRADDFRQFVAADVAWRQAAEDAF
YASLGDDDAERDT
>PFR_JS22-1_1192	PFR_JS22-1_1192	Hypothetical protein	1360386:1360601 Forward
MPNEIPDRGIGPVEPLWCARDVSAFLNVSQATLSRWRREKAGPPFLQVGGVSRYNPVTVR
AWVREQENAHG
>PFR_JS22-1_1193	PFR_JS22-1_1193	Prophage integrase	1360594:1361784 Forward
MADPRNHRMPPVGVNLTTDVERRVDGFRARVRWTDPSTKKRVGRVTHVRSTEEVEEFFDQ
MRTATQTGANTTVTLAEYAASIGDRWKRGLDPTSTAENYDIGLRLRVLPALGHIQLVKLT
AGMIDRTIDTWETQHSASTIKNSIAPLVRVLDEAVRDDVITINPAKHRARRNLGKQVTQT
TGALRQYAIPDLATLRTLADACGKVHQSYSDHVMLAALLAARGSEVAGLRAGDVDWTNRV
VRIERQHYPGKGGLVVKQTKGRRARLVPILDALEPVLERLTAEKEPDVPLLRGPRGGVLT
TATVRDATHWDDLVKDIGLPNLTRHGLRHTGATWLADAGIPLHVLQEILGHQSIETTKGY
LHPDHRHLAEAAKQANQFLSATPARREAPRRDAPRL
>PFR_JS22-1_1194	PFR_JS22-1_1194	S-ribosylhomocysteinase LuxS	1362344:1362808 Forward
MTQHMNVESFNLDHTKVKAPFIRVADVKHLPQGDTLTKYDVRFCQPNVNHLDMKAVHSVE
HSFAECVRNHSDSVIDFGPMGCQTGFYLIMVGEPDVPRIADLVEQTFRDILALDAVPAAN
VVQCGWGANHSLQGAKDAVSTMLRHRAEWEQVMA
>PFR_JS22-1_1195	PFR_JS22-1_1195	Antiseptic resistance protein	1363000:1364580 Forward
MPLNPTQHTGINPDRRRWIALIVLSLALFMASMDNTILNVALPTLGRELGATTDELQWTV
DAYQVTYAGFLLVAGGLVDRWGRTRTFVAGVAVFGLCSLAAGLSTNTTMLILARGLTGIG
AALLTPSTLALISVLFRRPGERTTAFAIWSGANSAGAAVGPLLSGGLLAHFSWGSIFLIN
VPVAALCLVGAVFLLPRVRAERDEDHIDWPGTGLSIAGLCAVCWAVISAPGLGLFSAPII
FAFLGGIALLVGFVWWQHHASAPLLRLSLFRSRPFAVSVAVSGLVTAGGAGALFVLTQFL
QFVLQFTPWQSGLSIMPVAAMMLVGAILAPISLKRIGIKRAVIAGLICVALGFTLLSLTH
VGMTYLQMLPGAMFFGLGAGLLMPAATQAVMDSLPSESEGAGSATNSALMQVGSAMGVAI
TGSLLAWRYREVMSADAAVRGLGEPLHSDILASVGRAFDLSSGGAHPDILAALKRGFVSG
MQVGLGASAAVVVLATIAVAIFFPRHPVAPDEAEIEDSEPKASPAP
>PFR_JS22-1_1196	PFR_JS22-1_1196	Nitrate/sulfonate/bicarbonate ABC transporter, permease protein	1364887:1365777 Forward
MASSRFTRHPAPTGVRIGAPLVVGALLLLAWHAVVSTHTVPLTLLPTPGSVWSRLVHDIV
HGELLARTATTIWEAVLGCIVATVFALPVGYLVARVRLAEAAISPYLAASQAIPAVALAP
LLVIWVGYGLTPIVLLCSLIVFFPLLLSTVLGLRSIDHEVVEAAELDGASGWRMIRYIEA
PLSRAALLSGVRNGFTLSVTGAVVGEFVMGGTGLGLVVSMQSASADTTGLFSTLIVLCVL
AMVIYLGLIAVERFTDPYRVPRAAHPVPLETAPDLRLVAATQAHQSHTSAQKELVA
>PFR_JS22-1_1197	PFR_JS22-1_1197	ABC-type nitrate/sulfonate/bicarbonate transport system, periplasmic component
(Precursor)	1365774:1366781 Forward
MTRHSRLTRFLLVLLALTLGTAMSACGNQSGSSSASSSAGIPLTVGLTYTPDIQFSPFYV
AVQKGYFADEGLNVTLRHHGASESLMGALQSGTEDVVYAGGDEMLLSRSQGVDVVNFATM
YQSHPAELIVPQGSSISSFADLRGHSIGIPGPFGENWYALLAMLRQAGLTQGDVNIQSIG
YTQQAALMGNKVDAVVGFSNNDAVKFGQAGFPIREIRLDAATPLVALGLGASKATVTDKQ
DQLKAMMRALDKAVAYCTSDLDGTVALTEKYVPALSDDAQRAAARATLEATNKLYGSQLG
KQDAQRWSDMATFMAESGIISKPVDAKESFVSLVG
>PFR_JS22-1_1198	PFR_JS22-1_1198	Homoserine O-acetyltransferase (Precursor)	1366963:1368216 Forward
MGHPGDGDDAASASRGIPGMTSSRHQYLPPTPEDIVETKFMDLFDTPGEPMHLVRGGTLP
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    GITVAYETYGTLNERRDNAIYICHALTGDAHAAGYHEGDDRPGWWDALIGPGKAIDTDRW
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    GGSLGGMQVLDWALTHPEDMNQAVVIASSSRLTAQNIAFSAVGREAIMSDENFMNGAFAE
    NDTNPDVGLAVARMMAHITYTSEEGFEEKFGRRPQFDAQQPGFGVDFAVESYLDHQASSF
    IGRFDALSYLYLTRVMDYFNPFADAHALDRLVATPVRFLVMSFDSDWRFGTAHSRRIVRR
    LQDAALPVSFREIHAPWGHDSFLLHIPPYLDSVRAFVEQPAVPRPTIRRRRLRKWGR
    >PFR_JS22-1_1199□PFR_JS22-1_1199□Methionine biosynthesis protein MetW□1368213:1368899 Forward
    MSQSSARDSVIGGANRLGEGLLRQDLQSVARLIRPGERVLDLGCGTGDLLAYLIGAMGCS
    GTGVERDPDAVLQVIGRGVPLIELDLDTQLEEFGDDSFDVVVLSRTLQAVLKPKEVLLQM
    RRIGQRMIVTMPNFGYWRHRLRLLTGRMPQSKDLPYTWYDTPNLHHTTLVTLEELFDDCG
    LDIERRIPLDGDGRRPRLPLELTQHTANVLAGSAIYVLTRRDAADAPA
    >PFR_JS22-1_1200□PFR_JS22-1_1200□Transcriptional regulator, AsnC family□1369035:1369448 Forward
    MSFTEIGRETGLSTSAAQQRVRRLEQRGIITGYHARIDGAALGHTLAAFIEIRPLGQVDE
    SLVDVLASMPEIVSCYSVAGDASHLCLAEVTSTQELDDLLTRIRTAVNVSTSTTVVLRTL
    FRDRPPIDDPDVPAAKR
    >PFR_JS22-1_1201□PFR_JS22-1_1201□Hypothetical protein□1369542:1371176 Forward
    MNTTSDIVAAGSPVALRGWSRLLRGDHAPVRLHWALASLLSLVAGALLALGFQPFGLWPT
    TVVGIALLSWLSDQARARRVAWCGLLAGLALYSMTVSFQAVVAWWLPVLMVPVLACWVLL
    TALGQHYVQFLRAWPLWSASIWTLVEALSARFPFGGFAWDRLAFTLPDQPLGGYLWLVGA
    AGAGWLLALSGCLVVVVVRAVVARGGRWLPRMAAGIAAMGLLAAVGAVLSAVPATTGAGR
    GVTVGVVQGNVDGSAGPHTMGYARSVTDNHLSETIMAMARARTGLDAMPDFLAWPENSTD
    MDPNQDEETHQLIADAQAIAARPILVGAVTLGPGDDGRQTAGLWWDASGETARYAKRNAV
    PFGEFTPLKDLVFAIAPMAREVGRQTIPGTAPGVITGTLPDGSSVRVGDIICYELAFDST
    VYDTVRHGAEVVVVQSNNATYAGTMQPRQQFAITRVRAMEMRREVVVSTTSSLSGLIDAR
    GRVVEHSQEDTAWARTFTVPTRQGVSAGVSTGPAFEAIACAVAAVAVVAGLVAPRRARRG
    GSLH
    >PFR_JS22-1_1202□PFR_JS22-1_1202□ApolipoproteiN n-acyltransferase Lnt/dolichol-phosphate-mannosyl transferase Dpm1□1371263:1372069
    Forward
    MVDHSESLDKVLVIIPTYNEAENIESIVERLRQAVPQADALIADDNSPDGTGDIADRLAA
    DDDHIHVLHRAGKQGLAAAYVAGFRWGLERGYDVLVEMDADGSHQPQFLPSMLNALRDAD
    MVKGSRWMPGGEVVDYDKKREWLSRLANIWVQASMNIPVRDTTGGFNAFRASALRKMNLD
    TIASKGYTFQIDLTRRVLDDGGIVREVPISFPDREKGESKMSGSIIGEALLRTTQWGAQR
    RGAQVAQFAREAADRVEPLVDRVKDKLD
    >PFR_JS22-1_1203□PFR_JS22-1_1203□PF13397 domain protein□1372165:1372503 Reverse
    MADRALRGMGLGAKSFEDEEGVEFATRKVLGFTCPKGHHFEVTFSTEADLPTEWECPRCG
    AVATRSDGTKAEDKQVKPPRTHWDMLLERRSVSELEDLLAERLEVVRKSPHY
    >PFR_JS22-1_1204□PFR_JS22-1_1204□Glycerophosphodiester phosphodiesterase family protein□1372610:1373407 Reverse
    MVSRRRTADDYEFFDAPFAAMAHRGGWDALVPARFENSLLAFEHAVNDLGYRYVETDGHA
    TADGVLVALHDTRLDRVTDMHGAVAGLPWRVVRRARIGGSEPVPTMDEVFEALPNTRINI
    DIKESGAIAPLAAAIRAHRAEDRVCVASFSPRRLAGFRALMGDRVATSVSVGAVAWSAYV
    PWLPRVLNSGAQVFQIPTSQAFGAVGIPVLTRNLARVAASRAMRIHVWTIDQSDEMVQLM
    DSGVDGIVSNRIDVLRRVARERALW
    >PFR_JS22-1_1205□PFR_JS22-1_1205□Hypothetical protein□1373452:1373976 Reverse
    MEYVSLTSTDRSLRCAHLTRLRQRASVMATHGISPALPRRDIPRRERFAWRARIRANPPA
    LLAYRVVVAIIGFAFIIAAGLTGWLPGPGGIPLFLAGMAILASEFRWAHSLTIRAMGVLR
    AFGRQSRRRKTLLVCGFLAAVLLLGYVALIIVGPPGWLPGWLHAALAMLPGVRG
    >PFR_JS22-1_1206□PFR_JS22-1_1206□Pyridoxal kinase□1374114:1374983 Forward
    MTRVLSVQSEVSYGFVGNSAVVFALRRIGVDVWPVNTVQFSNHTGYPSWRGPRLTPIDEA
    EIVRGLDELGILGQLDGVLTGYLSGPSMGRQIMAAVQLVKRRRPTALYCCDPVLGDDETG
    FYAAPGTLELFREQALPLAQVITPNRFELAALTNLPTSSLEEILIAADTLLDAGPSTVVV
    TSVPSLRPSQGAGHDDRIAMVAVQRDGAWQVSTPRLPGEFSGAGDLTSALFFAHSLAGES
    PGQALSHTASSIHGVLGATVAAGSRELELVAAQRELVHPSAVFEAERVR
    >PFR_JS22-1_1207□PFR_JS22-1_1207□UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA□1375074:1376543 Reverse
    MTQNQLAEELSTSQSAIHRIESGHQNLSLETINRIAGALESPLIVPGNSSTLNFRIGGET
    HLSGSIETRSSKNAAVALLCACLLNQGRTVLKGIAHIEEVNRLLEVLTSIGVDASWSPDG
    KDLTLQRPETLDLENMDVAAARRTRSILMFMGPLSRFFSEFRLPYAGGCDLGVRTVEPHM
    QSLRHFGVNVLATEGFYRASVTRTGPDTRHIVLTERGDTVTENTLMAAAVSPGVSVIRNA
    SSNYMVQDLCAFLMLLGVEIDGVGTTTLTVRGLSEAPSMDVSYEISEDPIEAMSLITAAV
    VTKSELTITRVPIEFTEIELSILGEEMGLHYGLSSEYKSGNGLTRLVDLTIYPSELKAPP
    DKIHPMPFPGLNIDNLPFFAVLAATAHGQTMIHDWVFENRAIHLLQLNQLGAHVQLLDPH
    RLIVQGPTRWRGREMVSPPALRPAVTIMLAMLAATGTSVLHDVYVINRGYEDLPARLNAL
    GADIETFYD
    >PFR_JS22-1_1208□PFR_JS22-1_1208□Dihydrolipoyl dehydrogenase□1376756:1378156 Forward
    MSAHYDVVVLGAGPGGYVAAIRAAQLGLKTAIIEKKWWGGVCLNVGCIPTKALLRNAELA
    HLVQKEADTFGISGQVSFDYGKAFTRSRQVSERMVKGVHYLMKKNKITEYNGWATFSDAR
    TLQLAGNDGTTDTITFDNVILDTGATVKMLPGTSKSANVLSYEELIMSDSLPESIIIGGS
    GAIGTEFAYVLNSYGVDVTIVEFLDRMVPNEDADISKELTRQYKKLGIKVLTSTAVQSVV
    DTGSGVDVTIAPAAGGEAQVLHADKMLQAMGFAPRTEGYGLENTGVALTDRGAVAIDDFC
    RTNVPGVYAIGDVTAKMMLAHTAEAQGVVAAETIAGAETMAVDYRMIPRATYCQPQIASF
    GLTEQQARDEGYDVKVAKFPFSANGKAVGMGAPDGFVKIVADGRYNEILGAHMIGEGVTE
    LLPELTLAQKFDLTTEEISRNIHSHPTLGEAVKEAAEGIEGHMTNL
    >PFR_JS22-1_1209□PFR_JS22-1_1209□Extracellular ligand-binding receptor (Precursor)□1378352:1379515 Forward
    MRRAVSAVLAAVVGLGMVACGPNKVNSAVGDTIKIGVNYELSGTVASYGSSNVKGIEMAI
    DEINAAGGVRGKQLKEVKYDSKSEPAEATTLATKLTSQDKVVTIIGPATSGSFKATIPVA
    NKHEVPVVSGSATANDATVLHGKVQPYAFRTCFSDNYQGTGMADYAVKRMKATRAVIIKD
    NSSDYSKGLAESFRQKMTEEGGTITNEVTYNTGDQDFNAILTSIKNQKFDVIYLPGYYAE
    AGLIIKQARAQGIDTPILGGDGWDSPKLEDLAGDSALNNVFFSNHYSSLDPSAQVQDFIK
    AYKARYGAEPDAFNALGYDTAKFVADSINRASSIDGPSIAQAMATTTNFSGVTGTFSMDA
    NHNPVKSIVVVGLTNGKQASSESYKAS
    >PFR_JS22-1_1210□PFR_JS22-1_1210□High-affinity branched-chain amino acid transport system permeaseprotein LivH (LIV-I protein
H)□1379612:1380496 Forward
    MDQILQQLVNGASLGSVYALIALGYTMIYGIIQLINFAHGDVYMVGAYVGYACMAHFHLG
    FFTSLVVAMAVCTVLGVVIERVAYKPLRKSSRIAVLITAIGVSFLLEYTMMFFVGADVRS
    YPPLPHWMQVSWHLGGVIITSLQVLIFAIAVALMIALQLIVRRTRLGKAMRAVSQDADAA
    RLMGINVNNTISFTFALGSALAGAAGVLVAVYYNSINPLMGMVPGLKAFIAAVLGGIGLL
    PGALIGGYFIGVVETFVSGTGFSTFKDAVVYALLIIILVVKPSGLLGKNEKEKV
    >PFR_JS22-1_1211□PFR_JS22-1_1211□Branched-chain amino acid ABC transporter, permease protein□1380493:1381512 Forward
    MTMSGSQTLGLDTSTTPSRSFVHASWFRKTVLLAAVYLVVLLLVQADVINDYRLITIATI
    CINIVLATSLNLITGFTGQFSLGHAGFMAIGAYVTALVTIQIDSVWGFVLGLLAGALLAS
    LVGLLIGLPTLRLRGDYLAIVTLGMAEIIRIVLLNLKVTNGAAGLQGIPQFVNWTWLFIL
    TAGSVVLISNYLHSRHGRDSIAVREDEIAAESIGVNSTRTKTMSFMVGAFFGGIAGGMYA
    SFFYFIKPDTFNFMKSVDILVIVVLGGLGSLSGSVIAAILLAIVSTLLQPFPEIRMILYA
    LILILIMIFRPQGLMGSRELSVKLFSRLIPGRARKERTR
    >PFR_JS22-1_1212□PFR_JS22-1_1212□Branched-chain amino acid ABC superfamily ATP binding cassette transporter, ABC
protein□1381509:1382300 Forward
    MSQPILTVEHLTRNFGGLAALSDMSMTLNRGELVGLIGPNGAGKTTVFNMLTGVYAPSSG
    SITFDEHGTAVELGGRKPNAICRAGVARTFQNIRLFKELTVLENVVSAMQLQESYGLLAT
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LDEPAAGMNPAETAELTTLISWIRENFDLTILLIEHDMSLVMTICERIYVLDHGIVIASG
TPDEVQHDPQVIEAYLGQEASDV
>PFR_JS22-1_1213 PFR_JS22-1_1213 Branched-chain amino acid ABC transporter, ATP-binding protein 1382293:1382997 Forward
MFEIHDLQVNFGGIQALKGISLSVEDGQIVTLIGANGAGKTTTLRTASGLERPSGGTITL
AGQDITRASARERVKQGLVQVPEGRRVFPKMSVLENLELGAFLRKDRAGITRDLRDVYER
FPVLADRLKQQAGTLSGGEQQMLAMGRALMSRPKMLLLDEPSMGLAPLFVQEIFDIIKAI
NEAGTTVLLVEQNANMALQIADHAYVMETGRIVLSGTAAELSASDEIKRAYLGG
>PFR_JS22-1_1214 PFR_JS22-1_1214 CBS domain protein/ACT domain-containing protein 1382999:1383649 Forward
MFIRDHMTANPFTVTPDDTVPKAVEVMKLNQVRHLPVLRDGKVVGVIANSDIAKASPSQA
TSFSIGEITYLFSKLKVGKVMSRDVYTIAADALLEQAAVLMRDHKIEMVPVMEGDKLVGV
ITESDILDSFVDIMGMRMRGTRLVLEATDAPGQLSRITGLVADHGMNITHLAVYPGSGTS
QIVLGVNSLNTADLETQLVGLGYRVIARLRNEPGKD
>PFR_JS22-1_1215 PFR_JS22-1_1215 PTS system fructose IIA component 1383681:1384103 Reverse
MIRVVVAAHGNLASSLVKSTAMILGSNPDVVAIDFDPEGDVHALYRSVQDATKDAAGVIF
LVDLLGGSPYNAAVRWCSRHLDSDVVTGVNLPMVIDVSTLAQQETHVPRAVSAAKAAGVS
SVASWRTGPASRHHTVTDDR
>PFR_JS22-1_1216 PFR_JS22-1_1216 Dipeptidase pepE 1384576:1385709 Forward
MTTDGLLRTASVDELTARQQMLRARAARSGVDAVVISTGADMRYLLGRSQGSHERLTALV
VPTKGSAFLIVPELERPGWEGSSAESMGLEMSTWPDGDSPYRLLAARLGPIAELAVDDVM
PVRHAHEIRTAVDCRVEPAGELIGGMRVVKTDEEITALTAVAAAIDRVHRRVHEWLRPGR
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GYFSDSTRTYCVGSPGDPEFATVHDIVRTAQQKAFETARAGVSAAAVDQAARTVIEQAGY
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DGSPVRLNHSPTRWELP
>PFR_JS22-1_1217 PFR_JS22-1_1217 Putative integral membrane esterase 1385739:1387055 Reverse
MTQLSRTWRSFVNWLMARNIVGPKELIPAAVIAALVVAWLVIRRHRGWTRTVAICAGVGA
VVGVIAWFLGEKVLNLTLGPMPMLGRIWVVAFFIGLGLVVANFRWSTWRRKVAAVLAAVV
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RGGLGAGLEWLYPRTGLS
>PFR_JS22-1_1218 PFR_JS22-1_1218 Integral membrane lysyl-tRNA synthetase 1387052:1389187 Reverse
MGPFPRSWALPWRRRGGGGFNHLWRVRTRWIGLAITLTLGFYDASTFAAMTLGSMVAGLV
IGAFWWRGAERFDLWPRFRERRVLVSLVIACASLGPLLAAWSTRAAGPLEEIAGYVRTGQ
FESREAHAICRLASSHACTLAHLHQNLGWPVLLMSVLPAVIMLVLCLGLVRARRSAWFCA
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VRLFPVRLPRRVAVGQLVRYVALFGVATIVYVVVGMLLAAQWSPQASVVALLHDVVTRVF
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YLVYQDPTDLPKIGRALTTAYVTTEPTVRISRIIKYFRGRRGSTDENGSDT
>PFR_JS22-1_1219 PFR_JS22-1_1219 Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B 1389751:1391262 Reverse
MSVQYSDDRLMDYDEVMARFDVVLGLEVHVELNTESKMWCGCSTKFGAEPNTHTCPVCLG
LPGALPVVNGKAVESAIRIGLSLGCSIASWCRFARKHYFYPDMPKNYQISQYDEPIAYEG
EVRLDVEGTQYTVPIERAHMEEDAGKSLHVGGATGRIQGSDYSLMDYNRAGVPLIEIVTK
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VVAGADQAAARKWWLGELSRRANETEVELAELPISPVQVAQVGKLVDSGKLTDKMARQVI
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VMKQMHGQADAARVRELILKALQ
>PFR_JS22-1_1220 PFR_JS22-1_1220 Glutamyl-tRNA(Gln) amidotransferase subunit A 1391259:1392791 Reverse
MTNDILTTPALELGRRIAAREQSSTEVTGAFLDQIDAVEPAVHAFLAVDRDLALRRAGEV
DAQIAAGERLSPLAGVPVAVKDLLCYQGLPTTAASRILEGWMSPYDATVVRRLQAGGLVI
LGKTNLDEFASGSSTESSGYGPTHNPWDLERIPGGSGGGSAAALAACEAPLAIGTDTGGS
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TSLDRPVPPVRQAAERADVTGMRIGVVRELGGEGYAPGVEARFGEAVAQLEAAGAEVIEV
SCPRFEQALATYYLIMPSELSSNLARYDAMRYGLRVGDDGHHSVEQVMRLSRGQGFGAEV
KRRIILGTYALSAGYYDAYYGSAQKMRTLIARDFAAAFDRVDALVSPVAPTTAFKLGEKV
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RLVGPGYDAALSDRAAALPGSLVSMGKDAK
>PFR_JS22-1_1221 PFR_JS22-1_1221 Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C 1392799:1393101 Reverse
MALTPHDVSRLADLARIELTDDELAELAPQLDVILNAVAGVAEVADEDIPPTSHAVPITN
AFRSDAMKLSWPAGEMLRSAPAEQDQRFRVPRILDDSDEQ
>PFR_JS22-1_1222 PFR_JS22-1_1222 Amino acid-binding ACT domain protein 1393322:1393948 Forward
MLLLRVELPDRPGALGQVATAMGGVGADISAIEIVERRSDGHVIDDFILAMPPGSLAETI
INACAEMPDVKVLWLSRYPDQWNLESDIEVINRMSKQRARAAEILTEDAPTVFRCEWASL
VDRKGLKVLHATERAPEFTADQLRELGDLAKAGRHAMGEDWMPDWGDVAVAAAPVDEDRT
LLVGRQGGPEFLDSELFRLEHLASVARA
>PFR_JS22-1_1223 PFR_JS22-1_1223 Hypothetical membrane anchored protein 1393969:1394172 Reverse
MRRFSSDLDLTGGAPVRARPSIGEWGPDQVPTTAQKKRLRIWVSIALVAATTAIGVLMYV
FYKLLGY
>PFR_JS22-1_1224 PFR_JS22-1_1224 Methionine synthase, vitamin-B12 independent 1394241:1395227 Reverse
MIATALGSFAGTDLRATARAVLGELPDRAPIVELPDRGPQASMIARTAAMLPDMPFDRRP
SGWRLAPGPSLVGRRAAALFNDDVTMTAEVIEDWQGTLTLTMAGPWTLLASLDLVRGGRA
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ITPACGLASADPVDAFRALADLAAVARG
>PFR_JS22-1_1225 PFR_JS22-1_1225 TRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase 1395273:1396346 Reverse
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FEAWSQEVTTCPVNA
>PFR_JS22-1_1228□PFR_JS22-1_1228□Hypothetical protein□1399582:1400454 Forward
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AGGSTATTNTAGTTATEFDSTAWTRWALSPCSTIMKPAANTGALFTPETKKQAATSQGID
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>PFR_JS22-1_1229□PFR_JS22-1_1229□Phosphorylase□1400619:1403210 Reverse
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PQKLLSRASRERLDTLAGDRRYLRHLELAAADLSDYVSGDRWYQGFVSRHPEAPKAIGYF
SAEFGVSSVLPQYSGGLGVLAGDHLKSASDLGVPIIGVGLLYTHGYFRQSLNAAGWQQEH
YPVLDPNELPVEMLREDGEPVTITLTINHRPVVAQLWVAQVGRVPLLFMDTNVDANDEAA
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LVRSCKSRGMSSEWVSNALNPHVLTIGFARRGASYKRLTLMIQQPERLKKLLNDPEHPVQ
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RPQEACGTSGMKAALNGAANLSILDGWWDEWYDPAYGWAIPSATNAASPEERDRMEAESL
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LLHDAAELGLATVATAAVAGQDR
>PFR_JS22-1_1230□PFR_JS22-1_1230□Alpha-1,4-glucan:maltose-1-phosphate maltosyltransferase□1403336:1405450 Forward
MVSKKKRQRSAQARVRSRVTVQASADPKPTDAQARPTEVPPQPAALSVPPPIPPGFGRIP
VHNVQPVLEGGDYAAKAVENGDLPVTANIFREGHDAVAAAVVLTDPAGATQRFEMAQIEP
IGLDIWMAWIRVGRPGDYSFHIEAYDDRWGTWRHNAGIKFSVGQDIALVCLEGLQLLDEA
RDAARAAGDDAAVTLLEQAASQLDPEQPMTVLASLPTREDLHQAMVRWCPRRLATPTREF
PLVVHRKAAQFSAWYEFFPRSIGAERHEDGSWTSGTLASSEEMLEHVAAMGFDVAYIPPI
HPIGHSFRKGPNNSLTAGPNDPGSPWAIGSADGGHDAVHPDLGTLEDFDHFVARARELGL
EVALDFALQAAPDHPWATQHPEWFTTRPDGSIAYAENPPKKYQDIYPLNFDNDPAGIYAE
VLRLMEFWIGHGVTIFRVDNPHTKPVSFWAWLAAELHSRHPEVLLQAEAFTRPEMMHALA
KVGFHLSYCYFVWRTTKQELSDYLNELAHETESFFRPNFFTNTPDINPKFTRSGNPAAFA
IRMILAATMSPAWGVYSGFELFEHAALVDGGEEYLDSEKYEYRPRDFTAEPNLNQLMTKL
NRVRHDHPALQQLNHTTVLETSSDQLFAFAKRSGDDRVIVVVNLDPDNTVEGTVYTDLGA
LGLPADARLVAHDELTDTVFDWNAAHYVRLWPAQPAHILTISWA
>PFR_JS22-1_1231□PFR_JS22-1_1231□Maltose alpha-D-glucosyltransferase□1405536:1407335 Forward
MTSDQHSETPPIRALLGEDEERTADARAKLEMALSLTQPTGAVDPHDTSWFETAVFYEVM
VRSFADSSGDGIGDLAGLTEHLDYLQWLGVDCLWLPPFFASPMTDGGYDVADYRAISPDL
GTLSEFGDFIDKAHDRGIRIIIDFVMNHTSDHHPWFEESRRHPDGPYGDFYVWRDNPDGY
PDARIIFIDTETSNWTFDPVRGQYFWHRFYSHQPDLNYENPKVLAEMLDALRFWLGFGVD
GFRLDAVPYLVEEEGTNCENLPGTHDILKQVRKMVDEEFPGRILLCEANQWPHDVVEYFG
DNDECQMAFHFPVMPRLYMGVARHTREAITTILASTPPVPQGCQWATFLRNHDELTLEMV
TEDDRQYMWREYAPDPRMRLNLGIRRRLAPLMGNDPDKIRLMNAMLLSLPGSPVLYYGDE
IGMGDDIWLHDRDGVRTPMQWTADPSAGFSTATPDKFFLPLLADPYSPQQVNVTDQMADP
GSLLVWMRSMLTTRRQFPVFGRGEFIDMGGQNDAVLSFLRVLDDDKHGSQRLLCLNNLSP
EEQDVLLYLPDDAGTKPVSLLTSQAMAPIAANGEFHDTLPAWGFAWLDLSKGSDEHESE
>PFR_JS22-1_1232□PFR_JS22-1_1232□Maltokinase□1407351:1408688 Forward
MVAPNDDPRWRYASTARWFAGKGRGGVARRIEALDWYRAPEPGHLGVRSEIITIAYPDGA
HDYYHLPISYRTAPLSDALIGPADDPQLGYAHDATRDPEAMELLIASLGRRVNSGDWSAM
LPRGDRLTGPMPARPFTGEQSNSTVFLGSTALVKFFRHLEVGNNVDIPLHEALGRYRVRD
VDELYGWVTAHFRAISGRAVHADLLMITEQLKTLGEGWPMAVESATADTDFSAHAAGIGR
ALAHVHLALVQAFPPVMLKGDDVADGMVARLDRAIEAVPALSDYRSMLVVGFNRLRGHRL
PAQRVHGDFHLGQTLLTPGGWRIIDFEGEPLRPLADRTLPDSVWRDVAGMVRSLGYAAAQ
DGSPDAPARQHWLQRSQAAFIAAYLEITGVHDQVDLLDAYVADKAIYEVVYETRNRPDWV
HIPMAAITSWHEHQFQAPRGRTHHA
>PFR_JS22-1_1233□PFR_JS22-1_1233□1,4-alpha-glucan branching enzyme GlgB□1408681:1410585 Forward
MHDKFGNLTGTDLEGFHSGGDTEAWRRLGSHVVTVHDDARGDLSGTRFAVWAPNAQRVQV
IGDFNWWQGDDMEFVPGSGVWGLWKEGVGAGARYKYKIQHRDGSWQEKADPFAFSTEVPP
ANASVVFEREHAWAPSEESWLAHRAQADPYHSQMSIYELHVGSWRKGLDYRQLAQELPAY
LTWMGYTHVELMPIMAHPLEASWGYQVTGYYAVDPRHGSPDDLRVLIEALHAAGIGVILD
WVPGHFPKDDWALGRFDGTALFEHADPRQGEQLDWGTYVFNFGRNEVKSFLISNALFWVS
EFHIDALRVDAVASMLYLDYSRPPGGWVPNKYGGRENLEAIDLLRYINRHLYRRQPGVMM
IAEESTSFPKVSAPVDVGGLGFGFKWNMGWMNDSLEYIKLDPIYRQYHHNEMTFAMVYAY
SENYILPISHDEVVHGKGSMVNKIPQDDWRKFATLRSFYSFMWAFPGKQLLFMGQEFGQR
SEWNEAVGLEWWVDSLQWHKGLRDMMREINHVQARTPALYELDSEPEGFRWINDNDWMAN
TFSWLRFDRQGGMVACVANFSPEPYPEYGLRVPRAGRWREILNTDEQRWDGSGEAANGTR
IAQPVDGEEGAELVISIPPMAGVWLRFEPEATDS
>PFR_JS22-1_1234□PFR_JS22-1_1234□Hydrolase, NUDIX family□1410621:1411406 Forward
MDDFKVNVVVDAGIGTLHWQGTVDQKTLDEAVSLAADDALIGHELHRVEASITADDLMAM
RALHRAGFRREGRRRQAVRAEDGSWHDALLYARLIDDQVYGAGGFTAVMDTVMATHRLIG
HVLIRDEHGRVLFVETTYKEDWELPGGIVEAGESPRVGAERELREELGVDIRINQPLVAD
WMPPYLGWRDAMEFIFDGGQLPSSTMQRFERPAQEIRSYHWVAPEEIAEHVTPLSARRLA
LLVAGTAPAYTEAGSAVTPDA
>PFR_JS22-1_1235□PFR_JS22-1_1235□Phosphoglucomutase PgmA□1411522:1413153 Reverse
MADPRAGQPAQPSDLIDVDALIAAYYDKRPDPTNPDQQVVFGTSGHRGSAFDTAFNEAHI
AAITAAIVEYRASQGTTGPLYLAKDPHGLSLPAWKTAIEVLVAAGVHVLAEAEDEYTPTP
ALSRAVILHNRGRERDLADGIVVTPSHNPPRDGGFKYNPTNGGPADTDATGWIAGRANEL
LGNLEGIKRIPYERAKDQVEHFDYRSRYCEDLRSVVDIEAIKASGLHIGADPLGGASEQY
WEYISEHMLPNLSVVNKVIDPTWYFMTLDTDGQIRMDCSSPDAMASLVAKRDQYDIATGN
DADSDRHGIVTPDGGLMNPNHYLAVAIQYLFGNRPRWASNTAVGKTLVSSTMIDNVAGLL
GRSLYETPVGFKWFVPGLISGELGFGGEESAGASFLELGGKTWTTDKDGLIMDLLASEIT
ARTAKTPSEHYRELEARFGTYYYARIDSEADRAQKARLKALSPSDVTATVLAGDPITHIY
TNAPGNDAPIGGVKVTTEGGWFAARPSGTEDKYKIYAESYRSAQHLSELQDGAREVVSDA
LKG
>PFR_JS22-1_1236□PFR_JS22-1_1236□Thioredoxin□1413286:1414278 Forward
MSQPLTPRQPSGPQGPARGQSSATPQGHAPSAHSDFSRPGAIDLSKIAATSPAAPQPGQA
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GASTGSYVVDVTEAELNDVIQQSVNYPVILALLSANDPGSNQLRSMLTRLADESAGRWLL
AVVDIDTQPRIAQALQVTAIPTVLALLAGQAIPLFQGTADEAQVRGVLEQVMASAVANGV
AGHVKPVSHGEAGPDPRFAAADTAMEAEDYDRAADEFGKLLAANPKDSEAAAGQATARLM
SRAANADPEATLAAAKAAPDDVPAAMAASDVDMIAGRPKDAFGRLIGLIRTTAGDERDAV
RRRLLELFETMDQADPELLAARRALGAALY
>PFR_JS22-1_1237	PFR_JS22-1_1237	4-hydroxyphenylpyruvate dioxygenase C domain protein	1414510:1414956 Forward
MSNEDLFICIDHVAYACPDADEASKYYQETFGWHELHREENPEQGVVEIMMAPAAKLTEH
MTQVQVMAPLNDESTVAKWLAKHNGRAGLHHMAWRVDDIDAVSATLRERGVQLLYDEPKL
GTGGNRINFMHPKSGKGVLIELTQYPKN
>PFR_JS22-1_1238	PFR_JS22-1_1238	Putative phosphate acyltransferase	1415112:1415687 Forward
MMRVRRAIARIGWALSPYQLVGRELTSEPGVVLGAPHTSNWDFIAFLGVSWYYRVPLKVL
VKKSWMRGPLWALGKALGAVAVDRAHPGQVVEHLVAQAEQGHSFKLVIAPKGTRSPRQYW
KSGFYRIALGAGLPVTLAGIDAGRRQVEVGPTIRLTGDVHADMDRIRAFYDRFDGVHPQL
RSDPRLREEDS
>PFR_JS22-1_1239	PFR_JS22-1_1239	Hypothetical protein	1415846:1417639 Forward
MSQYDDSHTGDDQSEETGLNLFDDRASAAGSFPHAMMGYDRSTVDNYVRDLEQRLSAARQ
LNRDRLRDLESLKSEQGTTDFTRLGAHATNLLRAAEAQADDLVTKAGVEAERIKEEGRRV
AADLRANAQTEADDVRVSGLTNLRNLRKETEQQTQSVIAHAKEQAATVVASAEQQAQAVI
QEAEQQAEILAHKADDAAKASEQQNQQKAAQTALEAKNRAQEIEAQAHIQAEQILAGARR
DGEATKAKAQQALTDAHAQADQVLADARREADATRAKAEAALADAHAKADEILADARNEA
QATKANAESTLADAHTKGEEILADTRREADATKASAESQASELVDKGKQEAADARAQGQA
QAKQILDQARAQADQIQADAHDAAQKALDAASAQADKVRKDIDALLAQSTKTAQESAARV
KAQADQVAELSAKALAAAEQSKTDGVREAESQVAAAHRQSAMMKDRLEEQYAWRKEQLER
ETHALELRKDAVLAQLSNVRALAQESVADFPNTDSLTNAALSLADGTSTGPDATMALKAT
VGPEGQQSGGHEDDQQWLAHSGDNGATDASPDEETTMLKTKDPQGEPRSSRRNKKSR
>PFR_JS22-1_1240	PFR_JS22-1_1240	Endonuclease NucS	1417680:1418327 Reverse
MAKRLIIIKSDGSVAVHSDDRAYKPLNWMSPPCTLTVLDAPQDLAATTADLDAEIDQVWM
VKARSGDILQIAIAEIIDDHEYDLGIDPGLQKDGVEAHLQALLAENPQTFGKGYRLVRRE
FPTAIGPVDLLLRSDDGGYVAVEVKRRGEIDGVEQLTRYLELMNADPLLAPVRGVFAAQL
IKPQAKVLASTRHIDCVTVDYDALRGIDNAEERLF
>PFR_JS22-1_1241	PFR_JS22-1_1241	Hypothetical protein	1418484:1418762 Forward
MGHHRPSKHLRAARPLNVGAMRTAVQKYDGRWIVQQIVAGRSVKEYRCPECNRMIPAGTA
HVVAWLETPPIGAISPVEFRHHFHTSCWNRRP
>PFR_JS22-1_1242	PFR_JS22-1_1242	Abhydrolase domain-containing protein 11	1418759:1419589 Forward
MNQSSGSLHVTTIGSGPATAVFLHGLLGQGKNLAGAAKALDGVATSLLIDAPNHGLSPWT
GEFDYRAMGDAVAAELEHRGAARKPVVLIGHSMGGKTAMCLTLDHPELVEKLCVVDIAPV
RYSHSKFFTGLISAMRGLDLAALGSRRQADQSLTQQIPDPVIRGFVLQNLHHGPSTPALG
DRGPETWHWRANLALLARALPQMEAFPDFAGRHWDGPTLWVSGGKSDYVQPAYHAAMQAL
FPRVELVTVPGAAHWVHADEPAEFGQLLRNFVTHGE
>PFR_JS22-1_1243	PFR_JS22-1_1243	ATP:cob(I)alamin adenosyltransferase	1419668:1420276 Forward
MVNITRVYTRTGDAGTTRLSNNEVAPKTDPRVQAYGQVDETNCTIGVALTLDPSDDMQKV
LAIVQNELFDVGADLSSPVVSDPKFRPVRVDQTSVDRLEKWIDEFGEDLPALRSFILPGG
SPLAAQLHVARSTCRRAERAAWEAVEAFGGEDGSSEPKGGVSLIAVKYLNRLSDLLFNLS
RHANYEAEHDEVLWVPDGEREV
>PFR_JS22-1_1244	PFR_JS22-1_1244	Lipoate-protein ligase LplJ	1420448:1421512 Reverse
MAEAALRGEYKVRGGKLVAVDLEIVDGRLARVHVSGDFFLEPDDALDEINAALEGQPANA
SVADLAAAIRARLSPDARLIGFDPEAVGIAVRRAVRGALGWNDLTFEVMGPKVMDPTLHV
ALDQVIPDEVSQGVRGPVFRFWDWDRPLVVIGSFQSVRNEVDEANARKYGIKVVRRITGG
GAMFMEQGNCITYSMVVPGSLVEGLSYEQSYAYLDDWVLGALAEVGVNATYKPLNDIASD
QGKIGGAAQRRLVDGTVLHHVTMSYDIDADKMMEVVRIGREKLSDKGTKSANKRVDPMRS
QTGLPRDEIFTRFLAYFKNRYNCVDSDYTPEEMARAQHLVDTKFNTPEWTYRVP
>PFR_JS22-1_1245	PFR_JS22-1_1245	Hypothetical protein	1421536:1421994 Reverse
MIAALEIVAAVLALAVVASLGVLIARRQWLLSREGIFSCEVRQRLPRNGSRWVPGVARYS
GNSLLWYKMLSASFRPTLVIRRRGARLTDHRAPSPQDGLLAVNSHRIVRLEVHTPGGAEH
VMELGLAPESLMGLMAWLEAGPPGGESYREFD
>PFR_JS22-1_1246	PFR_JS22-1_1246	ATP synthase F1, epsilon subunit	1422036:1422503 Reverse
MPNLLQVEVVAAEGKVWEGQAVSLIARTTEGDIGILADHEPFMAALVPSAVQVTTPEGID
EIIAVSDGFISVFRNRVSLLSSFAELAQEISVEQARVTVANLHERIDSSEATTDEAREYN
RALAQLRAAGQYQAKMKGQSYSEITPQPAKIAPGD
>PFR_JS22-1_1247	PFR_JS22-1_1247	ATP synthase subunit beta	1422503:1423954 Reverse
MTATQTAPEDAGTAGTGHVVRVIGSVVDVEFPSGRLPEIDNALHVSLDSGDGSTTITMEV
ALQVGDNTVRCISLKPTDGLRRGTEVVDTGAPIKVPVGDVTKGHVWNATGDLLNADPATV
KIDERWSIHREPPAFDALEPESQMLETGIKVLDLLTPYVQGGKIGLFGGAGVGKTVLIQE
MIYRIAHNFGGTSVFAGVGERTREGNDLIHEMEEANVLKDTALVFGQMDEPPGTRLRVAL
SALTMAEYFRDVENQDVLLFIDNIFRFTQAGSEVSTLLGRMPSAVGYQPNLADEMGQLQE
RITSTRGHSITSMQAIYVPADDYTDPAPATTFAHLDATTELSRDIASRGLYPAVDPLSST
SRILAPEYVGKEHYDVATEVKQILQRNKELQDIIAILGIDELSEEDKIVVGRARRIQQFL
SQNTYMATKFTGVEGSTVPVAQTVESFKMIAEGKCDEIPEQAFFNVGDMDDVNKKWDQLK
KEG
>PFR_JS22-1_1248	PFR_JS22-1_1248	ATP synthase gamma chain	1423955:1424890 Reverse
MATSLRELKQRRNSVATTMKITKAMELIAASRVTKAQQRARNADEYTRELVRAVSTVAAY
TREDHRLTQIKEHSKRAAVLVINSDRGLAGGYPANVMRASEGLLKHLAEGGLETDIYTVG
RRALDYFNFRHVPIKQSWQGFSEDPHYANAHDIGRVLIDQIMKDTEAGGVDEIHVVYTRF
LSLVSQRTELVRLLPLQVVRDQEETAHAGDDVVSDNAEIAPPYNFEPDAETVLDALLPLY
VIDRIKYMLRESAASELAARQQAMHSATDNAQQLIDTLTRQANTARQAEITQEITEIVGG
ASALSESTQEM
>PFR_JS22-1_1249	PFR_JS22-1_1249	ATP synthase subunit alpha	1424893:1426530 Reverse
MAELSISSDEIRDALDTFVHNFTPTQAAPEEVGHVTTSGDGIARVEGLPNVMANELLRFD
NGTMGIALNLDEREIGVVVLGESEGIDEGSIVRGTGEILSVPVGDGYLGRVVDAMGNPID
GKGAIDGIAGRRALELQAPGVMDRQEVTEPLMTGLKAVDSMIPIGRGQRELIIGDRKTGK
TAIATDTIINQLDNWRSGDPKKQVRCIYVAVGQKNTTVAEVHENLRKAGAMEYTVIVNAP
ASDPAGFKYIAPYSGSSIGQHWMYEGKHVLIVFDDLTKQAEAYRAMSLLLRRPPGREAYP
GDVFYLHSRLLERCAKLSDELGAGSMTGLPIVETKANDISAYIPTNVISITDGQIFLLSD
LFNANQRPAVDVGNSVSRVGGAAQTKAMKKVSGTLKIDLAQYRDMQAFAMFASDLDATSR
RQLDRGARLTELLRQQQAQPLPMEEQAVSIWAGVNGKLDDVPVDDVLRFESEFLDFLRES
TDLLTTIASSGALSDETVASLDDRIASFKQTFRTSDGQLLAGARDSEKVGNEDINQAKIV
ATKRS
>PFR_JS22-1_1250	PFR_JS22-1_1250	ATP synthase F1, delta subunit	1426605:1427375 Reverse
MNGTRIERLDEAADKLVATSSLSTELFALVDELNAQPDLGRALTDPALEADGRGKLAGAL
LGKRLSGPTVDFVVQALALDWASGREFTSGLARQAIRIALRSTDADQVRTELNVVRETLA
THDELRVAMAGHTAGEEARAKLVDQLLGDKVDPVTAMLVGRAVRDGEHVQDALWSCMELA
SQVLGRILARVTVARPLPAYQMAELGEQLRRLYGQPVDMAEHVDPSVLGGVRVELGDDVI
DGTVATKLSEAQRELA
>PFR_JS22-1_1251	PFR_JS22-1_1251	ATP synthase subunit b	1427382:1427936 Reverse
MTPNGLVPHIDLGPLLPELPEFLAGLLLLGLMWIIVAKAVAPRFEQLYEKRSSEIEGGIQ
HAEQVQAEAAKAREQYQAQLSEVRESAAKAREDAKTRSAEILRDAKNEAAQEQARMIAEA
RAQIASEREIAAGQLTTQVGGLATTLAGRIVGESLDDDERAKRTVERFLKELENQPARNQ
TIGK
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>PFR_JS22-1_1252□PFR_JS22-1_1252□ATP synthase C chain (F1F0-ATPase subunit c )□1427947:1428165 Reverse
MTPLEISGSLNVIGYGLATLGPGIGVALIFAAAIQGIARQPEARGYIMTPVYIGFAIVEA
LAILGFVLAFIK
>PFR_JS22-1_1253□PFR_JS22-1_1253□ATP synthase subunit a□1428211:1429092 Reverse
MSNEATVVDAPETSKGHPVAIVVTMLVVWIALTFLAERIGGGVSSWHAPSQEDFEFSGWF
GTTWFNKPMLLAIIGFVGVLAYWLIASRRLKVIPSKAQFFAEYVVDFVRNIGRDMIGPGY
RRFTPYLLTLFSFILVSNWFGETFVFMFPTFSRVSYAYAGAILTFLAYVISGFAKHGLGY
LRVALIPSGVPPWLYPVIIPLEFLSSFITRPLTLSVRLFANMFAGHMSIMVFVGGGAALL
GWVHNSFYNVTGVFALLFGVAMLCLELFIGFLQAYIFTILAAQYIGSSVGAAH
>PFR_JS22-1_1254□PFR_JS22-1_1254□Hypothetical protein□1429085:1429309 Reverse
MSEPVEHDEHPDQAQPGSGLQSVSYLLAGIALYGGLGWLADKLFNTVWFLPAGLLIGTAA
AVYLIVKRFGGRHE
>PFR_JS22-1_1255□PFR_JS22-1_1255□Hypothetical protein□1429306:1429743 Reverse
MNPSVNSAWLRSMTRRGLLFAMVCAVPAGVVNGIVGGLESVIGWLLAVGLVGLYFIAGVV
GDALAVRRADAFGMTMLLAGFLVRAAAVALVLWLLASHGLLAGANRGNGFVWTVLAMVIG
WTAGLVDAHRRARLPIYASVGRETP
>PFR_JS22-1_1256□PFR_JS22-1_1256□Glycosyltransferase, group 4 family□1429821:1430957 Reverse
MREYLLVMLTAFAATYLFAGLCRRVAIRTGAMAPVRERDVHATPTPYLGGVAMLVGVGAA
FLLAAHMPFLGRHPTVSRDALGIFLAALVICVIGAIDDAIDLPWMAKIAGQVLAAGVAVL
NGVRMYWVSLPHQIFALDEPTSILITVLYIFVCVNAINLIDGLDGLAAGVVGIGSLAMFV
YTYLLAYQQQFVVATTASLVTATIAGICAGFLPHNFFRAKMFMGDSGAMLLGLLLACSTL
SLTGQIDSSALTPSRGDALPALLPIVLPIAIMALPLIDMTMAYIRRTWNGNWWFVADKKH
LHHRLLQRGHSQIKAVLIMYMWTAIIAFGVIALGLAWYWPVILAVAVAIAIAIVLTVVPM
RQPKSPARRLVEPKPVER
>PFR_JS22-1_1257□PFR_JS22-1_1257□TRNA threonylcarbamoyladenosine biosynthesis protein YwlC□1430966:1431844 Reverse
MTHVSGAQTNKTDQMGQGTSAASPQEGGSGEESFRRFDLATQRDEALRAAQAAVGAGQNI
VLPTDTVYGIGADAFSADAVQGLLNAKHRGRDMPPPVLIAEPAMLPALVSSIPLGAERMI
KECWPGALTLILNAATALHMDLGETAGTIAVRVPDNDDARALLLHTGPLAVSSANISGQP
SATDVGAAIAMLGDSVAVYLDGGRTPGPVASTIVDFTVAPAGRILRQGVIGFDQLEGLSP
GLEDLVTEQVQADQAAAATPPSSSPDAPSGSGPSGTPDSSADAAAGSGSGQD
>PFR_JS22-1_1258□PFR_JS22-1_1258□Release factor glutamine methyltransferase□1431841:1432719 Reverse
MSTHRPAALIKQGINELTSAGAQSPRAEARHLLAAAADLDPAGLATTREVDDAVADRYAD
LIRRRAAGEPVQYLTGRAWFRKIDVQVGPGVFIPRPETEAVVHFALDQLLNLRADTGPSP
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QLEGKVDLVISNPPYLPAAHADELPADVLDYDPHEALFGGDDGLETIRGIVPVATRLLRP
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ARELANDDPAFAAEADQISARLDEVTDKLTALLAPRDPLDSNDAIMEIKSGEGGEESALF
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RVQRVPVTESQGRIHTSAAGVLVMPDVEESEIEINPDDLRIDVYRSTGKGGQGVNTTDSA
VRITHLPTGVVVTSQDQRSQLQNKEQALRVLRARLVAAAEEQAAQQAEQARKSQVRTVDR
SERIRTYNFPENRITDHRIGFKAHNLDAVLGGELEPLIEALQAADLAERLGQATESEKQ
>PFR_JS22-1_1260□PFR_JS22-1_1260□50S ribosomal protein L31□1433902:1434126 Reverse
MKNSTHPEYHDVKVVCTCGNEFTTRSTFPGDVMSADVCSNCHPFYTGKQKILDTGGRVAR
FERRYGKAKAAATK
>PFR_JS22-1_1261□PFR_JS22-1_1261□Transcription termination factor Rho□1434263:1436218 Reverse
MSETTQAVAENGPADPMSTLSAMRLTELKQVAAQLGIRGVSAMRKGDLINAIDSRRGGSG
AQPAQQQPTRHEEGPAERRTRSASRASREATGEEGPARDVSTADAIAARLEAAEHSSGRS
RRERNTDSESGTATERSTDNDRGGRSERNSTRTNNSRSDGAHNEGPRTSNQGVDDEVGAR
LEQLSGRGNRSEKNERNRDERPERHHNQSNRNHSESTRNDSNRNDSNRNDSGRRDDDEYS
GGRRSRRRRQRDRQGRRGNRNSPMNEMETTTVQEDDVLIDVSGILDVLDNYAFVRTSGYL
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PDFGKLTPLYPQERLRMETVSTNMTGRIIDLVSPIGKGQRGLIVSPPKAGKTMVMQNIAN
AITVNNPEVHLMVVLVDERPEEVTDFKRTTTAEVIASTFDRPADDHTTIAELAIARAKRL
VELGRDVVVLLDGITRLGRAYNLAAPTSGRILSGGVDSAALYPPKRFFGAARNIENGGSL
TILATALVETGSKMDEVIFEEFKGTGNMELKLSRQLADKRIFPAVDVEASSTRREELLMS
RQELDIIWKLRRALSGQKEQQALETLLSRMKKTRNNSEFLVLISSTTPGSD
>PFR_JS22-1_1262□PFR_JS22-1_1262□Phosphoserine phosphatase/homoserine phosphotransferase bifunctional protein□1436612:1437235
Reverse
MHIACLDLEGVLVPEVWINVAERTGIDELKLTTRDISDYNELMDHRLAVMAKHGLTLSAI
KKVIADMGPLPGAKEFLDWLRARWQVVILSDTFYDFADPLMEQLGRPTLFCHSLVVRDDM
VVGYQLRQPNGKYEAVRAFQSLNFTTLSTGDSYNDTAMLNQADYGALFNPPANVIAEFPH
LPVAHDYEELKEQFLAASEQLESGLQA
>PFR_JS22-1_1263□PFR_JS22-1_1263□Homoserine dehydrogenase□1437244:1438569 Reverse
MNQDARVTAPTRALRVALLGCGTVGRQVAGTLLDKAEDLAAKAGCHLELIGIAVRNVNKP
REGIPPELLTDDAAGLVANGGADIVIELIGGIDPPRELIVSAINHGASVVTANKALLAAH
GEEIYAAAEKNRVDIYFEAAVAGAIPIVRPLRESLVGDEIRSVMGIVNGTTNYILDKMTN
DHQDFEEALATAQQLGYAEQDPTADVEGYDAAAKAAILAGLAFHSPVSGSDVFREGITSV
STADIEAARASDCVVKLLAIAKIDEHDRISVRVHPAMVPYSHPLAMVNGPYNAIFVEAAN
AGRLMFMGPGAGGSPTASAVTGDLVTVARNRMRGVVGPAHSVYQAHQLAPMGETRTRYYV
RFRVADQSGVLASVASLLAKHHVSVHSIRQTPIEDGREAASARVSMMTHEAQESDMMVCL
EELEKSDYVLGSVRLMRAEGA
>PFR_JS22-1_1264□PFR_JS22-1_1264□Diaminopimelate decarboxylase□1438580:1439974 Reverse
MHVAGAIHADVSTPGPQWLTKPADLNELDPALWSRNVSRDEHGRVGVAGIDVVDAIEREG
SPLYLFDEDDFRHRARDFKSAFDGWNVYYAGKAMLTRTIARLVMEEGLGMDVCSGGELQV
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GLTEPIMAGE
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alpha-N-acetylglucosaminidase□1460637:1461584 Forward
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AEHVKLVN
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TETGDVEELRGDEKTDEDDLFAGIGRNDPCPCGSGKKFKNCHGRNPNIR
>PFR_JS22-1_1320□PFR_JS22-1_1320□Putative ribosomal S30AE, sigma 54 modulation protein□1514614:1515210 Reverse
MDVIVTGRRISINDATRDLVSRRLNDSIVKLKDRVIRTEVEFTANESKGDPSNAIRCEIT
VRGKGPVIRAGGMAEDKMIAFDQALDRLIAQLRKAADRRKRRRGGQRLADLPVAVEDQSV
KTAEDAHEVAGMTVDGDGPMVVREKTFETTPLTLAQALDQMELVGHDFFLFVDAASGKPS
VVYRRKAYDYGVIHLEVQ
>PFR_JS22-1_1321□PFR_JS22-1_1321□Phosphoribosyl transferase domain protein□1515366:1516175 Reverse
MNLSHVIAAGQDLLLGSECVACGSPGPVLCAPCDRRLDDGPLVREPDGDDLVDGMVPVWS
GSRYDPIAGKLVIAFKDRGAWTLAAPLSRLVSRALAGLLLAGPGGDASPLWGARGPTAGA
GGEVPILVPVPADPRRVRARGLDHTTTITRRAAAVCGLEWCKLLRRVSATRDQIGLGSAA
RRAGQHGTMSIGSPRWCLPRTRGPQLWQARPIVVVDDVVTTGATVREAVRALRAAGARVW
GVACAAQTELAGSVPRRVGSPLAPGDQTR
>PFR_JS22-1_1322□PFR_JS22-1_1322□DNA-binding response regulator MtrA□1516257:1516997 Reverse
MTDIEVGGPGLVLIVQDDAERADELHDLLSELGFATRWCASASIALKSFHETRPDLVVME
VGLAGRSGLDVCREIRRESDVPIILVSTGSATEDIVEGFRAGADDYIVEPFAGAELLVRV
QARMRRRRNGIQARHTVMVDDLEVDVDNRQVRRHREPINVTPTEFKLLVTLVERPGHVFS
REELLAEVWGYGHAGDERVVTVHVQRLRAKIEADPDRPRIVTTVRGLGYRLGHTTDVRWI
PEPLTV
>PFR_JS22-1_1323□PFR_JS22-1_1323□Conserved protein, DUF179□1517133:1517699 Reverse
MNFSSSPHAGELLVSSEAAGGGFFDQAVIFLLDNDENGAIGVALNKPSTTPVAEVLPAWA
GELNPPSVLFAGGPVAPNGAICLAKVMDSGEEPPGWRPVLGDVGLLHLDTPVEIAAGAYS
DVRVFAGYSGWDPGQLSDELDRGVWLRAPARDEDVFGAQAEGLWRRVLRRVGGDAGLLSG
YADKPALN
>PFR_JS22-1_1324□PFR_JS22-1_1324□Hypothetical protein□1518405:1519046 Reverse
MPSGSPIPGFTPESFGAAGRDLLDAPITEEQRQRSERYLQDAYAEGRLSHEEFGRRIDKV
LRARTRRELNAALEGFVKAGLASQVVGQFGAYPSVVVPREVRRRAGRWAGAAAHWSGAFT
WIVGPAAVYALSKPHSYPHREAAKAFNTQIAIAIVSALVVGFSALLGLGWIPFAVWSALA
LVLIVVSGLNASDGKDSRNVLQRVLPIRVLDEK
>PFR_JS22-1_1325□PFR_JS22-1_1325□TmRNA-binding protein SmpB□1519136:1519618 Reverse
MPREKGEKMIARNKKALHDYSIGERLEAGIVLTGTEVKSLRDGRASLVDAFATIDDNEVW
LRNANIPEYTLGTWRNHSAMRKRKLLLHRQEIKRLERALGDSGGRTLVPLSIYFKDGNAK
VEIAVGTGKREWDKRQTIRERDMNREAERDLADRNRRHRH
>PFR_JS22-1_1326□PFR_JS22-1_1326□MutG family lantibiotic protection ABC superfamily ATP binding cassette transporter
permease□1519769:1521721 Reverse
MTAGRPGARQRPPGAAPHRRTGGATRAALMGFLALLMVALGLTAAPQRALAQTSDSFDSW
TADYTVGTDGTTHVRETLVYRFASDSARHGMYRTLLTREPDGDNKNQDIVYDVSNVQVSS
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DERFLGVPPGTVPVDVDAAQVGPASKHDVVPVRFDPPQIPVALGGLLVDGQVDSQEMTAT
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PGSMSDASSELAREVAATATNQGLMKRIGQVGTKRSGAVIGSFVVLIGAWFGGSLLSNTA
ALASNAAGLTALMIIGALVVVGIITLLIRSSIARRGTRTAMGRAYTDQVQGFEEYLKTAE
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YFTSGVLSGVDSGISVPESSGGAGFGSGGSAFGGGGFSGGGGGGGGAGGW
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FHVYVNGATDDPQNWITVA
>PFR_JS22-1_1328□PFR_JS22-1_1328□Efflux ABC transporter, permease protein□1523291:1524208 Reverse
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CTADSATESAGGNCEAGQDTTASQRDAIRSRLTANPDVSNIYYETKQEAYDEFQRVYKDN
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VVLAAASMSALQYFVIDRVRSQLAIQSLGWITWGDTAVAVVWVAVVGVLLSIIPTFVATR
RYLRV
>PFR_JS22-1_1329□PFR_JS22-1_1329□Cell division ATP-binding protein FtsE□1524247:1524933 Reverse
MITFEDVSKLYPRQTTPALRHVSVDIDKGEFVFLVGVSGSGKSTFLRLILREYRPTTGRV
FVAGKDLGRLHNWKVPALRRQIGTVFQDFRLLPGQTVYQNVAFALQVLGRPMREIRQQVP
ATLELVGLANKGERRPEELSGGEQQRVAIARAVVNNPKILIADEPTGNLDPATSVGIMKL
LDRINRRDTTVIMATHDSTIVDQMRRRVIELDKGELVRDQKQGAYGNL
>PFR_JS22-1_1330□PFR_JS22-1_1330□Peptide chain release factor 2□1525085:1526194 Reverse
MALDELTEHLSQLNKSLSSIEAVVDVPAKNKQIEELETEASAPDLWNDQEHAQSVTSRLS
RLQSSVEKVQTLRSRLDDASTLLELASEESDADTAQEAEKEIATLADEIDTLEVQTLLSG
EYDERDALVTIRSEAGGVDAADFAAMLLRMYERWAERHAYSYEVYDISYAEEAGIKSATF
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WRRQEEQAA
>PFR_JS22-1_1331□PFR_JS22-1_1331□YqeY family protein□1526289:1526750 Forward
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TREESAETYAAAGREELAAKESAEAELLKKYLPEQLDAAQLQQIVDDVVAQASTDGKPTM
KQMGQLVRAANEQVKGRAEGKAVADLVRKAITG
>PFR_JS22-1_1332□PFR_JS22-1_1332□Fructosamine kinase□1526939:1527931 Reverse
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>PFR_JS22-1_1333□PFR_JS22-1_1333□4-aminobutyrate aminotransferase gabT□1528049:1529386 Forward
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SIIDLGAGIAVTSVGASAPRVVENVQKAVANFTHSSFATTPYEGYVAVCEQLAELTPGSF
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PGYLPALQAWCRAHGIVFVIDEIQSGFCRSGKWFASEYEGLEPDVITTAKALGGGLPIAA
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>PFR_JS22-1_1334□PFR_JS22-1_1334□Aliphatic amidase□1529565:1530425 Reverse
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>PFR_JS22-1_1335□PFR_JS22-1_1335□Putrescine importer□1530422:1531813 Reverse
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FSIYAVAHHGQQLLSLTPFTGKPFDVLALSAGAATAAYSFLGFDAVTTLTEETVDAKRTI
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GQFASGIAAQASASRLMFAMGRDGVLPKRFFGRLSPRTNTPINAILVVAAVGIIGCFLDI
STSTSFINFGAFIAFTMVNVSAISLTRRQIARGEHVNPLTGYVVPALGALVVIYLITELD
LPALLVGGTWLFIGICVLVGLTHGFHRPPPEMTDSTEVEELAA
>PFR_JS22-1_1336□PFR_JS22-1_1336□Hsp20/alpha crystallin family protein□1532086:1532538 Reverse
MSTAIYNPFREMDRFFNQVAKTVGPDTRYMPLDLYRDGDQFVAKMDLPGVDPATIDIDVD
DRTLSVRAERKAEQVHKDDKSHWVSRERSYGTYARQLTLGPGLDLSRINADYSDGVLTLT
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>PFR_JS22-1_1337□PFR_JS22-1_1337□Putative ABC transport system□1532788:1534581 Forward
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VRLAAVLLAFDLANTVTSNIGGYLGDNMAMRLRAGLSKRYFDKLLGLPQRYFDDELSGTI
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VVLLWQRNDTDVADSLVDAMRDMGNNGYIWLFTPKIGRPGYVEPSELSEGAEVAGLTLTS
AVDVADDWQATRVVRPHHGRR
>PFR_JS22-1_1339□PFR_JS22-1_1339□Hypothetical protein□1535046:1535180 Reverse
MPPRRTPPEVSPDPGKGGHSVVKASTRRGAAPRRVEFRGAYVVK
>PFR_JS22-1_1340□PFR_JS22-1_1340□Pyruvate dehydrogenase E1 component□1535143:1537890 Reverse
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LDVHATEEDTAGGES
>PFR_JS22-1_1341□PFR_JS22-1_1341□Aromatic-amino-acid transaminase□1538145:1539341 Forward
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AAKPATYPPMDGLPDYNADAQRVVFGADCEAVASGRVVTGQSLGGTGGLTLAADVYGSVS
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>PFR_JS22-1_1342□PFR_JS22-1_1342□Transcriptional regulator, PucR family□1539427:1540641 Forward
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GIDNFISWFADDAKADVNPGSLFNAAPRALTRKVSLHQTVDLVRTTVDVVGEQINELVPP
QERRALELAIVYFSRDVAFAAAELYARAAELRGGWDERMEALIIDAVVRGEADDMVVSRA
SALGWHSQGAVMVVVGPSAAGADLESYRHAAEALGLAVLASRQGGRVILIGSGEQLTDRD
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PERALANQDDAREALLEEIYKPLADAGGELLHTAASFLEHGSLEATARSLFIHPNTVRYR
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>PFR_JS22-1_1343□PFR_JS22-1_1343□Malonyl CoA:acyl carrier protein malonyltransferase□1540798:1541754 Forward
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PLLMGAGLYAGLALNTESEHGAFALADVVAGHSVGEITAAAGVGVLDHAQAAVFIRERGR
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>PFR_JS22-1_1344□PFR_JS22-1_1344□3-oxoacyl-[acyl-carrier-protein] synthase 3 2□1541758:1542762 Forward
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>PFR_JS22-1_1345□PFR_JS22-1_1345□Acyl carrier protein□1542824:1543075 Forward
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DDVKSLRTVQDAVDYIEKAQKKA
>PFR_JS22-1_1346□PFR_JS22-1_1346□3-oxoacyl-[acyl-carrier-protein] synthase II (Beta-ketoacyl-ACP synthase II) (KAS II)□1543127:1544386
Forward
MTTVVITGLGALTPLGNDVATTWQGLREGRSGIGVIDEDWASELPVHIAGSSLVDVTSHL
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>PFR_JS22-1_1349□PFR_JS22-1_1349□Pyridoxal phosphate enzyme, YggS family□1547242:1547994 Reverse
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NSPDRERVAACFDRLVALQSRLRDDGVLGSDWAELSMGMSGDYPLAIEHGATTVRVGTAL
FGPRDYGTPA
>PFR_JS22-1_1350□PFR_JS22-1_1350□Von Willebrand factor type A domain protein□1547991:1548956 Reverse
MTPLMSFMNPDRLWWLAVPVAIALLYLVLAARRRATSGGSTNSILRRVLPRDAALKRHLS
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>PFR_JS22-1_1351□PFR_JS22-1_1351□Von Willebrand factor type A domain protein□1548956:1549930 Reverse
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>PFR_JS22-1_1352□PFR_JS22-1_1352□Protein containing DUF58□1549930:1550994 Reverse
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>PFR_JS22-1_1353□PFR_JS22-1_1353□Transcriptional regulator moxR1□1550991:1552043 Reverse
MSSDSGHPMSTADAAHKLGEAISQVQRVIVGQEHMVEQLMVGLLAKGHILLEGVPGTAKT
LAVRTFATVVGGTFARIQFTPDLVPSDIVGTRVYSASKESFDVELGPVFTNFVLADEINR
APAKVQSAMLELMAEKQVSIAGKTYPVPNPFIVIATENPIESEGVYPLPEAQRDRFLLKV
DVPYPKGSEELEILRRMSVTAPTATQVLDPDLTRSLQDQAANVFVHNLIAEYVVRLVLAT
RNPSEFNMPDLAPVIQIGCSSRATLGLVASARALALIHGRDYVLPTDVQAVALDVMSHRV
ALTFDAIADNVTPAQVVERVLAMVPAPTPVWNKGQQPPASAQAGSGRAAS
>PFR_JS22-1_1354□PFR_JS22-1_1354□Hypothetical protein□1552288:1553214 Forward
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MSDEESTAGPGGAATPSAGRPSVNAFPLLPTDPPRIGRWWLDARLVARPSGVAFLAHADG
QASTMLILLSRGAAGDAAARDRLAGEINRMSEETVIARGGQGQDQGRLAHLFVSQADDPV
GPGHAATAPWTVLAWDDSDNALREADRLLRSVDLSGSPELGTPSGPAFSLPWIGHSTPGN
WRLWPPSWPDRKDRTGWVPMLASWLLMILAATLALLIAVLIFQNPPPGGGGGGGASGSGS
ASGTGSASSSEGSGTEPSSGSPSGSGSGSGSPSSSGGQGSPTKTPSMNAPGQGSATTTQS
ATPQQSRL
>PFR_JS22-1_1355	PFR_JS22-1_1355	HAD-superfamily hydrolase, subfamily IIB	1553222:1554064 Forward
MTGTVPHEDIRLIATDLDGTFLGAGGRLVARNVEAVRAAAAQGITIVVATGRPYRWTDVI
DPLADIHPLLLSSNGAVIADPATGRVLHHWPIDPADGLAFGAALVRRVPDAGFAVEFASH
GWGADARYVAAHPEGEPDLVAPLADLMAFDDVVKLLALSPSTHTEALAAAAVEPAAGRVD
PTFSFVRDEGLVECSAPGVSKASALKVVMAERGIDSGQAMAFGDMPNDLPMLRLVGHPYV
MANGHRIMLEAGFPIAGYSDDGAMGAVIDRMLHIAGPRRP
>PFR_JS22-1_1356	PFR_JS22-1_1356	Mercuric reductase/transcriptional regulator, fusion	1554085:1555515 Reverse
MDANSVQPETRDYDVVVIGAGPAGENVAQYATQHSGLTAVLVEAELVGGECSYYACMPSK
ALLVPLEIANQADHMHGLEPERLSNEQLLKRRDHWVSHYRDAGQVSWAQGVGLDVVRGAG
RLIGDRLVQVDGAEPVVLRARQAVVIATGSEPVVPAVYQGIRAWGSRDATGVVEVPGHLA
IIGGGVVACEAATWMRALGSQVTMLVRGGSLLPKQEPFARELIAEGLRRQGIEVITGANV
SSCTRADPQDTGLGHIHGGPVTLHLADGSGPELVADELLVATGRRPELGNLGLDAVGLSA
QDITGGSTPEWLYAVGDASGGALLTHMGKYQARVIGERIAARAAGRTPDAVPESVPVPQV
IFTEPQLAHTGLTEAQARAVGIDVAVTAVDYNTVAGASLLRDDLVGRANLVIDRARKVMV
GATFVGPEVGELIHGATIAVVAATPIPLLRHAVPSYPTASELWLRLIEALPEEVLH
>PFR_JS22-1_1357	PFR_JS22-1_1357	Predicted metal-binding protein (DUF2284)	1555924:1556565 Forward
MLSYAVHEHHRCVPVDDYTRDFVDVPRFVEFCRACPQHDQTWACPEFDFDPRDVWARYSW
IHLIAFSMDFDPDQRRTGWERDELTREVMDTFHREKKRALRTMIRLRNRVPGSQVLGAGS
CELCRVCTRQQGRPCRLPQLLVHSMESMGADVEATSRELFDHPIEWSDGTSLPDSYVIVM
GLVCNQPDLPPDAWGTPRHGVAARPSARAVKAQ
>PFR_JS22-1_1358	PFR_JS22-1_1358	TIGR00245 family protein	1556573:1557331 Forward
MSVNPSWQLLAALILMVAMSVVASRIGHFKMGRGMAWAAVRAAIQLFVVSAIIVAAIAHL
WSSALFVGAMFAIAVWTTTGRVGTRNAWAWSALAMASGVIPLLIIVFATGTAPLNGYSLV
PIGSIFVGNMMTGHTLNGRRVFPALRDNIATYEAVLSIGLPRSNAIGMVLEPITGEAIVP
ALDSTRTVGLVTLPGAFIGVLLGGGSALQAGAAQLLVLVGIVAGQAVTVMVMNAFIRRAL
LLPRDLRARLRP
>PFR_JS22-1_1359	PFR_JS22-1_1359	Putative dGTPase	1557348:1558493 Reverse
MTDNVHDLDVTKRTRQWALTMAGHEHELGGDEVVRPHRDSHASIRPGEVIDRITREQREA
ATLRQGATLAHGAGNRDRTEAPDALRTCFERDKDRIIHSTAFRRLAGKTQVVVYPTDHQR
TRLTHAIEVAQVATSIARGVGANVTLAEAIALGHDCGHGPGGHASEEAFDVFLPEGFDHG
PWGAHVALADLNLCHETLDGIANHSWSRPAPATIEGEIVSWADRIAYCAHDLEDAIHAGI
IRADQVPGTVHEALGVRLSQQLDALIGAVVTTSCRTGAIGMDTSTADALAALRRFNYEHI
YTRPESLAQSHTMIRVLQELVSFYFSHQDRLPPDHRDPDDPMLGVVTYVAGMTDRFAFDQ
AEQLLGWQRGRLPQGVGHGAD
>PFR_JS22-1_1360	PFR_JS22-1_1360	TIM-barrel protein, nifR3 family	1558544:1559731 Reverse
MRSAYYGAVAQIQPLTLVSPSGGVVQIDTPVVLAPMAGVTNAAYRTLCYEQGAGLCVCEM
ITSRGLVVGNVKTDSMLTFFDDEPHRSVQTYGTNPRVLARAIDELCTHYRADHVDLNFGC
PVPKVTRKGGGGVLPWKLDLIREIIRQSVRAADAHGVPLTVKTRVGIDDDHTTFLDVGRI
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CAGVEIGRGCLGRPWLFRDLAAAMHGQQVQTLPTLGEVAAIVRRHGELLVRQMGVKHGLT
DLRKHMSWYFKGFPVGGELRHSLGLIDSFEALDALLARLLDKAGADCPYPTRELGRPRGR
QGTPRHKVVMPYGWLDDRGGLDLDLSDAELAVSGG
>PFR_JS22-1_1361	PFR_JS22-1_1361	Succinate dehydrogenase/fumarate reductase iron-sulfur subunit	1559808:1560566 Reverse
MKVTLDIWRQAGPRAKGEFENYVVNDAEPEMSILELLDRLNDQIIEQGGEPVVFESDCRE
GVCGCCGFLVNGKPHGPLANTPACRQHLRAFPEVTHFKLEPFRSNAFPVIRDLAIDRTAL
DELIQAGGTVNVMTGTAPDADTSPQPHQVAELALDFASCIGCGACVAACPNGSAMLFAGA
KLAHLAKMPQGKEQRSSRARRMVAELDEDFGPCSLYGECAISCPAGIPLTAIATVNKERW
RSVFRGRHSQDN
>PFR_JS22-1_1362	PFR_JS22-1_1362	Succinate dehydrogenase flavoprotein subunit	1560563:1562647 Reverse
MNIIKNLFSGAAGKAASTPSAPKPARASAHRPASHLTGEAARDHLGPAQKAAGYEVGAEI
DGHVPAGDVLHTWEHRQDDYRLVNPANRRKMKVIVVGSGLSGAGFAASFGQLGYDVDCFC
FHDSPRRAHSVAAQGGINAARARKVDGDTLKRFVKDTVKGGDYRGREADVVRLGTESVRV
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KMHNRTEMLDLIVKDGRAQGIVTRDLLTGEIKAWTAHVVVLCTGGYGSVYHWSTLAKNSN
ATATWRAHKQGAYFASPCFLQFHPTALPVSSHWQSKTTLMSESLRNDGRIWVPKKAGDDR
PANDIPENERDYYLERKYPAFGNLTPRDVASRNARTQIDSGHGVGPLHNSVYLDFRDAIK
RLGKETIAERYGNLFDMYLDATGENPYEVPMRIAPGAHFSMGGLWVDYDQMSNLPGLFVG
GEASNNYHGANRLGANSLLSASVDGWFTLPLSVPNYLADYVGKPPLAVQDPAVKDALGRV
QDRINAFLTSKGTHRPEWFHRKLGDILYAYCGVSRDEAGLTKGLAEVRALRKEYWNDVKV
VGDDHRLNQELEKAGRVADFIELAEVMILDALDRRESAGAHFRTEYATSEGEAKRNDADW
CAVSAWETRPDGVHVRHSEPLEFSLIDLQVRDYR
>PFR_JS22-1_1363	PFR_JS22-1_1363	Succinate dehydrogenase cytochrome B subunit, b558 family	1562644:1563399 Reverse
MSVGLTTSGGQGDVVTRHKLKQRPSNVTLKVTMAVTGTIFALFVFVHMVGNLKAFMGPED
YDAYARFLRTLLYPLLPYEGGLWIFRLVLSACLVLHVWAGITVWLRGRKARGKFGRYGAK
PKSFFARTMILSGLLILVFVVVHLLDLTIGAGLSSQYYQPAVHLGGDQVQIHAYENLVAS
LSRPWMAIFYSVIMVIIGCHIGQGAWNTINDFGGTGPRLRKVWFLIGLLIALAIVVANGA
LPMLILAGVIS
>PFR_JS22-1_1364	PFR_JS22-1_1364	NUDIX hydrolase	1563647:1564399 Reverse
MTTQAPDQPPVARFRHEVLAVVFRALAQAGTRLEVMAWRRHRAPFKDEWALPSGPVNAGE
TMDQAVQRHLAARLDLTSIRYSEQLATFSDPGRDPFERTIASAYLVLLGQSGPVPGGAAE
WLDTRALPPMAFDHAAVVQAGIRRLRSKMSYTNIAFALAPDEFTLKELRDVYVGVLGHDV
DVTNLGRVLTRRGQIAPTGRRRRSGSGGGRPARTYRFVEAAYEVTDPFATLRPAETPLPG
QAAGEGKATR
>PFR_JS22-1_1365	PFR_JS22-1_1365	Quinolinate synthase A	1564466:1565446 Forward
MTDTAISQDLWADEIHDLARSRDAVILAHNYQSPQIQDVADHVGDSLALSRIAAEATAST
IVFAGVHFMAETAKLLSPDKTVLIPDANAGCSLADSITAEQLRAWKAEHPGAVVVSYVNT
TAEVKAETDICCTSSNAVEVVASIPEDREILFCPDQFLGAHVRRQTGRENIHVWLGECHV
HAGISPDELIARVHDHADAELFVHPECGCTTTALWLAGRGDLPAGRTKVLSTGGMLDAAR
TTQAPEVLVATEVHMLHQLRQANPQATFTPVNPRATCPYMDMITPQKLLDCLRGGHDEVT
IDPAIAERARASVERMISIGNAGRGE
>PFR_JS22-1_1366	PFR_JS22-1_1366	L-aspartate oxidase NadB	1565443:1567125 Forward
MTMGTSTQGAELAHGTPAWHDDATVVVVGSGAAGLMAAVELAGAGVDTMVLSRGRVTDSS
TDWAQGGLAAVWSDQDSPDLHVSDTLTAGAGLCAEDSVRILVNEAPAALRRLIELGAVFD
KDRTGGIDLHLEGGHHARRILHAGGDQSGHEVERTLVQCVADAVDGPLSVREGVRAVDLL
VDAQGRCNGVRALDAQGRLGEVRAASVILATGGIGQLWTTSTNPPVATGDGLAMAWRAGA
VLSDLEFMQFHPTILVVPADHRIPGDRGVLISEAVRGEGAFLIDHRGTRVMAGLHPLADL
APRDVVSAAEHAHMARTGERNLFLDATAFGAQAWEHKFPSILAMCRERGVDPVTEPIPVR
PGAHYHCGGVRADMDGRTSIEGLFAIGEVACTGVQGANRLASNSLTEGLTMGRRVARLIA
TGKGVPTGPASGGDAARRQLPPQDPALFDAVRRTMTAAGSVLRDARGLDNARRALADRAT
PAGTLTNATLDATNAAQVAELLLAAAALRRESRGSHRRSDFTERSAQWQCHQDWSLDAHG
LPEMTIRTIGHEQAPERSAA
>PFR_JS22-1_1367	PFR_JS22-1_1367	Nicotinate-nucleotide pyrophosphatase nadC	1567122:1568042 Forward
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MSPDVAVGQQRIDPGDVPGALRDAGLEPEDVGATIDRALDEDLAYGPDVTTEAIFDPADR
ATAWVASRQDGCLAGLPVAAAAIHRLAARQGTTARVTLLAHDGQRVHPGDRVLLIEASLR
CLLTSERTMLNLLGQLSGVATQTARWADALAGSRAVIRDTRKTVPGLRTLQKYAVRCGGG
QNHRMGLGDAALIKDNHVAAAGRIAQAIRAVQSHAPQVACEVECDTLDQVREAVGAGAHL
VLLDNMAPDVMRRAVAICRPAGVRTEASGGLLLADAPAVAPTGVDYVSVGALTHSSPVLD
LGLDMD
>PFR_JS22-1_1368□PFR_JS22-1_1368□Glycyl-tRNA synthetase glyS□1568167:1569555 Reverse
MAESKLDKVINLCKRRGFVFPCGEIYGGTKAAWDYGPLGVELKENIKKQWWRYMVTSRGD
IVGLDSSVILPREVWVASGHVAVFNDPLVECQNCHKRFRADQLQEEYAFRKGIADADTVK
LEDIPCPNCGVRGKFTESRDFNMMLETYLGPIHDEAGLHYLRPETAQGIFINFKNVLTST
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VGLGIEEDNLRLFEHPKEKLSHYSKRTVDIEYKFGFAGSDWGELEGIANRTDFDLKTHTE
HSGTDLSYFDQAQNKHYIPYVIEPAAGLTRSFMAFMVDAYTEDEAPNAKGGVDKRTVLKI
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VTIDFDTFDDDAVTIRERDSMAQERVPLSGVSEYLSSRLLGC
>PFR_JS22-1_1369□PFR_JS22-1_1369□Metal transport system ABC transporter substrate-binding protein□1569788:1570735 Forward
MNFTPRTRLSRWAVGLVLGALIVPLAACSTPSSSSSASAGKLNVVTAFYPFEFVSQRVAG
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RIAKVQDLAKQNNVTTIFYETLISPKVAESIAGDLHLKTDVLDPLEGITDKSRGSDYLQV
MDSNLTALKTANGCS
>PFR_JS22-1_1370□PFR_JS22-1_1370□Metal transport ABC transporter□1570830:1571618 Forward
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GGTAELFGTPLSQFKDWNRLGYVPQRGHSQVANATVREVVATGRLANRHFFSRMHKQDRD
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ARLFERLKSDGLSMLVILHELGPMERLIDRSIMIQLGHKIYDGPLMAGPAIDSGHHHPAP
IGADQAVISGPEMRRPHLTKEA
>PFR_JS22-1_1371□PFR_JS22-1_1371□Metal transport ABC transporter□1571620:1572627 Forward
MSVFALAFMQRALIAALLSGFMSPAVGTYIVQRKLSLLGDGLGHVAIAGVGLALLTGWAP
TPVAIVICVVGAVSIELLRQSGRAPADVGLAILFYGGLATGVLLAGISGQGTGVLSQYLF
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SVTVAVSMRTVGLLLVSALMVVPVAAANNLVTGFYRSMFTAIGIGVVVSFIGVTGSYYWN
TASGATIVVSAIAVFALSWPVGSLLNRRRLARSQRIPDPETARDNAAEVAAHRPVDPSEL
VGDDGNHPRIQHGDHVDYLHGNHRHAPHGDHFDEH
>PFR_JS22-1_1372□PFR_JS22-1_1372□Fe(3 ) uptake regulation protein□1572593:1573105 Forward
MPHMEIISMNTERDPGPEQETTPAAPRSTMGREEAPRPRPRQTKQRQLISRMLENQSRFR
TAQQLHADLRAAGDSASLATVYRVLQSLAEHGEVDTWRTPGGELAFRHCSPTHHHHLICY
RCGRTVEIDAGPAEQWASRVAAENGFIHAEHQVEVYGLCPQCAAEIGEGH
>PFR_JS22-1_1373□PFR_JS22-1_1373□Phage integrase□1573358:1574032 Forward
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RPFTRAELEVAWVQWSALDPRLADTVLVLAHTALRWDEARALTVDDLVPHAHQIIVRAHC
PGRVRRPLAPALHRRVPVSLRIRQALRRLASTPGPRGLVFTDPDGAPLRRATVRRVLDWY
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>PFR_JS22-1_1374□PFR_JS22-1_1374□CoA-dependent propionaldehyde dehydrogenase□1574246:1575655 Reverse
MTISPELIQQVVRETVREVISRQDSGTDAPSGTDGIFTDMNSAVDAADVAWRQYMDCSLR
DRNRFIQAIRDVASEPDNLEYMATATVEETGMGNVPHKILKNRYAALYTPGTEDIITEAW
SGDDGLTTVEFSPFGVIGAITPTTNPTETVINNTIGMLAAGNAVVFSPHPRAKKITLWLV
RKINRALAAAGAPANLVVTVEEPSIDNTNAMMSHEKVRMLVATGGPGIVKAVLSSGKKAI
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CFELKDRAVMDKLAALVTKGQHANAAYVGKPAAQLASEVGLSAPKDTRLLICEVPFDHPF
VQVELMMPILPIVRMPDVDTAIDKAVAVEHGNRHTAVMHSSNVNALTKMGKLIQTTIFVK
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>PFR_JS22-1_1375□PFR_JS22-1_1375□PduO□1575652:1576737 Reverse
MAAIYTRTGDKGTTGLFGGTRVPKQDPTVEAYGTLDEANATTGEAKARVEDPDMRAALQH
IQQRLFVAAAELASDEAGRAVIANTISPDDVADLERLIDDSMAETGPQRNFVVPGRDLVS
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GAELHGIQNSNDGRVVVFGGGLPVFVDGVLCGGIGVSGGTVDQDVTIASFAMSRAKEASR
S
>PFR_JS22-1_1376□PFR_JS22-1_1376□Propanediol utilization protein PduN□1576740:1577012 Reverse
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SSARFAADRKDAPIDSTIVGIVDTVEIGPA
>PFR_JS22-1_1377□PFR_JS22-1_1377□Ethanolamine utilization flavoprotein□1577014:1577898 Reverse
MNPDQLRAIIRQTLVELLAPAPRRALVVFTGGLLGFDECLGGLRALADEGVALDVVQTPS
ARRILDQHKIGALGLPQVDDHLVANHQMLIAPTLTANVAAKVSHGIADCLASNLFSEFIM
SNRLVVASSTAVSPDEAPKRSIYPEMPSGYAELLRANLTALTSFGVRLARSQALARTALA
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GPVTGAPSTLKLISQGVVQKLDPGSCLAIRPDTKVTAAARDMAASRNIQITVVV
>PFR_JS22-1_1378□PFR_JS22-1_1378□Ethanolamine utilization protein EutJ□1577895:1578752 Reverse
MAMTGMVVTTHVELPEQAIMRFAEQVRTGAIDEPTGQMRLGFDLGTANIVVAVVDAANHP
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>PFR_JS22-1_1379□PFR_JS22-1_1379□Propanediol utilization protein PduJ□1578899:1579177 Reverse
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>PFR_JS22-1_1380□PFR_JS22-1_1380□Propanediol utilization protein PduK□1579222:1579839 Reverse
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AAAERALDPADPPRDAEPAAPTTDPAPAPDPAPAGPVADDPAATAPAVPSQPKISPSQER
PDKGTAGPSRNRRKAPQAGREAGKK
>PFR_JS22-1_1381□PFR_JS22-1_1381□Glycerol dehydratase reactivation factor DhaG□1579856:1580200 Reverse
MNTDKPTINMRVSDQITADQIADICFGMEEEGVPSTVTWQASINPLELAHEASVESRLGV
GIGVALSYAVITTEKLPAERPYIAVNLSRDAARNRAIGANAARLVKRIPLLPMN
>PFR_JS22-1_1382□PFR_JS22-1_1382□Putative dioal dehydratase-reactivating factor, large subunit□1580197:1582011 Reverse
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EAGR
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SGRALSDFTFDKVKSGELTAKDFRIAPETLEMQAQVAESADRDALARNLRRAAELIQVPD
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>PFR_JS22-1_1384□PFR_JS22-1_1384□Dehydratase medium subunit□1582589:1583272 Reverse
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>PFR_JS22-1_1385□PFR_JS22-1_1385□Glycerol dehydratase large subunit□1583283:1584944 Reverse
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>PFR_JS22-1_1386□PFR_JS22-1_1386□Propanediol utilization protein PduB□1584959:1585768 Reverse
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QAIIAARATGLELLGAMGDVPTSTTTPYI
>PFR_JS22-1_1387□PFR_JS22-1_1387□Carbon dioxide concentrating mechanism/carboxysome shell protein□1585783:1586067 Reverse
MQDALGMVETKGFVPAVEAADAMVKSANVTLIGSQRVGSGLVTVLVRGDVGAVKAATDAG
AVAAQNVGELVSVHVIPRPHADVEKILPSFADQK
>PFR_JS22-1_1388□PFR_JS22-1_1388□PduU protein□1586394:1586735 Forward
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LVSVGKKNGYGHPAAATLELLMRQQMTIMRTDEQGALAVARHSDRSLQVVSQR
>PFR_JS22-1_1425□PFR_JS22-1_1425□Putative competence protein ComEA□1623663:1624574 Reverse
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TVNINTANAAALDQLPGVGPVTAEKIIAWRTQHGKFTRVDQLREVDGIGAKSYERMKDSV
TVG
>PFR_JS22-1_1426□PFR_JS22-1_1426□Malic enzyme, NAD binding domain protein□1624759:1626513 Reverse
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EELGLIGLLPPGVTNVYDQVKRIYRQYKTEPNPMARYVFLTALKDRNEVLFYRLVSEHIE
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>PFR_JS22-1_1427□PFR_JS22-1_1427□Dihydroorotase□1626531:1627823 Reverse
MSELLLHNVDLLGEGLGDLFVRGERLADPAEASSQVPTVDCSGLIALPALVDPHTHLRDP
GQGNAETIATGLQAAVRGGYGAVFAMPNTDPVADSAEVVEYELDTARQVGICDLYPIGAV
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YDPGRHFSLA
>PFR_JS22-1_1428	PFR_JS22-1_1428	Leucine--tRNA ligase (Precursor)	1627880:1630408 Reverse
MSQGEPKHDAATVSEERSGYDAPAAEAKWQKYWAEHETFKASDAPDDKRQRRYVLDMFPY
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VTMVVQVQGKVRAKLSVSPQITEQQAIEAAMADSNVQRALNGRPVVKTITKLPRMVSLVP
GK
>PFR_JS22-1_1429	PFR_JS22-1_1429	Hypothetical protein	1630725:1631783 Reverse
MAETLPGDGRAAHTAGMNDHEVHLHITTPDELVALIPYWLGYHPHDNVVILAERHGRVEL
GCALTTDQVGQADVLADLADMLSTRVGDAMLMVVGYGPARSTDEAVACVEIALGAQQIDI
SLVVSDRRFWVRSAGERVEWSPGHRFDPRASVAATAAVSAGLQVLGGRDQVSALVAGPGA
DDRAIADAWRTARQQASAWSPGQREEFLDDCLTRSVDHAEDLSRDELTQLGALVQCLELR
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VDPDYSMLAVLREVHDLAVPPSMWKRMGRDRRDRHRRLRQPAPPVIADPQAS
>PFR_JS22-1_1430	PFR_JS22-1_1430	Hypothetical protein	1631952:1632692 Forward
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SRTDTPAPETPPPAINRFQVRSARGPVVLVVVVALIIVAVLVTLAVRSPKQGAQAASPSP
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LGFSFFALDTDGGSNQYKASGALATGTVTAGGTTTGRVHFNKSHQTTLVILANSYGRQIT
ALTVDA
>PFR_JS22-1_1431	PFR_JS22-1_1431	NADPH-dependent glutamate synthase beta chain and oxidoreductase	1632995:1633915 Reverse
MQTALGANGQIAEELTRELHRNVTHDIRLVSRHPRAVHETDELVSADLRDTRATADAVAG
SDVVYLTVGLPMDSAMWQEQFPVMMGNVIAACRQHHCRLVFFDNTYMYPRTAAPQTEQTP
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QQLVEG
>PFR_JS22-1_1432	PFR_JS22-1_1432	Hypothetical protein	1634030:1634467 Reverse
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PLYQQLGLDSVGFELLDHQQLSATVVLVHVRWLFLDATGELLTDAVSYYLLRADDDGLRA
YVCIETDSAEKLAELAERQGITLPR
>PFR_JS22-1_1433	PFR_JS22-1_1433	Phosphoglycerate mutase family protein	1634527:1635135 Reverse
MSAPTRLVLWRHGQTDWNLAGRFQGQTDMPLNVAGLSQAEAAAGHVAALGPEAIVSSPLR
RALETADTLAELTGLAVTTDDRLQEINVGQWSGLRAAEVFAQDEIARFRATGQDFRYSPT
GETRCEVGERVAPALREIAAAHPGQTVAVVSHGVAMRMGAARLCNIDYQGAQDLGTMANC
AWSILEPGQGRWHIVDWNVSAS
>PFR_JS22-1_1434	PFR_JS22-1_1434	Ribosome-associated protein, iojap family	1635135:1635518 Reverse
MSATEHAVEMTRVAAEAALGKLGEDLVAFDVSEQLAIADVFLIVSGHNERQVGAIVDAIQ
DALIDRGEKVLRREGQGGNHWVLLDYGDLVVHVFRTDDRANYALERLWRDCPEIPLPQET
PTAREQN
>PFR_JS22-1_1435	PFR_JS22-1_1435	Nicotinate (Nicotinamide) nucleotide adenylyltransferase	1635515:1636285 Reverse
MTQGRSESASDDEEAGLNLGLVRANTWRRYRLGVMGGTFDPIHHGHLVAASEVAARFDLD
EVVFVPTGVPWQKAGRRVSKGEDRYLMTVVATASNPRFTVSRVDIDRKGNTYTVDTLKDI
RRERGGNLDLYFITGADALASILTWRGASELFDLAHFVGVTRPGVNLGQRDFSHLPSDKV
TFLEVPALAISSTECRNRVAEGLPLWYLVPDGVVQYVAKRGLYDANDGDVLVLDEPVDER
GYTTGTDEPGSDGSNS
>PFR_JS22-1_1436	PFR_JS22-1_1436	Gamma-glutamyl phosphate reductase 2	1636359:1637603 Reverse
MVEVYEIASRARTASRTLATLTRERKDAGLRAMAAALEQSSDQLLSANARDVEAAVAAGT
PDAMIDRLSLNPQRVSGMAQGLRDLAGLADPVGQVVRGWNLANGVHVDQLRVPFGVIGII
YEARPNVTADAAGICLKSGNASLLRGSSSALESNRAIVTALREGLVRADLPADAINLVEG
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VLVNASSRFVDGGEFGFGAEIGISTQKLHARGPMGLQEMTTTKYVLTGQGQTRH
>PFR_JS22-1_1437	PFR_JS22-1_1437	Hypothetical protein	1637610:1638278 Reverse
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NVWACNIVVLCCAAIILIVICRDRKLSWNVWVLSVLVAGALVTVDSVFGAVAYGMLIIVP
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LCLGLYMVKRAGVQLPGLPATSPPCPPAERQMGHGLAPWGPL
>PFR_JS22-1_1438	PFR_JS22-1_1438	Glutamate 5-kinase ProB	1638311:1639480 Reverse
MTDQVPSVVPALDTEESVRAAIGSARRIVVKIGSSSLSSARRGLDDARLAALVAALADVH
DAGRDIVLISSGAIAAGLKPLGLTRRPRDVAHQQAAAAVGQGLLIERYTEMFAHRDIRVG
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>PFR_JS22-1_1439	PFR_JS22-1_1439	GTPase obg	1639473:1641074 Reverse
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DYHHQSQRSATNGQPGQGKHRSGANGADVVLPVPEGTVVSDLDTGEVLADLTGDETEYVV
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MGDDRDADWRRIHAAELDKLRAGEGDDGEGVEVNWVGHDPNEDLESYTEGDDD
>PFR_JS22-1_1440	PFR_JS22-1_1440	50S ribosomal protein L27	1641223:1641486 Reverse
MAHKKAGSSSRNGRDSNAQRLGVKRFGGQVVNAGEIIVRQRGTHFHPGEGIGRGKDDTLF
ALVGGAVQFGTHRGRRVVNIQPVETTA
>PFR_JS22-1_1441	PFR_JS22-1_1441	50S ribosomal protein L21	1641500:1641847 Reverse
MPQAAARYRKWVSVYAIVRSGGRQHKVAVGDVLEVDKMVDEVGASVKLEPVLVVDGKDVT
SDKAGLDKVDVTAEVLGQTKGPKIHIMHYKNKTGYKRRQGHRQQYTRIKVTGIKA
>PFR_JS22-1_1442	PFR_JS22-1_1442	Hypothetical protein	1642044:1644830 Reverse
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PQDESPTDQP
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QGVDRSTMTAQTQHLEKRGYLVREPSQRDHRVIMVGLSAMGERIAQVLRAAGRSAFGRAM
GDWSPQEREMLDRLLSRLLAGLERSAQGDPG
>PFR_JS22-1_1445□PFR_JS22-1_1445□Integral membrane protein TerC□1646570:1647826 Forward
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TEMGSEYFAGYITEKALSVDNLFVFLLIISSFAVPRKDQQKVLLVGIVFSIIARTGFIFL
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FLAANP
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>PFR_JS22-1_1450□PFR_JS22-1_1450□Protein FolC□1652931:1654436 Reverse
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DLFRDAHGGAQAGLKAVWLDRIGEDGTPDSEHQVRSGDQAVPMIGGLDQLDVRLP
>PFR_JS22-1_1456	PFR_JS22-1_1456	Phosphofructokinase	1660709:1661830 Reverse
MSMRVGILTSGGDSPGLNAAIRGFGKAAVSTYGMELIGFRDGMRGLAENRFMQLDSHALS
GILTTGGTILGTSRDKVHKMLVDGKVQNMIPVIKKNYEKNKLDALVCLGGGGTAKNAKRL
SDAGMNVITLPKTIDNDLVGTDQTFGFATALEIATDAVDRLHSTAHSHHRIILTEIMGHR
AGWLALGAGIAGGADVILLPEVPYNVESIAAAISRRSAHGSNFSVVAVAEGARNERDAAE
LAAADALVREADSPVARDAAKTHRANVEASHRAHTFTLATELEKATGLESRVTILGYVQR
GGTPCGRDRVLATVLGTAGADLVAKGVFGVMVAAKGDGAEPVPLEEVAGKIRRVPVDHPW
IRAAKEVGTGFGD
>PFR_JS22-1_1457	PFR_JS22-1_1457	Threonine synthase	1661909:1663351 Reverse
MRYVSTRAASADASEPFSDILLEGLAPDGGLYLPVTYPRVDAQTLTRWRAVLAEQGYAAL
AAEVIGLYIDDIGHDDLLELCRRAYTAEKFGDPQIVPVTRIGDEPLWLGHLSNGPTAAFK
DMAMQLLGEFFEYELRRRSSWLTIVGATSGDTGSSAEYAMRGRDGLSVVMLTPAGRMTPF
QQAQMFGLQDPNIINVAVDGVFDTCQDLVKALNADAEFKHRWHVGAVNSINWARLVAQVV
YYFACWLRVTTSADEQISFAVPTGNFGNVCAGHIARSMGLPIKRLIVATNENDVLDEFFH
TGRYRVRGAVETVATSSPSMDISKASNFERFIADLFGRDGATVRRLFDQLARTGEFDISG
TAQFTAVIQQYGFVSGHSSHADRLATIKRLWTTDQILIDPHTADGVHVAEQFAGDEQIVV
LETALPVKFADTIKEATGELPPVPPRFAHIGEGPRRVIEMGDDLGALKKLVADTVGTLRA
>PFR_JS22-1_1458	PFR_JS22-1_1458	Hypothetical protein	1663440:1663784 Forward
MNVAGRKIGPMPSFRVQFQVSGLRPGHRPDEVLEVARAAVVAPLHCDDVRLDMPAGVPTV
TVRFTIAGSHDADEDARARRHGAQITHQVSQVAVVSPPRVLRRRGGSWLPIPAL
>PFR_JS22-1_1459	PFR_JS22-1_1459	ATP-dependent Clp protease ATP-binding subunit ClpX	1663896:1665173 Reverse
MARIGESGDLFKCSFCGKSQKQVKKLIAGPGVYICDECIDLCNEIVEEEFSESTEKEQGG
ELPKPAEIVSFLNSYIIGQDAAKKALAVAVYNHYKRVQAQADSSSKHDDDVELAKSNILL
IGPTGCGKTYLAQTLARMLNVPFAMADATALTEAGYVGEDVENILLKLLQAADFDVKRAQ
TGIIYIDEIDKVARKSENPSITRDVSGEGVQQALLKILEGTVASVPPQGGRKHPHQEFIQ
IDTTNVLFIVGGAFSGLEEIIADRVGQGGVGFTNDSVKRQPVGLDPFAGVRPEDLHTFGL
IPEFIGRLPVITTVPRLDADVLRRILVEPRNALVKQFEKLFELDGVELELTDDAVSAVAE
KAVTRNTGARGLRAILEETLLDVMFEVPSHEEIGQVVITGDVVHGDAQPTMLTRAEIAER
HKLSA
>PFR_JS22-1_1460	PFR_JS22-1_1460	ATP-dependent Clp protease proteolytic subunit 1	1665295:1665984 Reverse
MTNNVTPGLILPTAGQSPVAPGGLATSPSAEYYIPQWEERTSYGVRRVDPYTKLFEDRII
FLGAPITDDVANAVMAQLLSLQSMDVDRPISIYINSPGGSFTALTAIYDTMQYLKPAVQT
ICLGQAASAAAVLLAAGAKGQRLALPNSRILIHQPAISGEGSYGQSSDLEIQAKEILRIR
SLMEQMLADATGQPVERINRDVERDKYLTAEEAKEYGLIDDILTSLKDS
>PFR_JS22-1_1461	PFR_JS22-1_1461	ATP-dependent Clp protease proteolytic subunit 2	1666008:1666643 Reverse
MNDIAKNPVLPSLAAGGASGFGLSDNVYQSLLANRIVFLGSEVKDENSNAICAQMLLLNA
EDPHRDIYLYINSPGGSIDSGMAIYDTMQWISNDVATVALGLAASMGQFLLSGGAKGKRF
ALPHARILMHQPSGGIGGTASDVKIQAEQSIHLKHEMAALIAGHTGQTVEQIEKDSDRDR
WFTAQQALEYGFIDHVYERASKISDTDAPNQ
>PFR_JS22-1_1462	PFR_JS22-1_1462	Pheromone autoinducer 2 transporter	1666730:1667962 Reverse
MQSDQDQFGTAGTSSQDDTGRTSPDVGGAATARAEDRPKKAGSSGATRSTSVAQGPFRGQ
PRWLPRMSVIFIAMIGIAGSIWLFRQLSWLLAPVFLGLNLVIAFYPIYSGLTRRKWPRAL
AAIVMALALLSVVILAVASMAWAVGTLIGAIPSYVPRIQAMYGDLMQFLVQHHISADAVS
GFYSRIDPNNVLSALTGVLGSISGSIGAGTVALTTILMLLVDSVGWKRRLGMVEVGHPRA
IGAIRDFAHGTRRYWLVSMVFGAIMAGLNAIELKILNVPLMGVWVVLTFITTFIPSVGFF
FAMVPPVIVALVVNGWQNALWLMAIYFVTTWIVQGFFQPKFTGNAVGVNITTSFISLLFW
AWVFGPLGALIALPATQLVKSLVLDADPKSRWVSALIAPEPSVVGADPQT
>PFR_JS22-1_1463	PFR_JS22-1_1463	Inner membrane protein YhhT	1668195:1669388 Reverse
MSQPEEAEPVIPDGATAAYALAEDDGTTVAGPTSPTQAAAPPTRSPGIPRYLQIAGGIVL
SLGALLLLKEFGSTFAPMFLALNLMVTAYPLHTWLVRKGCPSPLSAVTTALVVFVVLLAM
VAGLVWSVNETVTLLPQYADEFTGLFNWFIDRAAQLGFDQASLMQAFKSIDPNSIFSAAS
SVLNGASGFVAMLAILVTTLVFMAMDTSGFAARIRIAGATHSRMVTGLVSFSRGIRRYWV
VTSVFGLIVAVLDVIAVAIIGVPLPIVWGLLSFLTNYIPNIGFVVGLIPPALVALVALGW
KQALVVVVLYCVLNFVVQSIIQPRFTGESVGVTPTISFISLLVWGLVLGGLGTLLALPMT
LLVKALIIDTDPRARWVNAFIASNPGDAQGAAQQAEL
>PFR_JS22-1_1464	PFR_JS22-1_1464	Trigger factor	1669613:1671196 Reverse
MPSTVEKLNPTRVKLTIEMPFAELQPKIDAAYKQISEQVNLPGFRRGKVPARLIDQRFGR
GAVLQQAINDAIPDAYSKAVQDNELFPLGQPDIEVSKLEDGDVVELSAEVDVRPDFDIPD
FSGIKVEVEPAKVSDEDVNERVELLRERFANLKEVDRAAKDGDVVNFDLSATQDGEPVPD
AESNGMQYRVGAGGMVDGLDEALVGMKAGDEKSFSSKLVGGSHGGQDVDIKVTVNKVNEQ
ELPALDDDFAQLVSEFDTVDEMLADLRDNLERMARIGQANEARDKIVEQVVEKVPFELPP
AVLEADVKGYHDQIENQLNQSGLTLEQYLEEAEDEKADTPEEFWAEIDKRAEQGLRAQIV
LDKLAEEQNVGVSQEEFTQLILQKAQQNGTTPEQELQHMSEHNHMPEWMGEVRRGKALNT
IVDEAVVTDTDGNAVDLKHLQADGTIAEPAADEKAEDADKAEDAKADKPAKKPAAKKPAA
KATKAAASKAAPKADKKPAAKKPAAKKPAAKKPAAKKADEAPADDAK
>PFR_JS22-1_1465	PFR_JS22-1_1465	Quaternary ammonium compound-resistance protein SugE	1671932:1672246 Reverse
MSWIVLVVSGFLEAVWALALGRSHGFTRLVPTVVFALALVASMAGLAFAMRRLPVGTSYA
VWTGIGAALTVTISMLTGQEPVSAMRIVFLAMIVGGVVGLKFVA
>PFR_JS22-1_1466	PFR_JS22-1_1466	Hypothetical protein	1672374:1672565 Forward
MMLRAAVERAALRMAAVGWPISRTRSARSASTKGVMPSRPNSLGRASFDRPDLPRASADP
LSC
>PFR_JS22-1_1467	PFR_JS22-1_1467	Hypothetical protein	1672800:1674353 Forward
MRRQMEWHHLRLTAGSHAGSVTLSDAEDGRPLGTLTVDFPTPWVPGPATLDDDEFEWQWT
RDDQPADDATAPAHLSSTRPSSTDLLSSHQPSTRQPDSTRATVRISTQPGFSLRVALATH
AATVAVEPPTLLWTPPGPARRWVGGSSALLVLDDRPGDGLVTAAHLSHGQAWPDEAGTTP
PPSRTRTPGGSATHRIALGPPLLTLTPERGYSTTWVIERFASLMNATSTLPGWLPPDCTP
RAGEPLFIDLPDAAVTGDVEIVTDEHGTQLSAAGGTHDIGIHGPGIDSSFTITWNAGTDR
VLRDVAAAILGQVDPRTARGSDAALIDRADTAHLIPHDDAERFLDDFFQELSDAPPGNSI
APEATAALLHWAFADATRMAAALQRLDGLAPGPGPMLAWLSASLAARAAMLDFDATVPMD
PHDPLCGALHAILTRADSPTPAVWQTIGLLHGPLPGPLPDGDSVRTAQACAILALAPTNW
QVEQRLGASLAHEIEDTRAWLAASSPDGPTLSWLLWA
>PFR_JS22-1_1468	PFR_JS22-1_1468	Transposase, undefined	1674350:1674934 Reverse
MLHVDVKKLGNIPDGGGWRYVGRRQGEKNRAATPDKAKNKWRDPLMGKAYVHTAIDDHSR
VAYAEVHDDETAFTAAAVLVRAVEWFNACGVTVERVLSDNGGAYRSHLWRDTCAELGIRH
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KRTRPYRPQTNGKIERFRRTLSDGWAYARCYTSETERRGELEGWLHNYNHHRPHTACGNQ
PPFSRLTNVSGQYS
>PFR_JS22-1_1469	PFR_JS22-1_1469	Hypothetical protein	1675172:1675336 Reverse
MTHTNAALTPRHRLIVARLVVEEDWPVSEVAARFQVSWPTVKRWADRYRAGQSM
>PFR_JS22-1_1470	PFR_JS22-1_1470	Permease of the drug/metabolite transporter (DMT) superfamily	1675403:1676275 Reverse
MCVAFVVAWSSGFVGATLADRTGVGTWSLLAWRYLATALVLLVGCLLVPSLRHSFCALGR
REVLQQVILSVLSHVLFLGGVFLAAEEGLDAGLSALVCALQPLIVTVAGRIFFGDRVRIV
QWVGLLIALGGVSLSVGGISAAGVGSVGLVAMSLLGLSTASLLERSWNPQVPVTVSLTVQ
VSVAAVIFSGVALVTGGLALQVTGALVLAISWLVLLSGLGGYATFIWCLRHVGATTTSTL
LYLTAPVTMLWAWCMFGQQPSPLQWIGLAVVLSGVGLATRRTNHREQGTA
>PFR_JS22-1_1471	PFR_JS22-1_1471	Transcriptional regulator	1676354:1676920 Forward
MDIDLEVFEPVDTTPVGRRILDAAAELFRDHGITATGVDSIVEHAGTTKRTLYQRYGSKD
RLIVCYLQQRAHAWQGELLETLTDASPAQALDIVYQHTAQWATSTPRGCAFVNAWSEIGA
SDHEATKFIRAEKAWMLALFTQIASGDENTGTLLHLLHEGAQVTASIQGDPRVFAQACNA
SQELLVRR
>PFR_JS22-1_1472	PFR_JS22-1_1472	DNA ligase	1676988:1679282 Reverse
MTAHEDPDEDIPTGLDAAVTVKVAGVDQQRRHAELVKEIDDAQEAYYGRDKPFITDALYD
ELMLELQKLEAEYPSLRTPDSPTQRVGAPQEETDFSPLTHPSQMLSLDDVFSIDELKEWM
TRTEAALGHTPEWLCEVKIDGLAIDLQYVNGRLQTAATRGDGRVGENITPNARTIKAIPQ
RLRPDPAQDFLALFEARGEVFVPLKEFAAYNDKLADQGKPQFANPRNAAAGSLRQKDPRV
TAQRPLSSICHGLGVADGLAVTRQSDAYAVMKAWGLPISPYNKVVHSLDEVLDFITYYGQ
HRHDLIHQIDGIVVKVDSFAEQQQLGVTSRAPRWAIAFKYPPEEVNTRLLDIRVKVGRTG
RVTPYGVMEPVQVAGSVVSSATLHNAYEVERKGVLIGDMVVLRKAGDVIPEIVGPVVEMR
TGAERPFVMPTHCPSCGTKLASEKESDKDIRCPNSKSCPAQLRERLFSLAARSAFDIEAL
GYQGADAILRAGVLDNEAQLFNLTPEQLVTVPFYTRGATPRELKEPALVPPPGIRDGRVL
SANGRRLLENLRTARHQPLWRVLVALSIRHVGPTAARALAARFGSMDAIRAAGVEELADT
DGVGLIIAEAVRDWFTVDWHLEILNAWAADGVSMADEKSARPAQTLRGLTVVVTGSLQDF
TRDSAKAAITDRGGKAAGSVSRHTDYVVVGENAGSKQARAEQLGVPMLDEAQFRELLEHG
PTPASETPASETPAPETPAPETSAPTTRASGAPGTPPETRDRRS
>PFR_JS22-1_1473	PFR_JS22-1_1473	Hypothetical protein	1679359:1680153 Reverse
MDEVGRAIEDNDEMGADEQAGADYTPARRAIDPMAGAVARVTASYSARRAMPDPSSQLDW
DDFLRGGAAGYEAQRTVTGLRALIDRLLGRSNEEAARRLDQDADELLAQELLRLAALDPR
WGFLQLARSNSGLSALQHMVVGPGGVYLLNAKNHPGAKLFVEGDTFLVNGHDRPYVSFSR
VQASTARTLLSRDSGLDLGVTGIIVPVKDRRLTIQQAPDDVEVIERNGLAEWLLNQPEEL
NEHEVVKGFTVAREATSWRPRWSE
>PFR_JS22-1_1474	PFR_JS22-1_1474	DSBA oxidoreductase	1680377:1680991 Reverse
MSDSTQTVDFWFDPACPWAWMTSRWMLEVEKVRPVHTVFHVMSLAVLNEGRDLDAGYRKM
IDTFWQGARACIGVEQEHGPEALRNFYTELGTRYHLHDEPRGDIEVIRAALRAQGLDESI
ADKSDTDVYDEALHASHHEGMDPVGDDVGTPVIHMNGMALFGPVISPAPKGEQAGDLFDG
FSKMVAYDGFFELKRTRTREPIFD
>PFR_JS22-1_1475	PFR_JS22-1_1475	Aminopeptidase	1681334:1683937 Forward
MNPANLTRDETHARSAMLSVTSYRVSVDLTGGDGFGRALAEPDETFVSTSIVNFSTSGGD
TWIDLIADSVVSAELDGTRLDASTFTGVRLPFSAEAGEHELRINALCRYSHTGEGLHRFV
DPADQRVYLYTQFETADARRMYACFEQPDLKASFQLSVIAPSAWTVVSNSPTPPATATDA
PAFQRWDFEATAPISTYITALIAGEYFVNQGTITSTKGELGANIVCRQSVAQYLDADRIR
TTTQRGFEVYEEAFGRPYPFAKYDQLFVPEYNAGAMENAGAVTIRDEYLYRSKVTSADYE
QRDNTILHELAHMWFGDLVTMRWWDDLWLNESFAEWCSHFAQKRIVDRFGGIDPWVSFAN
AREGWAYVQDQMPTTHPIAADMVDLETVDQSFDGITYAKGASVLKQLVAYVGEQNFLAGV
REYLTEHAYANAEFSDLLGALQKASGKDLDGFAEQWLKTSGVNTLRAQVEVDDSGAFTRF
DIIQTAPVEHPTLRTHHIGVGCYELRDGQLVRTTSLELDVSGERTSVDALVGQPRPALVL
LNDQDLSYAKVRLDKQSLDAAIEHITELADPLARAVVWTCVWDMNRDAELTTDEYISTVT
RGIGSETDMTAVRTQLRNALGASKAYTPPAHREEANRALVAGIAAELEKAEAGSQHQLAF
TDALIGSVDSPEGITLIRGWLSNEEVPVGLEIDQDRRWAILSSLARMGAVDDDAIAAEEQ
LDKTISGSERAAGARAALNNAEEKARAWALATEDPKVPNATHLRICAAFVQYGQEELLAP
YVDRYLQVCELISAQQGIWATQGHAASQAVLTYLWPSPLADRAFIERVDKWVESSELSES
VRHVITERRDASLRAIAAQEFAASQLG
>PFR_JS22-1_1476	PFR_JS22-1_1476	6-phosphogluconate dehydrogenase, decarboxylating (Precursor)	1684150:1685607 Forward
MTQTAPSSQTKANIGVVGMAVMGSNLARNLAHHDYTVAVFNRTYARTQKLIAEHGNEGSF
IPSEKIEDFVNSIATPRSIILMVKAGAPTDATIDELLPLLSPGDIIMDGGNSYFGDTIRR
EKAIAAKGFHFVGAGISGGETGALEGPSIMPGGSPESYKILGPMLETISAHYHGDPCCAW
MGPNGAGHFVKMIHNGIEYSDMQVIGEAYELLRGVGLTNAECADVFAEWNKGDLDSYLIE
ITSIVLRQKDPRTGADLIDVIKDRAQMKGTGTWTVQTALELGVPTNGIAEAVFARAESSH
DDLRAAARKYLAGPDGTVSVDDRTAFIEDVRKALWCSKVVSYAQGFDEIRTGGQEYDWNI
NVAEAAKIWRAGCIIRAKLLERIRQAYTDDPDLVSLMAASSVSAEMEANQSAWRRVVSKA
AESGVPAPVFSATLAYYDMARAPRVNAALTQAMRDYFGSHTYERVDDHGHFHIEWTGDHS
ETRID
>PFR_JS22-1_1477	PFR_JS22-1_1477	Putative phosphomethylpyrimidine kinase	1685737:1686558 Forward
MTKIALAIAGSEASGGAGAQTDIKTFEQLGVFGATSLTCIVSFDPNNDWGHRFVPVDPQV
IHDQIEAAVAVHGHIDAVKIGMLGTPTTINVVAEALKEYDFDQVIVDPVLICKGQEAGAA
LDTDNALRAQVMPFATMTTPNLFETQILSGMDEITNVSQLKDAAKRIHDQGVPNVLAKAG
TLFDTGTALDVFYDGSTLEVLEVPAIGEERVSGAGCTLAAAVTAEIAKGATPLDAARTAK
QVVVSSIEHRMHGNAPFDCVFQGYYREPALATN
>PFR_JS22-1_1478	PFR_JS22-1_1478	Acyl-CoA thioester hydrolase, YbgC/YbaW family	1686705:1687586 Reverse
MASFHATIPLRWSDLDPQGHVNNVVVLDLAQEARARFMAGGSHPELLLHGSVVVKQRSEF
LRPMMLDGGPVEVELSTTSIGAARFIMSYRMVQRGELCVRAATSMCPFDFPHQRVRKLTA
GERDALATISAPDEPWSPLPAMRLDEHAVETAFQPRWSDQDRYGHVNNVRTLDWLQEARV
EATTAMAPQMARAGMVDAAQRLPGSWVVARQDTEYRHQLRWQSSPYLMRTGVLRVGASST
TLGCAIIDPDDRTAHVRARTVLVHAGANGRPEPLPADVREQLRSYLPTPGDGA
>PFR_JS22-1_1479	PFR_JS22-1_1479	AMP-dependent synthetase/ligase	1687592:1689481 Reverse
MNSVREEILSACPPSYPASFRARVARAPHAVAYRVPQHQEPEVWKDLTWSQVADEVDQIA
AGFIALGVQPEQRVAIAAMTRIEWVLADLGIACAAAATTTVYPNSQPDDELFILQDSESV
IVVAENWKQLQKVVDQSELNAQVHHIVLFDDDRPIDRADAGGDRVVTWDALHALGRDYLA
AHPTALDERLDLMEPDTLATLVYTSGTTGRPKGVRIPHRAWTYQGEAMHHMWRGIIDDRD
VVYLWLPLSHVYGRDLLAAQMAIGFIMPVDGRIDRIVEGMGETHPTIMVGVPRIYEKIRS
AVITQSPANGIQGRIARWAFAVGRESRPYRLAGKHAPWPARLRYAVADRLVFSKLRDTLG
GSIRFMISGSAKLSTQVQTWFYSAGLLVLEGYGLTETAAIAAVNLPDKPKFGTVGPVTPG
IDARIAADGELLLSGPIVADGYYHLPEETAEAFEDSWFHTGDIGHFDEDGYLTITDRKKD
LMKTSNGKYVAPQKVEAALLANVPYISQAVAVADGHPYVIALVTMDHDQLMRWGKNHGHP
NDDYATLSQLPEIRESIDKFVRKANERLDRWETVKRYAILDHEFAQDTGELTPSMKVKRP
VVLARYEKTIDDRYEQTTVSDLTPFTGGK
>PFR_JS22-1_1480	PFR_JS22-1_1480	Transcriptional regulator, MarR family	1689658:1690116 Forward
MSGATNPPWLTAEQQRIWRSCLAGVARIDSHLNLALAEFGLDLNEYEILVTLSESDDHSL
RMSDLAQRVYQSRSRLTHTAKRMEEQGLLRRERANDDRRGVVASLTDEGMALLVEAAPTH
VRSVRDILIDVATPDDLRALGRVMGAVLEVAD
>PFR_JS22-1_1481	PFR_JS22-1_1481	FAD linked oxidase protein	1690122:1692950 Forward
MSASVQSIPVNELSDRVDALRRELGSDDCLDTSTLTRALYSTDASVYRVVPTVVATPADT
DQLRHVVQAALAVGLPITGRGAGTSCAGNAVGTGIVVDMRRHLNKILSIDPDARTATVQP
GVVQDVLQQAVRPFGLRFGPDPSTSSRCTIGGMIGNNACGPRALGYGRSADNTISLDVIT
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GAGQELRVGPGESNDFPQLNELVESNLGMIRTECGRFTRQVSGYSMEHLLPENGRDVARF
LSGTEGTLAIMTQATVRLVADAPHKIMVALGYPTMVDAGAATPKILEFKPTAVEGMDSRL
ADLVATRLGPSAVPPLPRGEGWAFVEMVGDDPAELADKAQRLTRESDCLEGWVIDDPAQA
QRLWGIRSDAAGLAGVALKNPAYAGWEDSAVPPAQLGSYLADFEKLLEEHNLHGLPYGHF
GDGCLHCRIDFPFDQPGGTDRYHDFMIAAGKLVASHGGSMSGEHGDGRARSELLPLMYSG
DMIKLFGQVKNLFDPKNLLNPGVIVDPRPTDVDVRVAETINAPLRLSDPLFTRHVHQCTG
VGKCLANSTKAGGVMCPSYQATGNERDSTRGRSHVLQEMINGRLITGGWRAPEVAEALDF
CLACKGCRRECPTGIDMAAYKSRVLYEKFKHHLRPMSHYAMGHLPTWGRLVTKLHVGALG
NLFTQTPGLRHVVRAMAGVDQRRPMPKFRKGASARKDAAREIARREPQGKPVAIWADSFS
DAFEGNQLLGLVATLISAGYAPRMIEQDACCGLTWITTGQLDGAKAHLRKALDVLYPIAK
AGTPIVGMEPSCMAVWRSDAGELLEGDERVAEVAHATHTLAELLGKTEGWNPPDLSGHTI
VAQPHCHQSSVLGWAADQKLLERTGAKVVTLGGCCGLAGNFGVEKGHYEVSIKVAEHDLL
PAIDAAGPDAILLADGFSCRKQINDLRQRQALTLGELIAAHL
>PFR_JS22-1_1482 PFR_JS22-1_1482 Peptidyl-dipeptidase Dcp 1693071:1695107 Reverse
MSSSLPLQSEFELADFAALAPGDYEQIVHDAMAAELSGLRLVSDNPEPATVANTIEAWER
AELALSRATAAFFTLHDADTSPELDAVAERLSSELAAHHDAIMLDAGLYDRVRDLSQAVE
AGAEPGDEQVTWWLHERLRDFRRSGVALSPEDQERLRVLNARIARLESQFGQRVVAGRNE
AAVHITDPAELAGLSEEQRTEAERAAGARDLDGWLLELVNTTGQDWLASLSHQEVRRRVF
EASMSRGATGGNETGSLVVQLARVRADRAALLGYASHAAYVADGGCAKTVDAIRGLLDPF
SKLSVHQASEDSLRFREIFTDLAVGKEFGPWDWSWVASRERARAELDDEALRPYLEFEQV
LTRGVFEAAHRLYGITVERREGLTGYTPDVRVYEVHEQDGTVLGLLLLDPWARPSKQGGA
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PSLAGTNTPIDYVEFPSQVNERWARDPELLAHYARHWRTGEPLPSDLVGALVNTDQGNVG
FDDLELVAAMQLDQAWHSSSPEQLPTQPGQVDAFENEALEERRVAFVLVPPRYRTRYFSH
IWTTGYDGAYYAYLWAEVFDADASAWFDEHGGLDRAAGERFRREVLAPGGSVDVMADYRT
FRGADPDVKYLLARHTRG
>PFR_JS22-1_1483 PFR_JS22-1_1483 Hypothetical protein 1695164:1696534 Forward
MPTLGLTEAIRTMPDGTVKQVNPLSGVEVWTVPGRGNRPLATPVNDPRALSADDFGHSCA
FCADRMAETPPEKARRVHGADGWQTLTGVLPEHLHDTVAEFRRIPNLFEIVGYPYWVANY
DYKPSPAAMARYRAYRNDAGGREHLLAISRTKLAASGLAPAQVRATPDDELLDDAIGFFA
GGHDVIVARRHFVDGATDSSQLAGSGALSPDEHAEYMRFTVDTLADLYRQNRYARYVAVF
QNWLRPAGASFDHLHKQLVAIDQHGTQAAGEVERLRSNPNIYNDLLLGTAVQHNLVIAEN
DSAIVFAGFGHRYPTLEIYSKSATCEPWNQSDKELDDMSALVHACHAATGMDVPSNEEWH
HRAPDMDVPMPWRINLKWRVSTLAGFEGGTKIYLNTIDPWHLRDRVVPRLHALRRQGRLA
DNILLDIECPAQYNSLMYNPLLQRRDTNRDRPIRIR
>PFR_JS22-1_1484 PFR_JS22-1_1484 Dihydroxyacetone kinase subunit M 1696521:1698041 Reverse
MIALLVVSHSRPLAQAAVELAVQMVPPDQRPPIRIAAGLDDGSLGTDATAVSAALEELAG
ADGVLVFVDLGSALLSAQMALEFVDPDLAARVVISPAPMVEGLVAGVVTAAGGAPITRVD
AEARSSLNAKIEQLADESPSRDTAPSADGLPSKDSTPAVAVGAGGPTQADGHRLVWDYTM
TNVHGLHARPAAAVVSALSGLDARVVISNATSGAGPADARSVSSLAALQLHQGQVMHVEA
SGAAAPQARQALDELAARQFGDATNGNPSEAGNTPGRASEGERPQQDASPAPVATAVVEG
PVHIIDPDPDVAGYRAGSAAIEQARFDQARHHVAGYLDDQASGPFAAIFNAQKALLNDAS
LRTGVSSAIDKGASSIEAVSATMAGLSASFDKLSDPYLRERGQDVRSLDRLLRSAIVGAS
LRWPREAPAGVWVLPELDALSAATADTARCRAIITLRGGDTGHGAIIARQRGIALLLGYP
DAARFTEGQEIRVDTVARRARPVNES
>PFR_JS22-1_1485 PFR_JS22-1_1485 Dihydroxyacetone kinase, L subunit 1698054:1698683 Reverse
MGDERVTKVAAWLHDYADTITEHSQELTDLDREIGDADHGFNMERGVKAIAALDPAQFAD
PGAYLKKVGMTLVSTVGGAAGPLYGTLFLRMATALPTDTALTTATFAKALRAGLEGVTQR
GKSAVGDKTMVDALAPAVERLEADAAAGDKLANALKHASTAAQQGRDATVDLVARRGRAS
YLGERSKGHLDPGAASLTMLIESAARTLS
>PFR_JS22-1_1486 PFR_JS22-1_1486 Dihydroxyacetone kinase, DhaK subunit 1698683:1699678 Reverse
MKKLINDAEHVVADSLRGVAAAHPGVQRVDLDNKIVYRAQPKQAGRVAVISGGGSGHEPL
HSGYVGEGMLDAACCGEVFTSPVPDQMVAATKQVDNGAGVLQIVKNYTGDVMNFDMASEL
SQADGIDVESVIVNDDVAVEDSLYTAGRRGVGLTVLLEKIAGAAAEEGRDLASIKQLSEK
VIATGRSYGCALTPCTVPAAGKPSFELADDEMELGIGIHGEPGRKRVKMGTAAQIAAELV
DPVLADLDFTGPVIAMVNGMGATPLIELYLMYGEIEPLLAARGITVARNLVGNYITSLDM
AGCSLTLLRADDDLVRLWDAPVNTPGLRWGI
>PFR_JS22-1_1487 PFR_JS22-1_1487 ATP-binding cassette protein, ChvD family 1699850:1701538 Reverse
MAEFIYQMHDVRKTVGEKVILDGVTLSFYPDAKIGVVGPNGAGKSTLLKVMAGLEPINNG
EAYLAKDATVGLLQQEPPLTEDKTVLENVEEAVADLKGMLNRFNEISAEMANPDADYDAL
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DLLLLDEPTNHLDAESVNWLEAHLKAYPGAVLCVTHDRYFLDNVVTWICEVDRGRLFPYE
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ERSRKLDTGEINIPPGKRLGAEVLDANKLHKGFDGRILFNGLSFDLPRAGIVGVIGPNGV
GKSTLFKMIVGEETPDSGELKVGKTVEISYVDQNRSGIDPEKNVWEVVSDGLDYIKVGNF
EVPSRAYVAAFGFKGPDQQKPSGVLSGGERNRLNLALTLKQGGNMLLLDEPTNDLDVETL
QSLEDALLEFPGCAVVISHDRWFLDRVATHILAWEGEGEDGNDPQWFWFEGNFADYETNK
VARLGEEASRPHASRYRRLTRD
>PFR_JS22-1_1488 PFR_JS22-1_1488 Hypothetical protein 1701734:1702234 Reverse
MDTAISMAGNVGTEVDYTSGEGYSFASFRLAATPRIRRGGEWTDGETVWTTVQAVNRTAE
NVRASVHKGEAVVVVGRLRARRWVGQDGQQHERLVLEAKSVGHDLARGTSRFTRNERVAP
AEPPADSGPAPQSRPDGERCEPDDEAESLPAESLASVEDGVAEPAA
>PFR_JS22-1_1489 PFR_JS22-1_1489 Hypothetical protein 1702451:1703113 Reverse
MSGNVDLGIGALETLRTVPFWRTDEVPRHVARRMLVIPGVRYSCDRPLLNWTSTIAHQHG
WWVQQAQWDLTPQTNQDEIIARALELLDHDAPDADQTMVVAKSMGSRAASTASANGWCGI
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WVDVAGANHSLEVPDDWRASLAVQRSLFELADGFIDVLSQ
>PFR_JS22-1_1490 PFR_JS22-1_1490 Dynamin domain protein 1703110:1704753 Reverse
MIFGRRQKSGQVPLGERITALSQAADLCRGRVDDALVDAALQAAQRADERLGLGGEYTVV
ALAGATGSGKSSLFNGLAGAQIATAGVRRPTTDRTLAAWWGDTEPAELLDWLNVPVRRPL
GRGRPELSGLVLLDLPDFDSTSARHRVEVERLLGLVDMFIWVVDPQKYADAALHERYLAP
LAAHAGVMTVVLNQADRLTPEELRAASGDLRRLVDADGLGSTPLMVTSAMSGLGVDDLRR
RIARAVRDRKVVTERLATDIDQAAVALAGQLGEPATMRLPRERLDALDQALAEAAGIPLV
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LAMGRGRRWWGVVRIVQWFLFAVLVVGAGWMIINALLGGDLLPVPRWRQMPVPVLLMVGS
ALGGIVVAGLARLGVEVGARHRSADAQEALMLAVARVTDVAVIAPVESELERYEQARQAV
ATAKGEQ
>PFR_JS22-1_1491 PFR_JS22-1_1491 ATP-binding protein SCC61A06c 1704750:1706597 Reverse
MGIAEGRATAGARDRADESLSESLGRLRADLGRVRLPLELADAPDRERQAAAMAAQLTDY
VLPRLANIDAPLLAVVGGSTGAGKSTLVNSLIGRTVSRAGVIRPTTRSPLLVHNPADAAW
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GRPLLAEDPQLGHTSADFAARVGVEVRDWQGEVLELVREQGHGRRRTARIAAAGVNGVGA
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TARDDTARDDEAGQQ
>PFR_JS22-1_1492	PFR_JS22-1_1492	Protease PrsW family protein	1706667:1708169 Reverse
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LWRVYLMFRVQTITSVAQATEKAGQRMEPTVGQFNEAVVKCAQLAAISLAIGLFLYFLID
RIHRTGFLLKVICVFWGGAVAVYFAVFVNSWVAALLGDSANDESASTKAAIYVAPFVEEF
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SSLFFGDDAGAAMTFLLIFGASGVIGLLIRYFIHLRSEGRLVGQRLADFVREGWLDPRDP
HVFSGFFRRVKLLLAALLRGPRTLIATVRIQRAMIELAYLRASVTWGTVDEAGQLRSREL
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PVMPPSPQAGQPVGAGQRWG
>PFR_JS22-1_1493	PFR_JS22-1_1493	Transporter, major facilitator family protein	1708223:1709674 Forward
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LLVTKQRWGRTLFAVYGPTLMASIGFGAVIPLVAIQARALGASVGLAAFITALNALAQVM
GDLPAGIVADRLGEKYAIVAACLIDTCTMAMVFVARSLVVLAIAVFLQGLTAAVFSLARQ
TYITERIPVHWRARAMSTLGGVFRIGWFIGPLAAAAVITRWDLITAFCFAGAMSFLAAVV
TLAMPSLPGEPTGLRGIRQRQQEDHPATFDILRQHRHVLLTLGVGCLCLMLIRSVRQTII
PLWCEAHGISPAATSLIYSISMGFDVLLFFPGGWIMDRFGRWFVSVPTIAVMSLCLLALP
LSHTAGTIALVACLLGFGNGVSSGIVNTLGADMSPSYGRPQFLAGWRVFGDGGAALGPLI
VSAATALVSLPFASILVGAIGLAGTGWLARYVPREVVPDEAEVTVGAGGGPGPEPSGDAS
TRG
>PFR_JS22-1_1494	PFR_JS22-1_1494	Oligoribonuclease	1709686:1710366 Forward
MKDMLVWIDCEMTGLDLANDELIEVACLVTDGELNVQGDGIDVLVQPSKHALDHMGEFVT
EMHTKSGLLAELKNVKTTMREAEEQVLAYIKKYVPTERKAPLAGNTIGTDRTFLAKDMPE
LEAWVHYRNVDVSSIKELAKRWYPRTYYQAPDKHGNHRALADIQESIEELKYFRAAIMVP
EPGPTASEARALAHKYQGSLTGFSDPDEPPEADFAGEPDTGSASKD
>PFR_JS22-1_1495	PFR_JS22-1_1495	Metal dependent phosphohydrolase	1711104:1711610 Reverse
MDNVDDGALTSTDAVGLAREVATRAHAGQVDKAGEPYIGHPRRVARRAGELAGGRGSGFR
DAAEAVGWLHDVVEDTELDGPDLRRLGFSDEVVAAVLALTRRVGEPEPDYAARVAANELA
MVVKRADLADNTDPARTALLDEETRVRLAEKYRVFRGLLDAALFEAGE
>PFR_JS22-1_1496	PFR_JS22-1_1496	Putative excision nuclease ABC subunit	1711685:1714018 Forward
MIRVQGARENNLKNITLEIPKRKLTVFTGVSGSGKSSLVFDTIASESRRLIDETYSAFLQ
GFMPTLGRPDVDLLSGLTTAIVVDQAQLGANPRSTVGTVTDADAFLRVLFSRAGSPHIGS
PKAFSFNVATMRGGGTMTVKKGTTGQAQAVKRSFNVVGGMCPRCEGRGTISEFKLAELYD
EDLSLSQGAMLAPGYKAGGWNYRIYAESGMYSPDKPIKQFTKKELNDFLYHEPERRKIAG
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LSIADANALQVTELADWLGGLELPGLGPLVTTLRAILTAFDDIGLGYLSLNRASGTLSGG
ESQRVKLIRNIGSPLTDVTYVFDEPTAGLHPADVHRMNQMLLQLRDKGNTVLVVEHEPET
IRIADHIVDLGPGAGSHGGELCYQGDLAGLRASDTLTGRHLDDRVAAKQAWRTPTGTLPI
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EGKRFEPGVLLYKLAGLDISQVLALPFDEARDYFGTGPAKIAAAQKIVGRMVDVGLGYLS
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IVVEHDLAVMAHADWIIDMGPGAGNQGGHVTFEGHPADLAATGSGPTARYLAAYLGS
>PFR_JS22-1_1497	PFR_JS22-1_1497	Putative secreted tyrosine phosphatase	1714088:1714933 Forward
MTANPASQPTPGQSTPSQPAPGAHIELESLPNLRDIGGYPITGGGRVRTGVLYRSAALSR
LSPADADALQRRDIRTIFDFRTEVERTAQPDVVPDGMHVVLADVLADAASAAPDEMLEAI
KDPLRASQLLAGDQTAAIFDETYRQIVSSDSALAAYRSFFTDIADPANRPALFHCTSGKD
RTGWAAAALLLLLGVDEADVFHDYELTNQYLPRSAAAMIKKFTDGGGDPSTLTPVLGVDP
KYLRAALTEMTSRFGSITGYFRDGLGMEDDAQDTLRAALTA
>PFR_JS22-1_1498	PFR_JS22-1_1498	Mur ligase middle domain protein	1715037:1716359 Forward
MGAMPSNSSRPAPGRAQPINALPFGTGLGRRVWRDAAIGLGNLAALASRAAGRGTGTSIR
GQVITKLYPPAFDELIAGRRIAAVSGTNGKTTTTHLLTAALRAVKGDQNVVTNADGANLR
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DGADVSWLWDVDFEQLAGKHVVCTGPRAQDLAVRLSYAEVEHSIVPDLSEALHGDYPGQV
DVLATYTAFLNLCRMGGVTW
>PFR_JS22-1_1499	PFR_JS22-1_1499	CobB/CobQ-like glutamine amidotransferase domain protein	1716353:1717126 Forward
MVKPIKIVVVYQSLLGIYGDRGNGMVLAKRLSWRGIASELIMVEPGQPVPTNGAVYLLGG
GEDQAQIAAVDALRADGGLFRALDDGAVLFSVCAGYQILGNSFTVGDDDTVIEGLGLLDV
DTRRGPVRAVGEVLSHWMTPEGDDYLLTGFENHGGYTTLGPKAAPFARVELGVGNRGDGT
DGAVQGRVMGIYPHGPLLPRNPLLADYLLGVALDRRLEPLPNEQVNDELATLRHQRINVV
RHTKSLSEDTRWLGERS
>PFR_JS22-1_1500	PFR_JS22-1_1500	10 kDa chaperonin	1717388:1717837 Reverse
MSDDQIPVTPATAGANPVPVAQDAQDTSSTLQAAAPADVPDAGHLEEPPIRMLHERVLVS
MESEKGEHRSEGGILIPSTVQMAHRLAWARVMAVGPSVRAVKVGDRVLFDPAERSEVEVR
NKVYVLLRERDLHAVADEQLSDAETGLYL
>PFR_JS22-1_1501	PFR_JS22-1_1501	Hypothetical protein	1717864:1718163 Reverse
MAQPETNIDRIRERIAASRDDLTYGIETLISTVHPTALKNRAIDEGKEFASEKADEAKSA
FIDENGPRWDRIGTVALAAAGVIVLAISVRGLGRVIRGK
>PFR_JS22-1_1502	PFR_JS22-1_1502	Bacterioferritin comigratory protein	1718337:1718825 Forward
MSTLAPGDPAPEFALPDADGNIVRLSDHAARTVVVYFYPAALTPGCTVQAIDFTASLDEF
TQSGVDVIGISPDTTDKLAKFRMRKNLRVTLLADPQHTAIDAYGVWGTKLIFGKPIDGII
RSTFVVDVDADGRGTVREALYDVRAAGHVDRLRKKLGIPAAV
>PFR_JS22-1_1503	PFR_JS22-1_1503	Class II aldolase/adducin family protein	1719118:1719810 Forward
MATLKDFSQATRAEVRAVREVVAALHDQLVAWNLVMWTAGNVSQRLHSADLLVIKPSGVR
YEHLTPESMVVTDLQGNLVDGAGSPSSDTSSHAYIYRHMPEVFGVCHTHSTYATAWAATG
KSIPCALTMMGDEFGGPVPVGPFRLIGSEAIGAGVVDTLKQFPRSPAVLMQNHGPFTIGR
DAEAAVKAAAMTEEVAHTMWAAQQLGGVIEIAPDDVDKLNDRYQNVYGQH
>PFR_JS22-1_1504	PFR_JS22-1_1504	Precorrin-6x reductase cobK	1719791:1720558 Forward
MSTGSIDPEVLVLGGTRLARQLARTLTDAGISALTSLAGRTRAPRQLPGPTRHGGFGGVE
GLARWLHDNRPRVVVNATHAFAATISAHAARACRRADLPLARLVPTSWAAQPDAATWIWV
ADNASAVRAVRALPDPVLLTVGRQATAEYLALGDRDITHRVIDAPDEGLPPRWRLLNARG
PFSEAAEEALMDDPGHRIATLVTKDSGGDQPAAKLVVAARTGARVVMIARPPVPDYGIVL
HDVADTLDWVRSALG
>PFR_JS22-1_1505	PFR_JS22-1_1505	Precorrin-6Y C5,15-methyltransferase, CbiT subunit	1720631:1721221 Forward
MTTDPDSSLLGRTPGLPESHFVHDGLITKHPIRAVALAALRPLPGQMLWDLGTGAGSIAI
EWCRTDPGCGAIGVEQRPDRAEHARQNAANLTLPGQVTIVESDIEQALPQLPDPDAIFIG
GGLTASLAARCIDALHTGGRFVVNAVTLEAELVIGQLALDHGGELMRLEVHNGDHIGALH
GFKPLRMVTSWTWVKP
>PFR_JS22-1_1506	PFR_JS22-1_1506	Precorrin-8X methylmutase	1721318:1721971 Forward
MSDYLNRGSDIYRESFRIIRDEADLSRFPDDLEPVAVRMIHAAADPAIAADIAFTTGVGE
AARTALRAGAPILCDSSMTATGIIRSRLPRDNEVITHIKDPRLAGIAEEKGVTKTSAAVD
LWHEEGRLEGSIVAIGNAPTALFRVLELVHETGEKPAAVIGIPVGFVGAAESKQALVDDD
AGLDYLTLLGRRGGSAIAVAAINALASSAELTNEHRE
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>PFR_JS22-1_1507 PFR_JS22-1_1507 Cobalamin biosynthesis protein CbiD (Precursor) 1721968:1723260 Forward
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TSGREAQLTSSGLRPGWTTGACAAAAARAAWSALHTGNFPDPVEVELPAGRRPAFALTFE
QLGDDTAMAAITKDAGDDPDVTDGAVIRATVERGRPGSGITFRAGSGVGTVTRPGLPLSV
GEPAINPVPRTYIAENLAAADRSVGGNGSPDVVLTLSIDDGEQIAQRTWNPKIGILGGLS
VLGTTGVVVPYSCSAWIASIHEGIDVARADGASHAAACTGSTSQRIARELYPDVELLDMG
DFAGAVLKYLHSHPLPRLTICGGFAKMSKLANGYLDLHSHRTRVDQEQLARLAREGGGDD
ELVAAVGAAHTASQAYQLSHDAGIELGDLVARAAARQAAITVDAPIDIEVICTDRAGTII
GRSPFTAAAH
>PFR_JS22-1_1508 PFR_JS22-1_1508 Sirohydrochlorin cobaltochelatase 1723292:1724533 Reverse
MTDLVPLVIAAHGTRDAQGLAQTRAFADEVRAALPGVHVELGFVELAEPDVAGAVHNALA
HIPDAVPSDEPELVVLPLMLNTGGHVNSDIPEFIEAGRDGHRVSYGGPLLPDPRVRQVLE
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VVRPSVPEALTMAVDAGATQLLVGPNFLFRGRLRTWLSEQVDAWLETHPGIEVRISDVLG
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ARVHVVAPNAGIRVARLAEQGRVDWQQRGFTESDVDEVWFVLAASNDPEVNARVSAEAER
QRVFCVRSDKSSDGTAYTPATEEAGGITVAVVGHRNPRRSVRVRDELLKALQV
>PFR_JS22-1_1509 PFR_JS22-1_1509 Bifunctional cbiH protein and precorrin-3B C17-methyltransferase 1724526:1727186 Reverse
MIRVHGFLGGISEALRADLATADLVVGGRRQLDDAGVLAAQRVELGALAPAIERLKALDD
DKLAVVIASGDPGFFGILRPLRRAGLHCEVVPTITSLQAAFAAVALPWDDAQLVSAHSGG
IEAAIRIAGVHPKVGVLTAPGKGLAQLVAALRGRDKHFVVAERLGEADERVRVFDEAAAL
TVDEDDLASPYVVLILDAAPESAEAVGHSPQLAGDPNAPGPDDPKPASNTRADGSDRAPI
IGQVVNTTRARHQADQIDQALGVESKRYDGPASAGLVAAWGECDLIVSHLALGATTRLIA
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ALDQLGWAVSGDVAGVTAAIIDGAPVSVLREHLWPMPPLPGNVLVPAPGEPAAPGTVGRV
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GQAAPPAEAAQPPTTQSQVTPSQATQSRTTAAQPGSDVPTQENSHD
>PFR_JS22-1_1510 PFR_JS22-1_1510 Tetrapyrrole methylase, precorrin-3 methylase, CbiF 1727183:1728142 Reverse
MSDTRSHEPDPAAGNEAAPLRGKVVFVGAGPGAADLISVRGAHVIAQADIIIWASSLVLP
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HGAGNDTTGAHRSTEGEQA
>PFR_JS22-1_1511 PFR_JS22-1_1511 Precorrin-2 C20-methyltransferase CbiL 1728172:1728945 Reverse
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VLDVAPEVAERIVRVPFSMAQRRGVGPKRSGSWQASARAALDAFEGGARAVVLATVGDPS
VYSTFSYLRGTVAEALADIAFEVIPGITAMQAISAASDLPLVEGREILALVPATVGPERL
DAVLDVADSVTIYKGGRTLPQVIAQLNAHDRNSVVGTDVSLPTQSLVDADELSADETLPY
FSTILSVPKRKSTGGAL
>PFR_JS22-1_1512 PFR_JS22-1_1512 Hypothetical protein 1729517:1729780 Forward
MNHIVGNVARKHAPTQREVNASLPCHCGAAPGHRGSPTPDGLIAAHEDPVALLVVPCPAW
HARHRIARQSVTGTPRGALTLSGAGVA
>PFR_JS22-1_1513 PFR_JS22-1_1513 Methylmalonyl-CoA mutase small subunit mutA 1729777:1731693 Forward
MSSTDQGTNPADTDDLTPTTLSLAGDFPKATEEQWEREVEKVFNRGRPPEKQLTFAECLK
RLTVHTVDGIDIVPMYRPKDAPKKLGYPGVTPFTRGTTVRNGDMDAWDVRALHEDPDEKF
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GVYERSDKPAKDLALNLGLDPIGFAALQGTEPDLTVLGDWVRRLAKFSPDSRAVTIDANV
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REAWARIGEVFGVDEDKRGARQNAITSWRELTREDPYVNILRGSIATFSASVGGAESITT
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LRAARMLWAKLVHQFGPKNPKSMSLRTHSQTSGWSLTAQDVYNNVVRTCIEAMAATQGHT
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HLTLVPALRKELDKLGRPDILITVGGVIPEQDFDELRKDGAVEIYTPGTVIPESAISLVK
KLRASLDA
>PFR_JS22-1_1515 PFR_JS22-1_1515 LAO/AO transport system ATPase 1733869:1734882 Forward
MPRPFNVPELVDEVLANKRPGLARAITLVESTLPAHRPLARELLAALLPHSGNAIRVGLT
GVPGAGKSTFTDAMGVRLIDRGHKVAVLAVDPSSSRTGGSILGDRTRMGKLAESDSAFIR
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DQLQGIKRGILELADVIAVNKADGDNAGEARVTARDLSIAMKLINDEADGWRTPVLTCSA
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MRATASILHLDLDAFFASVEQRDKPSLRGKPVAVGGVGDRGVVATASYEARKLGLHSAMS
TSQARHLAPHAAYLSPRGDAYRQSSRIVMALLGELSPLVEPLSIDEAFVDLEAGGQDTSP
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LPANAIPGVGPATMDRLSRLGIRTVGDLREASVAELVRELGQAVGESLHVLASGRDDRAV
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TLSRSRTLSGATDNPERIAATAQALITGVRIGQGFRLIGVGVGGFAQAAQEELFVLDDQQ
ASVAPVMEERQVASALRRGSQSWSPGAEVEHDEHGRGWVWGSGLGVVTVRFETRRTGIGP
VRSLRADDPALHRAGLLPMEFDHPDEEAEPEHGPGWARLRPTSPTPDTGADRGTSTPGTS
DPG
>PFR_JS22-1_1517 PFR_JS22-1_1517 Dihydrofolate reductase 1736541:1737143 Reverse
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PLIMGRRTHDAMGLLTGRTNIVVSRTPQAVTWPDQAPEGSHGIAVSSIEEALAVASGLDQ
RIYVIGGGQIYKAAWDWLTDLDITAVHEPADGSVTFPEISAQDWSQTSSEPHGEFDFVHY
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>PFR_JS22-1_1518 PFR_JS22-1_1518 Thymidylate synthase 1737258:1738070 Reverse
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MRQYLDLLTRVMDEGIDKSDRTGVGTRSVFGHQMRFHLADGFPLVTTKKIYTRGVFGELL
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NDPNSRRLVVSAWNVAEVDDMALPPCHLLFQFYVTPGEDGQPGKLSCGLYQRSADLFLGV
PFNIASYALLTHMVAQVCGLGVGDFVHTLGDAHIYHNHFDQVAEQLSRTPKALPRLALNP
QVRNIDEFELSDITVEGYEPDPAIKAPIAV
>PFR_JS22-1_1519□PFR_JS22-1_1519□Non-canonical purine NTP pyrophosphatase□1738072:1738878 Reverse
MTSEVLLATNNAKKLTELRRIIVEYDMDIQVLSLKDIASYPEPEETEWTFQGNALIKARQ
GMIHSGLPALADDSGLCVDALGHMPGVRSSRWDGPEQEDIANMELVLRQIEDVPRGRRQA
QFVSVMALVMPDGREFTTRGEMTGHLTTRPKGSHGFGYDPIFVPDEQVPDSEGRLRTAAE
MSAAEKDAISHRGRSVRAMLPILAAQLGLAAPKELDDEEEIVPGSQNSGPAPTAPPSEWT
ASIPAVGKPTSGANLGDLPSGGVTPLEP
>PFR_JS22-1_1520□PFR_JS22-1_1520□TRNA nucleotidyltransferase□1738875:1739636 Reverse
MSESTKSVTRSDGRSLDQLRPVSITRHWLDHAEGSCLIEAGRTRVLVAASVTEGVPRWRR
GSGLGWVTSEYEMLPRATNTRNDRESRRGKISGRTHEISRLIGRSLRAVIDYKALGENTI
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LDLAYDEDSTADVDMNIVATGTGDFVEVQGTAEGATFDRKLLGRLLDLADKGNRELTDLQ
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LDSLVARGVKSLVIACNTGSSAALHDARERYDLPITEVVLPAARKAARITRNGRVGVICT
RGTAISRSYNDALAASPVKLFTQVCPRFVEFVEAGITTGPEVLQLAREYLAPLQADDIDT
LILGCTHYPLLSGVISYVMGEDVTLVSSSDECARAVFAELTRDDLLRTEPHEPQREFFTT
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>PFR_JS22-1_1522□PFR_JS22-1_1522□Hypothetical protein□1740696:1741304 Reverse
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AELENQMGCEVKADFATNPEVDPVLRRLFPDAYRDDEGASTEFRRFSQASERDEKLDAAV
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VHMEGKAVVSSGGREEMERDVNAMHGFGLWATVSRAE
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RFDDEQIDYLVGAGVADDMLAEYLASYRFTGNVTGYPEGELFFSGSPLLQVEGSFAEAVL
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>PFR_JS22-1_1525□PFR_JS22-1_1525□Naphthoate synthase□1743158:1744243 Forward
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F
>PFR_JS22-1_1526□PFR_JS22-1_1526□O-succinylbenzoic acid-CoA ligase menE□1744316:1745548 Forward
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VRLPDDVRLVMRTSGSTTGHGRLVGLSAAQLRASIRATDQRLGGPARWLLTLPAHHIAGL
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>PFR_JS22-1_1527□PFR_JS22-1_1527□Isochorismate synthase□1745659:1746882 Forward
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>PFR_JS22-1_1528□PFR_JS22-1_1528□Hypothetical protein□1746998:1747474 Reverse
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>PFR_JS22-1_1529□PFR_JS22-1_1529□Putative excinuclease ABC, A subunit□1747645:1750215 Reverse
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SVIGRYLREDQAPRHR
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Reverse
MSNTADPQNPPQARSGEPAAAVGQAVPGGPPVRSAALARALVTALVAHGLRDVVYCPGSR
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SIVEVELPPVG
>PFR_JS22-1_1531□PFR_JS22-1_1531□Mandelate racemase/muconate lactonizing protein□1752103:1753101 Reverse
MKSAALTHVQVPEALRRRGIDEVLVFQAGLRHRFRRIEVRDGLLLHGEQGWGECSPFWDY
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GATESASWLHAGLEAATRPLPAPVRDLVEVNVTIPVVSPTQARRLIAASGGCMTAKVKVA
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RRVEADQPVHQDVPRALVDRWVERLTAICHEL
>PFR_JS22-1_1532	PFR_JS22-1_1532	4-alpha-glucanotransferase malQ	1753098:1755287 Reverse
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ESRPLEDRA
>PFR_JS22-1_1533	PFR_JS22-1_1533	Hypothetical protein	1755417:1756469 Reverse
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IRNGVYALIQAASYVVGFLIVVNGLWPLFQRRRQTWHDMVARTQVVSIRP
>PFR_JS22-1_1534	PFR_JS22-1_1534	Multidrug resistance efflux protein	1756643:1758154 Reverse
MRITDGGLARELPIGLPGLIGWTIVTNAIESRTGESRTRPNRGLIVAILVGVLAIAFEAY
GTATAMPAVAGQFHRLDLYDWAFTIFTIAQVFAIVIGGRMADRTGVVVPLVAGSVIFGIG
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IISALRIGPVRNDVAGVGPQKSW
>PFR_JS22-1_1535	PFR_JS22-1_1535	PF11238 family protein	1758213:1758476 Forward
MTQLAPGSETITKERTQPLREEGDEERFSHYVPKGKLMEAMVNGTPVVALCGKVWVPSRN
PERFPVCPTCKEIWESMKPGKDKGPDA
>PFR_JS22-1_1536	PFR_JS22-1_1536	Cation diffusion facilitator family transporter	1758632:1759672 Reverse
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LSEAIHSFADTGNQILLLIGGRQAKKQANRAHPFGYGRQRYINAFLVAVILFSVGGLFAL
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ESAEQLADTIDAAEVNIRTAEPMCRYIYLEPDIRDEDYHPARPTTA
>PFR_JS22-1_1537	PFR_JS22-1_1537	SIS regulatory protein	1759784:1760800 Reverse
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IVAAEEDSLVARAARSSATQLVATRTGDPLAAAIAVMSILHDIRLGPEVVPADTAEVADM
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VTLDAGRGSDLDCYVSLLQQGRYGAAYLSIGLGRRLGA
>PFR_JS22-1_1538	PFR_JS22-1_1538	Hypothetical protein	1760808:1761008 Reverse
MALTAELEMPTTFLEIAACPQCHSKLAVDYEHSELACTNSLCGLAYPVRDGIPILLVDEA
RSTKKI
>PFR_JS22-1_1539	PFR_JS22-1_1539	HAD-superfamily hydrolase, subfamily IIB	1761069:1761884 Reverse
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LERMPADAPLGNLHLMPTCGTRYERFTGEGWHEAYAHDLDAAERDQAIASLEARAKQLHL
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TGPDDTLEYLHRLIPSLRAGKPADLELLPSA
>PFR_JS22-1_1540	PFR_JS22-1_1540	Hypothetical protein	1762000:1762500 Reverse
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PDSTAVVGPLSGEVEPGTYDLCADHARTLSVPRGWQIIRLADIAETVPVPDDDDDLLALA
NAVREIGLGGAPMPAPAPVRQPDESGIVELAHRGHLRVIADQKRAR
>PFR_JS22-1_1541	PFR_JS22-1_1541	Hypothetical protein	1762567:1763007 Forward
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DIGVDEVPDVRALWSNGDYGDAIPLASATDAQPGQNARIVLFRRPLEHRAADQSQLRELV
HETLVDQLVALTGRSIDEIDPDDGDQ
>PFR_JS22-1_1542	PFR_JS22-1_1542	Hypothetical protein	1763112:1764464 Reverse
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PASVPVSIGLSKSCAATEPGTLLATASQGQLRVSGASTQTLDSPLSQQVGAGSERISPAD
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TQTGLTLIPAQPIRATQGELAARPAVDLGR
>PFR_JS22-1_1543	PFR_JS22-1_1543	Putative glycosyltransferase	1764461:1767712 Reverse
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LPDRAWNVRHAADTLAGRMGDAVYELRNDEGGSGLDELTGSDYANVAVTRRVLSARLLTV
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>PFR_JS22-1_1545	PFR_JS22-1_1545	Hypothetical protein	1768502:1769584 Reverse
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YIDEVARQIPEVESRNLLGEPVGRDSLNAVAWPAAVLARRDPGAVTAMITADQIIEPVEV
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HDCLLINADVGDSVLAVAGLRDMAVVRTAAATLSCPLKDSQQVKTLVGRVAHEVDAELA
>PFR_JS22-1_1547	PFR_JS22-1_1547	Cell envelope function transcriptional attenuator common domain protein	1770786:1772144 Forward
MAEQNDEGEQKADLDWLYRRGPEEAPDPLAGRPARVTSTFNRADVQRHEQEFLAERARRQ
AQQQARPAQVQPGGSAQYASRGQQPGGYGAANAVPRHAGSGPTGGGNGAPPRRPVPAPVP
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VANPVRWWNVNEALSKAITRGKDMGPGVALGAGRGMVSVAGGKGLTLQVPVSNSSGWSDD
GQSVVIWDSARASRMFGLLAQGDTKDMDQFAS
>PFR_JS22-1_1548	PFR_JS22-1_1548	Phosphoribosylaminoimidazole carboxylase, catalytic subunit	1772182:1772742 Reverse
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RMPDEMLAYGHRAHERGLRVIIAGAGGAAHLPGMLAAVTPLPVIGVPVALKNLEGMDSLL
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SKTVRA
>PFR_JS22-1_1549	PFR_JS22-1_1549	Phosphoribosylaminoimidazole carboxylase, ATPase subunit	1772735:1773907 Reverse
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GADLADVQERARAAAHYLMGDDDVMEDDGE
>PFR_JS22-1_1550	PFR_JS22-1_1550	Peptidase family S51	1773985:1774701 Forward
MSTHIVAMGGGGFSMAPNSAPTSLDRYLVDVSGERSPLVCFVPTASADSAPYINRFLMAY
SGLGVRTMVLTLWQGAAESVKRLPEADVVLVGGGNTVNMLALWDAHGVSRTLKLMAADTS
RTMVLGGLSAGGACWFEGCLTDAFGDLRGWRGGLGMLSGSFCPHLDGEDRGAIYTQAIAT
GMLPGGYAVDDGVAVHFENGKYTDVLAEREGPTALRLMPSTEPTASGVLTEILEPEVL
>PFR_JS22-1_1551	PFR_JS22-1_1551	Transcriptional regulator, TetR family	1774771:1775355 Reverse
MPKINAPTVREHHERVLTSLIDAAEQVLRYEGPDQFTTSAVSARAGVARNSIYRYVDSVD
DLRGLVVERYMPAWFRAVQEAMDATSDPAQQIVAWALTNLEQATIAGHGWLMKVGDKRLN
QQAAGTVNQAHQNMFAGLGEAWAQISAPNARLGAAMTGGLLNSCMKQVEAGMDSHEVAAG
LERAVRALVEAFRS
>PFR_JS22-1_1552	PFR_JS22-1_1552	Hypothetical protein	1775437:1775940 Reverse
MGWRRHLGDDETVIADLRAHPKALVVPVVFLFALAAACGVALAMVPAAVEPWAGWLIAVI
TAALAIAFVQRPVLAWATTRYGFTDRRLVVRAGLLRRRRSDLPYSRITDVSYARGLLDRL
WGSGTLVVTTASGARLELIGMPQVIALHQAVSQLVAESRPAAPDLPY
>PFR_JS22-1_1553	PFR_JS22-1_1553	Biotin apo-protein ligase	1775974:1776765 Reverse
MPTTAPVDPVELEQLLGKNSYWGPIQWRPETGSTNDDLVALAKKGAATGLVVMSEHQVGG
RARFDRVWQDTAGTSVATSVLVAPTPPPLQWGWLSLLVGVAVREGVENYTGAVPGRVTLK
WPNDVLLDERKICGILSERVGDRAVLGWGLNVSMSQEELPVPTGTSLLLAGLPHAKTPLM
AAVLQALDHWFAVWQRRGEIREEYARVCATIGRRVTVHLDFEHPDRGSITGVATGVDRNG
ALVVDDDQGTRRVLTAGDVVHLR
>PFR_JS22-1_1554	PFR_JS22-1_1554	Transcriptional regulator	1776915:1777520 Forward
MNDDVVSSISQRIKRAIRAAALELALRDGADKVTVDQIAVAAGVSRRTVFNHFATKYDAF
MPEVAAYSDSALKDFSSGREPDLIRALGDVIGNRIDQVQFTSDQVRAVRKLAQDSPGLHN
AMRGRSGALDARLQAAVMRRLGSTPDDPSTTMTLALARSIWRTTLDAWLTTPDEFNQDSL
RRCLAKSMETLEGLVRSNPGA
>PFR_JS22-1_1555	PFR_JS22-1_1555	Transcription regulator	1777534:1778112 Reverse
MAVSTHAEGEQDSAGPSEPRDEQGISEFVSHFGGLMAASGMPGLTGYVFALLLAQPDAEL
TAQQIGQALNVSPAAVSGATKYLADIGFTRRLRRPGSRRVVHALSSDDWYDALLGRSNVI
EGSKRLFLEGSRAAGGVGTPAGRRLWLNAKWFTKLGDAIEREMAAWPAEREELLRSLGEL
DDADPHDGPAES
>PFR_JS22-1_1556	PFR_JS22-1_1556	Hypothetical protein	1778227:1778745 Reverse
MAVRRMFADDVHDGGVQIFVTWAGFLGAWLLVAGPLLQGAIELWEIGRKGQGDVKLKPAD
RALWLSPPAYYFVARARIRRWERGSGRERARSVLTSYVNRATGWFTVAGGASLMALEATW
ELAEIYHWGVAGFWLIVAGLMVASHLNVAIRMWRLMREVPPQGSNPEVSPTS
>PFR_JS22-1_1557	PFR_JS22-1_1557	Tetronasin ABC transporter ATP-binding protein	1778850:1779794 Forward
MSPTRVSTAIEINGLVKTFGRVTALDGVDLSVQSGEVHGFLGPNGAGKSTTIRILLGLLR
ADSGSARVLGADPWADVRTLHERLAYVPGDVNLWPNLTGGQVIDLLARLRGDLNPARRDE
LLERFDLDPTKKARSYSKGNRQKVALVAALASDAELFLFDEPTSGLDPLMEAAFDTSVQE
LKGRGATVLLSSHILSEVEELSDRISIIKAGRIIETATLEQMRAMHTTSVSADVQREAPE
LGTMPGISQLRTVGGHVSFVVDAAHLDQAITVLTRAGITSLVSEPPSLEELFLSKYADPV
PTGTPAAPSAGDQR
>PFR_JS22-1_1558	PFR_JS22-1_1558	Putative exporter of polyketide antibiotics-like protein (Precursor)	1779791:1780873 Forward
MSRQTFATRRGRGADATRRRGSGVASLLRLALRRDRILIAVTLVLVWALNYYSAEAMGSL
YPHPADLVAANTAANASTGVVAMYGHISDVGSVGGVGSTKMAMINFIILAFLVVALVRRH
TRAEEETGRQELIGSAPIARHAPLTAAVLLAGATSVACGLVTWLCVWAGGWPSAGSMLYG
LALAGVGLSFTGITAVAVQLSANNRTCGIWAFSAIGLSFVLRMIGDVYWNRPAHVLSWLS
PLGWGQQVRPYDGNHAWALVVPLAFFAATVTLAFVLLSHRDLGAGLFAERAGTAHTRMGS
AAALAWRLQRGSFIAWLACYVIFGALAGGMSGSMQGMINADGEAMLRAMGGVGSTTSTSR
>PFR_JS22-1_1559	PFR_JS22-1_1559	Hypothetical protein	1780930:1781427 Forward
MRSEESSGHLEQLLATPLTRTRFAGSYLVQAVLGSAVLVALLGATAATLHTTSPGGGGWW
RVFSGALIGLPGIWLLTALAFVALAWLPRLDWLGWAFLGWVVVVDELGALLKFPGWLLKA
SPFAHLPKLPVEPMTWAPVLVITALAAVLVAIGFVGYRRRDMPVV
>PFR_JS22-1_1560	PFR_JS22-1_1560	Integral membrane protein	1781535:1782881 Reverse
MIDDSRHDRDFIDGTEAVVRLGSMLLSAGTGAYRVKHAMARAAEAIGMDRHDASVSLTEI
ITTTHKGDNFRTVVREVPRVAVDASRIGALERLARALPDGSTARELEDQLDHIARHVRGR
WPWWVNMLAAGIACAAFAVLNHFSLTDAVLVFFGAACGQGVRRALAKRGINQFGTAALAA
ATASSVYLLLTLACRTIPWHVLHGVDGTGYVAAILFLIPGFPMITSILDIARLDFTAGLP
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WRRSPHAFLSSDAEFAKRDIDYSAPSDE
>PFR_JS22-1_1561□PFR_JS22-1_1561□Carboxyl transferase domain protein□1783013:1784587 Forward
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GRHRSTKFGMEKRRPYGDGVIIGVGAIHERPVCVFSQDVGIFGGSLGQVYGEKICKIIDF
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SKHLGADVNLAWPTAQIAVMGASGAVNILYRKELAEADDPDAERERLMGEYEEEMSNPYV
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>PFR_JS22-1_1562□PFR_JS22-1_1562□Hypothetical protein□1784593:1784847 Forward
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>PFR_JS22-1_1563□PFR_JS22-1_1563□Septum formation protein Maf□1784898:1785626 Forward
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GISLPLVRQMLLDLGVSWFSLWDRPLSEAWQERHGAIAATKPGVPAESGSPQGPGAPADR
GE
>PFR_JS22-1_1564□PFR_JS22-1_1564□Hydrolase, NUDIX family□1785630:1786130 Forward
MTTPDFVLRLRAAIGHDPLWLIGASAIVLRPGDTGQQVLLGKRSDSGRWSSIDGIVEPGE
APEETAVRECLEETELAVEVERLVMTGVLGPIRYPNGDVCSFVDHVFRCHVTGGRAGTGD
RENTAVRWFGVDTLPADIDPVVVRRIRVAVENPREVVLAGRYPEYA
>PFR_JS22-1_1565□PFR_JS22-1_1565□Hypothetical protein□1786221:1786700 Reverse
MQASHPSRSTRWCALIAGCLGSALVLSACSAGSGGSTAPASSSRAASAVASPISQAPSVD
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SLGFTLTAASGDSLIFDAPGWEGAFTMDDQLAGLTLRHL
>PFR_JS22-1_1566□PFR_JS22-1_1566□Hypothetical protein□1786981:1787196 Forward
MSLSVGEVAILCGWALSVLLSVWFCYRYPVSRIHMVLMLVVAVALPVVGALINTAYVVFN
LSRRRSSEPRS
>PFR_JS22-1_1567□PFR_JS22-1_1567□Endonuclease VIII and DNA N-glycosylase with an AP lyase activity□1787347:1788162 Forward
MPEGHVLHRLAARFNELFADEQVQVSSPQGRFAESAALIDGSTLVQAQAWGKHLFVRFDA
PIADPIVHIHLGLIGKLSFTELAPPVGQVRVRINDDTWAADLRGPQICRLISEDEEAAAT
KKLGADPLRSDSDPERAWTKVHRSGKPIASLLMNQAIFAGVGNIYRAEVLFRHRIDPQCP
GNKLHRASFDLMWNDLVQLMRLGVRDGRIDTVYPEHTPEALGRPPRVDAHGGEVYVYRRA
DQPCLVCGSPIHETTLEGRHLFWCGRCQRRH
>PFR_JS22-1_1568□PFR_JS22-1_1568□Phosphoribosylglycinamide synthetase, ATP-grasp domain protein□1788318:1790099 Forward
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GATPAETYLDIDKIIAIAKRSGADAVHPGYGFLSENSNFAQAVVDAGMVWIGPPPAAIES
LGDKVTARHIAQKVGAPQVPGTTDPVKNADEIIEFAKTHGLPIAIKAAFGGGGRGLKVAR
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YGHPAPVPHLSLDRLSPQVSVQSTRALLGKLVPAHCRADRIQLCWYESDHCRVLDEWELR
>PFR_JS22-1_1570□PFR_JS22-1_1570□Genome sequencing data, contig C257□1790722:1791729 Reverse
MTTNVDISTNYLGLELKCPVISSASPLNAHVDKLRAIEAAGAGAVVLPSLFAEEAEDEEL
EAAGLLDSGDEFAEFASSPLVEVDQGDQGTNRHVLLVQQAKQALTIPVIASVNGSHPGNW
SGYAGMLARAGADAIELNLYNVAADPGQSPEAVEDDYLTIITDVKKAIGDLPLAVKVSPF
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YESVDQLRGSMNASSVDDPEAFERAQYMQILHSWN
>PFR_JS22-1_1571□PFR_JS22-1_1571□Pyruvate-flavodoxin oxidoreductase (Precursor)□1791733:1795452 Reverse
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DAWSAAGRTNLWGGVPQVVEMQSEAGAAGALHGAVTKGVLGTTFTASQGLLLMIPNMYKI
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DSWAHLPVEIQQIILDRKLDVWVIDATAIAIKTKLGHRINTIMQPCYFYLSGVVDQAEAI
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>PFR_JS22-1_1572□PFR_JS22-1_1572□MutG family lantibiotic protection ABC superfamily ATP binding cassette transporter
permease□1795764:1797551 Forward
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RRRRVPLRTEPPEQTLPGEVGFLLETHTETDQITATLIDLAVRGFLTVHREDDSSWTFRR
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PQGSAVLEQAEGFRQFLSDPDPELIDWKHSGDVFSRCLPWAVVFGVDAQWTALFQKLTDE
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>PFR_JS22-1_1573□PFR_JS22-1_1573□Chlorophyll synthesis pathway protein BchC□1797689:1798732 Forward
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>PFR_JS22-1_1575□PFR_JS22-1_1575□Puromycin N-acetyltransferase□1799583:1800203 Forward
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H
>PFR_JS22-1_1579□PFR_JS22-1_1579□Hypothetical protein□1802560:1803015 Forward
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DPDKARAIVG
>PFR_JS22-1_1584□PFR_JS22-1_1584□Hypothetical protein□1807834:1808349 Reverse
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RQVFNDVHRFEFELTDFRGFADGLVYLAPEPAEPFKQLTERLVEAFPAWQPYGGQFDEVI
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>PFR_JS22-1_1585□PFR_JS22-1_1585□Ribonuclease H□1808426:1809457 Reverse
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>PFR_JS22-1_1586□PFR_JS22-1_1586□Basic membrane protein□1809529:1810473 Reverse
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SPDQSDALAAAARANTDLHFALVGVTKPVSEKNLKLVRFQSSQVGFLAGYLAAASSSSGT
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>PFR_JS22-1_1587□PFR_JS22-1_1587□Phosphotransferase family protein□1810723:1812012 Reverse
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QAARTEVLIRRLLASFDARVDPVQLRLRAAGVAISLASGPYQEQAPDWKHQTQGILAGAE
NLIRRAEQL
>PFR_JS22-1_1588□PFR_JS22-1_1588□CBS domain pair protein□1812093:1813613 Reverse
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AVQIGVTLAGFLSSAFGTDSLAGAWVAPAFARWGVAPGLAGVLAVIVVTALISFFSIVIS
ELFSKRLALQRPETMALVLAPIVNGLAKVFRPVIWALGASTNALVRLVGFDPKAGKEGVS
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GAPHSRYPVIDGSPDRVLGFLHVRDLMGVGSTPRNTPISKLVRPVLSLPETVRVPRALSD
MRRAHSHLAIVLDEYGGTAGVVTLEDLVEELIGDITDEYDVVDDDTRKHRQLSEIDGLTT
LEDFEDATGHVIPEGPYDTVAGFFMTERGEVPTVGDSIKVSLDSDAPVSDDDEDEEKLRG
DDYELTVTQMDGRRIAWLRLRALSDTAELGAGVIEPAAAQAATKPATELAADGDPNTVAH
LTETLARNKVATDVGKADPGGNAQRP
>PFR_JS22-1_1589□PFR_JS22-1_1589□AzlC family protein□1813907:1814575 Forward
MGLAISVATGMYGISFGALAVTAGLTVWQACALSALMFTGGSQFAFIGVIAGGGTGAAAW
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>PFR_JS22-1_1591□PFR_JS22-1_1591□Isocitrate dehydrogenase [NADP]□1815044:1816261 Reverse
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>PFR_JS22-1_1592□PFR_JS22-1_1592□Malate dehydrogenase□1816439:1817425 Forward
MSTTPVKVAVTGAAGQICYSLLFRIASGSLLGDTPIELRLLEITPALPRLEGVVMELDDC
AFPNLAGVEIGDDPEKVFDGANLAMLVGAMPRKEGMDRSDLLGANGKIFTGQGKALNKVA
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>PFR_JS22-1_1594□PFR_JS22-1_1594□Bifunctional protein FolD□1817936:1818796 Reverse
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GIESYRVDLPADATPEQVERSIRVLNDSTMCTGYIVQLPLPPQIDPNWALELIDPDKDAD
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VGDFTADVWDVASYVTPNPGGVGPMTRAMLLVNVVERAEQIAAQEQ
>PFR_JS22-1_1595□PFR_JS22-1_1595□Bifunctional purine biosynthesis protein PurH□1818870:1820423 Reverse
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>PFR_JS22-1_1597□PFR_JS22-1_1597□Hypothetical protein□1821167:1822645 Reverse
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SGAADPVHGDEG
>PFR_JS22-1_1598□PFR_JS22-1_1598□ATP-dependent DNA helicase PcrA□1822739:1825228 Reverse
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>PFR_JS22-1_1599□PFR_JS22-1_1599□Phospholipase D domain protein□1825365:1826618 Forward
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QGPHGPLAVYY
>PFR_JS22-1_1601□PFR_JS22-1_1601□ABC-type cobalamin/Fe3-siderophores transport system, permease component□1827475:1828593
Reverse
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TFLIVLLRKGRL
>PFR_JS22-1_1602□PFR_JS22-1_1602□ABC-type enterochelin transport system, permease component□1828586:1829617 Reverse
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TWLLSVVGSCLVLWVYNKVSSRS
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>PFR_JS22-1_1606□PFR_JS22-1_1606□Sensor histidine kinase□1832103:1833446 Reverse
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>PFR_JS22-1_1607□PFR_JS22-1_1607□Possible stress-response transcriptional regulator protein PspC□1833688:1833978 Forward
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DGVDGSKGLDAVKRTINGFRDKNDGPQDFNPYDDTK
>PFR_JS22-1_1608□PFR_JS22-1_1608□NADPH:quinone reductase and related Zn-dependent oxidoreductase□1834275:1835219 Forward
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IGIEAVGRVHATSPASGLEVGQRVVTLMGGLGRDFDGSYQEYALVPNSQLYPVGIEMAWN
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TSTEMGKIVVSVAH
>PFR_JS22-1_1609□PFR_JS22-1_1609□Protein containing DUF1963□1835270:1836157 Reverse
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>PFR_JS22-1_1610□PFR_JS22-1_1610□GMP synthase (glutamine-hydrolyzing)□1836362:1837801 Reverse
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>PFR_JS22-1_1613□PFR_JS22-1_1613□Putative sugar ABC transport system, ATP-binding protein YtfR□1840290:1841180 Reverse
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VETLFSVMRRLRDQGVAILFVSHFLD
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>PFR_JS22-1_1619□PFR_JS22-1_1619□Class II aldolase/adducin family protein□1845896:1846543 Reverse
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GKHAREAVKAAVMVEDVARTAHYARVGGEAHRAAR
>PFR_JS22-1_1620□PFR_JS22-1_1620□Ribulokinase□1846540:1848309 Reverse
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TAVPAFSSTGAQVLAINGQPNGLNINENAGSTHIGGLQKRVVAEGADMGFAFDGDADRCL
AVDADGHVVDGDQIMAILALALKDEDSLAEDTLVATIMSNLGLIQAMRAHGVKVDQTKVG
DRYVLEDMVANGFSLGGEQSGHVIMSEFATTGDGVLTALHVASRAAQTGKSLAELAGVMH
RLPQALVNVPNVDKLRAALDPVIQSEANAANKKLGNSGRVVLRPSGTEPLVRVMVEAATQ
DEADEIANALAKVVAERVGLSKAGRAS
>PFR_JS22-1_1652PFR_JS22-1_165230S ribosomal protein S91886439:1886990 Reverse
MSAPTNEDSTVSQTTNDDVETGTTPFTDENNREIAYRADSTGAAPNASTSRSAVIAPGIG
LGRRKEAVARVRLTPGTGKYTVNGKTLEAYFPNKLHQQLINESFVVSGSADAYDVVARIV
GGGISGQAGALRLGIARALNQIDEEVNRPGLKKAGLLTRDSRAVERKKAGLKKARKAPQY
SKR
>PFR_JS22-1_1653PFR_JS22-1_165350S ribosomal protein L131886987:1887430 Reverse
MSTYSPKPGDITRTWHVIDAEDVVLGHLAVAAATLLRGKHKPTYAPHMDTGDFVVIVNAS
KIAISGNKREGSLRHRHSGRPGGLHTTSIGELLDSDPRKAVELAVWGMMPKNKLSRQQMS
KLKVYAGPDNPHKAQNPEPYEIKQVAQ
>PFR_JS22-1_1654PFR_JS22-1_1654Elongation factor G fusA21887731:1889827 Forward
MRTVSSPTDLRNVVLVGSAGSGKTTLFENLLRARIPGYRGERDDAERASALTLATIGNHN
DTAGSDVVINLLDAPGHPDFYGDLRAGLRAADGAVFVVSAADGVDPITAALWAECAEVNK
PRAIVVTKLDTDKADFFATTELIHEAFGAGTHPAYLPLLREEGGEVIGNISLLTGHVHDY
SSGQRVTRDTTPLERAEMDAFRADYVESIITESEDEDLLERYFNGDDLETGKVVEALFRA
LYHGTFFPVIPVLMDGIGVEELLGMIHRGFPMPNRRVLPAITTAGNDLVEPELGDPAGPL
VAQVIRTVADPYAGRLSMVRIYSGTLRTDATVHVAGHREAMTGRALDHYPDHDDEERVGQ
ITVPVGTDTAVQDAAIAGQIVYVARMAHAQTSDTLSDTDAPMVVEPWPLPRPLLPLALHA
TSRNDDDKLSNALQRLLVEDPTVSVERDPATDQLVLWTMGQAHLDLLLARLTGRYGVNVE
REEIKIPLRETFIAETVGHGRHVKQSGGHGQYALANVRIEPGERGSGFVFAEEVVGGSVP
RQFIPSVEKGVRTQLDRGVLSGYPVVDVKVTLTDGKAHSVDSSDMAFQAAGAAALRDAAS
AETVALLEPFDEVTVVCGNEYVGAVMTDLGSRRGRVTGQHGGDDGRTTVTALVPASELTR
YAIDLRGLSHGTGRFEREPAGYELMPPELAQQVLDERG
>PFR_JS22-1_1655PFR_JS22-1_1655PF03733 domain protein1889959:1890354 Reverse
MPKPLATLLNVIWLVLGGVWLALGYVVAGVIGCVLIVTIPAGIASFRMARYVLWPFGRTV
VPKPGAGAGTAAMNIIWMIVAGWWLALLHIISALAQAVTIVGIANAVVSLKMIPISVMPF
GKQIVSTTSNR
>PFR_JS22-1_1656PFR_JS22-1_1656TRNA (guanine-N(7)-)-methyltransferase (Precursor)1890567:1891421 Forward
MSDNSRVHHAMADGAAGGRVGPGGTSSDPSGTSHSSVDPINGRRGVVSFVRRSPRMNESQ
RQALASHSSEYLVEVPHDRLSTSVRHGATMSWPQVFGRQAPLVAEIGSGVGDSLVAMAGA
RPSDNVIAFEVYLTAVASTMGKLARADVHNVRLVVADGGEGLRELVRPGELSELWTFFPD
PWPKKRHHKRRLVQPGFAALVADRLAPGGLWRLATDWADYADQMREVLDAEPGLTNVYSD
RPGGWAPRPDRPFTRFEKRGLDAGREVRDLAYRRVHPEGDGENG
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>PFR_JS22-1_1657	PFR_JS22-1_1657	TRNA pseudouridine synthase A	1891414:1892292 Forward
MGDRRFRLDLSYDGTHFHGWAMQPGQRTVEGELATWLTRIAGTAQPVRLVVAGRTDAGVH
ARGQVAHADLPATMDAAELKRRLLRALPPDIVVRRLTVAPPGFDARFAAIWRRYVYRLWD
LSSHPDPLLRGMVTTKSLDLDPELMTAAGSRLLGLRDFAPFCRRREGATTIRTLLQCEAR
RVADGCGTIELTVRADAFCHSMVRSLTGALVAVGSGTQSMDWLDEVAAGPTRAGSVTVMP
ARGLCLEQVAYAPDHELAQRARAAHARRTLPAGPETTTGPVDSDDCGCGFEG
>PFR_JS22-1_1658	PFR_JS22-1_1658	Methyltransferase small domain protein	1892330:1892929 Forward
MTQYFVNPEGPAKYHQLHATIWGHDYEFRSSNGVFSQYRLDLGTSVLLRTLDPPVDRPAR
FLDLGCGFGPIAVALATECPRARVDAIDVNERAVELTAMNAKALGVASQVSASAPDQVPA
DVRYDEIWSNPPIRIGKPALHELLDTWLNRLTDDGVAHLVVAHNLGSDSLAKWLTGQGWQ
VDRLGSAKGYRVFDVTRRH
>PFR_JS22-1_1659	PFR_JS22-1_1659	Hypothetical protein	1893239:1893790 Forward
MKSSPTLAVAALGLCAITALAGCSSSTSGSSSSPSNTATALSMKDCTSQGKVWLVVQTDQ
DKTLANQCVGTPSTGTAALEAANVAIGRSSDGKMICTLGDYPNPCPATFTGAYWQYYTAT
PNGSWTYSDKGADDSSPKAGSIEGWCYGTTCTPKLDGVSAAPSASQSAEASATNSATSSV
SGS
>PFR_JS22-1_1660	PFR_JS22-1_1660	Cobalt transport protein	1893836:1894936 Forward
MVAAPASVHRMARRSTHPWAWWCWAIGAAAAVSLTHNLALIVLVCAAVITVVMVRRSDAP
WARAMGLYITLALVIVTIRMLFQITIGGIRYGRVLFTLPQLQLPGWMAGIRLGGPVTLEG
LVYTAADAGRLGAMIICLGAANALANPKRALRSVPSALYEVSTALVIAMSVAPQLVESLL
RIRRARRLRGGTVRGLRGLGALIIPVLQDSIERSMSLAASMESRGYGSTRDKARVGRGAG
FAMLASLALLCFGAFSLLSLANGAVLGISTLGAGVVAAVIALRSSGRQLAVTHYRPDPWR
ARESITALCGLAVIGVTVQLGIIAPKVLTPPAQPATWPALDPLMIVIIGLILAPIAATTT
PPAGEA
>PFR_JS22-1_1661	PFR_JS22-1_1661	ABC transporter	1894933:1896549 Forward
MIEFRDVSFTYTGASDPVLHDVSFQIPEGDLCLLVGRTGTGKSTLLRSINGLVPWFDGGR
LTGTVQVDTMVTSQHRPRDLARVVGSVGQNPLAGFVTDKVEDEIAYGMEQLGVAQPAMRR
RVEDTLDLMGIADLRHRPLTDLSGGQQQRVAIAAVLAAQPRVVILDEPTSALDPTAAQDV
LSSITTLVHEVGLTVVVAEHRLERVMAFADSVAWLPGDGSVQVGPAGDVLARADVRPPLV
GLAQALGWSTVPLTVRDARRRVKAEHIVLTDPPQAPAPDGPVVLTATKLVVDYGETRAVN
AVTTAFRAGEITALMGRNGAGKSSLMWAMQGAVASSGTLEVTGADPRTVSAEKARELVTL
VPQTAADLLYLPSVGDECRQADKESGRDEGTAAGLLSELGVALDMGRDPHDLSEGQRLAL
VLAIQLSSRPRVVLLDEPTRGLDYTTKAHLATMVRTLASRGVCIVVATHDVEFAAASTDR
TIVMAEGDIIADDTTREACTASPTFSPQLAKVFWPQPILTVADVRRGRRQQADGAIRP
>PFR_JS22-1_1662	PFR_JS22-1_1662	Substrate-specific component CbrT of predicted cobalamin ECF transporter	1896546:1897397 Forward
MNLLTRHREPATAGGYLMPLEPRKRLSARTSVMLAVTAVLGLVAFCWPLFVRPGAVLGSD
SSGRTATPFVMGAIMAVVLALLIAELSNEDLDVKALAMLGVLAAVGTAVRPVSAGTAGIE
TVFVLLILAGRVFGPSFGFMLGILTMFSSALLTGGVGTWLPYQMLGAGFVGLLPGLLPRR
WPRPGSAGEIVVLCLYGFVAGFGYGYLLDFAFWPFTTGLGMGAPGFDPEASPWRNLHTFF
VLDTVTSAGWNMGRALTNAVLIALLGRPLMRILRRTSRQARFD
>PFR_JS22-1_1663	PFR_JS22-1_1663	Putative integral membrane transport protein	1897412:1899004 Reverse
MVGTLAKLQLTLAWRGVRSSTGRIIGTVIMGIYGLGLTALLVFGLVMMRTPAMDAWRGPV
LTLAFGLVTLGWPLITMFTAGSNELLDPGRFALFPVTARQLIPGLFAAAMLGAGALDTAL
LALGTVISWSGGLGTAMAAAVGAVLGVATCVISARALTALMSRVLASRRFRDVGGVAFFA
VIMAVSFGMQFGSRIFADSGAPQDVIFIAARITSWTPFGWAWALPWDVAQGAWLPAAAHL
VLAAALVWALLRLWERSLARALVSPLDSAAVGGTVKSGRFDFLAPRGPIGAVARRDLRYW
RRDPRRLIQLLAVIVVPVFMFAPGLAQGMSQGSNFAVDFAAVLGGVIVASTLAWSISYDG
SALWMQVLSGVTGREDRIGRCWSVTIVTAPYLLVVLFGSLFLTGDWQLLPGLIGALITAF
GSSLGVGSLVGALWQQAMPAPGGNVFSRGSGTTAENFLGSMIAMIAPIVLTAPNLALAIV
SWWKPWAGWAAIVVGLVIGSLACWAGVRLGGRHLDNHWPEVLNKVKETHA
>PFR_JS22-1_1664	PFR_JS22-1_1664	ABC transporter domain-containing ATP-binding subunit	1898974:1900014 Reverse
MSEQTPPPGGTSGPDPAREEPVISAFTEPQESATTPSGAHIPTPVPMPGFAPPPPMPAPT
AAGIIGDDPSLDEPVPTSVAPGRTRPVRPPGPPALSIVGLRKAFGAKLAVADLSMAVPRG
CMFGLVGPNGAGKTTTLSMATGLLRPDAGQVLVGDVDVWADPARAKALMGVLPDGLRLFD
RLSGRELLKFVGQMRRMDEATITDRSNQLLSTLGLSEDANTMVADYSAGMTKKIGLACAL
IHRPRLLVLDEPFESVDPVSGETIREILHEFVAGGGTVVLSSHVMELVETLCDAVAVMAA
GRLLAIGDTDDVRQGKPLQQRFLELVGAHHLEGGGLSWLGRSQSSN
>PFR_JS22-1_1665	PFR_JS22-1_1665	Superoxide dismutase	1900213:1900821 Forward
MAVYTLPELPYDYSALEPYISAEIMELHHDKHHKAYVDGANTALDKLAEARDKADFGAIN
KLEKDLAFNLAGHVNHSVFWKNMAPKGSAPERPTDELGAAIDEFFGSFDNMKAQFTAAAT
GIQGSGWASLVWDPLGKRINTLQFYDHQNNLPAGSIPLLQLDMWEHAFYLQYKNVKGDYV
KSWWNVVNWDDVALRFSEARVA
>PFR_JS22-1_1666	PFR_JS22-1_1666	Resuscitation-promoting factor RpfB	1901116:1902201 Forward
MKNGLKTLLIGGVGIATLAVGGVGTAIADNEVSLNVDGQQKTVHHFGGTIADMLDKQGIQ
LGDHDQVIPDASQKLHDGENVTVRFGRQITVTFNGQTHTLWTTSTNLAEILAQLGVSDDA
KLSVDRSMNVGREGLTFTAVTPRHVKVIADGRTVEVSSTDPTVGGLLKGLGIEVGGDDVT
SAPLESLPVEGMTLTVQRGHVDEKTVDEPIDYDTVRQEDPSIPSGTTKVKTAGVEGARTV
TYRIKTLDGKEAQRDVLSQTVHKQPVSKVVLVGTGQAASGGATDTANSGIWDRIAQCESG
GNWSINTGNGYYGGLQFAASTWAAYGGTAYAPTANLATRDQQITIANKVYAASGLSAWGC
A
>PFR_JS22-1_1667	PFR_JS22-1_1667	Glycosyltransferase, group 1 family	1902311:1903552 Reverse
MRGTDRVFSRPGPGAAGGAYVAGLRPGDHNGPMRIAQLANFVAPHSGGMRVALDGLGREY
VAAGHERILIVPGLRDAEVETASGVVCQIASPRVSGTYRMIVRPGAVRRALRRFRPTNVE
CSDKWTLAWTGRWATHHGVGSVLFSHERLDDMLAGWLRARRPMRRMVGFLDRRIVPRFDR
VVVASQYAAEEFARWSPRVRVVPLGVDLSEFRPLPPTPRDAGAPLRLVLVSRLSREKDPQ
LAIDAVLELHRRGVPVRLDVFGSGPDEEALRSRARGGPITFHGFIADRGELSARLGAADL
SLSVSPKETFGLVVLEALASGTPVLTSNRGGAREIITPGAGVVDEPASGHVPWGAWAPSR
PTALAEAIEQLIGRLGPGMRRAARQRAEQFSWQDCAHRMLQVHQETLGDGGRQ
>PFR_JS22-1_1668	PFR_JS22-1_1668	50S ribosomal protein L17	1903593:1904180 Reverse
MPKPTKGPRLGGSPSHQRIILANLATQLFEHGKITTTQTKARRVQPFAEQLITKAKRGDL
HSRRLAAKTVKDKFVLHRLFDEIAPTMAEREGGYTRVTKIGNRKGDNAPMAVIELITEKP
SVKAAPKAADKAADVKADIETKAEKKADKANEASSEKVEAVEEKAEEAKAKSAEVKEAKK
AERTVQESVEKSDHE
>PFR_JS22-1_1669	PFR_JS22-1_1669	DNA-directed RNA polymerase, alpha subunit	1904224:1905243 Reverse
MLIAQRPTLSEEVVNDFRSRFVIEPLEPGFGYTLGNSLRRTLLSSIPGASITSIKIEGNQ
HEFSTLPGVVEDVTEIILNLKGLVLSSEEDEPVAMYLRKSGAGEVTAADIAVPTGVEIYN
PDLHIATLADDGSIEMELVVERGRGYVSSTLNNNPDAEIGRIAVDSLYSPVLTVSYKVEA
TRVETRTDFDRLIVDVETKPSIRPHDAVASAGKTLVELFGLFRELNVEAEGVEMGPSPVD
EQLAADMALPVEDLNLSVRSYNCLKREGIHTVGELVSRSEQDLLDIRNFGSKSIDEVKEK
LGDLGLTLKDSTPGFDPLAAADRFEDEDDGADYAETEQY
>PFR_JS22-1_1670	PFR_JS22-1_1670	30S ribosomal protein S4	1905368:1905973 Reverse
MARYTGPMTKKSRRFGTDLVGNDKAFERRPYAPGVHGRGRTKDSEYSLQLKEKQKARYAY
GVLEKQFHRYYEEASRRPGRTGDLLLQILESRLDNVVYRAGFASTRRQARQMVSHGHILV
NGKKVNIPSFRVTPLDIIDVRAKSQEMTPFVIARETFGERDVPGWLTVKPNKMRVLVHQL
PTREQIVLDVNEQEIVELYSR
>PFR_JS22-1_1671	PFR_JS22-1_1671	30S ribosomal protein S11	1906004:1906411 Reverse
MATTSRKAASKTKVRRKVKKNVVTGEAHIKSTFNNTIIAISDPNGAVIAWASAGTVGFKG
SRKSTPFAAQMAAEAAGRRAMDHGMKRVDVFVKGPGSGRETAIRSLGAIGLEVGTISDVT
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PVPHNGCRPPKRRRV
>PFR_JS22-1_1672	PFR_JS22-1_1672	30S ribosomal protein S13	1906457:1906831 Reverse
MARLQGVDLPREKRLEVALTYIFGIGKTRADAILEATGISPDIRVKDVTDAQLVELRDFI
DANYEVEGDLRRSVDADIRRKIEIGTYQGRRHRAGLPVRGQRTRTNARTRKGRKKAVAGK
KKAR
>PFR_JS22-1_1673	PFR_JS22-1_1673	Hypothetical protein	1907084:1907197 Reverse
MKVRPSVKRMCEHCKVIRRRGVVRVICTNPRHKQRQG
>PFR_JS22-1_1674	PFR_JS22-1_1674	Translation initiation factor IF-1	1907290:1907511 Reverse
MAKKEGALELEGTVVEALPNAMFRVELDNGHKVLSTISGKMRQHYIRILPQDRVVVELSP
YDLTRGRIVYRHK
>PFR_JS22-1_1675	PFR_JS22-1_1675	Hypothetical protein	1907870:1908154 Forward
MAFFAVNYTYDPAKDVEAVRPRHREFLRGLAERGVLRASGPFPGLEPQRALLIFEADSAE
EVATLLDQDPMHTEDILKVREILEWNPVIGIFAV
>PFR_JS22-1_1676	PFR_JS22-1_1676	Hypothetical protein	1908185:1908571 Reverse
MSQLPIGSRPPRDPQRPVADAQRDDLTQRLNTAYERGDLSLEDYQGLLAQLFEAHTTGDL
VPVVQALPAQYRVPSAPQGAEVDTNLAPGEVNQSRKRADLSLPMAKVGIGIAAVLAIIVV
AIVIGVAL
>PFR_JS22-1_1677	PFR_JS22-1_1677	Methionyl aminopeptidase	1908597:1909430 Reverse
MERIEVKSLDQIKAMRVAGLVVAEGLAAMGDAVRPGITTGEIDQIGRDVLAAHGATSNFL
GYGTEWGLPPYPGVACISVNEVVVHGIPGSRVLLQPGDIVSIDYGAIVNGWHGDAARTFA
VGEIDSDSQLLSDVTRESMWAGISTIGTGRRIGDVSHAVEESIDSHGRDFGIIRDYTGHG
IGTAMHQAPDIPNYGKAHRGPKIGPGMCLCVEPMVTLGMDDTAVLDDEWTVVTVDSSRAA
HWENTTAVLPNGLWVLTEPDGGRAQLEAHGASYAGLD
>PFR_JS22-1_1678	PFR_JS22-1_1678	Adenylate kinase	1909442:1910002 Reverse
MGAPGAGKGTQAVGIATHYGVPAISTGDMFRDNVKNGTPLGKQVDAIMKAGDFVPDELTE
QIVADRLDQPDAQGGFLLDGFPRTMHQVDALDDYLDKHGHSLDAVISLDVDPEDLIARLL
KRAELEGRADDNEETIRHRMEVYTSSTAPLLDAYKSRGLLVAVDGNGTVDEVGARIAAAV
DAKVGR
>PFR_JS22-1_1679	PFR_JS22-1_1679	Protein translocase subunit SecY	1910014:1911327 Reverse
MISGFLNAFRTPDLRKKMLFTLFILVIFRIGSTIPAPNVNIAAIQKCASDATTGDQAGVY
AMINLFSGGALLHLAIFALGIMPYITASIILQLLTVVIPRLEALKKEGATGQETITKYTR
WLTIVLGVLQATSFTMMAVSGQLYRTCTESVVYSDGVFPIIVMILTMTAGTSLIMWMGEL
ITDRGVGNGMSILIFTQIAARFPSSMWSIKTAHQGNQGWLLLVLVVAVGLLVMAGVVFVE
QAQRRIPVQYAKRMVGNRLMGGSTTYIPMKVNQAGVIPVIFAASMLYLPMLYAMFRPEGA
AATWIATNLNGRGDTVWYNVIYVAMIIFFTFFYVSITFDPVEVSDNMRKFGGFIPGIRAG
KPTEDYLAYVLSRLTAPGSLYLALISLIPTVAIVLLGADQNFPFGGTSLLIMVGVGLDTV
KQIDSQLHQRNYEGFLK
>PFR_JS22-1_1680	PFR_JS22-1_1680	Hypothetical protein	1911627:1912145 Forward
MTPTRGLADNATESDAAEQSRTARRPRGAGVIKYLLRRVLGWIGMIFLATNLTYFLANLF
LDPKANYLERNPPIPDDQIDRMLHPYNLDPTVSLIDRWWTWLQDVLLHWNWGMSPDGQAV
NTQVAFRVWNSAQLMLGATILACAVGIAVGVYTASRQYKLVTASSRRSRSWP
>PFR_JS22-1_1681	PFR_JS22-1_1681	Oligopeptide ABC transporter, permease protein AppB (Fragment)	1912142:1912699 Forward
MNTHIVVASMVAVIVAIAINGAAGQRIFFVTGSASIGVHGFFPVLLDKAQHLILPTLCLL
FINYASYHFMQRSLLLDNINADYVRTARAKGLTKPQAIRRHALRTSIIPVATQVAFAIPG
IFTGAVLTEKIFGWQGMGDYFVTTIAKNDIHGVVAVAAFAAAMTAVGAILADIFVVLLDP
RVKVS
>PFR_JS22-1_1682	PFR_JS22-1_1682	Oligopeptide transport system permease protein OppC	1912701:1913687 Forward
MSQTPDQLVPDELGYVATADGDQNLNLPAHRTRRMRLYVRRFWRNKPAVVGLGVFAFLVL
CSLVGGRFTPFRYTDMDFGALGAQPGTPGSVVRPDGTLVNATHLFGTNSGGIDVFAMLMH
GIGRSMTIAVSVSLVTTLFAAFISALAAYLAGLTERIVLAVINFLLILPSFLLMALIANH
YSGAWQMLIVVMIVFGWMYPARVIWSLSTSVREREYISAARFMGARGPSVVIRHMVPNIG
SLLVIQFTLGVVSTVMTETGLSFLGFGVKIPDVSLGTMLQSGVSAISSTPWLFWFSAGTL
TLLTVSVALISDGLRDALDPNSAAGGRA
>PFR_JS22-1_1683	PFR_JS22-1_1683	Oligopeptide transport ATP-binding protein	1913684:1915783 Forward
MTDPILSVNDLHVSFPSEAGVVDAVRGVSFDLYPGRTLGIVGESGSGKSVTSLAIIGLLA
DSAKVTGSVTFDGTELLGLSDQQMTRHRGNDIAMIFQDPLSSLTPVFSVGDQIIEALKAK
NPHISESDARARAIELLGLVGIPNPATRVKSFPHEFSGGMRQRVVIAIAMANNPRVIIAD
EPTTALDVTIQAQILDLLKVAQRETHAAVILITHDMGVIAGSADEVLVMYAGKPVEQAPV
YEVFSHPRMPYTLGLLGAIPKVHHNDNAPLVPIKGNPPILINLPDGCPFAPRCPVAVDHC
RTREPALEVIDTIDQTVSHPDTAPGEAELVHSSACWRSGEIHGGEIDGKPVFPVPPRPAS
DIRETPRDERATTIKVDHLVKTFPLIKGALLKRRVGSVYAVDDISFDVRAGETLSIVGES
GSGKSTTLLEIMAMSHDTVGEIELDGKRLKTLSRAQRRAERRNIQMVFQDPMGALDPRFT
VYDIIAEPLHTLGFPRDGIEARVNELMNLVGLDPAHIDRFPGAFSGGQRQRIGIARALAT
NPKVLALDEPVSALDVSIQAGVINLLAELQAKLELSYLLVAHDLSVVRHISDRVAVLYLG
GIVEIGDVDAVFDESRHPYTQALLSAIPIPDPTVERTRSRVVLKGDLPSPTDNEPGCRFA
SRCPLFQTLPEQDRARCLHETPALHGGEGADHLVACHFR
>PFR_JS22-1_1684	PFR_JS22-1_1684	Oligopeptide-binding protein OppA	1915854:1917572 Forward
MRSTTTKAFAGVAVLALALAGCGSNSGSSTKSADSNAKLSYSINEQAATNLKDGGNLNLS
IEEITPQLNMFQANMTVDTSTLWNWYNPQLIKFTPSGDMKLDKNYLESVNSELKDGKTVV
TYKINDKAKFNDGTDLDWTAFQATWQANSGKEQEYNANTIDGYDQIDSVKAGDNAKTVVV
SFVGPYPWYSSLFNNVLHPAVNSADIFNNGYTGGTLASAHPEWGAGPYALTGFDANAGVV
TFERNPNWWGDKGKLDKITYTVRADVQAQVNAYKNGEADTVETSTSELLTQVTSVADTDI
RRGTRAANYLLTMNSKSELLSDTAVRKAIATGINRAQLQQVLFQGLDYSEAIGGSLTLYP
FQKGYQDNLSKVVAKTDTAAATKALEEAGYAKGSDGTYAKDGKALSLRLPLFSSSTTSKA
MYQAFQTQMKAVGIDVQIIQKSSKDFSTTVKNRDFDLLISGWASTDPNGVAFFCQKFCSD
STLNKSGTGTAELDNLIKGPGGLTSLQTAEDQESKANELEVQALGTFGILPIYNGPEIFA
VKKGLANVGAGVYATTRAQIGDFPENIGWQKD
>PFR_JS22-1_1685	PFR_JS22-1_1685	Putative luciferase-like monooxygenase, FMN-dependent, CE1758 family	1917823:1919019 Forward
MDTTENRVPVQIGIFSVSDLTPDPTTGITPTEHERLKNYALIVKKAEEIGLDAFALGEHH
NPPFVSSSPTTTLGWLAAQTSKITLSTATTLITTDDPVKIAEDYAMLQHLADGRVDLMLG
RGNTGPVYPWFGKDIRQGINLALENYNLLHRLWREEVVDWQGKFRTPLQGFTAIPRPLDD
VPPFVWHGSIRSPEIAEQAAYYGDGFFHNNIFWTMNHTKRMVDLYRRRYEHYGHGRYDQA
IVGLGGQFFMRKNSQDAIKEYRPYFDNAPVYGHGPSMEEFTEYTPLTVGSPQQVLERTLS
FKDDVGHYQRQMFLIDHAGLPIKTVLEQLDLLGEILPEMRKGFLEGRPDDIPDAPTHASL
VAARDAAGVAPVEHVKVGADDVTGTSDAPEPPDSVFEK
>PFR_JS22-1_1686	PFR_JS22-1_1686	FMN reductase	1919130:1919777 Forward
MKVLAISAGMGQPSATRMLVDRLAAATVKHAGAAGLELDEPIEVIELRDIATELMSSEIS
RVPSPRVAGAIESVEAADTLIVVSPIYNTQPAALLSLFFEVADDAILRGKPVLLGATGGT
ARHSLAIDRALLPLFHYLHALVVPTSIFAATDDWGSPASLDKRTEDAAGSFVGLLAMRAG
VPNTDELSGSDTDKASHGDDDFELENDFETMLKSI
>PFR_JS22-1_1687	PFR_JS22-1_1687	50S ribosomal protein L15	1920134:1920577 Reverse
MAIKVHHLRPAPGAKQTKHRVGRGEAGKGGKTAGRGTKGTGARKNVPENFEGGQMPLHMR
LPKLRGFQNPFRVSYQVVNISRIADLFPAGGAVGVDDLVKAGAVRDGQLVKVLGDGDITV
KLEVTADKFSASAKEKIEKAGGSVTVQ
>PFR_JS22-1_1688	PFR_JS22-1_1688	50S ribosomal protein L30	1920579:1920761 Reverse
MAQLKITQIKSTVAEKPHVRSTVKALGLKRIGDVVTKPDRPEFRGMAQAARHVVTMEEVK
>PFR_JS22-1_1689	PFR_JS22-1_1689	30S ribosomal protein S5	1920761:1921372 Reverse
MNTQAQGRGRGQGNDRRGRDDRRGRDNDRNRDQYLERVVTINRVAKVVQGGRRFSFTALV
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VVGDGEGTVGVGYGKAKEVPAAIAKGVEEAKKNFFKVPMVQRSIPHPVQGEKAAGVVMLR
PASPGTGVIAGGACRAVLECAGIQDVLAKSLGSPNAINVVHATVAALKMLEEPEQIAKRR
GKSVADVTPAALLRARQEVEVKA
>PFR_JS22-1_1690	PFR_JS22-1_1690	50S ribosomal protein L18	1921395:1921778 Reverse
MAININHRRNLAQRKASQMRRQKRVRKHIFGYPERPRLVVTRSARHMFAQVIDDVAGRTL
ASASTMETELRGMSGDKTAKAEKVGELIGQRAKEAGISQVVFDRAGNQYHGRVAAVADGA
RKAGLGL
>PFR_JS22-1_1691	PFR_JS22-1_1691	50S ribosomal protein L6	1921781:1922323 Reverse
MSRIGRLPITVPSGVEVNLDGQKVAVKGPKGNLDWNIPEPITIKKNDEGQLELSRPDDER
EHRSLHGLSRTLVNNMIIGVHDGYQKDLEIIGVGYRVISKGPTQLEFALGFSHPVTVDAP
EGITFEVKTPTSFTIHGIDKQVVGEIAAKIRKIRPPEPYKGKGVRYAGEHVRRKVGKAGA
>PFR_JS22-1_1692	PFR_JS22-1_1692	30S ribosomal protein S8	1922354:1922761 Reverse
MTMTDPIADMLTRLRNANQAFHDETSMPSSKIKAGIAEILKQEGYIADYAVKDPEADEVG
KKLVVTLKYGDDRKRSIAGVRRISKPGLRVYAKSNQLPKVLGGMGVAIISTSQGLMTDRQ
AHEKSVGGEVLAYVW
>PFR_JS22-1_1693	PFR_JS22-1_1693	30S ribosomal protein S14 type Z	1922921:1923106 Reverse
MAKTALKVKQARKPKFAVRAYTRCQRCGRPRSVYRKFGLCRICLRTLAHAGDLPGVTKSS
W
>PFR_JS22-1_1694	PFR_JS22-1_1694	50S ribosomal protein L5	1923115:1923777 Reverse
MARKNADAGLAVAEVAQATAPEMPRLKKKYREEIVKALHDEFNYDNPMLIPGLTKIVVNM
GVGDAANDRKILDGAVKDLTAITGQKPQTTKARKSIAQFHLREGQAIGCHVTLRGDRMWE
FADRLLSLALPRIRDFRGLNSNQFDGHGNYTFGLTEQVMFLEIDQDKIDRVRGMDITFVT
TARNNEEGRALLKHLGFPFKATDDAKVPSARDFRRNGNRK
>PFR_JS22-1_1695	PFR_JS22-1_1695	50S ribosomal protein L24	1923777:1924148 Reverse
MAKMKLKKGDRVQVIAGKDKGVVGEIIAVDPANERVTVQGANIVRRHTRDSADASGAQVK
GGIISVEAPLHVSNVQLLVKDGSKDVLTRIGAQRQKVSKRRADGSEYEGTRGVRIARKTG
KEI
>PFR_JS22-1_1696	PFR_JS22-1_1696	50S ribosomal protein L14	1924150:1924521 Reverse
MIQQESRLKVADNTGAKELLCIRVLGGSKRRYAGLGDTIVCTVKDAIPGGSVKKGEVVKA
VIVRAVKSHRRVDGSYIKFDENAAVILGGTTSEPRGTRIFGPVARELRDKHFMRIVSLAP
EVI
>PFR_JS22-1_1697	PFR_JS22-1_1697	30S ribosomal protein S17	1924652:1924927 Reverse
MSQTDSTTERAGRKVREGVVVSSKMDKTVVVAVEDRVKHGLYGKVITKTIRLKAHDENNE
AGEGDRVRIMETRPLSATKRWRLTAVVEKAR
>PFR_JS22-1_1698	PFR_JS22-1_1698	50S ribosomal protein L29	1924924:1925172 Reverse
MAKTESLKAADLRAQSRGDLNDQVVKLKEELFALRFQAATGQLENHSRLREVRKDIARIY
TVLQERNLGIVDDPDREGKAEA
>PFR_JS22-1_1699	PFR_JS22-1_1699	50S ribosomal protein L16	1925174:1925593 Reverse
MLIPRRVKYRKQHHPNRRGMAKGGTELAFGEFGVQALEPAYMTNRQIEAARIAMTRYIKR
GGKVWINVYPDRPLTKHPAESRMGSGKGSPEFWVVNVKPGRVLFELAGVTPDVANEALRL
AIHKLPFKARIITRDEGEI
>PFR_JS22-1_1700	PFR_JS22-1_1700	30S ribosomal protein S3	1925599:1926417 Reverse
MGQKINPIGFRLGITTDHKSRWYAEKQYSELVGEDDKIRAWLVKNLERAGISSVEIERRS
DRITIFLYAARPGIVIGRNGAEAERVRGELEKMSGKQIQLNILEVKNPETDAQLVAQGIA
EQLGARVAFRRAMRKAQQSAMRSGAKGIRIRCSGRLGGAEMSRSESYREGRVPLHTLRAD
IDYGFYEARTTFGRIGVKVWIYKGDVTGTRAERAAQKAARQAAPSRQRSNRRPGRGERGG
RRRADAAREQAPRSDAATSAPAAAPATENAGA
>PFR_JS22-1_1701	PFR_JS22-1_1701	50S ribosomal protein L22	1926420:1926905 Reverse
MSNTTQRPSRRVALLGDRPGSYAIARHVRMSAQKVRRVADTVRGMDATQAIATLRFAPQA
AAEPVRKVIESAVANAETSEGLHNEQLVISQIYVDEGVTMRRIRPRAKGSASRILKRASH
ITAVVEPAETAGHPPLKKASSAKNSSKATAADTTSDDTKEA
>PFR_JS22-1_1702	PFR_JS22-1_1702	30S ribosomal protein S19	1926931:1927212 Reverse
MPRSLKKGPFVDGHLQKKIDVQNENGTKTVIKTWSRRSMVTPDMLGHTIAVHDGRKHVPV
FITEGMIGHKLGEFAPTRTFRGHVKDDKKARRR
>PFR_JS22-1_1703	PFR_JS22-1_1703	50S ribosomal protein L2	1927230:1928066 Reverse
MAIRKYKPTTPARRGSSVSDFNEITRSTPEKSLLAPKSKTGGRNNSGRITTRHIGGGHKQ
AYRIIDFKRYDKDGVPAKVAHIEYDPNRTARIALLHYADGEKRYIIAPQGLEQGATVYAG
VGADIKPGNNLPLRNVPIGTQVHSVEMRPGGGAKLGRSAGASIQLVAREGQYATLRMPSG
EMRMVDVRCRATIGSVGNAEYSNIHWGKAGRSRWKGIRPTVRGVVMNPVDHPHGGGEGKT
SGGRHPVSPWGQKERRTRSKNKASSKLIVRRRKSGKKR
>PFR_JS22-1_1704	PFR_JS22-1_1704	50S ribosomal protein L23	1928105:1928416 Reverse
MSDFKIRDPHDVLISPVVSEKSYGLIDENKYTFIVDPKANKTEIRQAVEAVFGVKVVGVN
TANRKGKKRRTRYGVGRRPDTKRAIVTVAENDHIDIFGNAPAE
>PFR_JS22-1_1705	PFR_JS22-1_1705	50S ribosomal protein L4	1928413:1929114 Reverse
MNETTSIDVVNAEGKKAGSVELPGELFDAQANVPLMHQVVTAQLAAARQGTHSTKTRAEV
SGGGKKPWRQKGTGRARQGSIRSPQWAGGGISHGPQPREYSQRTPKKMVATALRGALSDR
AREGRIHVVSEFVGGDKPSTKSAAKVIAGLGDYGRVLVVLERSDENNWLSMRNLIGVHVV
SWDQLNTYDVLLADAIVFSESAIKAYVAGPAKGKSVKAVATSREAEAVEEKAK
>PFR_JS22-1_1706	PFR_JS22-1_1706	50S ribosomal protein L3	1929111:1929770 Reverse
MTTEHKVKGLLGTKLGMTQLWDENNRLVPVTVIQAGPCVVTQVRTPDTDGYSAVQLGYGA
IRAKSVTKPAAGQFARAKVTPRKYLAEIRTSDASEYTLGQELGPDTFRTDDVVDVTGVTK
GKGTAGVVKRWGFKGLGASHGVHRKHRSPGGIGACATPGHVFKGLRMAGRMGNARKTVQN
LAVAGVDADKGLILVRGAVPGNKGALVVLRTAAKKGEAK
>PFR_JS22-1_1707	PFR_JS22-1_1707	30S ribosomal protein S10	1929782:1930093 Reverse
MAGQKIRIRLRAYDHEVIDSSARKIVDTVTRTGAKVAGPVPLPTEKNVWCVIRSPHKYKD
SREQFEMRTHKRLIDILDPTPKTVDSLMRLDLPAGVDIEIKLP
>PFR_JS22-1_1708	PFR_JS22-1_1708	Aminotransferase, class IV	1930528:1931400 Reverse
MIISVLGTGVVDSNAPIATADDLALTRGEGVFDSTVVYRQVTGPRILHLDWHLARLERSA
QGMGIECPSRDAWRRAIDDALDVWHGHNAVIRLILSRGREVVTDDPAQHLAYVLLSDIKG
KRAHPAQIRVTQLSIGRPHDAFVDAPWLLGGVKTLSYATNMSAFRYATARGFDDVLFTTT
DGYCLEAPRAGLIWAKDGRLGTTSREGTGVLDSMTVRAAVAGARSEGFEVVDGLLGAEEI
FSADGAWLVSVSYGCTPIIEVDGRPLSVHEHLTQRMAVWTKQPYNDDALD
>PFR_JS22-1_1709	PFR_JS22-1_1709	Putative insertion element ISCmi2 transposase	1931550:1932545 Forward
MTHANAPLTPAGRRRLAIVVVEEGWSLRRAAERFQVSAGTAKRWADRYRAGEPLTDRTSR
PARCPGRLDRRTERRIIGLRTTRRWGPHRIAYHLHLARSTVGRVLTRYRMPLLAHLDRAT
GAAVRRPPAVRYEKASCGELVHVDIKKQGRIPDGGGWRIHGAGSRQHIANGRARYQRARA
GKTVSGYRYLHHAVDDHSRLAYSEILDAQDADAAAGFMARTLDWFSAAGIAVAAVMTDNG
WCYRSKAFARALGPITHVRTRPYRPQTNGKVERFNRTLSDEWAYARAYYNEEDREQAYYA
WIHEYNHHRPHTSLNGLTPSDRVPNLAGKNN
>PFR_JS22-1_1710	PFR_JS22-1_1710	Glutamate--tRNA ligase (Precursor)	1932542:1933936 Reverse
MALFDKAWAVRTGGQFVLRIEDTDRNRLVPGSEQQIVDSLNWLGLTPDESPEQGGPYAPY
TQSQRLDTYRPVVDKLLASGHAYHCWCSQERLAAMREEKAAKKQDTRYDRLCYGMTKEER
AKLPGFTETPVVRMYIPDDAPLVFHDLIRGEVKAPFPDDQVILKADGFPTYHLAVVVDDH
EMKINTVVRGEEWISSTPKHLLLYKWLGWELPAFAHMPLLRNTDHSKISKRKNPAARLMW
FKEQGYLPQALRNFLQLLAYPPAEGDQELESFADFVGNFAWSKVNTVGPVFDTKKLDWLN
GQYIRELSDSDLADQLVDFIAASRQWGDDPDPSWAEVIRRATPIIKPRLVKLSDAWDQIA
FLVEADDSVYIEDTARAQLKDNAGEVLDATAKVLATVEPFTADAIQQALRDELVDAMGIK
PRQAFAPLRVATSGRKVSPPLFESCEILGRASVLARIAGLRETL
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>PFR_JS22-1_1711	PFR_JS22-1_1711	Acetyltransferase, gnlAT family	1934162:1934851 Reverse
MAWRPAYCRGASKFVTAIACRGAYGHDCRVSDRDRAGDGGRTGDPGSGREHAAPRGPRAA
TPGHIPARAEVEIPTARLVLHGVDPAQAEQLARGISPLPCVAGYPHADSDTAARMQRHAL
EVDNWVPGYGLYLMVRRADGLVVGDIGFHTPPDQRGAAEVSYGVADSVRRRGYASEALVA
LTAWAHAHGASTVLAEVDPTNHASRGVLAKAGFLPVRSDGPKLRLRHQG
>PFR_JS22-1_1712	PFR_JS22-1_1712	Membrane protein, PF09852 family	1934893:1936323 Forward
MVTAPQRHPQLWLALICLIALAAYLVTSIVKFNRLRDGMDITIFDQAIRSFAQGHAGYTT
LKAPGMPIFGDHFHPIILTMVPLYWLWDDPRMLLITQGICIAWAGWLLGRLAIRRLGPGT
GLLIAAGFLCGIGTQYAIIFDFHELVLATPLMAMALASFIEARWTACWVWSASLMVAKED
MCFLVGGIALAMLVRRHWVRGLSLGIFAVAWTAIAVFVVVPAFNPDHVYPYLHAVGAVAV
AGVQTSAHGAWFGPLKTLGSAAILLSGTAFVALRSPLIWAFVAPFLTRAVSKNPQHWTTG
FHYNLLPMLVACYAFVEAWPRLVDAAGRTLPGRRGTLRRWWRAVALPMVGIVALASIPLG
PLWHEWTIGRCRDECRVFPAALAQLPAGSRVATDVYLTSHVAAHADVSQWRPPDYLDDRG
QPVTPDWLLLDRETISYQNKDSHWVDQFLADPVVRGTRYEVVWQRDPMVILRPAHS
>PFR_JS22-1_1713	PFR_JS22-1_1713	Translation elongation factor Tu	1936517:1937707 Reverse
MAKAHFERTKPHCNIGTIGHIDHGKTTLTAAITKVLADKYPQWNSFEAFDDIDKAPEERQ
RGITISISHVEYQTEKRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTHE
HVLLARQVGVPAIVVALNKCDMVDDEELIDLVEMETRELLTAQEFDGENCPVVRVSAFKA
LQGDEKWAEQIMKLMDAVDDYIPQPERDTDKPFLMPVEDVFTITGRGTVVTGRIERGVIT
TGETVELVGLADTQTTTVTGVEMFRKILDEGQAGDNVGLLLRGTKKEDVERGMVVTKPGT
TTPHTEFKGSVYVLTKDEGGRHKPFFSHYSPQFYFRTTDVTGTVVLPDGVEMVMPGDNTD
MEVELQKPIAMEVGLKFAIREGGHTVGAGRVTEIVK
>PFR_JS22-1_1714	PFR_JS22-1_1714	Translation elongation factor G	1937942:1940041 Reverse
MAIDLQTDLAKVRNIGIMAHIDAGKTTTTERILYYTGVNHKIGEVHDGAATMDWMEQEQE
RGITITSAATTCFWNNYQINIIDTPGHVDFTVEVERSLRVLDGAVAVFDGVAGVEPQTMN
VWRQASKYNVPRICYINKLDRTGASFDWCVQTIRERLHAVPVLLQLPIGAEADFIGIIDL
IDMDAKTWRGETELGEHYEVEEIPAELAEKAKATRAEMIETVAENDDTFMELYLGGEDWT
NEDLKAAIRRGVLANAFTAVVCGTSFKNKGVQPLLDAIVDYLPSPLDIPAVVGFKPGDES
VEIDRHPAKDQPLAALAFKIAADPHLGRLTFVRVYSGVLTTGESVLNSTKGNKERIGKIY
QMHANKRQEVEEMPAGMICAVMGLKNTGTGDTLCDPQNPIALESMTFPDPVIEQAIEPKS
KADQEKLGVAISRLAEEDPTFQVHTDEETGQTIIAGMGELHLDVLIDRMKREFHVEANIG
TPQVAYRETLRRPVTGIDYTHKKQSGGSGQYAKVIIDLEPQPAGTGYEFVNAVTGGRIPK
EYIPAVDAGIQEAMQFGVLAGYPVEDIKVTLTDGAYHDVDSSELAFKIAGSMVFKEAARR
ADPALLEPEFAVEVTTPEEYLGTVIGDLNGRRGRVKEMADEHGNKVIRATVPLAEMFGYV
NDLRAKTSGQATYTMEFESYGIVPKGIADEIIAKAHGTE
>PFR_JS22-1_1715	PFR_JS22-1_1715	30S ribosomal protein S7	1940212:1940682 Reverse
MPRKGPAPKRPVVVDPVYSSPLVSQLVSKILVDGKKTVAQSIVYTAMEGTREKTGVDPVQ
TLKKALENVKPAVEVRSRRVGGATYQVPIEVKPARSNTLAMRWLVSFSRDRREKTMAERL
QNEILDASNGLGASVKKREDTHRMAEANRAFAHYRW
>PFR_JS22-1_1716	PFR_JS22-1_1716	30S ribosomal protein S12	1940682:1941053 Reverse
MPTIQQLVRKGRSDKVSQSKTPALKGSPQRRGVCTRVYTTTPKKPNSAMRKVARVRLSSG
IEVTAYIPGIGHNLQEHSMVLVRGGRVKDLPGVRYKIVRGSLDTQGVKGRKQARSRYGAK
KEK
>PFR_JS22-1_1717	PFR_JS22-1_1717	DNA-directed RNA polymerase, beta' subunit	1941513:1945403 Reverse
MLDVNTYDTLKIGLATADQIRGWSYGEVKKPETINYRTLKPERDGLFGEQIFGPTRDWEC
ACGKYKRVRFKGIVCERCGVEVTRSNVRRERMGHIELAAPVTHIWYFKGVPSRLGYLLDI
APKDLEKVIYFAAYMITRVDEDARSRDLSSLEAKVATEHKHIEGRRDADVEKRMSKLEED
LAKLEEEGAKADAKRKVKDGGEKELKTIRDRAQRELDRLDAVWDRFKGLKVQDLEGDEVL
YREMKNRFGKYFDGFMGAEAVKRRLETFDLAAEADSLRETILTGKGQRKTRALKRLKVVS
AFLDTGNSPMGMVLDAVPVIPPDLRPMVQLDGGRFATSDLNDLYRRVINRNNRLKRLLDL
GAPEIIVNNEKRMLQEAVDSLFDNGRRGRPVTGPGNRPLKSLSDMLKGKQGRFRQNLLGK
RVDYSGRSVIVVGPQLKMHQCGLPKQMALELFKPFVMKRLDDLNYAPNIKSAKRMVDRQR
PQVFDVLDEVIREHPVLLNRAPTLHRLGIQAFEPLLIEGKAIQLHPLVCAAFNADFDGDQ
MAVHLPLSAEAQAEARILMLSSNNILKPADGKPIALPSHEMIIGMYYLTQDLDGLTGEGR
AFSSKAEAVMAYDLHQLDLRAKCKIRLSGVVPPVGLEDKQRADGSLLLDTTLGQVIFNEA
LPDNYPYVTSHVGKKQLSAIINDLAIRFPRPVVVATLDNLKDMGFRWGTQSGVTVSIGDV
QTPPNKPEIMASYEKKAAKIDKLYDRGAVTEEERRGELVQIWNDATAELTDAMEKNFTKT
NPIYMMVNSGARGNMTQMRQIAAMRGLVANPKGEIIERPIKSNFREGLTVLEYFISTHGG
RKGQADTALRTADSGYLTRRLVDVSQDVIIREEDCGTERGLMKAIAEPGADGMLVPAKML
DTSVHGRILATDATDESGKVVIEAGTMLDSTVVGNAIRAGITSIKVRSVLTCEATTGACA
KCYGLSLANGKMVEVGEAVGIQAAQSIGEPGTQLTMRTFHTGGVAGDDITQGLPRVVELF
EARTPKGKAPIAEADGRVKIEETDRGRKLTIVRDDGGEDVEYALPRRARLEFEDSNRVRH
SIADGVHVGVGEQLTGGTIDPQDVLRVRGLRKVQEHLVEEVQKVYASQGSPIHDKHIEIV
IRQMLRRVTVIESGDTPMMPGELVDRKTYEAANRKAVEEGGRPAEGRPVLMGITKASLAT
ESWLSAASFQETTKVLTDASIHGKSDHLVGLKENVILGKLIPVGTGLERYRDIRVEPTAE
AKANSFQVNYDPFDYDFGSGSGAAVPLDDLDFGDLR
>PFR_JS22-1_1718	PFR_JS22-1_1718	DNA-directed RNA polymerase, beta subunit	1945505:1948981 Reverse
MAASRTALNNSDVVSTTGRISFAKIREPLGIPNLLDLQVKSFNWLVGNENWQNEVDQALS
EGRTDVNTKSGLEEIFEEISPIEDFSQTMSLSFRDHRFEEPKYTIEECKDRDATYAAPLF
VTAEFMNNDTGEIKSQTVFIGDFPLMTDKGTFIITGTERVVVSQLVRSPGVYFEQTPDKT
SDKDIFTCKVIPSRGAWLEFEIDKRDTVGVRLDRKRKQNVTVLLKALGWTEERILEEFGE
YESIRMTMEKDHVTTQDEALLDIYRKLRPGEPPARDAAQTLLDNFYFNPKRYDTAKVGRY
KINKKLGLSLPYDQQVLTMDDIVAAIHYICALHEGKTELADGLPVEPDDIDHFGNRRVRT
VGELIQNQLRTGLGRMERVVRDRMTTQDIEAITPQTLINVRPVTAALKEFFGTSQLSQFM
DQNNPLAELTHKRRLSAVGPGGLSRDRAGMEVRDVHPSHYGRMCPIETPEGPNIGLIGSL
ASFARVNAFGFIETPYRKVDKGLVTDHIDYLTADEEDRFVIAQANATMNDKGELTEDRVL
VRVSHGDVDLVPADEVDYIDVSARQMVSVGSALIPFLEHDDSSRALMGANMQRQAVPLVR
NESPYVGTGMEYRAAVDVGEVTLASKPGTVTGVTGDLIDIACDDGTYQTFKLEKFQRSNA
GTCVNQRPIVTPGQHVEAGTPLADGPCTDQGELALGRNLLCAFMPWRGLNYEDAIIISQR
VVSEDILTSIHIEEYEVDARDTKLGPEEITHDIPNVSDDMIASLDDRGIVRIGAEVRPGD
ILVGKVTPKGETELTPEERLLRAIFGEKAREVRDTSMKVPHGEEGTVIGVRIFDREENDE
LPPGVNQMVRVYVAQKRKVQVGDKLAGRHGNKGVISRILPIEDMPFMADGTPVDIMLNPL
GVPSRMNLGQVLEMHLGWIAHSGWDLGDATDPWAEHLREVGLEHVDGDVRLATPVFDGAE
EHEITGLLAHGLPNRDGDHIVDSDGKTTLFDGRTGEEFPEEVGVGYMYMLKLHHLVDDKI
HARSTGPYSMITQQPLGGKAQFGGQRFGEMEVWALEAYGAAWALQEMLTIKSDDVAGRVK
VYEAIVKGENIPEPGIPEGFKVLVQEMKSLCLNVEVLGSDGAVIDLRETEDDYRTVDELG
IDLSRRPGTDSYKLESEG
>PFR_JS22-1_1719	PFR_JS22-1_1719	Hypothetical protein	1949307:1949933 Reverse
MARRHWWRRIIPGLSTSVRLVAIGVAVLVVAVMTVVNVMTSKNTNQPGSRAGTWNTALPS
TGVPTAASSSSNAVSTDSRAYSELVRLSDQGWTATQPLTNQWVAELGSSVVVPPSQPTPT
PSGSASPSGAPAALARFESAQKNDPGAGREVRLLRRSTYNPPVVDDRFTFVIIVSGTFST
ADDVRNWCSDQFGSAPPDRCDPLQLHPR
>PFR_JS22-1_1720	PFR_JS22-1_1720	LSU ribosomal protein L7/L12 (P1/P2)	1950204:1950599 Reverse
MAKLSTEELLDQFKDMTLIELSDFVKAFEDAFDVKAAAPVAVAAAPAAGAGEGEGAADDA
NAEVDVVLDSIDSSKKIQVIKEVRALTSLGLKDAKDLVESAPKIVLEKVNKDTANDAKEK
LEGAGATVSFK
>PFR_JS22-1_1721	PFR_JS22-1_1721	50S ribosomal protein L10	1950616:1951263 Reverse
MARPDKAAAVAELTEKFTESNATVLTEYRGLSVQDLQDLRRSLGDNASYAVVKNTLTKLA
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AKEAGVEGLDDQLTGPTAVAFISGDIATVAKGLRDFAKANPLLVIKGGVMDGQILDAETV
TKLADIGSREELLAKLASAMKASMSNAVATFAAPLSQAARLMGALESKAQGDPSVIGGAG
TPAADQKQDTAEESAPEAASAAEESADAADAASNE
>PFR_JS22-1_1722□PFR_JS22-1_1722□Lipoyl synthase□1951632:1952582 Reverse
MTTPAQGRRLLRIEKKNSQTPIEKGRPAWLRTRLSMGPEYLDVRERTGGEGLHTVCQEAG
CPNIFECWEDREATFLIGGEHCTRRCDFCQIESARPTGYDRDEPRRVGESVKQLGLRYAT
ITSVCRDDLPDEGAWLCAETIRQVHSQNPGVGVEMLAQDFSAKQELLDQVFEAAPEVFGH
NVETVPRLFKQIRPGFDYDRSLQVLTMAHEAGVISKSNLILGMGETDDEVAQALQDIHDA
GAELVTITQYLRPNVTLRPVDRWVTPQQFVEFGKLADQIGFMGVMSGPLVRSSYRAGKLY
RQAMSGREAAAQAAEA
>PFR_JS22-1_1723□PFR_JS22-1_1723□Octanoyltransferase□1952579:1953451 Reverse
MVAVTDQREEATVQPTTPQAVNGVLPPNWVPHPAGLDYERHCLDAAPGALYDYETGWEHQ
REILDAVAHHRSPNRVLYVQHESVYTAGRQTQPEDRPFDGTPVVDVDRGGRITWHGPGQL
VGYPIIFLQRGVGVVDYVRRVEEAVIRLLAQYGIATGRIPGRTGVWLASDGIRPERKICA
IGVRCAHQTTMHGFALNVDPAFDRFDNIVPCGIDDADVTSIRRELGRAPSLSQVADDLTP
HLTEMMSFAPYQMSPDVPRTQHAAFHHPTADHPAADHHQPQPNVVKEIRL
>PFR_JS22-1_1724□PFR_JS22-1_1724□50S ribosomal protein L1□1953618:1954328 Reverse
MKHSKRYRADAALSDPEQLYTPDEALAIIKQYTPGKFDETVEVSMRLGVDPRKADQMVRG
TINLPNGTGKTARVLVFAQGAKATEALEAGADEVGGDDLIARVNDGYLDFDAVVATPDLM
GKVGRLGRVLGPRGLMPNPKTGTVTMDVTKAVSDIKGGKIEFRVDRHSNLQFIVGKLSFT
TEALEQNFRAAADEVYRLRPSTSKGRYVKKITVSTTMGPGVQVDPVAARPASEVSS
>PFR_JS22-1_1725□PFR_JS22-1_1725□50S ribosomal protein L11□1954450:1954878 Reverse
MPPKKKVAAVVKIAIAAGSATPAPPVGTALGPHGVNIMEFVKAYNAKTEAQRGTIVPAEI
TIYEDRTFDFITKTPPAAELIKKAAGVQKGSGQPDKEKVGTITSDQVREIAETKMPDLNA
NSVEQAMKIVAGTARSMGVTVK
>PFR_JS22-1_1726□PFR_JS22-1_1726□Transcription antitermination protein nusG□1954988:1955875 Reverse
MTQTPDEGDNKPLEETELNLGSNDDQGDTDTGINLDFADFSDDDAKSGAELNLGPLPTEE
GEADKAEPAADQDAEKPDEPDEKAPSQEDEAVAKALEELHDDLVVKPGEWYVVHTYSGME
NRVKQNIDNRVKSLNMEDYIYETVVPTEDAVEMRKGQRKKVTRVFMPGYVLVRMEMTDES
WSTVRHTPSVTGFVGQGQTPAPLDLSEVEHMLTPSVTAQVVASGEAKAGADQEKVEVVDY
AVGDQVMVIDGPFAGVHATITEINTHNQRLKADVEILGRETPVDLTFPQIQKVID
>PFR_JS22-1_1727□PFR_JS22-1_1727□Putative SecE/Sec61-gamma subunit of protein translocation complex□1955895:1956482 Reverse
MADRSERAKRRAEQAQSGPVKRHRSTGEHMEADDLPGSMLPEANGEPDPAVIDDADAEEL
TNADDTVDSTPDKGDPDDVRIDDESQLDEAERRADEAQDEKPTPIVRKHSTSPVRKAGGA
RAKAGKPTQAKKGHKRAGPITFTKQSVGELKKVVWPTGEQTGQYFVVVLVFVLFIMAVVA
GLDFGLTRLLLWLFG
>PFR_JS22-1_1728□PFR_JS22-1_1728□Hypothetical protein□1956915:1958399 Reverse
MATRASSRLLEWGTSALVTALFVVLWWRQRAVSPATHEEASSLLHAQLGVGGLWTATAHA
DRSWFAYWLCLVPMGSGPDALTVARTFSLVCAAVMVFALAATAGRLWGTGGALVAGGFLV
ANPAIVTLALSARGEMLGLALLALASWLLVALLESYQDLGLGPGIVYGLLLAAMVVCDLT
LAPVMVAHLFYAATMRPSGEGWRQLVPGWLAGAAIAVLIWANGHAGYTVAPGPQDGSGQL
RAVVRLLLDASGDFPGQVMLGGAALIIIIAIVNTHGNAFFDTGLGLAVLMVVAQPGADLL
LALTGRATPPDQVLGATTLGAALLLGCAAGQWRGANMQSLVVLLLAAGLGIFGWRSYSQV
KPSWRNADGNPPLARDLMLTTAPGDVVAVDEKSGPGLTGAIALAMGDQRLWQEARDQLTA
ASPRVFLVAGHEPWASAPASTAQAGGNLTGAGLTGSVRWVSLDASSAPDWQHCTIKDSDP
YARATVTHLECAAS
>PFR_JS22-1_1729□PFR_JS22-1_1729□UDP-N-acetylenolpyruvoylglucosamine reductase MurB□1958421:1959554 Reverse
MSIADEEDYDLFDSCELDPTSGILPEREISDSPVLADHTSFHIGGRAKRFVVARTEAEVL
DEVKRADEAGEPLLVLSGGSNMLVSDDGFDGTVLQIATRGVEGEISGCGGAVMNIAAGEN
WDDFVQLAISREWRGVEALSGIPGMVGSTVIQNVGAYGAEVGELVYRVRTWDRQEKSYRT
FANADCKFSYRNSIFKQSRLPGSPTGRYVVLEVTLQFLLGNMSMPIRYAELAHRLGIEVG
EHAPAQKVRDEVLALRRSKGMVIDPDDHDTWSAGSFFTNPILTSQVAAGLPEDAPRFDAG
GGMVKTSAAWLIDHAGFHKGFGEGAATLSGKHTLALTNRGQATAADVVALARQIREGVHQ
ALGITLVPEPVLVGLSL
>PFR_JS22-1_1730□PFR_JS22-1_1730□MaoC-like protein□1959624:1960055 Reverse
MSAFDPAAVRAGDVLPPLTLTITRGGIVRYAGASTDFNPIHWSDRKARELGLPGVLAHGM
WTMGASLRIITDWCADPRRVLDYQVRFTRPVQVPDDDRGVQVQVSASVTGVEAGVATVAV
DARIDHEGKPVKVLGNARAHIRL
>PFR_JS22-1_1731□PFR_JS22-1_1731□UPF0336 protein□1960052:1960486 Reverse
MPIGPEHVGRTYPSTAPYRVSRAKILEFVKSLGDPNPAYLADDDTPFTAPPTFAAVIAAS
AWGAMFDDPDLGLSLQRTVHADQRFDIERLMREGDDVTATLTITKVHNRGLTDIVTIAVK
LDTVDGEHLCTATSTLLNSREAAE
>PFR_JS22-1_1732□PFR_JS22-1_1732□50S ribosomal protein L33□1960634:1960804 Reverse
MAKKAGDVRPKITLACTVCKERNYITKKNRRNTPDRLELSKFCPRDGRHTLHRETR
>PFR_JS22-1_1733□PFR_JS22-1_1733□Alkyl hydroperoxide reductase, F subunit□1961203:1962858 Reverse
MAVLDAALISQLNQLMDRVTHPVELVMSLDDRPESAQISDMLEQVAALSANITVRRDDSA
HDRRPAFSITRPGSDISITFAALPTGHEFNSFVLALLQVGGNPVKLDEKVVAGARAITTP
KNFVTYISLTCQNCPTVVQAINAMAVLNPLITNTVVDGSLFRDEVEAEKIKATPTMYLNG
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ALIGDRFGGQVNDTLSIENVISVPHTEGPKLASDLRTHASQYEIDMIDGVRASELLPTTD
GDDLVRVRLEGDAQLSADAVVLATGAHWRQMGVPGEQEYRNKGVTYCPHCDGPLFKGKDV
AVIGGGNSGIEAALDLAGVARHVTVVEFMPACKADEVLLDRVDQTTNITVLTNSAVTEVV
GDGSQVTGLHYDDRATGEHRELALDGVFVQIGLMPNTDWLKGAVKLDAHGQIVIDDRGAT
NVPRVFAAGDCTDVPFKQIIVAEGAGAIAGLSAWESLIREQSTAAPKGSDAASTTGSQDA
RKGEPQAAMAR
>PFR_JS22-1_1734□PFR_JS22-1_1734□Alkyl hydroperoxide reductase, C22 subunit, thioredoxin-like (Detoxification of hydroperoxides)□1963082:1963645 Reverse
MSLVGTQILPFKASAFHQGEFVDVTDEDLKGKWSVIFFYPADFSFVCPTELGDLADHYDQ
FQKMGVEIYSASTDTHFVHAAWHKESEEVKKVQYVMLGDPSGQLATNFQVLREGQGLADR
GTFLIDPDGVIQLVEVSADGVGRDASELVRKVRAAQYVRQHPDQVCPAHWDETGDTLTPS
LDLVGQI
>PFR_JS22-1_1735□PFR_JS22-1_1735□Hypothetical protein□1964169:1964663 Reverse
MLRHTGGMAREPQVFHADGPVRRTWASKLAATLAVLVVVALIVGPVVVRAVHRSNADAAE
ASLLLLGLACVVVGLVAVLCAFVAVVRDRGTSRVGALLFLADAGVQVVYGLIGISSTQMQ
GLADQAYSWSWAAISLLVTVVACAFTFMPPRPLTTRKDARRPVR
>PFR_JS22-1_1736□PFR_JS22-1_1736□Exodeoxyribonuclease□1964742:1965683 Forward
MLRLATYNVNGIRAAQRRGFTGWKQRCLPDVACLQEVRCPYEALPMEAFAGFHVAYDAGE
LKGRNGVAVLSRTPFDAVRVWSDQAMFISPAGDARMAGADELSVPDYPLARPLRSFNHEG
RYVEVDLADQPLTVACVYVPKGDSLLAPGIRSRDPLTDEQLAGVQRRYDRKMAFLAGFSR
HLTRARRAAHAAGREFLVVGDFNIAHTRLDVKNWRPAQKASGFLPEERAWLSEQLSPRTL
VDVVRAAHPDQDGPYSWWSWMGQAFARDTGWRIDYHLASPQLARRSARAFVDRDHGADER
VSDHAAVVVDYDL
>PFR_JS22-1_1737□PFR_JS22-1_1737□Hypothetical protein□1965742:1966128 Reverse
MANLQQAATSTTLTFTNRERLAVLITTTLGVIGVGWSAVGLVRDGISARELVGFIGQTLI
YLALLIGILQRRGWAVTLVRFFAFCTVAQIIVSPNYPTTARFLTTLVFLACVVTLLWSLK
GFRTVRRT
>PFR_JS22-1_1738□PFR_JS22-1_1738□Mannosyltransferase MptA□1966295:1967884 Reverse
MVVEGSRAVAWLANCWRDLADALRVRVVRRGLYGTLLIAIGALSPAYLPRSSPWWTWLSA
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RRAEGLPSKLIGTAATMAGLLLIMSAWYRLRPGARGGAPGDATGPAAYLTLKHWAVLAWW
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IKQPAFLAAYVVPMLARRWGSLKVGETAITVTRVLTSFAVSIAVFAGISIATGLDFGWYN
AVSVPGSVGSPAPASIVGNGVQWVMNLFGADPTAKLGISITQTVFLAVGAVVLALGAVTI
ARKRPATFISWGYLVVAIASPALHSWYMLWGGLTLPLAQPRRRLVAVAIWVNLALLCYDA
VDMAWRNDGVAIGVAAVAASVFMTWIHQASVRVTRHPGHATHLELPATS
>PFR_JS22-1_1739	PFR_JS22-1_1739	Oxidoreductase alpha subunit	1968056:1969945 Forward
MNPGQQTPQRQRLNRVVIRFAGDSGDGMQLTGDRFGAESAEHGNDIATLPDYPAEIRAPQ
GTIAGVSSFQIQFADEDIVTPGEHVDVLVAMNPAALRANLADVVRGGLVIVDKHSFAKRA
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GRPTEDTVHWLGETFASRPSVRDANIAALRAGENYGENTEQFAVRYEVPPAPVPAGRYRR
ITGNLATAYGLMVGAARAGMTLFVGSYPITPASDILHELSKRKAFGVITVQAEDEIAGIG
AALGASLGGALGVTTTSGPGFALKQEMINLAVMTELPLVIVDVQRSGPSTGMPTKTEQGD
LLQALWGRNGESPLPVFAPSSPSDCFQVTVDACRAAVENRTPVVLLTDAFLANGAEPWQV
PDLSQIAPIDPHFATGPNGFDEKGKPTFLPYKRDPQTLARDWALPGTVGAEHRLGGLEKS
VEAGTVSYDPANHEQMVHTRAERVARIPVPDALVGDPEGEADLLVVGWGSSWGPITAAVR
DLRAAGRHVAQVQLRTLNPLPANLDQVLHRYRRVIAPEVNLGQLALVLRAKYLVDVRTFS
KVRGQPLPVGELTQYLAGHLDEIEQEARR
>PFR_JS22-1_1740	PFR_JS22-1_1740	2-oxoglutarate ferredoxin oxidoreductase subunit beta	1969942:1971021 Forward
MSIDATQADEQANGLLGVPLATTPLNRKDFVTEEPRWCPGCGDYSILSAFQQVLPELGIA
RENTMVVSGIGCSSRLPYYLNSYGIHSIHGRATTLATGLAVTRPDLAVFVVTGDGDALSI
GGNHLLHALRRNVNITILLFNNRIYGLTKGQYSPTSAVGQVTKSSPMGAPDRPVNPVSYA
LGSEATFVARSLDSDREHLVSTIAAAAHHRGASLVEIYQNCPVFNDGAFEALKGPGADEA
VIPLVAGEQIRFGTDRELCVVPDANGGVRIAKVSEVKEADIVVHDPTNPDPTRAFALSRL
TDSGVMHRAPMGIFRDISLPSYDDQVRTQITQATHGEANPSSDPALQNLINGTDTWLVE
>PFR_JS22-1_1741	PFR_JS22-1_1741	Peptidase family M13	1971151:1973124 Forward
MGSLGQVSTPAFHFEDFDKSVAPTTDLFRHVNGTWLKNAVIPDDRSNWGAFAILRENSEK
AVHEIVEGLEAGDDPTTEQAKIANLYASFMDEETIEALGVSPLAPILARVDAIASVADLA
SFWGWSVRHGINPLADFDNDSDPGNPNRYLMFVGQAGIGLPDEEYYRLPDHEDLRALYLA
HIRKSFDLAGVADADGQATMAFELEKQIAACHWDKVRTRDMTQMYFPQTWDDFTAATPTL
EWDSFLAGAELPREAVSEVVNAQRTFLGDVAKLVIPENLDRWRAWARWQVVSGLSPYLNR
DLSAQSFEFYSKGLRGVPKQRARWKRGVSVTEGVLGEAIGKRYVAKHFPPETKAAADRLV
RNLLEAYRASISTLDWMTEATRAEALDKLSKFRTKIGYPDKWRDYSALEIAPDDLLGNVL
RADSFEFDHTIEQLSGPVDRDEWFMYPQTVNAYYHPLRNEIVFPAAILQPPFFNVDADDA
VNYGGIGGVIGHEIGHGFDDQGSTCDGDGRLRNWWTDDDRKAFEDRTHALIAQYNELAPS
VCPEVHVNGELTIGENIGDLGGLSIAYQAWLLSLGGVEPAPQDGYTAAQRLFLGWAQVWQ
NTTRPEQMRQSLAVDPHSPDEIRCNQVVRNISAFHEAFGTKPGDPMWLEPSDRVQIW
>PFR_JS22-1_1742	PFR_JS22-1_1742	Hypothetical protein	1974033:1974416 Forward
MRPGTQVGPQAQPTQEPAGSRDAFMPGPQDAEPTLLDTGAHHDARNGAEDDTVRLENPAA
SEQTVVLGDTAASESTVVLGDTTPVPTTDPDQFWASPGADSATRPPKNATPPPSGDDSQE
PPAVTGR
>PFR_JS22-1_1743	PFR_JS22-1_1743	Inner membrane protein YhaI	1974489:1974944 Forward
MSPLEAIKSCFRNYVNPNGRSGRAEFWWFLFFILVVDSVLGLLAVLTGDHTTLADDGWFY
AYMSHNVWFNALGWVFSLAMLLPFIMVQIRRFHDQDRSGWWLLLHFIPGFGNFIVLVFMA
IGGTFGPNRYGPGRYDPRAAFDPDTPLTPTR
>PFR_JS22-1_1744	PFR_JS22-1_1744	Polyprenyl synthetase	1975074:1976051 Reverse
MTQAEDEAFEAYVGDQLDAVERRLSAITLTAANPFLAEAAEHIIAAGGKRFRPMLVAVTS
QLGPQPNDAAAQIAAVVVELTHVASLYHDDVMDDAALRRGVPSANAAYGNSTAIMVGDWL
FARASNQVATLGNDFVRMQADTFAELVTGQIDEMRGPQPGHDAMLHYLNVVAGKTGALIR
TSAVFGAMTSGASREVLDALAQFGMQIGVVFQLADDLMDIMSDDSGKAPGTDLREGVSTL
PTLMLAASEDSDDDELKSLIAGDLADDDVLARTLAMLRANHVIEEARADIVQRAELARKQ
LDLLPDGAATRALSRLCDEVVSRSN
>PFR_JS22-1_1745	PFR_JS22-1_1745	NADH-quinone oxidoreductase subunit N	1976065:1977621 Reverse
MHTPTIEYGLIAPLIVLIVGAIVSVLAEAFIKRGKRFSVQFAIAVITMAVALGLVCFDWS
SQPGAAVMGALSIDGPTRVVWMLLLSFGLLSALLYGERRIGGGASSFAPQGHTVPGSLAE
RQAIAARQENSEVFALLEMSLFGMLVFSAANDLLTMFVALEILSLPLYVMCALARRRRLL
SQEAALKYFMLGAMSSAFFLFGAALLYGYTGSFNFALMDRSITLSTESIGLLLAGTALVT
SGVLFKVGAVPFHNWVPDVYTGAPTPVTGFMAICTKIAAFAGLLRVLYVALGGARWDWQL
VLVVIALATMLIGAVVGLAQTDVKRLLAYSSIAHAGFIMIAVVGAVTAAGGLAAGESGSV
SSVMYYLAAYGLATLGAFAILPMVRRAGGEANGFDAWAGLGRRRPVLAVIMTLFLASMAG
IPLTGGFIGKLLAFSAGWQGGYAWLAVVAICLSVVTAAYYFRVVWIMFFKEPDMEVDVVK
AGWPTWLVIIIGVVGTVVLGIAPGPVLDLFTGAAQFLR
>PFR_JS22-1_1746	PFR_JS22-1_1746	NADH dehydrogenase subunit M	1977625:1979166 Reverse
MTFPWLTVLGLLPLLGSVIVFALRGRGGKVAAMVFSLVTLVVGVATFFMTGLTEKVSWIS
PIGAWYALDLDGMSKVLVLLTVILVPIVLIAEWHVGDSSTQNQNAADTTSQVAPARWSSE
TFMALALMLEGFTLYVFMASDLLLFYIFFEATLIPMYFLIAGWGGARRAAAAMKFLLFSL
FGGFVLLLGVIGMYAVSAGAGKPSLLTADLAGLSMGQGMERWLFVAFFIAFAIKAPMVPV
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GAFMAIGSKNLLRLVAYTSVSHFGFMVLGIFSFTTESIAGSIFYMLAHGFSAAAMFLVVG
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FVAVAVVATVLAAVYIMLSYQRVFTGPATEQSEKHMTHDLTGRERLVIAPLIALLLFFGC
VPKPTFDVVNPTAKEAMVQVSMVDPQPTVKRGK
>PFR_JS22-1_1747	PFR_JS22-1_1747	NADH dehydrogenase subunit L	1979181:1981088 Reverse
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LLFISMMGSDEASRSVRVPVYTWVSAGAFSIDISMLVDQLSILFALLVTFVGSLIFIYSI
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LAAKKAFVTNKVGDLGLFAASFAMFSLFGSVRFDVVSNSVANVSPAWATALGCLLLLAAC
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FLGAGAVMHGMNEDTNMHHFGALAKAMPWVFGTFACGYLAIIGFPFFAGFYSKDHIIVAA
FDKGPIFGWLALIGAGITAFYMTRLMMMTFMGNKRWLPGVHPHKPGALMVVPLVILAIIS
VVGGLALNGWIQGWLEPAVANEIEPVHVFDTGWISLVTLLAVALGVVIGVVLYRSNIAQE
TPVSHNFFVLAGRNELYANQFNEAVLMRPGQALCNGLELTDNHLVDGTVRSSAAVVTGAS
GALRLLQNGYVRTYGVTMALGLVVIGVVMILGQLA
>PFR_JS22-1_1748	PFR_JS22-1_1748	NADH-quinone oxidoreductase subunit K	1981099:1981398 Reverse
MNPNAFIVLSAILFCIGVLGFLVRRNAIIAFMSIELMLNAANLSLATFANVHGNLDGQVA
AFFVMVVAAAEVVVGLAIIMTIFRTRRSASVDDENLLKH
>PFR_JS22-1_1749	PFR_JS22-1_1749	NADH-ubiquinone/plastoquinone oxidoreductase chain 6	1981395:1982264 Reverse
MIPLVTAQAVAFWVLGPLSVIAGVGMVVNRKPVHSALCLAGLMVCLAGLYASLDAPFLFV
AQIIVYTGAVMMLFVFTMMVIGIDTVDEMIETIKGQRVAAIIGVVGLLALLVLAVGHGIV
SSPAGLEQATGADGNVRSLAYLIFSDYVFPFEATAALLITAALAAMVLAHGEPLFKKEQQ
KERINRRTKEFGEKGTQPGPLPNPGVYARHNSVDYPSLLPDGSISDDSIIPTLAERGIVV
VDKNRLLTPTKSANKAIVDVRDDQKGIVPGDDELAAEPTDENGLKEVNR
>PFR_JS22-1_1750	PFR_JS22-1_1750	NADH-quinone oxidoreductase subunit I	1982261:1982833 Reverse
MGAWSGFGITFRTMFRKSFTQGYPEKGKERLVAPRFHGRHQLNRWPDGLEKCVGCELCSW
ACPADAIYVEGADNTEEERYSPGERYGRVYQINYLRCILCGMCIEACPTRALTMTNEFKL
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ADETRESLIYDKDRLLAPLLPGMEQPPHPRRLGDDEDDYFLGLPPSNQLDERGVVVAARA
AANNWTGVAK
>PFR_JS22-1_1751□PFR_JS22-1_1751□NADH-quinone oxidoreductase subunit H□1982834:1984204 Reverse
MIPQENMIFGADPWWVVLIKVVVVFVAVLLWIIFNVWFERRIIAKMQNRIGPIMNGPLGL
PQTIAEGVKLLFKEDFRPARTDKLVFNLAPMLIAIAAFSSWAVIPFGGEVTIFGHTTRLQ
ITDLPVSVLLVLAIASIGVYGVVLAGWASNGTYSLLGSMRATAQLISYEVAMGLSLVAVF
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GWWGLLWFVLKAQFLVFSFTWVRGAVPRVRYDQLMDLGWKVLIPINLVWILFLAVMRGGI
ANGWFANPAMRVIVGVIVVALLAYALWPRKKEAEPDDADDEVFDAFADGYPVPPMPGQKL
AAYAGIVASEPAPPSRAPSGGDPSGPDSGKSIKGVL
>PFR_JS22-1_1752□PFR_JS22-1_1752□NADH dehydrogenase, G subunit□1984201:1986612 Reverse
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RVCLVEVPDAGNGRAMKPQPACALSAMPGMKVETADSNPTVAKHQSGMIEFLLINHPLDC
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TQSSCEHCASGCELRVDHRHFQVKRRLAGNEPAVNEEWNCDKGRFGFRSGHGDDRITTPL
VRRNGALEPASWPEAIDAAAEGLSRAGESVGFLPGGRLTVENAFAYSRFARAVVGSNDID
FRSRAASAEEATFLTNHVVGRKLADSITFGALEKATKVVLVSFEPEDESPMVFLRLRKAW
RKNKLQVVSLAPFATRGSEKMGARLWPTAPGTEAAELDKLAAAGELDNQTIILVGERAAL
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TALLETAPAPSVRLAPADATGLGVADGQAVTVRVGGTTFTAPLTIVPSMVPGVVWVPGNT
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>PFR_JS22-1_1753□PFR_JS22-1_1753□NADH oxidoreductase, F subunit□1986609:1987949 Reverse
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GFPTGMKWSFIPQDNPKPKYLVVNCDESEPGTCKDMPMLIATPHTLLEGIIIACYAVNAH
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LSALEGHRGQPRLRPPFPAVEGLYACPTVVNNAESIASVPAIVRNGAEWYQSMGTEKSKG
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>PFR_JS22-1_1754□PFR_JS22-1_1754□NADH dehydrogenase subunit E□1987946:1988677 Reverse
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VSDAGMRAVAEIAGVNTAQVNGVATFYTMYKRRPAGHQHIGVCTTALCAVMGGDILLSHV
EKKLGIHEGETTPDGKFSLERLECNAGCDFAPVMMVNWEYMDNMTPAKADELLDKLAAGE
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VGK
>PFR_JS22-1_1755□PFR_JS22-1_1755□NADH-quinone oxidoreductase subunit D□1988733:1990106 Reverse
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PIFVRRNKGVAHMSLASAVMMGASGPVLRSAGYPWDLRKMEPYCGYENYDFEVCTADSFD
SYGRFVIRLNEIEQSLRILEQVRDELAESKGEPYRIEDADLSWPSDLTVASDGQGNSNEH
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TSGFEGMRRVISLTGSTEPPFGGWFDDVADRMAELVPGFATRVMVHRGEITFFVDRDKLL
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LPSLVPVYPMANFHERETWDMFGIIFDGHPALTRILMPDDWVGHPQRKDYPLGGIPVEFK
GAVVPPADDRRSYNR
>PFR_JS22-1_1757□PFR_JS22-1_1757□NADH-quinone oxidoreductase subunit B□1990867:1991424 Reverse
MGIEEKLPAGIFLTTVEQVQGWMRQASFWPLTMGLACCAIEMISYGGPRADCSRWGQEIF
RASPRQADLMIVAGRVGQKLAPVVRQLWDQMPNPKWCIAMGACASSGGVFNNYAVVQGVD
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KGLMR
>PFR_JS22-1_1758□PFR_JS22-1_1758□NADH-quinone oxidoreductase subunit A□1991443:1991808 Reverse
MNAYIPVIGLVALATLFVVIAAIVLSPLIGPHRYNRTKYDSFECGIQPTPQTLTGGGRFS
VKYYVTAMLFIIFDIEIVFLYPWAVAFDHLGSFGVIEMITFIIVVFVAYTYVLRRGGLNW
D
>PFR_JS22-1_1759□PFR_JS22-1_1759□Geranylgeranyl reductase family protein□1991865:1993196 Reverse
MVHGEVQMGDAPALASAQLSTADQDSFATEADVIVVGAGPGGSATAAFCAMRGLSVLLLE
KSQFPREKVCGDGLTPRAVRMLTRLGIDSTETAGWARNKGLRVYGGRTEPFELPWPELAD
FPDYGLVCPRSRFDDVLAGHAMKLGVTLHTGVNVTEPITADDRIVGVRDNQGREFRAPIV
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ALPMAFNRKPAYADGLLLVGDSGGMVNPFNGEGISYAMEAGELAADAISEAHSRGVGTPG
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>PFR_JS22-1_1760□PFR_JS22-1_1760□Chorismate binding enzyme□1993542:1994780 Forward
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DNVDEPAEIARLLSSQQRMHQHRLSVESAATALGAHMSGIHVPEAPFVLALPDMLHLVTD
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>PFR_JS22-1_1761□PFR_JS22-1_1761□ABC transporter, permease protein□1994826:1996631 Reverse
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QLLLLVKDWRKGRATRRLRDVITDAYVAMFTVVVVAAMIISGLLSAQNQASTCTSDGCVT
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K
>PFR_JS22-1_1762□PFR_JS22-1_1762□Heme ABC exporter, ATP-binding protein CcmA□1996628:1997320 Reverse
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KPTEGTIEVLGEKAKDTEISFRRNVATVIDDLDFFPDLSVVEHLDLLARAHGLEDTDELV
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>PFR_JS22-1_1764□PFR_JS22-1_1764□Nuclease, RecB family□1998330:2000099 Forward
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>PFR_JS22-1_1772□PFR_JS22-1_1772□Hypothetical protein□2006977:2007324 Forward
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AN
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AFEALTLGTLAFIIILSLVGYWRGRPVRQGLR
>PFR_JS22-1_1862	PFR_JS22-1_1862	Fructokinase	2115418:2116383 Forward
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FGAQLRSHLRANGVDDSLGVQTLAGSTSLSVVSVDSSGAARYVFHLRGTANFGWKPEEFP
QLDADDWLHTGSLVATMKPGRSALLDFVRTTPAHLSYDLNVRPTVEPDPDAYLALIDPFM
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TVRVPGFPAAVVDTVGAGDTFTAGFLQGWLRDADLTAALLRGCAAASIVCTQVGADPPTA
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>PFR_JS22-1_1863	PFR_JS22-1_1863	Hypothetical protein	2116524:2116922 Forward
MIVGMRFVSTAAGAAAVILGGWIAVMRFIPEIGGVKRDDLNKWLAIDTAEVATLAGLSVT
AAWRPSYSHVWALAGTALVVGDAALDVSIAKPGPDRDRAIGMATLIEVPSALALGSWTLH
RVIKRRRAARAA
>PFR_JS22-1_1864	PFR_JS22-1_1864	Integral membrane lysyl-tRNA synthetase	2116919:2119051 Reverse
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SVATAIVGLVLIALSTGLKHRKRVAWWLAVAMVVMTVLLHVVKGFDFEQSIAGLVVLALL
VAGHRHFTGIPDPRSRRSIWTTVILAPLAGITLGTVLLTATARTQAHDTTLVDRIVETVV
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>PFR_JS22-1_1865	PFR_JS22-1_1865	Integral membrane protein MviN	2119115:2121058 Reverse
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>PFR_JS22-1_1866	PFR_JS22-1_1866	Aspartate kinase	2121145:2122419 Reverse
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PQTRELDMLLTTGERQSAALLAMALNDLGVKARSYTGSQAGVITTERHGDARIVTITPGR
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GTGR
>PFR_JS22-1_1867	PFR_JS22-1_1867	Oxidoreductase, NAD-binding domain protein	2122588:2123574 Forward
MTVRWGIAGSGRIARIMATEFTAAQHAELVAVGSRSAERAGQFAAEFGLAHAHGSYRELL
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LDDSIAVAGAMTHALEQLGYRPLDDEDF
>PFR_JS22-1_1868	PFR_JS22-1_1868	Isoleucine--tRNA ligase (Precursor)	2123701:2126961 Reverse
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>PFR_JS22-1_1869	PFR_JS22-1_1869	Hypothetical protein	2127282:2128049 Forward
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>PFR_JS22-1_1870	PFR_JS22-1_1870	Recombination protein RecR	2128073:2128699 Reverse
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NVTDSDICRICRDPRRDHSSICVVEESKDVMAIERTREFRGLYHVLGGSISPIDGRGPGD
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>PFR_JS22-1_1871	PFR_JS22-1_1871	Hypothetical protein	2128701:2129009 Reverse
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VARS
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GLVWLWIAYGGFLAARGLTLALRARSGRWASTGE
>PFR_JS22-1_1924□PFR_JS22-1_1924□Methyltransferase small domain protein□2194792:2195781 Forward
MDPVDRMIIEESPESAKHLLVIDSPELADAASDVAGRVSIYCDDRRDADQVPRSLLIEAL
DAATLEGVDLVWMRLPKALAALDEYAERISAHALPGVHLVAAGRTKHMTLSMNDVLGKHF
KAVSASLGRNKSRALHAIGATPTELTWPRENLHPELSLGVIAHGAVFATNKVDDGTRLLA
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ERCADLHGNDLLDLGCGSGILATLLARANPEATVHGVDTSLAAVDSTRITSEANGRHVTV
HWAWNLNDWPADSLDVIVCNPPFHRGVAKDSEPALEMFTEAGRLLRPGGEFWCVYNSHLP
WKARLTASIGPTTVDFQNPFYTVTRSIAR
>PFR_JS22-1_1925□PFR_JS22-1_1925□Carboxy peptidase YwiC□2195988:2196761 Forward
MSTSIKHWIPNQHGAWAMLAVPFAAAVILRARVADVPAWTIPLAVLWLVGYLLFNAVLAW
RKTAPARRQPLRSPLICYSLVCLVAGVAILMTGGLPLALWIVLFAPLVVAALVLAAHKRE
RSVLSGLTTVGAACLVFFVVRCGGWPLLALGTDVWIGALLYGYFGGTVFHVKALIRGRRD
AGSARAGLIWHGAWLVVALLLGSAGLASWWWTPFFALLIVRTAAMKHATNTGHVLRPALI
GFTEVALSVVALVICMA
>PFR_JS22-1_1926□PFR_JS22-1_1926□2,5-diketo-D-gluconic acid reductase□2196938:2197771 Forward
MIPLTNGTRGETVNIPQLGFGTYKVPPADTQRIVEEALEVGYRHIDTAEMYGNEAGVGKA
IASAGIPRDQLFITSKLNNAFHDPKAAHKAFDDTMTALGIDVLDLFLVHWPMAKTTSLEA
TWTAMVDILGSGRVRAVGVSNYQPDHLRTIINATGVTPAVNQIEVHPYLTQEPLRELDKE
LGIVTEAWSPLARGVVLSDPTIDRIAGELSRTASQVVLRWHIQRGDVVFPKSMHRARMEE
NAKIFDFELTDGQMAEITALNRNERQGSHPDEVQGVK
>PFR_JS22-1_1927□PFR_JS22-1_1927□Hypothetical protein□2197900:2198508 Forward
MNPQPAPVGQPNPSGRDTAQTRTRRPMTDPLNPPRGFWECSCPALVMLVIGLAINVAAWT
QMPEVVPQHAGVTGQVDSWTSRNGFLAFTVISIVLFTAALLGASAAVGLSSEGLHAPGKR
AERVTYWQHPDRWPIFRPRLWSLMAWFTGWFIVAMAVGANVFALSPRFNLPGWLALVVIF
GAMGLELAWFVVRMFRLLDADV
>PFR_JS22-1_1928□PFR_JS22-1_1928□Isochorismatase hydrolase□2198576:2199238 Forward
MWAWRKPIRDPQADQLLTPQNSVVVLIDFQPGQYATVGSVSREEIDLGVVTLAKLAHTYD
IPTVVSTVAVGMGVNAPTVPQIMNELPGVDQIDRTGVNAWEDPEFRAAIEATGRRKIIMA
GLWTEVCLAFPALDMIEAGYEIYPVADAVGGVSQVTNDRAFDRMIQAGAHPTTALALGCE
LMRNWARPGTDDFRRIFNWYFHQQRSLGLLDAKILPSVGR
>PFR_JS22-1_1929□PFR_JS22-1_1929□Hypothetical protein□2199376:2200716 Reverse
MTIQAETTEPGGWSKRWARWRSYGLVENLFFVAAAAFSLMLAVVVLRKGVSRPADVLFLI
AFYLVLAYLALPRFHRILTALYVPDYYIGRTRTGDGLLGDPVNLALLGDGVQIRQAMEDA
GWVEADPVNLNSALRIIAGSVMRRSYPTAPVSPLFLFGRQQDMAFQQEVDGSPSKRHHVR
FWRCPPGWLLPGGARVDWLAAGTFDRAVGLSLFTLQVTHKIEPNIDVERDHIVATLEHAV
PQTKVNVLENFSTGYHTRNGGGDTLRTDGALPVIDLSAVPVHAEAPHEEQHQMLSDVGKR
PVSLILAFLLILIGIGITFSEVAVDAFHDVAGQVAASGGTRTEVIVANVVALVVLTGLQV
VLSTLVFKGFNWARVLLLAVTSVTLVTRLAGAIVRVPGSMDIVQMSVDVLIVYALTSLSA
RTWTHDRRTLRRELRRKRRDAKALGA
>PFR_JS22-1_1930□PFR_JS22-1_1930□Uncharacterized conserved protein UCP033563□2201029:2202219 Forward
MPRFEPFAALRYAPSADLDKVIAPPYDVLSDADIDELEARDPHNIAWVDDPRGGDDRYVK
AAALLRQWISEGVMVYDDQPSFTIYRMAFTDATGAHRVISGVLGGLEVVDEGAGGVLPHE
RTTKKAVTDRLDLTRATSTNGSPVWGLSLAHGLTDALAAPGEPVGEITVDGVRHSVERVV
DPGRVAKIQEILAADDVLIADGHHRYSISRTYRDEVRKATGRTGTPAEQTLAFVNELVEH
QLAIEAIHRLVDGISWDDLNKALSRYFDIDPIDEELTPATLSEMVAQARLVLLKPDGTAS
WLIPHEGAFDDMRALDGAWLEKALGDTDAQVTYQHGLDEMRTMVADHAAGILIRPTSLTE
IMRTAREGLLMPPKSTFFIPKLRTGFVLRPTASVSD
>PFR_JS22-1_1931□PFR_JS22-1_1931□Succinate CoA transferase□2202343:2203866 Forward
MNERISNEKLRGKIMTADEAAALIPNGAQIGFGGFTGSGYPKELPQALANRIKAAHERGE
EFTVNAFTGASTAPELDGALAGVDGMHYRMPYQSDPTLRKKINDGTTLYTDIHLSHSAQL
VAEGFMGKLDFAVVEAVRITEDGNIVPTSSVGNNKTYLDMAEKIIIEVNSWQSPDLEGMH
DIWNGYLTPPNRPIIPINNVGDRIGDTFLTIDSDKVVAVIETTDRDRNSPFKPIDDDSRA
IAGYLLDFYANEVKHGRLPKNLLPLQSGVGNIPNAVLDGLLHSDLENLTSYTEVIQDGMV
DLIDAGKLAVASATAFSLSPDYAHNMNENAKNYRKSIVLRPQEISNHPEVIRRLGVLSCN
GMIEADIYGNVNSTHVMGTRMMNGIGGSGDFTRNAYISAFVSPSTAKDGAISAIVPMVSH
VDHTEHDVMVIITEQGIADLRGLAPRLRAQKIIDNCVHPDFRAQLQEYFDHSLVTSKAKH
TPHDLRHSYDWHLNFIENGTMKLSHYR
>PFR_JS22-1_1932□PFR_JS22-1_1932□2-deoxy-D-gluconate 3-dehydrogenase KduD□2204094:2204906 Reverse
MAKDLPNDTTPTTAPSVTSLFGVSGRRAIVTGGDSGLGHGQAEALLEAGAQVVIMARTRS
KVDAALAGWARRGLEGHGVVADLSDAASRGRGFDEAVATLGGLDVLVNTAGMITRHRAED
YPLDEYRAVLAVNAEAPFGLSQRAARIFIAQGHGKIINMASMLSFSGGANVPAYAASKGA
IAQLTKACANEWAAHGINVNAIAPGYMATDLNTSLQGEDNPRYREITARIPAGRWGNADD
LKGITVFLASGASDYLNGAVIPVDGGYLGR
>PFR_JS22-1_1933□PFR_JS22-1_1933□D-isomer specific 2-hydroxyacid dehydrogenase family protein□2204946:2205992 Reverse
MADHLTVAVATPLSEELCLLIEAREPRCELIRDQSLLPPMRYPGDHAGDPGFRRTARQEE
AFRAMLTHADASYGIPGESPQLLAWTAEHNPGLRWVHTTAAGGAQVRQAGLSREQLDRIT
FTTSAGVHAAPLAEFAVFGVLAGAKLLPRLTAQKHDRTWGGAFLMRQLSQMTVLVAGMGH
IGNRCIDDFHALGARVIAYNRSVHDNPNVSAVYTTGQLGEAVEQADAIVVTLPGTERTNK
LLSAEILQQVRPGTILVNVGRGTVIDQAAMVNALADGRLAFAALDVVADEPLPTDSPLWG
LPNVIISPHTAGLDAHEDRSIAELFARSATLILDGREPLNRVNTVEFY
>PFR_JS22-1_1934□PFR_JS22-1_1934□Pyrophosphatase PpaX□2206071:2206724 Reverse
MSTQDLPWKLVLFDLDGTLINSIDLVVAAWQHAFADVLGKQLDRETVLPWIGLPLTDTIA
EQGGDKAEALRASYDQFMQANHDDMVTAFAGLPELLDDLAVYNVGTAVVTAKGRELAERG
LRVAGYPETLHVAAAMEDTREHKPNPAPLLAALAHEGAHASDAVYVGDAIYDLQAAEAAG
IPAIGVTWGAGKRDALHQQRALAFADAPDELRAQLLG
>PFR_JS22-1_1935□PFR_JS22-1_1935□Hypothetical protein□2207232:2208788 Forward
MPLVGDFVKGYGQLPLGLVAPTFGNDGYDALPVASDPSLPRSVDLRDNSQGFNQKVETAL
RDGQIYVRNIGDKQWREAPMPSCLAGQVVGISLNEDLLIALDSQGWIYTMGNLLSDPSKW
GWVRAWGSPFWFGDGLQSPTTEPNRWSLSVIGNQTDRTYTMPDGTQQPISLAKVTQVTAL
SPDGSKIYTLDPWLAQDYSYEVGTPFNSRFRATSLSSSGSVHFITNEYGDMYTKLSDFDI
NGSDPAQFRYTWRPDERPSATDALQHLLDPSTAAIQLPTADWAHQPKVPGRITDRISIHS
THAGSENRELRVEGESAAGMHGYWFKALDDPAWQFAPTGEEIQGRWLDNSERDRSTETLV
ADSPYDYVGTMPTGGELVIDNFAYASARHDAALRVGDKSYPLVLHTVDGRWGTALSMRMG
FVGKEGAFGARPAGLVNAVPRNYAAAIEVPYETMLASISDPVLGQFIERDLANQRMHEVF
LSVTPNTMKLYDSQHLGGDTTIPNFNKLVTLGEATPEV
>PFR_JS22-1_1936□PFR_JS22-1_1936□Hypothetical protein□2208973:2209665 Forward
MSSHDDAPRRTASGEGPATATTETSAGAEHADPESGSQGFGTPPATPIATLPPLSPHAGG
VPVSPRTGEPVRRRSIVATQVAFWASALCAGIGYSWYWFQAMHKGQFHTASWVTGWLHPR
PGGMWSLLLACGLAAVVAAMVALPCVTAYQAWTGHRFARTLSWWALGGSLLGVLFNWWAV
AAIPCALVGVVLLRLGSSRDYFAEWDTLRAPAPQPELPTDVFYGPLPRFQ
>PFR_JS22-1_1937□PFR_JS22-1_1937□Hypothetical protein□2210108:2210557 Forward
MTDSTDTTFSTRGEAIASIIDAIEAGGAVADARAEYDLDAIADELVTLHSEETSEGATIA
SSVHFSIEADEDAFWEAVADHELVGITAEFTSINTPTVIDGRATTTDTITITRDGVELDA
VDVESSEDEAPYDLAVRSIIGDQPFTWIR
>PFR_JS22-1_1938□PFR_JS22-1_1938□Hypothetical protein□2210627:2211067 Forward
MASTITWRPTDDMAAWMARRGADVAAPPSLSARTRTEMDLWREAQRIDLARTGWTLVELG
IIADATQAGMTADTVSQLPGGDITIALQDFTPDGTDSADLLSARDKASQLSACATIAMEH
ALTQWWDLGLDHTAEAWRSLGIRVVA
>PFR_JS22-1_1939□PFR_JS22-1_1939□Hypothetical protein□2211069:2211995 Forward
MAAPESWTWTPRGVPGLRRRFVRDSRHLDERLEQLAATHPDAVAEAMGDKALPMSGFGWS
AERLGNASLFWVSGEMAALALDAALDVPEWSPSQLITPTGLACFAKPLPGPKPRTFDLPG
GRTWQGNPPVWAIAWLPAPGGGTMIQLLGRLGDYPPGFADVDGPLVEILSILIRPESDLD
ATLSPEARMSASLLMAMSVLMDTPTVAERRTIDSRTGKAPGTEHRPRTPRPDRHVTLVDL
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RPVRTVVTDRDDGTGHKLTVRFMVRGHWTHQAHGPKHGLRKLIYIAPYLKGPEGAPLQAA
EKVMVWRR
>PFR_JS22-1_1940	PFR_JS22-1_1940	Hypothetical protein	2212155:2212493 Reverse
MIWTLAFWKGAGERAIKTAAQTAVGLMGTSTLIEQVPWTVVASGTAMAVVLSLITSIGNA
DFTAGVPTTAKGLEATTVGKTDTTPVTPPARVAEEVPAGFVPDTAPDPVPTV
>PFR_JS22-1_1941	PFR_JS22-1_1941	N-acetylmuramyl-L-alanine amidase, negative regulator of AmpC, AmpD	2212511:2213362 Reverse
MDWTNLNADVTKLMGVHFTPGREGRTIDKIVIHHNGGNLSIDQIWNVWQTREASAHYQVE
AGGRIGQLVNDLDTAWHAGDWDANLTSIGIEHADDSTDPWHVSDAAVDAGAHLVAALCRG
YNLGRPEWMRNVFPHSQFTSTSCPASLARDQLGDYMGRAQAYFDGAPVAAVHQSVPAPAP
APSRHVDLPAWNLPEGNFYGLVSGGNDSHGGFYPAERPAVRAIQLWLIRHGYAGAVPDSW
ADGIYEQPTADAVTAFQHAERPNSTDRWGEVWADDLATMAANN
>PFR_JS22-1_1942	PFR_JS22-1_1942	Hypothetical protein	2213413:2213688 Reverse
MNDFQTWITVLGGAGFLGALVTLIKGLVGWRTGKSGRKMRAAHDAIDSLNLAGLWAEAYW
HARGYCRSHHEWTSDYADGYPPPPDDTNTPD
>PFR_JS22-1_1943	PFR_JS22-1_1943	Hypothetical protein	2213685:2214131 Reverse
MSRDADVTKQGSLPRRVWDMLAEPKSVTVLMTIAYAALVALGFWAIDDASTMGVRDMMGG
LLIAGGVCGLIGCPWGQWWIERAGLVAIGAAFAVHLSFVVAISPPDGPWEVASALGLLLL
VATRWIRIRTLPADPTLPRPGPPEAGDE
>PFR_JS22-1_1944	PFR_JS22-1_1944	Hypothetical protein	2214128:2215819 Reverse
MATWDYGYAPADVVTDAAGDVLAGIELRVWDAEVAGKAVAVQQDRGDGWKPASRVLTDDV
GRYRFRAEAGPTVWVEDVSGRRWRMDAWQTLGTMIDSAQSATAAAESANSIAHEAMSVAQ
QAQTSAKAAADSAAAVQGVAPSDANVSPIITGGAKTAEAVRKAALAAFPTTGPTIFTHFL
TRDEALHVAISTDGVTVEDTGLRWKPKNDTTLGECFVRDPSVCFWKGAYWVAFTRPTKGG
GDAFGTTKSFGLMKTTDWRTFQELPPVVMPSQFQQTWAPQWFIGSDGVPHIFVALGTTTT
PNAYFTQYELRPLDDAMTSWSDPVVMSGLPANCIDVAVIEDAGTFHAFPSNQKTSTVEQW
TSTGLTGPYTKLAASDFPGAGVEGPQPVPLKTGGWRIYVDNYAETDSIYFAESTDLLHWS
ALRPVTLPMRHVGAVAVDSFGALRTRELWQPNIPGMRGMGAPFWGVPFAAGNVLKEFAQI
VSMRTDGGGEIDLAKAATLGFTGIDYISATAVANVEILQIEPDIRAVDSMIHGVALRGPS
TPQIDTDVKVAWRVLGWGDPSTP
>PFR_JS22-1_1945	PFR_JS22-1_1945	Hypothetical protein	2215819:2216430 Reverse
MATVYGPDKFTVPTGPDAPDVPATIITLLDSMRPSLIGHASSIADRTAKYGRASASSIQA
PKGTVVVSAELNAIWVKTSDTLDEWATIIQHSDEVATVSVVSTQSDQVTTVQKFTIPESG
IYALYASMNDQNGLDVDGSIREIHVLVNGTWKFGGIFPASKFWLWSGSRTTFLNKGDTYQ
IDFMQRSGGERSLKVTLSYQRIL
>PFR_JS22-1_1946	PFR_JS22-1_1946	Hypothetical protein	2216473:2216703 Reverse
MSAPDIALQGLIGEDTEQVALAQVLGVGVDGRSVRVQRGTLTHEVRRLDSYKPSAGDRAL
LLRLSGGEWVLIGALA
>PFR_JS22-1_1947	PFR_JS22-1_1947	Hypothetical protein	2216700:2217875 Reverse
MIEVSKRWASSVGAGARWSVMVSWSSDGGQTWHDVVPTACSVDESTGQQVRWKLSCTLRK
ADAEGLTVFGCRARVFVSMHHTDSWEETIQLGEFRIDTTSDTTLAGPSGAQVAAVQVSGS
SWEQQLMDSRLVEPREVSGAAIDVLGGLIREVLPDAEIVFDGGIDPGRNIPATVVERDRW
AFIDGSNSSETSVARMLGAQVSTDARGVWHVAPPPVLDGTAAWTIEAGKGGALLSAVASE
DRSTIRNAVIARGESTDKSVPVLGPVTVADHNAWSPTNVDTPVSRGGFGTVPIFYTSSLF
TDTTQVEAAAKAMLQPRLGVKRTLDLTTLFDPAKRAGDVGVVQTTDGPVTVVLESVSCDL
VAASMTCQTRGTTGTELITTETTTTTGEKIS
>PFR_JS22-1_1948	PFR_JS22-1_1948	Hypothetical protein	2217875:2218690 Reverse
MAIIATRRDWPEAPQRFQSADGRLVAELDPDRCGVRLRGTDLEAWSVTLTRDGEVIHTGD
PMVTPGGTGIAYDLSAPLDADVVYEAHAGGAVLTQVAVHTGGLPFEWGMVTPLADPDKGL
MLRTVADTPTLGRSARQKLSAVPSSRLQAGGWDVPTDAAQGWTWLAGFPDASKALAERDA
IMEALSLGPVYFRPETSIGFPPMWALPGDVSATKQGDAWTVSCTLTPITAPATADLPAWA
PGNSYARVAATRGSLAELARTSKTFLELVGF
>PFR_JS22-1_1949	PFR_JS22-1_1949	Hypothetical protein	2218692:2222786 Reverse
MALDLGTAWVQVSPSFRGFASTVNKEVGSAVGGAFKSAAKVGTTAIATIGAAVGGLALKG
GIDRALSIEQAQAKLKGLGHDAGSITEIMNDALASVKGTAFGLGDAATVAASMSAAGVKS
GEQMTGVLKTVADTAQISGRSLTDIGAIFGSVAARGKLQGDDMLQLMSSGVPVLQFLSDQ
LGVTTADVSDMVSKGQIDFATFSAAMQKGLGGAALAGGETFTGAMANVRAALSRLGEAAA
KPALDGLRNVFNALIPAIDAATNALKPIASALANRISQAAEAASASIGRLTGSLTSITNL
NTGMLGAAFSSMLPIIGALSGQLGSLLGGIPVVGQAFAGITGPVGLAAGVLVEIVAASSS
LRQALGTLVGVVGSQLSGVMTGIVAVFAGFRSVLGAVGDVLAPFVDRAADAANVVLPLLG
GALSAAGGILQSFAGFIERNHVALSILAGAVVAAATSWKIYTGAQDLARLATTKLGLATT
VLKGKLSSMGAAFKTNPFGVILMAISALVGAFSIAYQSSETFRNGVQGILGSLAPVFSSL
MGTLSGLFQQVAGAVGPVLSSIVSTLASVFSAIGPVLSQLAGTIGSVFSAIGPVLASVFG
SIGSVLASVFSGVMSVVAPMLTALQPLFTQLSASAGQIGAAFGPVGQALSSSFQQVGAAL
APLLPMLGQQFGAILSQLAAALAPVMGQLLAAAAQVLPTLAQAFGQVAGVLIGSLGQALT
QIAPLIGQLVGVLIGSLGQALTQIAPLVGTLVGVVAQLFAQLAPLVGQLLVQLVPVVAGI
LVAIVPIVGMLISQLVPVIVTLLQVITPIITMLISALVPVIQVVTQLVLAIIQAVIPLIS
AILPAISALISALLPVIVMIIQVVAQVLQWLAPLISTLITALIPVITTIIQVVITVVSTI
WSVVGAVIGWFQSTVVPIIGTVVGAIANAFGWVRDRISDAWNWIKDRIVAPVVEWFQSTV
VPKFEAVRDSVVRAFETLKDGVGRAWDALKDLAKKPVEFVVNTVAAGLVRAYNWVATKFG
ADEVKEPHVEFANGGFAGREAGFASSPILWAEAGPEAYIPLDPAKRTRSLGIWAKTGQML
GALPMADGGIIGNIIGGIGNAAAAIGNFIKSPIEWLMGRVRDLIDDVGSSPFAQIAAKIP
GKIADDIGAWVKEHMASIFGGGGSGSEAFDGWWNAAVAINPDMAPFKQIAATVAQNESGF
NPNVMNNWDSNAAAGTPSGGLMQFIQPTFEAYKWPGFDNWMGAVDQILAWWKYVNARYGG
PFNIPGIASLAGGGGYVGYAGGTLNAAAGTAWVGENGPELVDFGGGESVYNRSQIDGLED
RIADRTISRLQQLRVALIVDGHQMGQVIDGRISMAGAAAHGSRW
>PFR_JS22-1_1950	PFR_JS22-1_1950	Hypothetical protein	2222813:2223181 Reverse
MSLFQLLATHWEELEGDFQEAYRVDLRDLWRGRLSPARCWVLLTQLPPGSRLWRMLGGPM
AWGMVERAVREEGWRLASQNAGKELPRPEPPAPGWRDKQDDLRRREERRLARFMQRHAER
NN
>PFR_JS22-1_1951	PFR_JS22-1_1951	Hypothetical protein	2223181:2223534 Reverse
MAEAKKISAAEKARRETQSAKDTGTITDTTVQIGDIELTVPAAVFEDDWEFQEAILMAND
PDATDEDRARASMTLFRRLVGNRHREVLDQLRDESGRVPVSKVTETVKKVMDAVNPN
>PFR_JS22-1_1952	PFR_JS22-1_1952	Hypothetical protein	2223632:2224495 Reverse
MAVNSVNVHVFGSDDDVLYLGPSGLNLGNISLETAIPKEMIDTGWLTDDGVTLGMKDSVK
AIQGHQGHANVLQFMDSSDTTLEATLMESQLQTFLWNLDADAEDIDGVTKITAASSRKVL
NLCAIWDTFDTQHSGIHWRYVFPSLTLGERDDIPFKVGEASAYKYSLGVLEKFFVFTNAA
AMKAGGASAKTVTGVKITTTDGATVGLPSSLKVGEKVSLAAEISYSDGTKAVKQTNAVGL
TWTSSDKAKATIDGGVVTGVSAGKADITASIDGKTSEALSLTINTAA
>PFR_JS22-1_1953	PFR_JS22-1_1953	Hypothetical protein	2224505:2224873 Reverse
MKPPDLHTLVAHHLAELLDVPVVSTRPEGETAPSKFVRIISTGGAGRYGRVFQGIQLTIG
SYAGSAATARDLAMQVDEAMNGLPVSPLPVSKVTGNTPSDDPDPDTQQARHTATYQLTTL
IS
>PFR_JS22-1_1954	PFR_JS22-1_1954	Hypothetical protein	2224870:2225118 Reverse
MANFRFEPNTKAFTEWAQRDCDAHLIAGITASMGAKAGEGFSTMVSNNGDRTRGYLATAS
TKGRMRQAQGHVIERVIGSSGV
>PFR_JS22-1_1955	PFR_JS22-1_1955	Hypothetical protein	2225111:2225452 Reverse
MKRSWPTPVERLREGPPEIDRDGDPIAGSGVITKDPLPDALFAPGGSQILVAPGVAAVVD
EPTLYWRGSEVIDVVATDKVRIAGRVWTPEGNPARWPKGVVLKLKAQEAKNRG
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>PFR_JS22-1_1956	PFR_JS22-1_1956	Hypothetical protein	2225449:2225829 Reverse
MVAPDPELPFATVSDMESRWRSLSKDEHTRAEALLDDASGLIVDTCPRWEQASPATLRRV
TCSVVRRAMAADDEDIGATSLMDTTGPFTTQRAYSSPAGDLFLTKAEKAALGGVTGAFET
SLLGLT
>PFR_JS22-1_1957	PFR_JS22-1_1957	Hypothetical protein	2225816:2226016 Reverse
MKVTSTIPNLTVLDLDIQFVDGQADVDPHLAERLRRLEPLGVRVPTASRKPPTRSRRKQG
VSHGRT
>PFR_JS22-1_1958	PFR_JS22-1_1958	Putative phage major head protein	2226042:2227022 Reverse
MPGITGQGTTYNLPNYVGELFAASPEDTPLLSAIGGLTGGESVGARQFEWQGYDLRDADG
SRQRLEGANAPDGEERTRYSASNVVEIHQESVEVSYTKQAANRERATNGAATVQLAGSVL
PADELTWQIDQQLKQVARDVEKSFIAGTYQLPTDNAKPRRTRGLLEATTTNVAASTHTAK
ELTVEEILDLFQKVWENGGIQEAETRTVIVGAALKRTLTRLFITDVKYQEESRNVGGVNL
QTFETDFGKANIMLDRFMPSDTLVVASLEDLKPAFLDIPGKGHFFAEPLAKTGAADKVQI
YGEVGLQYGNQRKHGKLTVAPATPAK
>PFR_JS22-1_1959	PFR_JS22-1_1959	Hypothetical protein	2227039:2227671 Reverse
MHKKLMPWVRLIEAVETPAGAAPTPAIDPKDPAANPTTEPKPADATSEKPLGEAGKVALD
REREARRSADKRASELEARVHQLEDAGKTEAQKQADELKRTQSELETLRGEKARLEVASA
TGVPVDLLAGPGDDLDAYAQALNAWRDKQSEKPAAPAVDTPSPSPSGVTGQPVQPNRTVD
ELIAAAEKNGDLATAKQLKLMKLDALRRTS
>PFR_JS22-1_1960	PFR_JS22-1_1960	Hypothetical protein	2228001:2228765 Reverse
MTDRDDLNHFHEANDAIQRRAINDLNKFWARLAKSDPKAVRAAMDLFVPQLIASYGELAA
EAAARWYEELRPADKKNFQAELADPVSDDIIEADVAEALGTSGAWDTEAVRGSLADAIRR
QIFYMARATVARNIAHDPKRPRFARVPRGAVTCAFCTMLASRGWVYYTAKTAGITRPWHR
KCDCQIVPEWKRGNIHFAGYDPDKMFEQYAESVDAVGSSFDTKAILADMRRRHPEALTDG
VVNMSEGQGPVTSD
>PFR_JS22-1_1961	PFR_JS22-1_1961	Phage portal , SPP1 Gp6-like family protein	2228752:2230263 Reverse
MSLLVNPYASPSFFSSPSVVGLGADEQELLDELVALWARKKPRNVLRGLYLDGKQQIKNL
NIAVPDEIADSLQIVVGWPEKAVFGLSNLCMWDGVVTPTGDENPFGLDDLLSANRFDVEI
NETITSAMANSVAFLTVSAGNVSIGEPPVVIMPFSAEWASALWDRRTRSIKAGLTIGDID
YLGRPTSLSLFTRTATITCVGSRLGWMIEDRAEHGLNRVPMEPVPFRPTLDRPFGRSRIS
RQVMTIVDRAMRAALRMDISSELFTAPGLLLNGITPEQWAEIQKWTWKLGTVRGLTRDED
GETASVETIPQQSMEPFIAQLRELAEEFASATSMPLSALGVVQDNPSSADAIYAAKEDLV
IEATNANRITGYALSRVFQDAVMMRDGLTEMPDELGGVAAKWRNPAMPSIVSQSDAMVKQ
ISAIPGLAATDVAFEQLGYSAADIVRIRTQMRRAQAADGLTSLLAKPATSSTPGAEPSQS
ASPTEPAASTPLPDLEGAPGDRS
>PFR_JS22-1_1962	PFR_JS22-1_1962	Gp8 domain protein	2230260:2231714 Reverse
MVPSPQTKHGDRKLSEVAKHLILPEGIVSTGWPAVRDRCGEWGVVFDRWQDGMGRVILSK
RGSGLFAAGVGGVGMSIPRQTGKTFTVGMIILGLCSLSEELTVLWTSHHSKTTTKTFESL
RGMAQRKKVAPLIRQVRTGNGDQQIIFSNGSRIYFGAREQGFGRGFDDVDIEIFDEAQIL
SEQALSDMVPAANVSTNPLIIFMGTPPRPSDPSEAFANRRAEALAGDAPDAAWIEFGADE
HADPTSRAQWRKANPSFPHRTSETSILRMKKMLGPESFKREGLGIWDETASVRAIPAEGW
RVLTVKEPPADAIQSFGIKFAIDGSAVALAAALKPKDGPIYVEGIEQRSASDGIEWLADY
LTPLWRNTAQIVIDGKSGAGALVDALRRGGVAAKVILTPSVADVITAHSLTLEAIKTGGL
SHLADPELDRQVRIATKRKIGAAGGFGWQAPEGDTVALLDAITLAHWAALTTKRHPGRKA
VALA
>PFR_JS22-1_1963	PFR_JS22-1_1963	Hypothetical protein	2231668:2231964 Reverse
MAAQVRAVDPDERPPARKRAKTITQAAKSGTEVELLEALQARVARAVQDRDTPPRDLAAL
TKRLMDITRELEAARVKDQEAGSDGAVTADETWRPQAL
>PFR_JS22-1_1964	PFR_JS22-1_1964	Hypothetical protein	2231980:2232354 Reverse
MRSRTAWVRCDGKRPITLAGAPASSTDPGTWSGWSQVRRATAGDGFGTMLGDGLGCWDLD
HFDDQGARAFIDRIDKPIIFAERSVSGHGFHIFVRTDEAPGRRTGNIEFYSRHRFIRVTG
DQFV
>PFR_JS22-1_1965	PFR_JS22-1_1965	HNH endonuclease domain protein	2232729:2233067 Reverse
MSTSRTGTATWLRHAAQAKREAQARGLARCPLCGVWMDYEVGKRPNSAEADHIRPHSLGG
SDDIDNIRVICRRCNQSRGNGLKRPGRQRQRPIKRIELAQPARSGAFPAPPA
>PFR_JS22-1_1966	PFR_JS22-1_1966	Hypothetical protein	2233064:2233357 Reverse
MKQPGPHQRMRATFKADRGWRVACPRCAWHATSTHLAWLMDQASTHTCAPLLLSPTPPDV
ELAPAGDGLSVLWPEVDGDVQFTCIHTSTATCRQDAP
>PFR_JS22-1_1967	PFR_JS22-1_1967	Hypothetical protein	2233500:2233715 Reverse
MALALRLPKRVELTSDRQLLIDGELFKWPIEEDGTTISPGKLKDVSRLTLTVLLHPSCAI
IVDPQDCPDGG
>PFR_JS22-1_1968	PFR_JS22-1_1968	Hypothetical protein	2233820:2234536 Reverse
MEPSDTLDRLRQIPDMAAELWASGRATGDTGDPKPGQVRPHRAKPSTPIDLGRHDILRTD
EHGLLSEMSQAVRAVWEDNPGVALSNPPTWAGECGWLLANVELWDLDPFLSAFVSDAAWL
VWRTLDRALHHPAPARLTCPVCGGRLAESAGGWITCRDCASQFPGRERIATQMIHKRDMT
TDEIAAEFQIDPARIYKWRERGLIKPTNPGCKPATWRPWDVLAVLHPDIVEAIDEKAC
>PFR_JS22-1_1969	PFR_JS22-1_1969	Hypothetical protein	2234570:2234800 Reverse
MSNPEYLDPQATQGPQNRAQRSVQWIAIDPKAGMTLDEMAGLVQDAMRADIDGSTPIRVT
VGFRSQIRVATIGGVR
>PFR_JS22-1_1970	PFR_JS22-1_1970	Hypothetical protein	2234862:2235329 Reverse
MTTPITVVGNLTDDPTLRFTPSGKAVASFQVAVNRRRKDQSGNWVDDGADWHSVQAWGTL
AENVAESLTKGTRVVVTGRLESREWQDREGNRRTSWEITAQGVGVDLSFATATVTRSGPK
RPPQQAQGSQFAATPPQGEPPADPWAAAKTDEPPF
>PFR_JS22-1_1971	PFR_JS22-1_1971	Hypothetical protein	2235326:2235673 Reverse
MIQTEIERVALAVHGLRPDWPATSLRTFIENNLAGKAYQDVAVAFAWIACDPTTNTPKRI
LGAGPWWNATRAGVQHITDLPPRFTPEPTPKRDPAFRRELIDQFKQDLHQTKETK
>PFR_JS22-1_1972	PFR_JS22-1_1972	Hypothetical protein	2235670:2235882 Reverse
MSKQTGKQTGKQVLTELGKQNDQKRQALSKQTGKPIVTPYPYPYPYICSYVSTKSKFSTV
RAILDLEVER
>PFR_JS22-1_1973	PFR_JS22-1_1973	Hypothetical protein	2235863:2236228 Reverse
MAWFKVDDQFWSHPKVIRCSDKAIALWVRAGSWSSQQLTNGEVPVEALAMFKANRQTAEE
LVGTGLWKRNGTGFQFHDWSTYQPAGSEVEELRVKRAEAGRRGGKKSAQTRWGDRREQAN
G
>PFR_JS22-1_1974	PFR_JS22-1_1974	Hypothetical protein	2236228:2236608 Reverse
MSRSRRSARTAGTRFETSVADYLARHVDDGIERRARNGSKDRGDISGLRHMAGRVVVECK
DYGGQFKAAQWVGEADVERGNDDALAGVVVAKRRGTQAPQDQWVLMTLGELVALINGNRD
HYEKGE
>PFR_JS22-1_1975	PFR_JS22-1_1975	Hypothetical protein	2236850:2238949 Reverse
MSTPTIGSLFSGYGGLDMGVQSVTGGRVSWVSDVEPGPCTILDTHHPDIPNLGDVTAIDW
KAVEPVDVICGGSPCFVAGTSVLTHDGLRPIEDVQVGDLVWTHAARWQRVTHTMRRTSET
VQFRSGSYCTPEHRLWLRAPQRRWNNTIHHYRRHLDAPEWVEAKDAHNLFAASPVSVTHE
GVSKPDTLTWWQIGRFVADGYVNKQVNVYIRKGKESDADNFPGWTHHQQKTALCLTMPKS
AAERDWLTEHFGKLAHGKTIPAFLLAETEENRRAFLDGYWSGDGWKPEGRKFTESTSVSA
CLTTGIELLAKSLGYTCTVSQYQVAPTTVIEGRTVNQRQWWMVRATPDDGRFTETDADWH
WFKLRRAPKAGEVTTVYDLTVERDHSFIAAGIVVHNCQDLSMAGRRAGMRPGTRSGLWES
MMTAITTIRPRLVVWENVRGALSADAFTLCDLESESRHLGDRPAGPSLRALGRVLGDLAN
IGYDAGWCCLRASDVGAPHRRERVFVVAHPQGQPWGSGDGEYGVAANADGATIGQQSPES
PREETGPYPGDRPGHHGRERPAEEWRETSNPEASLTLLPTPIAERPDGHKSAAFTAGHTT
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FRDVIDRNRWGEFAPAIARWESTLGRPAPEPSEPGREGRRLSARFVEWMMGLPDGWVTDV
DISRTAQLRALGNGVVPQQAAAALKTLLMEADTSQVMVA
>PFR_JS22-1_1976□PFR_JS22-1_1976□Hypothetical protein□2238946:2239197 Reverse
MNTLRDDSIVWDAKDIRSACHALWQTAYIYRRVKVPDPTTADAVRLLRRWEANADHLDKL
IHGLEGLQRQQVQPRIKLTTEDA
>PFR_JS22-1_1977□PFR_JS22-1_1977□Hypothetical protein□2239242:2239535 Reverse
MSTPGSLRAALDQLDEIGIADHVQSLEWDRAGARTTAWLETCGDFAAACQWGDAAGEWVT
WDITDVAEADVSPRLRVKHMHLRARPCADAPAKAVAA
>PFR_JS22-1_1978□PFR_JS22-1_1978□Hypothetical protein□2239532:2240062 Reverse
MKATQYAKSTDPEVIATIEENELSRRAWIDDTKAWFGKTIRTGIPGAKLFLFSTRTAIRL
LGIVTSDEKKPAGWKFCWRSRSRFEPRKNNPLRATWDARRWQAASIPGLPVVLTSSVSGE
LQSWLRMYPCPFISSGAAWLDLEHMPDPDSPHFGPQWTEVRASQAMAAKEALKDAS
>PFR_JS22-1_1979□PFR_JS22-1_1979□Hypothetical protein□2240301:2240534 Reverse
MIFKDTTIGPLETRFTWSMRCDRCGTPLDWLVAASCKTERSEVIAVKFLRERARDGGGLR
EWGELDLCPSCFSVMDA
>PFR_JS22-1_1980□PFR_JS22-1_1980□Hypothetical protein□2240531:2240755 Reverse
MSANRSRRATYNHTGIFVHLREAAEPSEQPPSDQTCPALHVIAGLTPWADHQPRHALGVD
GRCRHCHTTIKGNP
>PFR_JS22-1_1981□PFR_JS22-1_1981□Hypothetical protein□2240752:2241312 Reverse
MSAPLTKAQKVAAVVEQLLRGGADTSTLLEATGADRPGRLRDTLRRAGRDDLAARIITTD
RAAQRRREVIEAVEKLVWVDRADEIAAELGYSSRYGLQQSLRGWGRRDLADQIVLTRETH
RDRVIADVEWIAGTRGPEDVARATGYRNAAALQAALTGWGRKDLADRIVGASRNDTGRFR
FTWRAA
>PFR_JS22-1_1982□PFR_JS22-1_1982□Hypothetical protein□2241309:2241641 Reverse
MSWPEEHHDVWAGVEDAIPEWVSDKVACSVRSDADWNADEDSRKAVAAVRICERCALTEQ
CLDWALAHHEAGIWGGLTASDRERIERGAPVRRVREIRRRRTAVRQVQES
>PFR_JS22-1_1983□PFR_JS22-1_1983□Hypothetical protein□2241638:2241802 Reverse
MSTLPADAAERWQQWDGLARTILALHLGLTDLEMVELVGGLIGAGWHQDGPVES
>PFR_JS22-1_1984□PFR_JS22-1_1984□Enterohemolysin 1□2241799:2242638 Reverse
MTETTPSTDIETTAPTPSGSIAAVGSETAGLTLQQKLDYASALADSELLPAAYKGKPANV
LVAMEYGGELGIGTLVAVNQITVINGGVSMEAKLMMTLARRAGHIVRLSGDDKQATCIII
RADDPGHESVVTWDEAKAKTAGLWGKGHWQKNPGLMLKYRAASENIRLTCPEVLAGIVYT
PEELDERTERAGRSTMRVHQVVAEPEKTAAYFMKALHLNGGQFKEFAQRVLGHPLKSWES
LAKADKQRVLGALASWENSGADPTTGEVLDAEPVEGGAA
>PFR_JS22-1_1985□PFR_JS22-1_1985□RecE□2242640:2243491 Reverse
MMPITKPCAVKDMPEGEYHSDPCVEPSLSSTMAKTIVSGEAGPARLREIMSHGQEHKAVF
DFGSAAHEKVLGRGAGVEVLDFPAWTTKASREARQAVWDAGGTPVLAKDSAQVDAMAEAI
LSNPVAGELFTRGAGSPELSMFTIDEETGRWQRGRLDFLADRKTIVDFKTSGQSVELPDW
IKHSWQFGYHIQAAAYMDQAISLDLVDEDAIFLHVVQETKPPFLLAIYQVSADQLAEGRR
QMRRALDLWDRCLTLDEWPAIPAVIQLSKLPDWVHTTDDEKDS
>PFR_JS22-1_1986□PFR_JS22-1_1986□Hypothetical protein□2243488:2244129 Reverse
MNRTYFKAVRADGTDFYTGKVRWLPDDGAPIPAGGWVVEHPTSERVGDDARTYLSVSTVE
TDCAGMGWPCRLLRVVPDGRQVSIPEPVGLPSTRASIRWRVIEELPAWQALGPQGREIEA
LLGQVESLTEDQTLEMSAARGFARGFARDVARFAALVASRGGALNAAQGGALGTALNAVR
DAVLGWLVKDFISDEEFRTLVGPWEQVMGRVIA
>PFR_JS22-1_1987□PFR_JS22-1_1987□Hypothetical protein□2244126:2244872 Reverse
MRPPAVETPDVKAPATPAGSRLFKAVRPDGFDFHSGTVRWLPADGAPIPEGGWLVEHPHP
GEVGSWDAAFYLSASSVETDCTGFQWPALLLSVEPVGAMWTPRPDKFPRKRAAHAWRVIE
ELPAWRLFGPQGRTVLDIIEQTAHLTKRQIAALNRALDAARDTVWDVAWNAAWHAARVAA
RVAARGAARGAARYAAWDAARGAAWYATWVAARGAALGWLVKDLISVEDFRTLTGPWEQV
MGPIEVAA
>PFR_JS22-1_1988□PFR_JS22-1_1988□Hypothetical protein□2244869:2244964 Reverse
MPDTQPRRARRRTLSEILAPAPAPRRAEATA
>PFR_JS22-1_1989□PFR_JS22-1_1989□Hypothetical protein□2244957:2245103 Reverse
MPSPRRFLILIALGAAAVGFAPSSIQFLFMAALVLGLTITCLKESNHA
>PFR_JS22-1_1990□PFR_JS22-1_1990□Hypothetical protein□2245096:2245311 Reverse
MKVDDFDDVRPLTQKDVAELLHASVGYVRSCRLATKPKGRVFPMPGWKTDGKRYLLPAWR
FREWVESLPDA
>PFR_JS22-1_1991□PFR_JS22-1_1991□Hypothetical protein□2245298:2245390 Reverse
MTSTLTGNIIALLIVAGVIVLAMGVRREGR
>PFR_JS22-1_1992□PFR_JS22-1_1992□BRO family protein□2245387:2246190 Reverse
MSILPFDYHGQEVRFITDESGEPQVVASDLAKALNYRNAPDMMRSIDLEERGTRPVRTPG
GEQEMLTLTEAGMYQAILQRQTGRMVDVAQRAAVKRFQHWVTHEVIPSIRKRGMYATPDA
VEAMLADPDVMIRTLTELKAQRARVAQLQPKADYVDAFVADEDLRLLRNVAKSIGVQEGA
IRDALLAHEWIYAEESSRWSNSQGCKVIEHRYSPRSDKARYFRPVPNHQAPRFKGEVMHT
LKVTPAGAEAISKMAKRWGLVVQEVAA
>PFR_JS22-1_1993□PFR_JS22-1_1993□Hypothetical protein□2246253:2246456 Reverse
MISAAIERSDTSRAEVATLTGIPLTTLRRKLMGRSPVNIEDIFLIAGALGIPPVSITPDV
LTSEAAA
>PFR_JS22-1_1994□PFR_JS22-1_1994□Hypothetical protein□2246586:2246840 Forward
MDQNQASKRDAIRAAIAAQLRAERAAKGLTQVETARLAGVSESTIIRIEQGKRDLPVALL
FELARVLDFEPGVFMDAAQARYQR
>PFR_JS22-1_1995□PFR_JS22-1_1995□Hypothetical protein□2247112:2247564 Forward
MTHTMRRKALVPIALLASLCLAGALTACDPQTSGSSSSASKTPKAAKTPTATKTPTASAT
PTPVEATTTGLTMTGATSGCGTYARDALGKQYPSLKIKVHSTVDSVAALNKTDDLWNVNI
GADVGSAKYTVHCDVTGTDQAPVVSNFQAW
>PFR_JS22-1_1996□PFR_JS22-1_1996□Integrase family protein□2247637:2248947 Reverse
MSRASYGDGTQPTRRSDGRWAASAYDGWQANGNRRRRWVYGRTQAECKRKLRDLKREIWS
DTQQMNVNPRETVKSWTASWLDDYRSIARPTTFATDESMVRNWIVPAIGARRLSELTARD
ASKLQRVCRDGGLSATTSHYAGLLLRRILKAARANGYRIPDSVMLARIPGIGASNRSALS
AIQAANLLSTANARDTWPEPPSLPDLPYGAISKLAPAEAQKREQLKMERLEWTAAQNTDP
SRWAAALMQGLRSGEARGLTWDRVDLDKGTITIDRQLQRIKPDAALPPGYKVTRLEGSHC
LVAPKSRSGIRRVPIVPWMGQALTRWRDIQGDSPFGLVWPLPTGAPPTRVHDLRAWRGLQ
RVAGVHKEDGNLYVLHEARHSTVSLLLAAGVPESVVIAIVGHASFAATEHYAHTDLEAAR
AALMKVQDRLGLELES
>PFR_JS22-1_1997□PFR_JS22-1_1997□Starvation-induced DNA protecting protein□2249638:2250165 Reverse
MTNTISAIHQAEVSTTNLQNAESGFVASDILRDSLQSVLVDLIALSFSGKQVHWNIVGPN
FRDLHRNFDDVVEIAREGSDTIAERMRALHVAPDGRTDVVSATTTLPELPAGEILSSDAV
DLVVKSIEATTRTIREVHDAVDSADPSTADLLHELINKLEQQAWFIAAEKRQPQD
>PFR_JS22-1_1998□PFR_JS22-1_1998□CAAX amino terminal protease self-immunity□2250323:2251378 Reverse
MTHDDQPAPAMPGGGGPGPSGAVPGSPSGTAPGVTRVRWLPIVVFYVLACALAWLVISPL
WISGKGLQNPLMGVLSPLMMYTPAVAALFVVMVVQRVRGRAVLASLGMWPIRPLKRTLLL
ALAALVGTALLPIVVTFIAAGLGLVRLDLVNFSGFAQVLQSQMPAGQTYPLSVRTTVIVQ
LVMLLPASATNAMFTVGEEIGWRGFLMSSLRPLGTWPALVISGAMWGLWHAPLILLGYDF
GRRDALGVLLMIVSCVILGTLFGWLRIRSGNIWPSVFGHAALNGTAGFLGLVVAAGESPS
VLATSPLGWIGWTLVALVVVVLALAGQFRGKDQWAVNVAKAPAVGPSPFQP
>PFR_JS22-1_1999□PFR_JS22-1_1999□Hypothetical protein□2251566:2251784 Reverse
MNDAQSAFDKAAGKAKEVGGKVTGNDEMAAEGTTQNAKGKVEGALNEAKDKVADTVNGVK
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EGLKGVFNKDES
>PFR_JS22-1_2000□PFR_JS22-1_2000□Putative long chain fatty acid-CoA ligase VraA□2251954:2253012 Forward
MNTSVIDTGPVCVLGEGPGVVHQFWQAHRRGRLIGLRTSGTTTGAGRVIVRSTDSWVDSL
DAVAQRCALTPHDRIWIPGPMGSTMNLFAACLAVHNGVEWSSDKPECATIWQLTPARLSS
LLDAGLPRSQRLREVIVAGDSLSRGLRDRATTRGINVVHYYGAAEMSMIAMGSCRDDLEL
FDKVEVRTTDGTIWVRSPWLAQGYLRATPDAPRQPESPAPLRRSDDGFVTVGDRGALAGR
RLIVAGRDGAVTTAGQTVILAPLLDRLRHRAQGELFLLGLPHATLGQVLTAVVTRREDLG
PVRAWAREHLTGGDRPRCWLWVPRPPLTASGKVDLRALALDLAGPTDGPDAP
>PFR_JS22-1_2001□PFR_JS22-1_2001□Putative acetyl-CoA C-acetyltransferase VraB□2253009:2254163 Forward
MSALADNPVIIEALRTPIGTTGGVFADQTTTDLAAPVLGELDARLPAGTGFSEVVLGNVR
GPGGDPARVAALAAGIDPAVPALTLDRQCGSGMAAIEYAWHRCRSQPGVVAAGGMQAAST
QPITLWPGRDGEPPTAFDRAPFAPPPWLDLDMGVMADQLAAELHISRERQDRYALRSHMR
AATARDAGDFDAEIVPIAGVGRDQRPRGDFTMARLARFPAAFRPGGTVTAANSCGINDAA
AAVTMVDAATHAHLPTPGLRVLAARTVGYDPDRFGLGLVPAVRAALDDAGLGLDQIDALE
FNEAFAAQVLACADALDLDEHRLCPQGGAIALGHPWGASGAILLVRLFSRLVREGAGRYG
LAAISIGGGQGSAVVVEAVHPRGN
>PFR_JS22-1_2002□PFR_JS22-1_2002□Sugar phosphate antiporter□2254558:2256006 Forward
MGSLKTAFNIVPAPKSDIPITTQRKRWLREFMKTYAVLIIGYGGFYLLRTNFKSAQPFLR
DQLGLTTTQLGTIGFGFSLTYGFGGLILGFFADGHNTKKIISALLIASGVVAITIGITLA
VTHNPYGYLILLWSLTGLLQSPGGPCCNSTMNRWTPRKYRGRFIGWWNASHNLGAMAAGA
LALWGANTFFHGSVVGFFVVPALVAIPIGIWGLFFGKDDPIELGWDKPEVIFGEPQAKAD
VVTQQVSKGRILMDYVVKNPAIWFLCIANVAAYVVRIGIDNWNVLYTKSELGFSDYTAVN
TTIALEIGGLLGSLCWGFFSDRLGGRRALTAAIGLALVVVPIFVYAHATTPTVVYAALFF
IGFLIFGPVTLIGISVIGFAPKTATVVVNAVPRAFGYVFGDSIAKVLLGRIADPKKQGLE
IFGHSLHGWGSTFTVLFVSAGVGLVCLVAVALFEERMIRADREFSRGHPAADAGISQGAD
DE
>PFR_JS22-1_2003□PFR_JS22-1_2003□YktC (Inositol monophosphatase SuhB)□2255999:2256850 Forward
MSEQLDIKALLAIAEQVVRRASAMALAGQQRDLQVQTKANRNDLVTRVDKDIEEFVAAEL
TSRTGYPVLGEEGHGVDSFAGRVWVVDPIDGTMNYVETRRDYAVSLALVSDGQPLIGVVA
DVVAGRLYSAVRGHGATCHQDERDWTRSDAGGPPTEPGRSTEELAQVPSDKGFRDSIIIT
DLKEIRAMPRLVAALVESRGHRRYGSAALECLEVASGRAGAFVHLWVSPWDIAAAMVICA
EAGVTVTRLDGTPLDVRHKGSILAGAPRAHAELLARLVSDPTQ
>PFR_JS22-1_2004□PFR_JS22-1_2004□Permease, cytosine/purine, uracil, thiamine, allantoin family□2257026:2258546 Forward
MTTAATSTGPAPDERLLEAPIKHGVLSHVEQRGIEPVPADKRNGTPGQLFWIWFAANISI
LGIPLGATLIALGLNLWQAVLATAIGAFGSFAVVGVISVAGRRGGAPSLTLSRAIFGVRG
NAGPTLVSLVSRLGWETVTTLTGAFALISLYSIATGTTADAKAHPVLTVVCIVIFVALTV
VVSATGHAFLLTVQKWATWVFGALTALVALYLATTVDWSAFIGNAPGPASAFVVGIGTIV
AGTGVGWANSGADMARYQKLSVKTRSLVASASVGAGIPLVVVIGLGSALTAGNSSIATAS
DPIAAVHQSLPTWVSVPYLIAAFAGLLMSNHISMYSAGLTTITLGVRIRRVYAVVVDIVV
TITGSIYFMLISDSFYGPFISFISVLAVPITAWIGCFLVDMAGRRSYDAHGLLDLRPGAR
YWYWHGISLAGTGSWLIGLVVGLLFMSAKISDTEVWFAGPLSHTWIGTNGLAWLVSLVVA
AGLYALFGGLRRKDDAAAALAAGAAA
>PFR_JS22-1_2005□PFR_JS22-1_2005□PfkB carbohydrate kinase family protein□2258543:2259547 Forward
MSEPVDRSRGRFLHLGQMIVDLTVYVDRIPERGGDVFADKATMNAGGGYNVLWAVKQMGL
SPDFFGAVGTGPMGDILRGAMHRIGVAAQGPTIAGLDTGYCVAMTEPDGERSFISVSGAD
AQMGPDEFAGLALRDDDLVYLCGYSFMSPGTRTAVERFAAARTEWTQAGGRVLFDAGPMV
AEFPGSSLQAMIDLHPMWSMNDLEGCLLTERLGVAARGEQERCRLLSQRLGAPVILRVGS
DGAWFADGDAARKVPTPRVGAVDTNGAGDAHAGVLGAALLEGIPRDRALVLANCAGALST
TRPGPATCPDRQAIEDAADKLVGSADSLVGSTDS
>PFR_JS22-1_2006□PFR_JS22-1_2006□NUDIX hydrolase□2259754:2260197 Forward
MGSVLYPKLQVLDVVAAVIVDGDHYLACRRDAGLDAGGKWEFPGGKVKPGETAQQALRRE
IREELGVDVEVHDMLTSSQTTKSDRIIGIRFYLATAAERPTHSDAHDKLTWLTADELPAL
DWATPDLAAVGQLNSKYALELSAPVLN
>PFR_JS22-1_2007□PFR_JS22-1_2007□Hypothetical protein□2260290:2260493 Forward
MRDSKNLPQDAVDMARAFIADYARRNDGDVTAGADFLKGPLDTMPEIVDEALRQMQEFPQ
ARRARVA
>PFR_JS22-1_2008□PFR_JS22-1_2008□Sn-glycerol-3-phosphate transporter GlpT□2260817:2262235 Reverse
MSTTDTARPARKRSWLSSPLPAPRLPDAEVKQRYPRMRFQVFMGIFVGYAGFYLIRNNIS
LVAPILLKDGHIDKVGIGLIANAVLIAYGLSKFFMATVSDRSNARYFMPIGLALSAVANL
LVAFVPALTGSIAIFAIMMFINGWFQGMGWPPSGRVLVHWFSTNERGWKTAIWNCAHNVG
GMAVGAAASWGLAITGDSWQSAFWLPALIALVVALFAFLTIRDTPASVGLPPIEDFRNDP
AKVEVDNSEIAQQSYWRVIWEHVLKNRTMVLLALANVFVYALRYGVLSWTPTYLSQVHHV
SVTKGIAGFSLFELAGLVGTLACGWVSDKVFHGNRTKTGITFMVGVGISLVAYWLAPVGT
PYWLLMVFLFFIGAFIYGPVMLIGLQALDMSARQVAGTSAGFTGLFGYVIGATLASTGVG
WMVQHFGWGVTFGALTVCVVIAIILLACIGPEEKRLIASHDAAVEESFQEED
>PFR_JS22-1_2009□PFR_JS22-1_2009□Mg2 transporter-C, MgtC family□2262525:2263253 Reverse
MPFLSSELALRELILLSIAFVLCSVVGLERSIHQKNAGYRTHVLVGMGACGLTLVSWYGF
GAGIAGHGAGIDPTRIAAQIVSGIGFLGGGVIFKGRNFVRGLTTAATIWITAAIGMSVGS
GLVVLGAMLTVAHLLTIFIVGPLIRKIPPADRRREMTIVYEDGQGVLRKILGAATDQGFA
AEVRSTRRLPRKDRDLISMELRFFGNQPLRELVVPMSEIPGVDRVLLHGVAEDEDDDDET
SA
>PFR_JS22-1_2010□PFR_JS22-1_2010□Metallophosphoesterase□2263260:2264954 Reverse
MSDISREATTDDDPADNGPAAGDTADTTNHRIVRAQPYQGRYVELTDAPGEPHVARDELA
PGIGDDPTSDWTPSGGPLLSLAQLTDFQLADLISPARTDYLQRRSDDPRWTRMTPSYRPE
EFLELHAIEGVAASIREFAEQHHLDVTVTTGDNTDSAQHNELATYMRLVTGGPVDPTALG
VGHPSSPTGLADDPAYWHPSGTAPDEFTDRGVPRRPGADAAAAKPFTATGVGTPWLTVYG
NHDALVQGRATGSSLYSEYVQGNRKPVEPPAGYEPADEALVDFVADPMVLTGGPSIPVPA
DPDRRVLDREGYVKGHLVADGLPVGHGFSELNAETHTAYYVWDAVPGMRIITLDTNNPAG
FWDGALNDGQFTWLAERLAEVSADSDDPRLVIIAAHHGLSTLTNGYRDAEHHEELHLADD
VEALLHRHPQVIAWISGHTHVNLVTPRARPTDGQQSSPGGGFVEFSTAAVSEWPVQWRHL
EVRIAPRGAVIRSTIHDSAAPLHAESWQTPLELASLHRAVAANDPDAVGGLEAQGSARDR
NVIVHVPLPPELVSAVLRASLTRD
>PFR_JS22-1_2011□PFR_JS22-1_2011□Putative metabolite transport protein YaaU□2264947:2266335 Reverse
MTSGTSPSQRSPQVLTTTGFDEVDTPQMRRFQRRVTLLSAGGTFLDGFDLTVIAVALPLI
KDEWHITALQQSIIVSAALVGSLIGALWLGHLTDRHGRKAMYVIDLLGFVVFGALTAFAP
SVLWLIIFRFLLGLGIGADYPISATLVSEFSSNKRRGMHSTSLAAFWFVGSVFAYIVGLI
VAPMGDLAWRAMLLVGAAVALVVFFMRIKLPESPRWLIAHGREEDAREVMHRVTGLQVAE
HIKLVVPEAVPARKLFTPRFLKRTIFTCGFWFCYSTAYYAISMYTPTILAPFTKGDRTAN
IVGSGVVAIIGLIGSIIGMNTVDRWGRRPLIITSFAGLTISLAIIGVNTSPSLGFLIVLF
SSAVLFANAGGGILNFVYPVELFPTNIRATASGLATSVSRFGSILGVLVFPNVVKAWGQN
SAIWIFAAVGALGTIICIALAPETKNRTLEELNPEPGEPAHV
>PFR_JS22-1_2012□PFR_JS22-1_2012□Hypothetical protein□2266493:2266645 Forward
MQPAVEQDPLVDAGTPESIQNDWDTSPVINRTAKDTKRWNTDFVTSENHA
>PFR_JS22-1_2013□PFR_JS22-1_2013□Thermostable beta-glucosidase B□2266745:2269129 Reverse
MPGQPARAASVPESEQRRQAHQIVSRLAPDEKAALLSGADAWHTVGLGRLDVAAVTLADG
PAGLRKVTDPEVGVMRFDNAVRATAFPVPAALGNSFDPDVVAMVGRAIGEEAREQSVGVV
LGPGINIKRSPLGGRNFEYYSEDPILSGQLGAAWVQGLQSCGVGACVKHFAANNQETRRM
TADALIDEQTLYEVYLRAFEHVVRTADPWTLMCAYNRVNGTYCSESHWLLTELLRDQWGF
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DGLVVSDWGAVLDRVRSLAAGVDLAMPPDLAHDAADIQSAIARGMLSPQGRDEACARVVE
LALKVTQGTTRELGRRVGAHHHVAREAAGRSIVLLRNRAVDANNHGSANPVLPLAHGAKL
AVIGEFAANPRFRGGGSSQVIPMLLDIPLDEIRGRADEPVRYEAGFLLSGESDDELADRA
VEAAEEAEVAVVFVGLPDDAESEGLDRTSILLPAVQTGLVQRIAAANPRTVVVLTNGGVV
QLAEWSSEVPALVEASLLGEAGGSAIADMLFGEVNPSGRLAETIPLRLQDTAAYFNFPGD
RNQVRYAEGLHVGYKWYNASQLEVAYPFGHGLSYTRFSYNGLHLAADESGLHARFTLRNT
GARVGREIPQLYVALRASAYRRAGFEFKASAVVQLAPGEQREVTLSVSPADLGVWDADLH
RWLVEGGDYDVAVGASSRDIRLNGIVTVRGEARPRTLDRNSTVSEWLSSPLMAQFLAVQL
ANLATDPAATDGAGPRDPQEFMRLAHDLRLSQLPVLAPQLHISHEQIDQLIAAAGMDARP
RPRRIDDSDSGART
>PFR_JS22-1_2014	PFR_JS22-1_2014	Transcriptional regulator TetR	2269498:2270190 Forward
MTLRHYPKGSAKRLEILDAALEVFTTEGYRATSLRGIAERAHITPAGIMHYFDSKEQLLS
AVLQHRDAMDVRRADLDTPTNPVETLAQVMDANMKVPGLVTLYLTIAAAAVDPHHPAHDY
LERRYRRLAGGLTAWITEMSQAGLVPKVVYPAGVATAIVAQADGIQFQWLLDPSVDMGMH
VRRGGRRLLGLPFDKPIPQLPNPWTMRRALQLYPVTMVTGERVGEAPVGH
>PFR_JS22-1_2015	PFR_JS22-1_2015	UDP-glucose 4-epimerase, galE	2270265:2271239 Reverse
MSWLVTGGAGYIGSHIVQAFQQAGIDPVVIDDLSSGHEHFVPEGVPFVRGSILDTGLVQR
TLDEHHCEGVVHVAGFKYAGVSVTRPLHTYDQNATGTVSVLRAMRSAGVHRYVFSSSASV
YGTPDVDEVTEQTALHPESPYGETKLIGEWLNHDMEPVDDQWQGVNLRYFNVVGSGSDQL
YDTSPHNLFPIVFDLLLSGGTPRINGDDYPTPDGTCVRDYVHVADLARSHVAAAEQMMAG
KKLEKAYNLGSGTGSSVREIMDAIARVTGIAFTPEIAPRRPGDPARIVARGDKAARDIDW
KMRHSLDQMVESAWNARRAHPQGA
>PFR_JS22-1_2016	PFR_JS22-1_2016	Putative Sodium:sulfate symportert	2271588:2272985 Forward
MRKNWIFLGVATLAFLLVRFAIPTTAALTPSAKGALAVAVFAIIVWVTQAVSDALSGFLI
ILLLVISSATNLAGSFAGFSNTSLWLIVVGFIMAAAMEKSGLSERIALSVVRLAGGSAIK
IYWAIAGVMAVLTFLVPSITARTLLMLPIIMGIGQAFGAERGKSNIVKALIFIVAMSGTM
MSIGVLTAHVGNPATVGLIQAATGHNVSWSEWFKVGGPPAFVLSALSVVVISLMWKPETS
RVEGARDYIAGELARLGPIKKTEWYTLAVFMATLVLWATEPPMLSTIVVGIIAVILLLLP
GLGVLNWKEAQEKVPWNVFMVYGAGLSMGTALTTSGAAKWLATTMFGPITQLSIPVQMII
LLWFITILQVFFTGGGPKTNALTPIILAHAGAIGANQASFGLILGMNMNHQYLLPVSNMP
NAVAMGTDFINTRELIRTGAVMSVLGAAFMSVMVLTYWSWLGMVG
>PFR_JS22-1_2017	PFR_JS22-1_2017	Polyphosphate glucokinase/transcriptional regulator	2273065:2273850 Forward
MLGIDVGGSGIKGAPVDLQAGELAVPRRKVLTPQPSTPEACAGAMATIIEQFADQIDGPI
GVAVPAPVLHGVTPFMANLDQSWVGLDADAYLSEKLGREVVLVNDADAAGVAEMQYGAGR
GKQGTVVLTTLGTGVGTALFHDGRLVPNTEFGHIEINGRDAESRAASSYMEREHISYKKW
AKHLQRYYSTLEKLLWPDLFIVGGGVSREYKRFLPLLNLQTPIVPASLRNSAGTIGAALA
ASLRVGADVPPGAQRIASVPA
>PFR_JS22-1_2018	PFR_JS22-1_2018	ABC-type Fe3-hydroxamate transport system, periplasmic component	2274021:2275016 Reverse
MTLRRAVIALIAAMSLLLAGCSGSSSSSKSSASASGGAAAGSFPQSVDTAFGKVTIEKAP
QRVVALGWGDAETALALGVQPVGASDWLNFGGEGVGPWAKGLYTTAPTIIGTMEPNYEQI
ASLKPDLILDVKSSGDKDRHDRLAQIATTVGIPEGGTSYLTTMDQEVTMIATALGQPAKG
KELLDAADASYKKVADAHPQWKDKTVTVATRTSEGWGAYIEGDTRLASLEKLGFKQNPTI
ASMTPSSSGFSVSVSSEQLSAFNADLIVAFPIYIDTTQITDDAQWKQLSTVQAGHDAVID
GDLSSSFAVGSPLAVNYMLDNMVPKLEKATA
>PFR_JS22-1_2019	PFR_JS22-1_2019	Ferric enterobactin transport system permease protein FepD	2275264:2276322 Forward
MTPNSSAPARTAELSSPHAPDATRRRLIGLVVGIALLVAACAASLAVGSATVPLQTVWQA
LTGAHDSEAARIITTLRLPRTVLGLLAGAALGVAGALIQAVTRNPLADPGILGVNSGSAF
AIALGVGLFGASSPGQYLWFAFAGALVATVVVYLIGASGSGSVSPARITLAGMALGAVLS
GITSAMRLADDRRFSVIQAWQAGSFADRGWDVIVPTLPFLAAGLVIAALLGRSLDAIALS
DDLARALGTNVNRARLLALAAITLLAGGATAMVGPIVFVGLMVPHVARWISGPRQGWIMA
LCVVWAPVLVLAADVVGRIILRPGEVAVSIVTAFIGGPVLIYLVRRTKAGKL
>PFR_JS22-1_2020	PFR_JS22-1_2020	Ferric enterobactin transport system permease protein fepG	2276364:2277389 Forward
MRPSVAMSTMAPWRHRIPRRMIIACAVICAACVAISLLALSLGDYPLSIPEVVSALFGDQ
GFATTVVTQWRAPRVVAGLVFGAALGLSGALFQTLTDNPLGSPDVIGFSTGSYTGVLIVT
TLGATSAVSTSVAAVVAGIVTALVIYLLAWRGGVQGFRLIVVGIAATAMLTAVNTFLLLR
MRTEVAMSASIWGAGTLSLVSWAKLTFALPAAALLVACTVLLARPLRQLELGNDTALAHG
TRVESSRLAILVVGVGLVAVVTAAVGPIAFISLSAPQVARRLARSAGIPLLTSAFTGALL
LVGADVVAQHLTTNPIPVGIVTIVIGGAYLLALLFREARSL
>PFR_JS22-1_2021	PFR_JS22-1_2021	Iron-siderophore uptake system ATP-binding component	2277386:2278291 Forward
MTIKSTPDSPTTAGRDVPHDAGADSAGTHGADAHSAGTHEAGTALVSRLGAEHVKLAYGD
RVVSDDLTVHIPPGSFTVIIGPNACGKSTLLRGLSRLLKPRGGEVVLDGKAISTYRTKEV
ARIVGLLPQSSTAPEGITVADLVARGRYPHQGLIRQWSHDDEMAVNDAMEVTGVSDLRNA
PVDQLSGGQRQRVWTAMALAQQTPILLLDEPTTYLDISHQYGLLNLFAALNRQGTTIVAV
LHDLNQAARYATHLIAMKQGRIVAEGTPREVVTEQTMREVFDVDALVMDDPITGTPMVVP
R
>PFR_JS22-1_2022	PFR_JS22-1_2022	YdjK	2278721:2280184 Reverse
MSNAVRDAGGTKPASQQENQLPPFTVGPHSKRLGIIAVIATFGGLLFGYDTGVVNGALTP
MKADLGLTSVTEGFVVSILVVGAAFGAIIEGGVSNRLGRRRSIQMLALIFMIGTTGCVLA
PTWQVLGIFRFILGLAVGGASAVVPVYLAEIAPVERRGSLVTRNELMIVSGQVSAFIINA
IIYQYWGDHLSVWRYMLLVALLPAIGLFFGMLKVPESPRWLMSKGREDDALAVLKLIRAP
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CALAIPDGVAAKPVVILVLVMCFVFSMQALIEPLTWLLLSEIFPLRVRSFAMGVSVFMLW
VANSIVAFAFPPLVEGVGVSTTFFIFAGLGVLAIIFMVRMVPETRNKTLEHFEEEMRQHG
EPTAAGS
>PFR_JS22-1_2023	PFR_JS22-1_2023	Inositol 2-dehydrogenase IdhA	2280288:2281286 Reverse
MTLRIGLVGAGFIGSLHARNLFASPRFDLAVVAEPNADHARAVEELTGATIVPDWRTLVD
DDSLDAVLIASPAEDHPEQVGAFARAGKHVYCEKPLGLTLEAADAAVAAVQEAGTLLQMG
FNRRLDPNMAALHANVADGRVGDPLIVNIISRDPGLPDASYQRGPGKMFMDTSIHDFDTA
RFLAGSEIVEVSAFSAALVDELARDAGDADTCLITLRFANGALGVIDNSRLATYGYDQRA
EVLGTLGLASMGNVPSTTTTVADGAGYLTPPLPDFFPERYAESYRIGLDVFADAIEKGSP
VASDGHDARQALAAAFAAEQSRRKQRAIPLNQ
>PFR_JS22-1_2024	PFR_JS22-1_2024	IolE protein	2281316:2282233 Reverse
MTTTDKAPATRARLGSAPDSWGVWFPDHPQQTTGTRFLDEIAEAGYHWMELGPYGFLPTD
PSQLADELAARDLHVSAGTVGGAFHKKDELEALTQEALRVAKLAAAVGGKYLVLLPAMYR
DLLSGDYLEDKTLDTEGWKQFIRSCEEVSRAVQQETGLRAVFHPHADSHVETQQQTYRWL
DDTDADAVGLCLDTGHIEYGGGDSAEIMRRYPQRIEYMHFKQVDPELMKTVRDKDLAFAD
AVKLGAICEPPKGIPTAESIAAQMHLLNPELFVIVEQDMFPCDPDDPLPIAARTCGYLRS
VPLAL
>PFR_JS22-1_2025	PFR_JS22-1_2025	DNA-binding transcriptional repressor of ribose metabolism	2282471:2283508 Forward
MTHTAGPGPENPSVTIRQVAARAGVSKSSVSRFLQGGTYLSDAAREAIQAAVDELGYRPN
AMARSLTERRTHAIGAMVNDLRQPWFGDFLGGLGAALHHHGYYMVVGDTRVDRHMDERLI
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LLERGGTPPTAVFVSNDFAAAGLLTAAADLGLRIPTDLSVATIDNSFLSRSGTTPLTSVD
THSEEQGRLAGESIIRRILQPASPPQRSLVAPSLRVRRSTAAPAR
>PFR_JS22-1_2026	PFR_JS22-1_2026	Arginine--tRNA ligase 1 (Precursor)	2283530:2285122 Reverse
MAGIDPEMRPATKPQFGHFQSNVALRLAKQQGKPPRQVAQEIVDKLDVGDLCEPVEIAGP
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GFLNFRLRADVLAGAVTDQLHDPRAGITPTELPQTVVIDYSAPNAAKQMHVGHLRSTIIG
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GRNALDPDEWERAGWRYAGMGRR
>PFR_JS22-1_2028□PFR_JS22-1_2028□SanA protein□2286762:2287433 Reverse
MRRRISHPLRVILVGMVVLACLVLTGSWALVHGAARDRVFTAQNAPSRDVALVLGAGLNA
DGSPSLYLAGRLRAAYDLYVSQKVKVILVSGDNRTVTYSEPGAMRSYLRLLGVPDRDVVA
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WRTGEMREIPANVKFVWDRVTHRKPILGQRETSVTDALAEHDR
>PFR_JS22-1_2029□PFR_JS22-1_2029□Protein involving differentiation□2287695:2289467 Reverse
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VAAELLSARVIQRITVVCPTEHLKTQWAEAAAKVGIQLDPGLGGSSRRGRSRQFHGTAVT
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>PFR_JS22-1_2030□PFR_JS22-1_2030□Hypothetical protein□2289471:2289713 Forward
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ATAVERVGPIGATSACTGAT
>PFR_JS22-1_2031□PFR_JS22-1_2031□Hypothetical protein□2290515:2291303 Reverse
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AQSPGGRCRPAEWSHVPFRRAGHHRPWPTLLLFYGTCGADTPLSLELQICDFWLHAGVHR
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>PFR_JS22-1_2032□PFR_JS22-1_2032□Ferredoxin-like protein fixX□2291573:2291866 Reverse
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VEYAACLECGTCLAVAPPGTLTWHYPRGGMGVVFREG
>PFR_JS22-1_2033□PFR_JS22-1_2033□FAD dependent oxidoreductase□2291880:2293184 Reverse
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VFPGFVDNAPVERRITRNVVSFANPTSTVNIDYWDQRLAEPVNAVSVLRAKLDAWLSEQC
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LRLDDLVAKGLASSDVHDHFLAHPAIAPLLEGGQLREYGCHLTIEDGPAMVAHELHRAGL
MIVGDAAGFTLNTGLTIRGMDLAAGSALAAASAAHRALTDKDYSDESMARYERNLERDFV
GQDMRTYAHMPELLDSPRMYGAYGEMIADVMHGMFNMDTRPRTHAIKVATRAFKKSSVRL
GELVRDGITALKAL
>PFR_JS22-1_2034□PFR_JS22-1_2034□Electron transfer flavoprotein FAD-binding domain protein□2293187:2294059 Reverse
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VADAVAAGDQDVVLAPNRPAERVLAGAVAARLNAPVLSSVKKVDAEGAHVARFGGITLQT
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>PFR_JS22-1_2035□PFR_JS22-1_2035□Electron transfer flavoprotein□2294096:2294851 Reverse
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>PFR_JS22-1_2036□PFR_JS22-1_2036□YqgX□2295035:2295679 Reverse
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>PFR_JS22-1_2037□PFR_JS22-1_2037□Metabolite transport protein YaaU□2295684:2297042 Reverse
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>PFR_JS22-1_2040□PFR_JS22-1_2040□Hypothetical protein□2299856:2300980 Reverse
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>PFR_JS22-1_2045□PFR_JS22-1_2045□Short-chain dehydrogenase, teichoic and lipoteichoic acid D-alanine esterification□2305142:2305882 Forward
MDISGRTVLIVGGTTGIGRALAQRFVDAGSTVVVGGRNIEQVDGVETVRIDVTDAASVAQ
ARDEVLAKHPELDVVVTMSGVMLTEDLRDPDHIAQAETTISVNLLGTIRVIDAFTPHLLG
RGAGDIITVSSGIGFLPFPLMATYGASKAAVHSYTESLRAHLAGTGIAVTELIPPAVANA
GQEKLNPNALPMGDFLDEVIGLLTQNPTPKEIVVERAKPLRWAEHDDTYEELLAARSQSL
SNLSGR
>PFR_JS22-1_2046□PFR_JS22-1_2046□Ketopantoate reductase (Precursor)□2305905:2306825 Reverse
MVTEQQPSSFRERKRVGVVGPGAIGTTVSALLHEAGNTPTLYGRTPRTELTLIDGDRRIV
VPGPVRTDPAAQPEKADVLFLAVKATQTAAAAPWLRALCAPGTVVCVLQNGVEQIAAVRP
HVPEGVEVVPAVVWFPAQSQEDGTILLRGEPRLTLPASPEAERIADVLRDTRCQVELAGD
FTTLAWRKLLQNAAAGLMALTGRRAGVFTRPDFADLTLDYLKECLAVSHAEGAALSDDVP
AAILARFQAFPADMSTSILTDREAGRPLEWGIRNGVISRLARRHDIHTPISDAITALLAA
TSDGPG
>PFR_JS22-1_2047□PFR_JS22-1_2047□Transcriptional regulator, RpiR family□2306939:2307733 Forward
MASEAKVVDLVLEDPLFVGRSTTAQVAERAGVSAPSVIRAARAIGFSGFAELKLEIARAR
GTAEFFAPPHTLTSTDSTRTIIDTTARTGIDALTALSGAIDPDALDQAVSAIRGAGQLLA
YGAGPSATVAADVVFRLRSLGVRTSGVVDHESAMIAARLLDPGDVVVAVSSTGRTDMTVA
IADAAATADATVIAITNQYGTPLTDVSAVALVVGGAPLTTQMAAAGSRLAQLVVVDALAA
ALALRDPDRVSRAERAGIDLPDIT
>PFR_JS22-1_2048□PFR_JS22-1_2048□Putative transporter, DMT superfamily□2307733:2308593 Forward
MPPVTVAIVLVAAVAHAGWNLVSKYKKGDTLLFVGAYTTASAILCLPLAIGAAVSGSQPI
TWALVAAAAVSAALHLTYSLTLQAGYDRADLGVVYPIARGVGPLLTIVIAIFLLGERPTA
LAIIGALVILAGILVVTGNPFQRTGSRPLRGIAWGTTTGATIAAYTLWDAFAIGSIGLAP
VSYYAGTLVVQVVFLAPAIIRRRAAFANTLRVNRAPIAAVAVLSPLAYILVLTAMQTSPV
ALVAPLREASIVIGALLAWRLFGEGHLARRLIGAVIVLAGIAGISL
>PFR_JS22-1_2049□PFR_JS22-1_2049□Hypothetical protein□2308894:2309055 Reverse
MASVGAGSRGYRYLHHGVDDHSRVAYSEILDDQRKQTAARFWERANAFFATSA
>PFR_JS22-1_2050□PFR_JS22-1_2050□Transcriptional regulator type FNR□2309221:2309904 Reverse
MPEDDLCVTRVPIFQGLTHEEQLRVADFARPVLAKRGEVVYAPGQPVSRLLVMHSGQLKV
SYVAANGQEQILRTVTDGDVVGERAFLTGHRPNDLAVALEESRICVFDHADLAVLLRDYP
DISQRMLRTLADRLSSVERLLAAVTSSDVNARVAAYLLELPGTVRDGAATVRLPMAKQEI
AAYLGTTPETLSRRLAALSVSGLIELHGRRNITILDIDALEHVATPR
>PFR_JS22-1_2051□PFR_JS22-1_2051□Heavy metal transport/detoxification protein□2310061:2310294 Forward
MTTATTTHTILRAEGFSCPSCVTKIEKQVGRLKGVENVKVHFASARIEIDHDAERVSVED
LVAAVVKAGYKATPAAF
>PFR_JS22-1_2052□PFR_JS22-1_2052□Cadmium transporting P-type ATPase□2310381:2312348 Forward
MNRLQKWVYGNWSVPVVSGVLIIISFAVQWLGGGVANLTVGPQWWLNAGTHATHANAVFT
LGDAFMIAAAVVAGYGIVVKAVRTLIARVIGIDLLVSVATIGSVIIGNFWEAAAVTFLFA
IGHALEAATLNKTRSALAELVAIAPDSATIVRDGQQQEVPAAQVRVGEMVLVKNGAKVPV
DGQVVSGTGVIDEASITGESIPVEKSKGGQVFAGTVSRGGFLQVLAMGIGADTTLARIIH
RVEEAQDAKAKTQAFIDRFSGWYTPAMMVLALAAGLISGDVVLALTLLVIGCPGALVISI
PVAIVAGIGRAASNGILIKGGEFLETSAKISAVAVDKTGTLTEGCPELTDVVILDSALER
SEVLRWAAAAEAGSEHPLARPILDTAQAEGVGPHGVPGSVTPVPGKGIVSDVDGRRVLIG
NPPLLLKYGVVDDGSAAQAAESLAADGKTPMIVAVDDKVIGVVAVADQIRQDAPEMIARL
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VNDAPALATADIGVAMGAAGSAVAVETADIALMGDNLLKLPEAIGLAKRTVSVMRQNIAI
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>PFR_JS22-1_2053□PFR_JS22-1_2053□Hypothetical protein□2312971:2313342 Forward
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EGLYTSLISSWRDQRDRGALEALGRSSGAAPATAAEKEAARLRRENERLTGELTVLPREV
VNG
>PFR_JS22-1_2054□PFR_JS22-1_2054□Putative insertion element ISCmi2 transposase□2313366:2314199 Forward
MWVTTLTLLTTEVFVTHANAPLTPEGRRRLAVLVVEQGWSLRRAAERFQCSPATVKRWAD
RYRAGLPVRRPKPKRYEVAAPGQLVHVDIKKQGRIPDGGGWRAHGRGSMQDRHAGVARDK
AARAGAAGSRGYRYLHHAVDDHSRIAYSEILDDERKETAAGFWTRANAFFAGLGVTVTAV
MTDNGSCYRSGAFADALGDEVKHKWTRPYRPQTNGKVERFNRTLAVEWAYAKPYASEAER
AAAYETWLHHYNHHRPHTGIGGQTPSARVHNVTGKYS
>PFR_JS22-1_2055□PFR_JS22-1_2055□Transcriptional regulator, RpiR family□2314161:2315114 Reverse
MTAPREVAPDSTVPSRLDDVSSQPADRDTSPNSTLLVERIRRARPSFSAMETAVADHLLS
DPSAVVSATTAELAKAAGVSQASVVRFARSLGYEGLPALRLSLARELTRLDVEHELSGVA
RGRIDASDSLHDLAHKIGFHEARSIEDTVSGLDLTCLDEVAHAIAARRPVTVLGVGASGL
VAEDLCQKLQRIGQQCQFTSDTHLQLVQAAMRTPQDVVIGISFSGRTVETHKALALAANA
GALSVAITGNPDSPIGQVVSHVLTTTAREDELRIGALASRMAQLAVVDVLFARIAQLRFD
DLDAALAVLPRDVVNAG
>PFR_JS22-1_2056□PFR_JS22-1_2056□Glycosyl hydrolase, family 2□2315463:2318531 Forward

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GPVETRATLLGADGTTVASGVLAEANDARGYSHAVELHVNRPRLWNPEHPELYTLLLEMP
DEVVTDQVGLREVSIDDVVLRLNDCPVTLRGVNRHDSAPATGPTVDVAHMRRDLELMVRH
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DSPDWTEATLDRVQRCVQREKNRPSIFSWSAGNECAYGCTLEVSLAWMKEFDPDRVTHYE
SAFYRNSKRSYDYSNIDLYSRMYPSQQEMLDYLAGDPDKPLVLVEYCHAMGNGPGDLEDY
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RPHPGLLELKNVQRPARVVAHDPGAGMLTLRNDLDFTNLDEVVDLSWELVCDGIVLDRGD
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EVNIWRAPTDNDRRIRLEWERARYPYAAVRAHECSAQTLDGSVVVRARMTLDAATIQPIL
RLDASWTIDVAGRLRCQMDVTRTPEFPTLPRLGLRFFLAPELDQASWVGLGPGENYPDKR
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TQEQLSITRHDVELDPDDQVVLCIDHAMAGIGSNSCGPELLARYRVDDETYHVDLVLAPT
RR
>PFR_JS22-1_2057□PFR_JS22-1_2057□Glycoside/pentoside/hexuronide transporter□2318554:2319942 Forward
MPTHAASSGKTYLTWGNKIGYGSGDIAGNVVYTFLSAFLMIYLTDQMGLNAGVIGTLMMV
AQLFNGVTDIGFGALLDRTHTRMGKARPWMLWPYIGCAVTLVASFAIPGGLSETGKYIWF
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LANKFYLIILVIYLVQQIFTATLNMGIYFMAYVLGDATRLGAFAWAINIPLIIGLLFTPV
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YGTPDVDLVTEDQPTAPESPYGQSKLIGEWLLADQARALELTDGATPLQHVSLRYFNVVG
SGTDEVYDTSPHNLFPLVIEALIEGRTPRINGTDYPTPDGTCVRDYVHVADLATSHVAAA
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>PFR_JS22-1_2059□PFR_JS22-1_2059□Uma4 protein□2321225:2322532 Forward
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LLETGGFRPQLHPRL
>PFR_JS22-1_2060□PFR_JS22-1_2060□Transposase, ISlxx5□2322844:2324097 Forward
MVGVSIPVASRWFRHAGGMPPISLVEPSGRYLSFAEREEIAILKAQGKGVRTIARALGRD
PGTISRELRRNAATRGGKLEYRAMVAQWKAHEAAKRPKEAKMVTNPRLRDYVQDRLAGKV
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QYFPKGTDLSRWTAEDLEAVAHTLNNRPRKTLGWRTPAEVFEEQLRSLEEAGVATTG
>PFR_JS22-1_2061□PFR_JS22-1_2061□Pyridine nucleotide-disulfide oxidoreductase□2324247:2325602 Forward
MDVDLLVIGWGKAGKTLAGRFAAAGKTVALVERSPEMYGGTCINIGCVPTKDLVVSAEER
RDSDDPQEFFRTAVAGRDALIGTLNAANHQMLEKPGVTLVDGTARFTGPRTVVVDTAEGQ
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FTHFGSKVTILDRGEEFLPRVDRDVAEAVRQTLLDMGVTIEQGVRPTSLDDDGTHAVVHT
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PQFTYISLDDNRIVWDAVMGQGTRRRSDRVAVPNTTFITPPLSMVGMDETQARKSGRNVL
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AKVSDLRDGIWTHPSSTEAFNEVLGTLEPLA
>PFR_JS22-1_2062□PFR_JS22-1_2062□Hypothetical protein□2326165:2326437 Reverse
MYECCRELHLDQSMGRTGVCWVNAMIESQWSVLKAEFYDRYEWDTPQQAIQGVEEWIYDF
YNTKRLNSAIGYQTPVEFEAQHAAALTRAA
>PFR_JS22-1_2063□PFR_JS22-1_2063□Transposase, ISlxx5□2326463:2327662 Reverse
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IEYRATVAQWKAQEAAKRPKIAKLVRNERLRDYVQDRLAGGVTHPDGTPVAGPAAPAWKG
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VERRSRTTILVHLPRLEGWGEQPPVKKGPSLGGYGAQAMNKALSASITSLPQQVRQTITW
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AVAHTLNNRPRKVLGWRTPAEVFDEQLRSLEQAGVATTG
>PFR_JS22-1_2064□PFR_JS22-1_2064□Putative IS1236 transposase□2327604:2328557 Reverse
MQAEKARYPIARMARLLKVSTSGYYAWVAAQQRDGDHLLPSLRARRRLDEAVRRIWVDSR
STYGYLRVCAQLRREGVVVDRKTVAASMRRQGLAGISPRRFRPVTTIPGTRTHSILDRVK
RHWDTGQVDRVWVTGITYLRTRAGWVYLCAIKDACSRKVIATAMSTTMTTDLVEEALRRA
RILRPNAPRKVIIHSDRGTQGGFNWSSQHLDVEGVGDGSERQGPEHEGRATGVAAPVACR
SSVAPTDAFPWAPTPVTFAASRTAVLAPDRHGRHNGGSLPRGRRVVPRRCALVSTRWRHA
TDQPGRAVRALSQFRRT
>PFR_JS22-1_2065□PFR_JS22-1_2065□Hypothetical protein□2328575:2328919 Reverse
MWRGLVALGEGVVMSTGNEKTRRQRRKFTAQYRHEAARMVIDSGRTIAEVAQELGLGPQL
LGRWVKAEKETMTPSTLSPDEREELKRLRKENADLRMDNEFLGKAAAFFAAKHQ
>PFR_JS22-1_2066□PFR_JS22-1_2066□Trypsin-like serine protease□2329137:2330504 Forward
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RAVSNAQAPNSPTPNGPVPDNRVPNGRALNSPTPNGPAPDTPAPDSPVPTAPFFIPGDYP
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EQTDASGDQIRGVAIVEAMLSVTEGSAGTGMVIGDSGIVLTNYHVVQGTNGTINVTIAST
GSTYSAKVLGHDKANDVALLSLNGASGLPTVKIDADGVRAGDQVTSVGNTDGRRKIMAAP
GEVLSTNESILTRDEGSTATNQLSGVYETSSRAMHGDSGGPTYDSQTEVIGLTTAGSADD
GSQFATAYVVPIARALDIANKISRNEPSGTVQMGP
>PFR_JS22-1_2067□PFR_JS22-1_2067□Secreted serine protease, trypsin-like serine proteases□2331057:2332499 Forward
MSERNDQYNAHSTEGAGTGSTTPAGSGPAMQPPATQQSSAAQQGWQAPRETWDAAWSPAS
PDDASSTFNANPSAAAAFNNAAGNGGGYGGYPPAPNGANWGVYPPSNNHKGPNTRLAALL
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  FVARCAGAQQAIRSYQTVMTTKTVTPQAGTQESTTTFQYDFADAARPKVRSITSTGTETI
  YIGSDMWTRSAGAGWTHTTNSASAVVSGKGMDNYVGQVAGEIASVVYAGDEDVNQVRAHH
  FVFKPVVAPGSASPSVLAHDETGYWVDQDFRPVRVQTSVTTGGITSTTIMDSTQYGASFN
  IQAPAA
  >PFR_JS22-1_2069□PFR_JS22-1_2069□Hypothetical protein□2333402:2336797 Forward
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  RIQRFLDDYLADCDEHPQLPRTTLVLDEPGLARGLSLPVDGDEFHSDIVASYRLVNGVLH
  NPKHDRRTTAGVFHISTGGLPIPQDKVEVDKNVYARILARAFQAPDEELALPYTANLPEQ
  AHCWASLLMRPTVLPAVPGRTAEKSYEVHFIVPGGLMCNLDFVEGIFGNAGDPYLPENDA
  SLDPDSWTGHTGCVILAPHLTTMTKKSLGMPHYDDATERQRRDGQCWRHEDDLYNDGKAF
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  AEQTIKLLAGKHYLSPDGYRIHAKHREMDATQWHLIGTSSRAVTCHKPATVSGGGKSEIS
  KSISDAFVFGNAFSHDIDSAMDQVQALFDTDFTNRFADASRNGTDHRPVLSIDRSLGSVI
  KLLTPSIQYNDEYNAFLEGIEPDVKELAFTVKRYYLPEWGEDWRSHFTVGIMNGRHGNMV
  RLDGKKIITNMLRVGFREDGSWRLFTLRPDYSPAVKVQTEDDITASTVTPPWEDAEGLPR
  KYVTNCEHLLFQRPDDAIHRGYDKQAEFDLASGTDTFISNFEPLTHEQARDLLTDVQAYS
  EFTKPVRKLIERVAAMPDDQSPEFWVCSDDPRHLPDGGRSKNPRYLQVRPTDSNPELTTV
  ADVAGKLARKLPLAGHAPQPIDVVAAGRRNNPPEDKVPALCAYNPLHYMELPELFMEYIS
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  DHDISMLIPELFSHMGPNDRNTKRLISEGYLEKMQDFDFDGHRVLASRLGYRINDRFVTH
  YFGRIFLHPDVVFSEEMLRPELQDEKIFADSIDVIVKTHQRVAQMYFDDGTVSLACPPIR
  ALLEIMAHGASAEGWTLDSPEFRKLFERESVLASDWYAARLDAKQAEDVKQTEEGVERLK
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  LLVDALAFLTCALSIGVSWGASAQGSAYLTYVPPIIVATCFATAALILRAEGQLARDHSQ
  PRL
  >PFR_JS22-1_2071□PFR_JS22-1_2071□Hypothetical protein□2337826:2338200 Forward
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  ISDPADDNPIWNNPKTWGGDWWRKGRRELKVFATIADMRGVLPDELVAAVGQAVEHPPVE
  DLDI
  >PFR_JS22-1_2072□PFR_JS22-1_2072□YeaE protein□2338290:2339174 Forward
  MESANEMEHTMRHLQISGVSVPAIGIGTWHMGGSPARFDAECDALRAGIDAGARVIDTAE
  MYGSGASESMVGTAIKGLDRSELFIITKVLPNNASRKQMEHSLDASLARLGTDYADLYLL
  HWRGEVPLEQTVEEMQRLWHSGKIKSWGVSNFDLADMEELAALPHGNHVAANEDLYNLSS
  RGIEFELIGWQRSLDIPLIAYSPLGASGGERGAREMRTSPAVNKVAEAHQVTPSQVLLAW
  VIRNGHTLAIPQTSNEDHMRDNIAAANLTLTDDDLTLLDQAFPPPRHKVPLDIL
  >PFR_JS22-1_2073□PFR_JS22-1_2073□Para-aminobenzoate synthase glutamineamidotransferase component II□2339217:2339861 Reverse
  MARILVIDNYDSFVYNLVQYLAQLGARVEVWRNDDARFATPGWANGFDGILLSPGPGTPE
  DAGVCVEVARTLGEQMPVFGVCLGLQAMAVAFGGRVVRAPEPRHGKMSMISHDGQGVFDG
  LPDPLEVTRYHSLAVEPGSVPDVLDVTATSLDDQVIMALRHRELPVESVQFHPESVMTSN
  GYQLLANWLAACGDLGAPQRAQGLSPLMTAVAGQ
  >PFR_JS22-1_2074□PFR_JS22-1_2074□Membrane spanning protein DUF881□2339974:2340708 Reverse
  MADKKPGRGRKITRRMATVLVGALAGLLFVAAATTSHGSDLRPTRQQDMADLVAAQATHN
  SQARSTASALQSQVNELSNHDAEAAGVASASMASAEAAAGLTAVRGPVVQVTLTDAPLDE
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  PPYVVAAIGDQQALEQSLAASRNVQIYKQYVLAYRLGYDQKRIADVTMPGYAGSVQLNQA
  TPVR
  >PFR_JS22-1_2075□PFR_JS22-1_2075□Hypothetical protein□2340887:2341174 Forward
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  IGGQQIPLMYALSNWNFVIGLGLIAGSFFVATLWK
  >PFR_JS22-1_2076□PFR_JS22-1_2076□Putative chemotaxis protein, resembles CheA□2341490:2342524 Forward
  MPDYEQIIPRILTGAGTGDRRQSAAPAKARVVGAYLSQPLEQVKRPAYAHAVLQLPGVTD
  LEIPLCTTMARDDAKWLMDVLPPGARNIATLMGACDEAAADDPAFGLASTDPAGRNRALD
  LLQQARHSIARMTERGQHVLALEVHSSPTHRDNVDGTSQEFAASLAQAADWDWGETALVV
  EHCDAARSSGGASKGFLTLDEEIDAVETVRALSPRTPVMMSINWGRSAIDTRNAGGPLTQ
  IDRLRRHGLLAGVILSGASDRASSYGAPWTDAQLPAAAPDGSGEASSLLTPQRAVEAMER
  AGDHLLFDGVTFAIMPQWTPSQERLRYVRGLLSVMPRGHLSVAF
  >PFR_JS22-1_2077□PFR_JS22-1_2077□Dihydrolipoyllysine-residue acetyltransferase component of pyruvatede hydrogenase complex
(Fragment)□2342749:2344098 Reverse
  MPEYNMPDPGEGLTEADIVEWHVKVGDQVKVNDNLLDIETAKSLVELPSPFAGKVTKIYA
  EAGATVAVGAPIVFIDDGTGPAPEHDGGAPAQGAEPGAQSSSAQSSSAQAGPAQPSSNRP
  GPAQPSAPAPAAQGSAKASRPDADEASAQRDLDGGMTGERLLSLDELPASKPTQQTVRQM
  LVGYGPADESTPSSTERRRRAHQVSRRGANERALRDEEIPVDTVRRLTARNVVHSRTSKV
  HTTAWVSTDVSGTMELVANLRKRREFKDLHVTALLVWCKAVCLAMRNNPMLNATWEDGSE
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  TFTITNVGGLGLDAGTPIINGSESAILAMGAITRQPWVVGRGEDEKIVPRWVTTLSISFD
  HRLIDGAIASRFLRDLAALVRDPAMAMAY
  >PFR_JS22-1_2078□PFR_JS22-1_2078□Transketolase, pyridine binding domain protein□2344109:2345083 Reverse
  MTTLTLAKGLNQGLHDAMDEDPQVLMMGEDIGKLGGVFRITEGLLDDFGADRVIDTPLAE
  AGIIGTAIGLALRGYRPVCEIQFDGFVYPGIDQIINQLARYRSRTHGRQSLPVVVRIPFG
  GGIGSPEHHSESPESHFVHTPGLHVVACSNPHDAYWMIRQSIACPDPVIFFEPKRRYYAK
  GEVDTSAPDLPLFSARIVRPGADLTLLTYGPMVQTCLDAARVASAEGRDVQVIDLRSLSP
  FDMATIRDALKRTRRAIVVHEAHRTLGPGAELAARLDEELWGELDAPVLRVTGYDTVYPP
  SRSEKGYLPDAERVLDAVDKSFDY
  >PFR_JS22-1_2079□PFR_JS22-1_2079□Pyruvate dehydrogenase E1 component, alpha subunit□2345080:2346192 Reverse
  MDSDDPTQPLQLLTPDGTLVDNPRFPWEGSDEDLVDMLRQMTTARRFDVEGAALQRHGEL
  GLWAPLSGQEAYQAAVTKVMKPQDMVFGTYREQSIALQKGVPLGDILAVWRGSSLSRWIA
  SDAQVAPYYMIIGAQPLHAVGYAMGVARDKAKHPTDPANDAVTLTIYGDGASSQGDVNEA
  LVFAASQQAPVVFLNVNNQWAISEPSSVQTRIPLYQRAMGFGIPGIRVDGNDPLACHAVL
  NWAFDEVRSGSGPVLVEAVTYRMGPHTTSDDPTKYRSSQVTEEWKAKDPIERLRSYLLER
  GLIDYAWTEKLNADLDTFGALVRDTCRALPNTPMSEVFDAVTADPGLYLSEQRADCLDWL
  ATPPSEGAAE
  >PFR_JS22-1_2080□PFR_JS22-1_2080□Methyltransferase type 11□2346337:2347059 Forward
  MSEFPHQEHPSDQFPGGPDEPTTSSPESVTEFWEERYAGPEHVWSALPNHTFVQVVASLT
  PGRSLDLGCGEGADAIWLATQGWQATGYDISQTAIGRAQQAAAEKNVADTTHFEAVNLDE
  WSQAPLPDDQGRGQYNLITASFLQSPVALDRIRILQRAARLLVRGGHLLMVTHAAPPSWA
  PPEMASQGDFPKPEEDLKALDPDPRFFEVKLAETRRRPATDPTGKPATMNDAVILIQRIR
  >PFR_JS22-1_2081□PFR_JS22-1_2081□Lysine--tRNA ligase (Precursor)□2347245:2348855 Reverse
  MVSEQRPEKAPQSRGNQSAGKQSGGNQSRKNEPRKNGAADVEQDLPEQMRIRAEKRQRFL
  DEGKQAYPVDLRRDHTLAEVRATWGHLAAGEETQDEVAIGGRVIFIRNSGKLCFATLQDG
  FTPDQDAERLQIMLSKAEVGDESLAAWKADVDLGDFVWVRGRVIASKRGELSVMASEWKL
  ASKALRPLPTLHNDLSEEARVRQRYNDLIVRPAARTMVRQRALITRKIRETLEEQGYLEV
  ETPVLQSVHGGAAARPFTTHLNAFDIDMYLRIALELHLKRVMVGGADRVYEMGRVFRNEG
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VDSSHSPEFTMLEAYQSWGDQFTIAETLKSIIMKVAEALDIFEIPTDQGVIDLKGEWIWL
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FVCDFPEIAQPLARRHRSKPGCIEAWDLIIGGMERGTGFSELIDPVIQREILTRQSLAAA
AGDPEAMQLDEDFLNALEQGCPPMGGLGLGVDRLVMLFTGAGIRETILFPLLRPLN
>PFR_JS22-1_2082□PFR_JS22-1_2082□VarM□2348996:2350690 Reverse
MSHTSVSPSAFTRAAPTVVVDHASFELPDGQPVLSDVSAAFPAGRTGLIGDNGTGKTTLM
RLIAGELTPTEGSVHVAGSCSYLPQDVTSAADISVADQLGITAIRQALTRIEAGSVDVHD
YDLVGDDWDVDARAVAELAGLGLRADVGWLDRSMSELSGGEAMGVALAATRLVRADVTLL
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FGGNFSQFEAQREVQRAAAERELRSADAEVHRARAQMRAEQQRQQQRDRSARRENARGNV
SKGERDFLANRAEKNTGGKKLMHNARLHDAEAARAAADAAARQPDVIRIPLPDTAVAPGK
QIVQVKVGAGQQLRIDGPERIRVSGDNGTGKSMLLKLITGQVDAVPAGLFAAPVGLQLAP
TVSTGVLSQRTDELDRFDTCIDALLDVAAQRTSGEARELLARFLITGDKAFQLPATLSGG
ERFRVAMARVLFTDPAPQLLVLDEPTNNLDMASVDHLLEALDGYQGALLVVTHDAHLAGG
LHFNRSWQLRRTDEGTVIEEQLGG
>PFR_JS22-1_2083□PFR_JS22-1_2083□SAM-dependent methyl transferase□2350982:2351899 Reverse
MASTGIATKGSAAGRRGRRRGWLRQAPEALTAETRTSGIPADEVPDARLQGHWLLASMGK
RVLRSGGLHLTREMLEAAAPHAGDRIVEFGPGVGLTAAELLAARPPFYVGIEPNTEGRAK
LDAVLAGRPARVVTAEASATGLDAGSADLVVGEAMLTMSSPQQRRAIVAEAARVLAAGGR
YAIHELALADAAPDPDRRTGRGEVSREISRTIKVGATPVKLAAWRALLTDAGFDVVWQGT
APMRLLEPSRLIADEGPIGFARFATNMIRRPEARRRVLAMRNSFRAYKADLSAVAMVAVK
RPTQH
>PFR_JS22-1_2084□PFR_JS22-1_2084□Conserved protein, contains double-stranded beta-helix domain protein□2351899:2352258 Reverse
MAQQTPVTQAGVFTNLASELPVVPKSTTSRVVLDNDLIRVVEFTFDAGELLTEHASPRAV
VVQLLEGTMSFTVDGAESTLHVGDVVYLAPGTPHALVATTACRMSLVMVEAGAHLAGEN
>PFR_JS22-1_2085□PFR_JS22-1_2085□Amino acid permease□2352423:2353925 Reverse
MSNQPDRPRGARPTTGGGATGQRVPSGAPSGLDDDPTTQPGLRRGLKNRHIQLIALGGAI
GTGLFYGSGQSIGQAGPAILLCYLVGGAAIFMVMRALGEMSVDTPVTGAFSYYAWRNWGE
RAGFVSGWNYWFNFVAVSMAELTVVGKYVQFWAPGVPAWVSAAAFLVVVTLVNLVSVKAF
GEFEFWFAIIKVVAIIAMIVLGALIITTGLGNGGHPIGVENLWVNGGFFPKGLWGVLLGL
VIVMFSFGGVELIGITAGEAENPRTTIPRAINQVVWRILVFYVGAVFVMLCLFPWNQLGT
SESPFVTIFDKIGITGAANILNLVVLTAAASAYNSGLYSNGRMLYSLARQHNAPRALMKV
NRFGSPWVGVLVSSAVTAVAVVLTFLFPDTVFLYVMSIALMAAMTNWVMVVYTDVKFRQR
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VKRWRDKHGIEAVSEDRWRM
>PFR_JS22-1_2086□PFR_JS22-1_2086□Dihydropteroate synthase□2354178:2355068 Forward
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DVGGVRAGQDGPWVGEAEEIARVRPFLAAARQRHPDTLFSLDTWRAGVARACAGLIDLVN
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LPVDQRLEGSLAATAVAAWQGAILFRAHDVQATRRVVDMVASIRGDRPPARAERGV
>PFR_JS22-1_2087□PFR_JS22-1_2087□Transcription regulator□2355147:2355839 Forward
MARAAPLPAEQRRASLIAAARPLLLAHGDGFTTKQVARAAGVAEGTIFRVFSSKQDLLNA
VVADVLDPTPVIKALDEMAPDASLDERVHHIIELLHRSISDVRAFFAAIHAIPAHGKLFR
GSTLSNPKNPDPHHPDACDDAGSASPAHPPVAPDEQMRAKRQQTDLASQAAVERALSPFA
DQLSVDLATAAGFLRSVTFATIHPFLMNGAPPMTPDQLSALLLHGLKKES
>PFR_JS22-1_2088□PFR_JS22-1_2088□ABC transporter□2355839:2357572 Forward
MLVRLIWRYLRHYKAAAAIVIAAQLVATVSSLLLPNLNAKIIDQGVSTGDTGYIWRTGLL
MLAISVGQIGGQMVAAFFGARLAMGVGRDIRAAFFDRTLTFSQQEVNRFGAPSLITRNTN
DVQQVQQLLLMTAIMLIGAPITMVGAVFMALREDMGLSWIILAAIVALGVCVGIIVSRMS
PLFGQNQLRLDAINRVLREQLSGIRVIRAFIREPSERKRFNAANTDIRQLGYRIGTLFAF
LFPVVGLVMNLSSAAVWWFGGMRADNGQVQVGQLTAFMTYLMQVLMSVMMATVMSMIVPR
ASISAKRIMDVFLTKSSVVQAEHPVTELTGPAEMDFDHVEFSYPGAEAPVLHDISLELRP
GTTTAVIGSTGSGKTTLVQLIPRLYDATKGKITINGVDTRDLDMDLLWSKIGLIPQKAYL
FSGTVASNLRYGKPNATDDEMWEALRVAQADDFVRQMDGQLDAPIAQGGTNVSGGQRQRL
SIARALVKKPDFYVFDDAFSALDVSTDARVRAALAPTTKDAAVLIVAQRVSTIRHADQII
VLDSGHIVGRGTHAELLESSDTYREIVESQMSALEAA
>PFR_JS22-1_2089□PFR_JS22-1_2089□Bifunctional ABC lipid A exporter□2357569:2359632 Forward
MSVTKDEDSTVSGKKNTNKPAANKRPDYAQSASHHRGPGPGGGRAAAVEKAVNFGPSLKR
LFGEMKPDRVLIVVVMVLGAIGVAANVYGPKLLGKAANAVFAGVIGKGLPAGVTKDQIVA
ALTQQGKTDQASMIAKLDVIPGQGIDFTHLGHILLLCLALYVTAAVLTFIQAFIVNRVVQ
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GVIAMMLTVSWQLTLVTLCIVPLSLAVSIPIGKAAQKRFVGMWKSTGELNAKVEESYTGH
ALVKVFGRRREVEASFHDTNEEMYKASFGAQFISALIMPANFFIGNLNFVAIAVLGGLRV
ASGTMQLGDVTAFIQYSRMFTQPLTQITSMTNLLQSGVASAERVFEVLDAGEQTPDEHGS
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VQGGKIAIDGVDIASVPRHQLRDQLGMVLQDTWLFGGTIHDNIAYGKIDATDDEVIQAAK
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YESQFSAAEQPEELAGSATSGAKRASS
>PFR_JS22-1_2090□PFR_JS22-1_2090□Transcriptional regulator, AraC family□2359924:2360823 Reverse
MTRTASQIALSDVAPLTGPLAAVETVARAPSGPVAHLEAKIVHVMNGRARIETARGELAL
SRGDVLVLAAGSVSSIRPDPWLRSWTVYVDETFFRHHMHWAIPEHAPLIQGVPPSSWDGR
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PRKNDRVRRAGKPPIRAEVRATMALIEERLSYPWRMNELATAVALSRSQLTRLSHRHLGA
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>PFR_JS22-1_2091□PFR_JS22-1_2091□Flavin reductase Short=FR□2360841:2361476 Reverse
MRVLIAGATGTVGQHVVAQALDRGHEVTAIARRPESLRTEHPRLRTFAADVLDPDAVEPL
LAGVDVVVSTVGIGTSKQPTTLYSEGTRNLVNGMARHSVSRIVTISSEVADHWAHQSPLK
LWVALPLLQRFLGATYDDMRRMDIVLWESDAQWTTVRAPYIRDRAGSGSYRIATDKPLRR
GFSITAPDMATALLDIVERNDLGRRFVFVAN
>PFR_JS22-1_2092□PFR_JS22-1_2092□MarR, Transcriptional regulators□2361578:2362027 Forward
MTDVDPITRVRQSLQRQVVAAVLGNEKVARAHGLLVTDLQTLHLLVLREDVRTPSQISDA
TGMPTSTVTKLIDRLETAGYVRRRPDPADRRKTVLELVAESIAPLRVLYGRTDQEFDDLS
RQFTDSELDTVARYLDAVSGFYQIDRLRP
>PFR_JS22-1_2093□PFR_JS22-1_2093□RNA polymerase sigma factor□2362439:2363011 Reverse
MTPDPQAQRLTEALRRESPDLLRYFRRRVTEPEDAADLLAETGLTAWRRVRDLPADDEGA
RRWLFTVAHNTYLNHQRGSRRRHALADRVRRILARAERVSPPSDDGIEVRDAIDNLTPEL
AEVVRFIHWDGLTVTEAAEVIGVSASTARARYQRARIELRDTLSVATAATSGGAHQRRVA
LSDPSPGATP
>PFR_JS22-1_2094□PFR_JS22-1_2094□Hypothetical membrane anchored protein□2363008:2363673 Reverse
MENRTSPEHDALDVLLDRSRMALAEPGDLDAAVEVMLADLADRPRGRVARLGRGRRVAAG
IALSAVLAGAGMSAAAATGLWSWWAETPDLAYEFTSPSGEQCEVRYGLMSTSPTTAPIDS
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DGLYAAAVEYAVSEVINDEVIARGLTGIAYGTESVCGEVMQ
>PFR_JS22-1_2095□PFR_JS22-1_2095□Polyketide cyclase□2363747:2364190 Forward
MVATFTLVTDCPTDAATMFDISLDIDAHVDSMSQSRERAIGGMMSGRIGLGQTVTWRARH
FGIWFTMTSKITTLDRPRSFIDEQVSGPFKTFAHRHTFEDTSGGCRMTDTITVASPIFGA
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LAERLVLVPYLRRLIQKRNAALIRKVG
>PFR_JS22-1_2096□PFR_JS22-1_2096□Hypothetical protein□2364194:2364631 Reverse
MFSIALAVGATLGAVTVFVSVFVSLRATPAARPDLDSWTGAANVAAVAAIVGAIVGLIVA
AASWSVAALVLVLVARRWRAPAVRVAAVALGSAAGAALVLWFFATRPGVMLDAGAFAALA
VVAAALAVVALLVSERRVRSLSPQS
>PFR_JS22-1_2097□PFR_JS22-1_2097□Hypothetical protein□2364699:2365139 Reverse
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LCTDAGCAPAEDVDMTGPLGFVSVEDQAGDSWTFSVGMMRLERFTVRTLAGDGTVLSDTE
VTPEWVRVGGSEQCGGPGEATVTVQP
>PFR_JS22-1_2098□PFR_JS22-1_2098□ATP-dependent exoDNAse (Exonuclease V) alpha subunit-helicase superfamily I member-like
protein□2365316:2367235 Forward
MKGGVILFRGTGADALRYLESDRARADEYYLEAGTALAEFTSVDAEGRVIGEVALSADEY
RQWVDWVNALTGESMGKPRLPGDGRRGSPRFAEMVVNVSKSLSVAAALHPEVSEALDAAQ
RDAVAGIRSWLGQHSVTRVGPRGAQEVVPVEQLETVAVSHKTSRAGDPHRHIHFQIGTRV
WAAGAWRGLDTAALFRQQGAIRALGTAVIAAHPQLAAMLDTHGLTLDPVAGEVAELEPWN
ALMSKRGAQVARNLAKFTAEWEAARPGEEPGPVVRARLHAKAWDHERPNKKPSQLGSEAG
WRRELQDAGYTPDLPRATVQPARTLDELAVQQIASRALDRAAAAASAWTVHDVQEQVTRI
VTEAGVRATPDELREFIGITTRLATGDCLSILPPGAPTPEHVAHLTTLHVVTVETELRDR
LVARATARASGTTPSVREPGLDADQARAAAAVSSSRPLVVVEGAAGAGKTTMLGAATRTA
ERDGRSVRVMTPTKKAAEVAAVELGVPTDSVAALVHAYGFRWNTDGVWTRLAPGDADPET
GAAYRGPAKENRLAHGERIVVDEAGMLDQDTALALLTVTDEAGATLALVGDRAQLPAVGR
GGRVRHRRRARAASVRPDEPAPLHRSRVRAAHPRPPNRP
>PFR_JS22-1_2099□PFR_JS22-1_2099□Hypothetical protein□2367278:2368585 Forward
MLHEDTETLRAAVAADRIDEAAITAATNDEARELNALIRENRVRAGLVDDARTVEGSDGL
SIGRGDLIQTRRNDSEAGVTNRHTWIVQQVGRDGDLWVRDTASDRKQQRTVRLPVEYVAE
HAHLAYAATAYGVQGLTAPESHTILSDALSAAGVYVGLTRGRETNRLHVVAADLGDAREQ
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RRTPHPRHHRGPARH
>PFR_JS22-1_2100□PFR_JS22-1_2100□Methylase involved in ubiquinone/menaquinone biosynthesis□2368767:2369366 Reverse
MVDYWNHNTAYHAELLDAVPPSGGDVLDIGCGDGLLVEKLATKATRVIGLDPDPRAINQA
RRRLTETPNAQVVLGSFLTAPELDGQSFDLITCVATLHHMPLFAALEQMNAKLKPGGGLC
IVGLSANKTAWDWIVSGVHVLPIRLLSKLRGESGYPGMAVARPSESLAEIRRISSKVLPA
SRVRRRFWYRYTLTWTKPE
>PFR_JS22-1_2101□PFR_JS22-1_2101□Filamentation induced by cAMP protein Fic□2369380:2370690 Reverse
MGGYVERLWHPEDAGGLSRKDRAPGRYLAYVPDELGDSLPMLGAEAQGAAEDALAVLARA
DERIGARGRYLNHLLIRSESISSSWIEGNRVTPKRLAIAELLHQGPRQALDVVANVRATE
SAIAELADHTRTIETSDIVDLQHVIEPRLERGVRQEQNWVGGPGWSPLRAAFVPPPETEV
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GARRQVSTTRRDAPGL
>PFR_JS22-1_2102□PFR_JS22-1_2102□Hypothetical protein□2371081:2371665 Forward
METERVRGNPPGITNTHVAANIRAARQAIGMDLRTMSDALDAAGRKLSPSGISKLENGDR
RVDVDDLTVIAYLLRTSPAALLTPPDEQTTLTGVPETYLPEEIEKWARGELVLTSHGLLA
YWQQEWVQNLNRIQYFESALRHGSPNQASHDDYKKRLADLKERQRLIRERGVQIDPTGRV
FDAADYLDRFGPAE
>PFR_JS22-1_2103□PFR_JS22-1_2103□Site-specific recombinase, phage integrase family□2371696:2372985 Forward
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DLGEKKFSRGGFSTAADADAALQDALKRRDQQEKFGGKVPTLGVYADAWVEGLKLADSTI
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DVDAATLKAIASYKVARAELSFELARADAYIFGDDDGQPRSPDAMTSRWDRRLKWAVKVK
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RFASRLAGT
>PFR_JS22-1_2104□PFR_JS22-1_2104□Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase□2373216:2374172
Reverse
MKGQGPYVDWFGVESAIQQAARRQAADHPGASVGQYLDHIRRDRFLSRVFADPESGWLLK
GGTAMLARVPTGRHTRDVDLSTTRATLDEAVEDLAHRVAVDMGDHLRFQLESERPGLAVT
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MEWTVGTGSPAAGPHRGV
>PFR_JS22-1_2105□PFR_JS22-1_2105□Hypothetical protein□2374169:2374816 Reverse
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VYRVCGAPATDFQEITATWLALSNPGRRLTAAGTTAATLYGIGDFLRTVPEFIVAGDPST
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QRVARALAPMAADHGLPDGDGSELLASILPAATAA
>PFR_JS22-1_2106□PFR_JS22-1_2106□Hypothetical protein□2375071:2375271 Reverse
MKLKNIIQALIALILIVAAVGLYKVGQVWPAWICVVVGIVVAVWGGTASGRTRSGRPRNP
ERTRSA
>PFR_JS22-1_2107□PFR_JS22-1_2107□Hypothetical protein□2375357:2375491 Reverse
MKSRTVARVVRVALVALCAIIGVVLLVMGRHVLGAVGRPPGAGQ
>PFR_JS22-1_2108□PFR_JS22-1_2108□Hypothetical protein□2375563:2375772 Reverse
MRGSTKMIIVGAVLVVAIMVAGEVWGAGSSSGGTTLWAALNPVTRFGLLLGTMLTAVGVG
IRVWMRRTK
>PFR_JS22-1_2109□PFR_JS22-1_2109□Hypothetical protein□2375807:2376106 Reverse
MKGSTKLLVIGVVLLVLGCGVTFLQYLNFTSADRQGPDGPELLPLAVLDFAMSICGYLGA
ALTAVAIGLKVAAGGDARAVLPDLDDELDDEIALGRGPA
>PFR_JS22-1_2110□PFR_JS22-1_2110□Putative aminobutyraldehyde dehydrogenase□2376657:2378081 Forward
MALLQNFINNRFVASTSTESFNLVDPATAEVTGQSPASNQADVDAAYAAAKDATRTWGKM
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SAALDFGCVWINCHIPLVAEMPHGGFKSSGYGKDLSKYSVEEYTRVKHVMSSME
>PFR_JS22-1_2111□PFR_JS22-1_2111□Dihydroorotate dehydrogenase 2□2378347:2379495 Reverse
MSINYGSDALAAAAASAAAKSVAGNATTDQLMAPREVNAQVTVPNTTDLSSNYMGLPLRN
PVVASAGPLAQTVDSIKTLEDAGVGAVVMHSLFEEQLRYESEQIVQQTEEQSESFAEALS
YFPVTAIASVGATLSSQYLQVLEDGAKALEIPLIGSLNGASGGTWTAEARRMQDAGASAI
ELNIYLVPGDTSITGREVEDRHVEILRAVKDVVNIPVAVKLSPYFSSFGEVATSLCDAGA
DGLVMFNRFLQPDIDVNKREVVSGFELSSPEIGRLPRTWAAVLSGKVKSSLAVSGGVETR
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DDIVKGLLAGADVVMTTSALVRHGAAYAGRLIDGLRDYLRRSDLTLDQLRGMLAVPSDAS
ASEYERSGYVSAIEKAKRRYGV
>PFR_JS22-1_2112	PFR_JS22-1_2112	Pyruvate-flavodoxin oxidoreductase (Precursor)	2379497:2383264 Reverse
MTTTTRGPVPGSNGMPANPGLSGEAATATPSPVDVAAGAKDAADELAQSRREQDITHQMI
CDGNTAASDVAFRINELCSIYPITPSSPMAELADEWSARDRMNIWGQVPHVMEMQSEAGA
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QDVMACRQTGWAMLCSTGVQQCHDNALISQVATLRSRVPFMHFFDGFRTSHELNTCIQLT
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DEFAAMTGRQYHLADYYGAPDADRVIVIMGSGAETVQQTVSKLNEQGEKVGLVVIRLYRP
FPTQAVLDCIPASVKKIAVLDRTKEPGSNGEPLFLDVVSAVSEAYSNGERDNLPAIIGGR
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>PFR_JS22-1_2113	PFR_JS22-1_2113	TRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	2383270:2384901 Reverse
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PEK
>PFR_JS22-1_2114	PFR_JS22-1_2114	Protein of hypothetical function DUF77	2385225:2385542 Reverse
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>PFR_JS22-1_2116	PFR_JS22-1_2116	Hypothetical protein	2386219:2386368 Forward
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>PFR_JS22-1_2117	PFR_JS22-1_2117	Hypothetical protein	2386668:2387012 Forward
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>PFR_JS22-1_2118	PFR_JS22-1_2118	Integrase catalytic subunit	2387009:2387917 Forward
MSEKYTLMQAEKARYPIARMARLLKVSTSGYYAWVAAQQRDGDHLLPSLRARRRLDEAVR
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AA
>PFR_JS22-1_2119	PFR_JS22-1_2119	Drug resistance transporter, EmrB/QacA subfamily	2388141:2389838 Forward
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>PFR_JS22-1_2120	PFR_JS22-1_2120	Succinyl-diaminopimelate desuccinylase	2389976:2391157 Forward
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>PFR_JS22-1_2122	PFR_JS22-1_2122	Cytochrome d ubiquinol oxidase, subunit II	2395250:2396383 Reverse
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GHYPPPAGITDIMGMEALGVIEKLGDGVEGHQVGEQVLALVSGGAYAEFFVVPAGQLLKL
PAGIDPLAAAGLVEVAATVVSNFDRVHLSAGETVLIHGGAGGIGTLAIQYAKALGAHVIV
TAGSAKKLAYCRKLGADEGFDYHDDWEPQVMMATQDRGVDVILDIVGAKYLEANVRCLAD
DGRLVIIGMQKGTKGTLNIAVLLNKRGTVTATSLRFRSLASKAAICRRVEEAIWPLLSSG
AIKPGNQTQVPMAHASKAHELLESGDNTGKIILVV
>PFR_JS22-1_2146□PFR_JS22-1_2146□Argininosuccinate synthase□2421418:2422854 Forward
MLDVVSKVLTSLPVGQRVGIAFSGGLDTSCAVAWMREKGAIPCTYTADIGQYDEPDIASV
PGRAGQYGAELSRLVDCRESLVEEGLSALACGAFHVQSAGRAYFNTTPIGRAVTGTLLVR
AMNDDNVSIWGDGSTYKGNDIERFYRYGLMANPSLRIYKPWLDEDFVSELGGRDEMSVWL
QKRNLPYRDSKEKAYSTDANIWGATHEAKTLEHLDVSLETVEPIMGVKFWDPSVTIDTED
VTIGFEQGRPVTINGKKFDSAVDLVLEANKVGGRHGLGMSDQIENRIIEAKSRGIYEAPG
MALLFIAYERLVNAIHNEDTIINYRNEGMRLGRLLYEGRWLDPQSLMIRESIQRWVASVV
TGEVTLRLRRGEDYTIVNTDGPAFSYHPERLSMERVQDAAFGPLDRIGQLTMRNLDISDS
RSRLEQYASQGQLTGGEAAKLVGALEPGKASEIADHPEHAGTSHATPLDNAAMETGAD
>PFR_JS22-1_2147□PFR_JS22-1_2147□Putative CONSERVED PROTEIN CPSA□2423509:2425218 Reverse
MSEEPQGGHVDDPSSASRARRAARAADDPGDGANTPRYADSAAKRRRGRLRPRWGRIAAL
AMALVLFVVVAAAGIYIWRANAGIKRSGAIADKTSQSSDLDLLVMGLDSRVDVNGNALPS
DIYDALHSGDASDGGLNSNVLMYVHVPADGSQASVFAIPRDDYVDFPGCPDGVCKGKIKE
AYGYAADAKTQELDKQGKTGQDAYQQARDAGRAAEVRTVEQFLGVEIDHFIEVTMVAFFQ
IAQVVQPITVCVNEKTVDTYSGADFKAGEQDINAEQAMAFVRQRRDTDNPDLAFTDLDRS
RRQQAFIASLLVKLKKTNLLTNPGQLDKLVQVAQQNTVLDKNLKISQLTSLATSLEGSKL
NFYTLPVESFGTADDGAAINVVDKAKIQGIVRSILHPGQSASPSASASASGSASYSPTYG
MGATVSVMNESGVTGAAASLVGQLTGFGFTAGQATNGADILQESSVSYGSAVAGQAKQLA
QQLGGLSANADSTLGANAVVVHMGTGFTGWPSASPSAASSAASTGGSSVSPSASSTAIPS
AVDANSGGQSGPEPSQLTQISGGGIPCVK
>PFR_JS22-1_2148□PFR_JS22-1_2148□Transcriptional regulator, Sir2 family□2425419:2426165 Forward
MSADQLSRILAPADHVVFFGGAGVSTESGIPDFRSATGLYKTQSGGEFPPEYMLSHSCWA
DHPEDFYAFYRKNMLHPEAKPNAAHYALARLEKAGRLTAVVTQNIDGLHQMAGSQKVFEL
HGLVLRNHCVDCHRSYPVEAIEQSTGIPRCTVCNGIIKPDVVLYEEGLDPDVMDGATRAI
MAADVLIVGGTSLNVYPAAGLLEYYRGDKLVLINKSATPADNRAQLVIHDSIGKVLGQAV
DEVLGDKA
>PFR_JS22-1_2149□PFR_JS22-1_2149□Probable thiol peroxidase□2426333:2426830 Reverse
MSTTAFQGTPVHTVGELPAVGSQAPAFELVGKDLSTITLKSLRGRRVVLNIFPSLDTGVC
ATSVRTFNKLAAGLDNTTVLAVSKDLPFAAERFCVAEGIENVVPASAFRKHSFSNYGVLM
TDGPLAGLLARSVVVIDENGTVVYNQLVPEIGNEPDYDDAVAALK
>PFR_JS22-1_2150□PFR_JS22-1_2150□Putative periplasmic or exported protein□2427163:2427810 Forward
MSRRFATTLAASALSLVVLAGCSTATAGPSSGTPSGTVTAGAASNTSSTAANGSVDVAKA
GVEELKGADARTLVDKLEATPLSQRRTDLRASVRADELQLSDTSGNKASVKMPADQFYLS
FAPYVNKTHDCTYHSLTTCKAELGNKQMHVTITDAAGATVIDQDLTAADNGFIGVWLPRN
ITGTLTVSYDGKSASQQISTAKADDPTCLTTLHLA
>PFR_JS22-1_2151□PFR_JS22-1_2151□Two-component system, sensory transduction histidine kinase□2427872:2429161 Reverse
MSEPRTPDRPAGTHPATPSAPDVPRDAALGDGRDAAGTGDRRDSRDSGAGVRRWWHVLTR
RSIARRFLTGAAVVVGVAVVTIFVVDALVSPAIFHAHLMQADLSNPETVLRHVEEGMRSS
NMIALAVAILIAVLAALLVSLYLATRVSASLAPLAAAARQVAAGDYTARVDAGPLGAEFD
ELTEAVNAMSQRLASVEQSRTRLFSDLAHEMRTPIAVVQAQLEGIEDGVVGVEDSIPVLR
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THARAQLDTARFAQVITNLLANALNATVSAGRGRTGDRGGHVHVGVRRHGNEVAVQVRDD
GVGISPEELPHVFDRFARVGPARDRSSGGFGIGLTVARAIMSAHHGRISADSPGPGRGAT
FTVTVPVLH
>PFR_JS22-1_2152PFR_JS22-1_2152Putative OmpR family two-component response regulator2429158:2429877 Reverse
MSAVQDAPGDAPCILIVEDEHSLATVMAGYFTRNGYRAEVVGDGLGAVAAARRLDPSVVI
LDLGLPSLDGVEVARRIRTFSDCYILMLTARADEVDELIGLSVGADDYLTKPFSPRLLIA
RVQAMQRRPRSAITPPDEQPLRIGELTIDPAAREVQLGTREIALTRTEFDLLAHLARNPR
RAISRDELIEAVWGVGWSGDDQLVDTHIGHLRKKLGDSAANARFIETVRGVGYRMGQGR
>PFR_JS22-1_2153PFR_JS22-1_2153Putative exonuclease of the beta-lactamase fold involved in RNA processing2429874:2431268 Reverse
MSKPVATLTFLGAARTVTGSKFLLDLNERRLMVDAGMFQGAREWRRRNWDDFPVDPATIT
DLLITHAHMDHSGYIPALVKHGFHGRIHCTPQTRELTAIVLRDSANLQVNEARDAARGGY
SKHNPPLPLYDEADVERSLPLFHDVAFDRDLDLGGGVHARFTRAGHILGSASIRVWLADD
PQISVLFSGDLGRDQHPVLRRREEPEGATSVLIESTYGNREHPTGDEEDHEALAGLIRRT
IARGGSVLIPAFAVDRTEILIKVLGEMQHAGRIPPVPIFINSPMGSAALDVYQGTGAHAE
LRADIDISALLNLPTLRDVRTKEESVALNRPAQPCIIISASGMATGGRVVHHLRHMLPDP
RNAVVFTGYQALGTRGRSLVEGAKQIKMYGRYVPVKAEVLLDTAFSVHADAPELLEWLAA
LSPAPQVVYCVHGEPKSAEHLADTISEELGLMAVVPRYGEVVRL
>PFR_JS22-1_2154PFR_JS22-1_2154PTS system mannose-specific EIIBCA component (EIIBCA-Man) (EII-Man/EIII-Man)2431518:2434505
Forward
MTSDINAPAEILASIGGADNVENLTHCATRLRFQLHDNSGIDEKQVESIPGVMGAVSQSG
NRYQVVIGGAVESVYNDIMALPEMKEGGSATGTQKSGSNADVKSAAKEKGPRGRFTWLDS
FFDFLGDSFRPILGSLLGASLIITFMALMGTLGVIGNWADPRTELSPTWQFINLCWRCVF
YFLPLMVAYNASKKLGADPWIGFAVMAVVMLPGFTSLGQYATHLTFAGSEINVVRLFGGH
LPLTIFDYGSQVFPPLLMAAVLGPLYKLLKKIISPNVQLIFVPFLSMLIMIPLTAFLIGP
LGVYAGAGLANGLKAVNDFSPFIFAILIPMLYPFMVPLGLHWPLNAIMLLNIQTLGFDFI
QGPMGAWNFACFGATAGVLFLSVRDRDVTMRQTATGALAAGLLGGISEPSLYGIHLRFKR
IYPRILVGCFLGGLVQGIGGGLTTNAFVFTSLLTIPAFSNIPLYAISIAVAFFSSMLLVV
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TVAAERAAQVATAVAPARTALAPNAVTQIASPVAGYVVPLDKVPDPVFAKGTVGLGVGID
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TTGDVLVRFDRKVIESAGYSMITPVLVTNPRKFASVTQAPATLSSALVAPGDTIITVTAK
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PGSTVPGVSAHGVSAHGDAQASPQGTGTADGARRAATTAGAADSSGSAAASGAAPGSALV
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AFGIKLDNGIELLIHVGIDTVNLGGTGFDVHVARGDRVTTGDVLVRFDRKVIESAGYSMI
TPVLVTNPRKFASVTQAAQGAVTPGEGIITVTAKQ
>PFR_JS22-1_2155PFR_JS22-1_2155Phosphoprotein 3 (GPP34)2434645:2435325 Reverse
MEHTVDLAGEYLLLVLDDHKGGFRQDLTTIDYTVAAAELVDLVGMGALEFTGTGENRTFV
PGEKAPQDPLLAELAELAAGRSYDEAITALSGGVSVGDDKPRSLRSLELERLVNAGILRA
QHGKLLGLIPRTRYPQADPTVELELRARLSGALVGTTDLDDRSRALIALLYAAHALGKAF
PDLDQKRIWRRGKEIANESWEDDGLALALAQYAIYMATLSAASLGR
>PFR_JS22-1_2156PFR_JS22-1_2156Seryl-tRNA synthetase SerS2435446:2436720 Reverse
MIDPKLLRTDPDRVRRSQRARGESVELVDQALAADEARRSSISAFEQARAEQKSLGALIA
KASGDERNALLSRTKELAAKVRELDASAHEADEHYTEVVKQFGNIVFEDVPEGGEDDLFV
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LLAHEKEFISALGIPFEVLDVASGDLGLSAARKYDCYGWVPSQDKYREITSTSNCTEFQA
RRLNIRMRDGKQVTPLATLNGTLCAMTRMIVMILENYQQVDGSVVIPEVLRPYLGGREVF
TPKG
>PFR_JS22-1_2157PFR_JS22-1_2157Diacylglycerol kinase2436847:2438472 Forward
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QVASAFAIVAHPAVMCLLLVVIAIWAWRRRLRHLAVTSLVSGALTMLICQAIKASVNRAR
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FDGWLMNAHHFTDIIAGVLLGAAVVSAVMLFARVRMLPLIAPRHPANAVRTRGGLCAVIY
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R
>PFR_JS22-1_2158PFR_JS22-1_2158Prephenate dehydratase2438352:2439338 Reverse
MLGYFGPEGTFTHQALLSVSEDEATPFSTVAAALDAVRAEEIDAAMVPIENSVEGSVSAT
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>PFR_JS22-1_2159PFR_JS22-1_2159Hypothetical protein2439880:2440560 Forward
MSQPMPPDSSGQNDPEGWVRDPTAPGGWAPIRGYQPRPGGHPGQGQYGRQGAAPDQGQYP
GARPDQGQYQAPPPLQARQSMPPQRPQAPMPQQRPQAPMPQQPQGRPQQPPRYSDEARND
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SISLGIAIPLTAIASDYGLVGMAMAWVGVLLVAFITTGFKWGRDDK
>PFR_JS22-1_2160PFR_JS22-1_2160Branched-chain amino acid aminotransferase protein2440853:2441806 Reverse
MTESQPADGASDGPGTPGGAELSGVVRRPFTPRALVWNGEAFVDDVRAIEPALDILAADS
WRSSHGAAAHFDLHCLRFEAGVARWALDAGLPIPSAREWASMRRAMIAAILTAHHDTHRD
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MVARRAASLGMQVVRANARTDDWGSGQGVWFLNSVQGISPVTRVVIGSRAMHLAPFVATA
EWRHWWGSQFRPYSPSL
>PFR_JS22-1_2161PFR_JS22-1_2161Aminodeoxychorismate synthase, component I2441799:2443532 Reverse
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AVAQHVGPRPAGTTSDRGRFSLLGTDAGDLSEVLRYCRHDDAGHTRLQRGHGAGRVSQTL
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LRDDVDLVGLLRATFPGGSMTGAPKQRTLQIIDALEPGPRGIYSGALGYLGYGRRAELSI
VIRTIVRNHDRLSIGAGGAIVLDSQAPAEFDEKELKAAALLRALRRAGTPAGRPAPYGGS
STREANSAPGAGHEDTGVHRAARDAHAADHQGGEPDD
>PFR_JS22-1_2162PFR_JS22-1_2162Hypothetical protein2443769:2444758 Forward
MKYAVIGAGAMGYRYGVLLQENAGVDVDFVDTWEPNLAKVAEQGGVYVSRDHEGRHLVPI
NLYSPEDYKGNPDVWIIFVKQMQLEGVLERCAHLFNDKQVVFSAMNGYGHFEKIQKYFSD
DRIYGGTAMIATVLNGPGDVDFIGKSGAGEMHMCAYTEKVTDIEKKIAEDFKAANLNPII
TENFMGTCMAKVIFNSVVNTLSTMYEITMGQFIEFDGAMAMAKQLIDEAYDVCDRAGIRL
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FLTRGVHLAELAWHIHKEEAEKVEAEQAA
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>PFR_JS22-1_2163	PFR_JS22-1_2163	ABC transporter inner membrane permease YbhR	2444959:2446146 Forward
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SRYPVAGQNLDISTAAGATDPEQLLRERRADVVVQAVEESTSATPSSAPISERMHVYADG
SRLFAAQAAQRAFTTLVAQDTQQHLARIQASAAAGASGGSATQGSAAAGGAAQAASNPGS
VVTVLFNPDLKTSWVMVPGLIGLILTFIGTVITSIGLVRERETGTLEQLAVMPLRSSSII
LGKIIPYFLLALFDMVLITAVGVWLFGVPFRGSLLLFAAAAVIFLFVVLGFGVLISTASQ
TTGQAIQLAIMTVLPQVLLSGLIFPLDSMAAGVRWIGYCLPLTWFNQIAQGIMLRDAPAG
SLLWPFVILAAMAVVFFGIATLQMRFSLTHGGARA
>PFR_JS22-1_2164	PFR_JS22-1_2164	ABC transporter multidrug efflux pump, fused ATP-binding domains	2446143:2447963 Forward
MITLRGASVHFGARAALDDFSGSFAPGQVTALVGGDGAGKSTLLRVLTGRVAATPAQSGA
VTPRTQLGYMPADAGVWNNLSVAQNIAFVARVFGMSPEQTRERSQLLLARAGLAQVGDRE
AGKLSGGMRQKLGFVLATLHSPSVVLLDEPTTGVDPVSRGEIWSLIAGAAAEGATVVFAT
TYLDEAERCDQLFLLDQGRLVTSGTPDEVIASCPGTVWQAPAGAGAGAADDVPRATSWRR
GDQLFVWTPSDREAPAGFTASVPDLENTSIALLLAGGATLGADSLDDAATAPGHPRASDA
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LFGQVPSIAVRRRLGYVAQGLGLYPTLSATENLRFTARVFGARSGGREFSAARGARDGVR
LGERALAYAHDLGRGPVGALPLGARRMLAYLCAIEHDPELLILDEPTSGMDPLSRARLWR
ELREVADRGVGILVSTHYMAEAAQCDRLEMLTAGHVSASGSVADITAGRRSLVVHAPQWQ
RAFTLLRDADLPVTLDRRMLRVPGASRDEIARVLDRLDGGYSIAEAASTLEETMMLAERG
GDAGGK
>PFR_JS22-1_2165	PFR_JS22-1_2165	Type I restriction-modification system, M subunit	2448018:2449586 Forward
MTESTKESERAELHKTIWRIANDLRGSVDGWDFKSYVLGMLFYRFISENLTAYINKGEHA
AGDVDFNYADLADSDAAMALRETVDEKGFFILPSDLFENVRRDAPHNPNLNETLANAFAN
IENSAAGTSSEGDLKGLFDDLDVNSNRLGNSVMQRNEKLVKLLDAVGDLPLGNFGEHTID
LFGDAYEYLMTMYASSAGKSGGEFYTPQEVSELLTRITVVGKTHVNKVYDPACGSGSLLL
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FEAIVSNPPYSIHWAGNDNPTLINDPRFSPAGVLAPKSKADLAFTMHILSWLAVNGTAAI
VEFPGVLYRRGAELKIRKYLIDNNFVDTVIQLPPDLFFGTTIGTCIIVLKKSKRDNSVLF
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PEDTTEKIDITELNARIAKIVARQSELRTQIDVIVADLEDAQ
>PFR_JS22-1_2166	PFR_JS22-1_2166	Type I restriction enzyme, S subunit	2449583:2450767 Forward
MNHIEELIERLCPDGVVFRELAEVFDLRNGYTPSKSDAANWNGGTIPWFRMDDLRERGHI
LEDSTQHVTLSAIKRGEPFPKNSLIVATSATIGEHALITVPFLANQRFTVLSLKPEFSKS
IDMKFADFYCFVLDDWSRRNTTTSSFATVDMNGFKRFRFPVPPLEVQHEIVKILDTFTNL
ESELESELESELESRRLQYQLYQDKLLTPASDTTLSALGDISSIKTGGTVSKKFIRNNPG
PFPVINSGKSPLGYVNAFNSEDDPIGITSRGAGVGSITWCPGRYFRGNLNYSVTIKSSKL
VNMRFLYHSLVHLQPKIHELSTFQGIPALNKANLQKLRIPLPSLELQERIVARLDTFDAL
VNDLNSGLPAELNARRQQYEYYRDKLLTFKELKS
>PFR_JS22-1_2167	PFR_JS22-1_2167	Type I site-specific deoxyribonuclease, HsdR family	2450764:2453802 Forward
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EAFNQINRYQRESFWADSGLYEYVQLFVISNGTLTKYYSNTTRATHVDQASGSKRSRSQV
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EKESIDDDVVFEIELVRQVEVNVDYILMLAEQYLEVKDGPRDKEIRAQINRAASASPTLR
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AITTTGTAVTRILPPASRFSKTNNHEQLKDRVLAKLQAFFDRYAGLLNDVRD
>PFR_JS22-1_2168	PFR_JS22-1_2168	DNA polymerase	2453876:2455444 Forward
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GVSACQIALVRVESGRVVDRFNTLLKPPSGFDDFEFTYLHGISARDTRTAPSWPDIIPAI
RGFAGDATVYAHNAPFDSRVWRQLDEFFHTRSLPDHFFCSYLTARRMMPGLDNYRLPTVL
ERCAPHFVLDHHKADSDAEACALIVAALQSNPELYARLEAHR
>PFR_JS22-1_2169	PFR_JS22-1_2169	Appr-1-p processing, ADP-ribose-1-monophosphate processing activity	2455559:2456512 Reverse
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DAGWTHGGRLAARYVIHTVGPLQPTSKKSEQLLASCYRRCLQIADELGIQTIAFPVIGVW
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LITNLTTPGEVADLLLGEVPYLAQKKSDPEYVVWYQALVSVCEGLEAQPWTSSDWVTPPG
WGIGQKVVFPYPPAPKG
>PFR_JS22-1_2170	PFR_JS22-1_2170	Transposase IS6110	2456940:2457827 Reverse
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WKAARRGGIMIGRDQTARLMRVAGIEGARRSKRVKTTRPDPASSRHPDLVKREFTATAPN
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GPWKTVEDLELATLGWVHWHNTQRLHGYLGDVPPAEFENAFYAVPNDSNLLIGIK
>PFR_JS22-1_2171	PFR_JS22-1_2171	IS3 family element	2457860:2458204 Reverse
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QADVDDGVVPGVSSAEEQRVKELEQENRELRRANEVLKRAASFFGAELDRHYRK
>PFR_JS22-1_2172	PFR_JS22-1_2172	Hypothetical protein	2458518:2459324 Reverse
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AGRDVPDEPTARLVRQWSSTTMDELDGAFTPEGFSTAWGARYAGLDAGYERLLVGSARWM
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MVLLGRAGTVALDHFECSELDGRYAPDQLRERAGSRAEGYRKRWQTILAYASDAAAGEGI
ADAPAGRITFDDVSDEQARRRLQGRLGR
>PFR_JS22-1_2173	PFR_JS22-1_2173	Gluconokinase	2459502:2461037 Reverse
MTETMMPGNQTTEIPEARPVPFARAIGPFVLAMDIGSTSTRAALYDAMARPVLEQNAVAE
HHFVEGADGTSEIDADQMADEVAETITGALAGLEPGTVSAVAMDTFAASLICVDAQGRAI
SPCMTYADSRSAPQLAELRKVLDLDEAQQAVGVRLHTSYHPPRLLWIKQNHPDFWARTAR
FVSLGEYVFTKLAGVDACATSTMAWAGMLNRHSGQLDDDLLSVTDTRADQYAQIVDPDQP
QTPDPGLIDDRWPALSGAKWFPTIPDGYASNIGVGAVGAETVALSAATSGAMRVIVPGTP
EKLPSGLWAYRVSRHESIVGGALNDVGRVMTWLTTTFAPVDATERDTALRAAPRPDTPLV
LPFLTGERATGWSGNARAVFCGVTAASGPWDMWRGTVEGVAISYRRIFEQLRSIDVNIER
ILASGGVTHHFPATLDVITNALGYPVHVVNMERMTMRGTAMMALGVINPEGKFATAPQHS
VNNPDPSQAPYYDDLRKRFEEVYDEVIAGKE
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>PFR_JS22-1_2174	PFR_JS22-1_2174	DNA-(Apurinic or apyrimidinic site) lyase	2461296:2462159 Reverse
MPELPQVEALADFLRTDLVGSVIERLEVGAISALKTFDPPPDALVGRTVTAINRFGKHLD
VDAGGLHLVFHLARAGWLVWREKVPSTVIKPGKSRIALRVRLQGGAGFDLTEAGTQRKLA
VWIVRDPQQVPSIASLGPDPMAPGFTPAVFRQILAGAGRAQLKGILRDQHVIAGIGNAYS
DEILHDAKLSPFKPAANLTDDEVERLYAAIRDGLAAATERARGLAARDIKADKRAQLRIH
GHAGDPCPVCGTPIASVNFADSSLQYCPVCQTGGKKLADRRMSKLLK
>PFR_JS22-1_2175	PFR_JS22-1_2175	Leucyl/phenylalanyl-tRNA--protein transferase (Precursor)	2462152:2462877 Reverse
MLAHVFGPEASWPSQDLVGFTEQIDAGLTMAAYASGLFPMPLHESEFHGMGWWSPMQRGI
IPLPSLRVSHSLRQALRRYRTTIDTSFDEVLAGCADPTRPGSWIDDDVKAIYTGLFERGV
VHSVETWDDDDRLVGGLYGVGLRGLFAGESMFHDREHGRDASKVALVRLVDTLSARPDGK
ALLDTQWLTPHLASLGGVEIPRHRYLELLDDALDAPETAWPAPGVFTRGRALPPAQGGSH
A
>PFR_JS22-1_2176	PFR_JS22-1_2176	Hypothetical protein	2463424:2465625 Reverse
MTQDNSGSAEKPFRLGTNYQVETPLGHGVVGTTWRGTGAGGAELAFTVLNKRFASNPQVV
RHLLAQRPVLATVRGDHVVPVVDMVADSDVVAVVSPYIKGTDLRSRLDDEGTLPPAEACR
IISETAQGLATLHATGLTHRDVKPSNILLDDTQQPASAKVTDYAVGGIVEEWAGGGHSAV
LASTPAYLSPEVIAGDPVTVQSDMYALGVVLYESLCGVTPFAPLQPEGTMQAILTLDPGR
PRGVDDALWEVLSMLLNRDPRQRGSADALSWRLSELQNALADAPKLPKLDVSPSPTPLPQ
VMAFPGAAPTTAPQIVGQVPAPNQPGPNQLGPNQPGPNQVGGGQPGAQGAGFQGPAAGVL
AAGAVIGAAAAAVPTQQAAAQPTQAASGPSDAGQVAGGQTAAGQAGPAQGQGGQGQPVQG
QPGQDQSGQGAQGQPLQGQPAQGQPAQGQPGQQPSPQSGAAGQAPGQPAADQPAPHQGAA
PQPVPHQVAASQPGGAPQGAPAQQPTAAFAAQQAPTQELPAQAAAQMGGAQTPPPVPPAP
QRAHPEPEPQRGRPLRRRPKFIVGLVLVIVIGLAAAAAIAVAVTRLNSSSSSSSASQSSV
TPTPSETPTPTPTPTPTPTPTPEVWPPDANAVICTSGGTMAVKRGTTYCTFGSTVQQALA
AGTLTAPSAAPGAAAATPATGATPATGTTPAAGGATVSLRNTQTGTSVAVSCTSGATITT
CSGNDGSVVWVRK
>PFR_JS22-1_2177	PFR_JS22-1_2177	Putative cell wall catabolism protein	2465940:2466548 Reverse
MSKTLSRIASVASVAALAGSITVIAGQNASADSVNWDAVAACESGGNWGTNTGNGYQGGL
QFSSSTWNAYGGGQYASSANQASRDQQIAVAEKVLAGQGIGAWPVCGANAGSAGSYTSTN
TGGTAASTSNAASSTTRSTARTESTYTPARAASTGGNYTVQSGDTLNTIAAAHGTTWQAL
YAANKSNITDANLIYAGETLNV
>PFR_JS22-1_2178	PFR_JS22-1_2178	Citrate (Si)-synthase	2466761:2468065 Reverse
MGETARLEIDGEVYELPVVQGTTGEKAIDISKLRNTTGLITLDEGYANTGSCRSAITHID
GEKGELSYRGIPIETLAEHSTFIETAWLVIFGRLPTELEREHFSELLSQNAALHTQMRAH
FAAFPEQAHPMAILSAMINAISTHDRPKIAPDDDATLERYAANLMSKVRTIAAGSYKTSI
GEPLIYPRRDLLYTQNFLHMMFSLPYQEYEASPQAVHALNLFWLLHADHEQNCSTSTVRM
VASGEANLYASCSAGVVALWGGRHGGANVATVQMLQRIRNEGLSPKQFLAQVKDKESNIR
LSGFGHRIYKSYDPRARLLEKAATELLDATDSKDPLLPLAQELAAEALSDDYFAERSLYP
NVDFYSGVILRAVGIPLNMFTVMFAIGRMPGWIANWREINNDPNGRIYRPRQVYTGPPYV
QWREYADRISQPGE
>PFR_JS22-1_2179	PFR_JS22-1_2179	EcsC family protein	2468568:2469371 Forward
MPTRKRSNTGSTVGAIGATVVAMAPTIAPGPSANLLRRLADYAIDGVGPLPGARIAAGHA
LEHKTGDVEAALDSLVRNHVAMAGAQGFVSNLGGVVTAIAAIPANLAAVAVVQTRMVATI
AHLRGYDLSDLRVREAIWMTLLGRHDVDDLVAAGKLPSTPLGVATAPVLDSALEQRIAEQ
VLATLVGRSGGKQTLAMMSKRIPLVGGGVGMATDGWFTWTVASYARDVFAPRRLPELPGP
EQVVDEEQPAPQPESDVRDAEWSEEDD
>PFR_JS22-1_2180	PFR_JS22-1_2180	Hypothetical protein	2469482:2470351 Reverse
MVLLAIVNLAAAVLLIAMGVLGQRHALPRNGWAGIRTATTMTNDDTWDAAHVAAAPAFVI
GGLVQLLLAATALVLAGNDDLNGAGVAIVFTVVWLVTLTAAVAMAAVVGVRASKAVLVRQ
QQQLVAVGAHGHSASASDEVLGAEPPGEWISRDPARTVAAIVMALVPAALMMVLRSSVFA
DLPAKVPQHWGLSGPPDAWVSSNTAFWLGFVAACVLGVAAISVLLVARTARARRGYYSLF
TIMAFIASGGWLASALYGIGIAIGGWQSGLIIAAAAVLGLVARYIVPDA
>PFR_JS22-1_2181	PFR_JS22-1_2181	Putative thermostable alkaline protease	2470530:2472146 Reverse
MDGWMHRIGSARRARTGRSRGGRRLAGRVLAALCALTVGLSSSAIARADDGLWYLDQFGV
RDAHAQGLDGSGVTISVIDSPLVSDYPALSDANISYDTVPQSTRAPGGRSEGYDACYQNG
QKIVASFKSGQAMDPDAPGDPIFITHGTEMTSRIVGNGKGYGSDPGFEGIAPRAAVKFFA
NSGGIGSGDVADNSCEGPDGSALGTDLATTGLGIARAVGAGARVVSMSFLTSVDADDYPG
FLSALQHGVIMVSARDNSQEPGLPDMVGDPSRLTGLPGLVTVNSIGPSGPLAPSSDTTDG
SVAILSPGNEVLIAPAMDTRVLDVANGGTSSAVANLSGMLTLALQKWPDATGNQIMQSLV
ANTRDSDGTATLDEGHERGFGVVDLTKLLAVDPTGYPDVNPILDQEVTRAAEHGETADMY
DAQCAADSAQTTEYQFGDVTMKVPCQAGQFKQELVRQQDAWAAVQQCRADGGADCMRLSA
TNTAPAVSKQAGAVQAPAAPVRTSTHAGVWVAAATGALAVVAVATGGVILHRRRRSSH
>PFR_JS22-1_2182	PFR_JS22-1_2182	Alanine racemase	2472156:2473304 Reverse
MLYTTHLEIDLDALRHNARAIKQLVGDRKVLVAVKADGYGHGAVPIARLFQREHLADWLG
VATVSEAMALREGGVTLPILKLSHAFPEELPTAIDADIALTVVDEQSADEAAEAAKVVGK
PVNVHLALDTGMRRIGAEPEHAVALARHIDEDALNLQGIFTHMPVSDTTQGYDFTVEELA
RFAKAVDDVQADRATRGLPAVPLVHAAASAGVLGHDLSGLTMVRPGIAIYGAYPDAQTPR
TAALRPVVTMRSKVSFIKRIRAGETVSYGRTWTAPTDRWIATVPVGYADGFNRLNSNRGR
MLINGRSFPVAGRVCMDQTMLDLGEADDHGVHRGDDVIIIGASGDEYISTDELAELAGTI
SYEVTAVIPPRVSRQYFDSAAE
>PFR_JS22-1_2183	PFR_JS22-1_2183	Hypothetical protein	2473477:2475030 Reverse
MTSASSTHSRERHILLGVTGSIAAFKAAQLASDWVKQGHQVRVLMTAAAAQFVSPLTFQS
LTHQSVRIAMFDDSGASQTATDDGMHVGITHIDDAKWADVFVIAPASADVIARIAAGMAN
DHLTATLLAATCPVVLAPAMNTRMYDNPVTQRNMTTCRQLGMSFVEPSSGLLACEDVGKG
RLAELSDIEWAVDEALEGMSAPRFDADVAGPGRSGAARAEAPRPTSDVESAGATPSDAGS
SDAGPIDAAVIDAAMADAEHSTTLVVPDSVTSDVVVPDAGAMPPLRAGGPAGGAEGLLSG
VRVLITAGPTREPIDPVRFLSNHSSGRMGYALASAAHDLGAAVTLVSGPVSLPEPAGVTM
VQVQTAAEMFDAVTARFEQADLVVMAAAVADFAVAAQADQKIKKRGRRALTLQLEATPDI
LAWCGEHRHPGQVLCGFAMETTELVAYATEKLARKGADMIVANSLTTPGAGFGTDTNVVT
ILTATDGEPHRDDLPMMTKRELAGQILARMAALRVSA
>PFR_JS22-1_2184	PFR_JS22-1_2184	MarR family protein	2475074:2475418 Reverse
MTASHDDCALESLLILNQCIPLFETLKDPERQSILVRLIEHGPLTVNEVAESSSLSRPAV
SHHLKILERNGLVSMTKEGTRRICRAETQTGLSLLKRLVSALEADLAEVPGVAH
>PFR_JS22-1_2185	PFR_JS22-1_2185	Possible FMN oxidoreductase CC3083, imported	2475421:2476068 Reverse
MRFLTQIYRAMRDALGDDFPIGLKLNSSDGVEGGFSEQDALSVIETMAAMGLDLVEISGG
TYTKPPVDVVDGVDPRRGTIFFLDFARRLQGRVDIPVALTGGFLAAPDMEEVLASGAADM
IGIGRGLVVSPDLPNKILDGGSHETVSLPRVTTPVSAVDRALGSILVISWYEHQMCRLAE
GKQVASSGDATVALMSTLRSHGLGALAPRRNSGRK
>PFR_JS22-1_2186	PFR_JS22-1_2186	Uma4 protein	2476192:2477499 Forward
MSHPTFTTPCLTTFCGLDELGLEAVGQRLDPDRAVIECRVVEPDRWCRECGCEGAPRDTV
IRRLAHEPFGHRPTTLLIRVRRYKCCGCGRVWRQDTTAAAPVRAKISRGGLAWGLAGLVL
DHLSVTRVAAGLGVSWSAANDAILAEGRRRLIDDPARFEGVTTIGVDEHVWRHTRHGDTY
VTVIIDLTPVRDKTGPARLLDMVAGRSKAVFKTWLAARPKPWREGIEVVAMDGFTGFKTA
AAEELPDAAPVMDPFHVIRLAGDALENCRRRVQHDVFGRRGMKGDPLYQARRTLLTGAGL
LTDKQQARLDALFAEDRHVEVEATWGIYQDMITAYRDKDRGLGRFFLAHTIDKISASVPE
QLVEIRKLARTLTQRASDVLGYFDRPGTSNGPTEAINGRLEHLRGTALGFRNLSHYIARS
LLEAGGLRPALHPRS
>PFR_JS22-1_2187	PFR_JS22-1_2187	Chondroitin sulfate/heparin utilization regulation protein	2477558:2478721 Forward
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MTPEVVRAVLQDAIDASPDTAIQFCWQGGEPTLRGLDFYREAFAVARRIVPPGRHFAWSM
QTNGVLIDERWAEFLARHDVLVGLSIDGPRDVHDRWRVDRGGRGTWAKVMRAARLLHEHG
VRFNTFTTVHPANQHRGAEVYRFLRDEVRSDFHQYIPIVVPDPARPGHVVRGLSVDPGAW
GEFQVDVFSQWLHRDVGQVFVMNVEWALAAWCGDEPASCMFREHCGDAVVVEHDGSVYSC
DHFVDPAHRLGRVGDDSLAAMVADPRQRTFGDAKADLPARCRECPVLFACHGECPKNRLM
GEAQLTGEDRLTGEDRLTRGPRSEGADPMAGPADGPKVNYLCRGYRHFFTAIDAPMRYLA
ACVLSGRDPARVMPWARQYRILVSPGT
>PFR_JS22-1_2188□PFR_JS22-1_2188□Carbohydrate kinase FGGY□2479151:2480707 Forward
MSERQRTQQGPLVVAIDSSTTSTKAIVVDTNGTVWATARRPIPLLTPAMDHYEHDPALWW
RTSHETIGEVLGGLSQADRDRVAAIGITHQRESFAPFSADGTPLANGILWLDGRAAEQIE
RHGSAHVHELSGKPAGVTPAIYKMAWVTQHHPEWFARADKVTDVLGAIVFNLTGRWASST
AAADSLGLFDIQRRDWSDELLQIAGVRRDQMPELVAPASPIADIRPELAAEWGLARPIPV
IAGLGDGQAAGIGAAAVDPGVGYLNMGTAVNAGVESGSYIYNPAFRTHVSGIPGNYVLEV
LQSSGSYLAGWVRDTFGDPDHPGDPDVERDNAAAAAIAPGADGLVTLPYWNAVQSPYWDA
LARGAVVGWRGTHTRAHLYRSVLESICFEMRRNLDELADGTGTPITQLRIMGGGARSGVW
RQIMADVTGVPLTVCLEEEISALGAAVLAMAAINAHAEPLADGSPDVASSAKAMASFGET
VHPDMELHERYRRIAAVHARLYPALRETFQELAALSQD
>PFR_JS22-1_2189□PFR_JS22-1_2189□NAD-dependent glycerol-3-phosphate dehydrogenase domain protein (Precursor)□2480760:2481812
Forward
MPTITVLGAGAMGSALCRPLADAGWDVRLWGTWLDDHLLDAVEAGKPHPRTNVPLAPGVA
TFRSAQLEQALDGTQVVVMSVASVGVPRVAELALPGIAKADALWMTSKGFSEADDGRIGL
LPEAIRSIAAAKGVALPPLVAIAGPVKANECAQALPTATIFGCRDREVSRSYAAQAATAN
YAIAHTDDETGVEVCAPMKNVYAIALGVADGLEEETGVPHHNLKAAAFAQAIAEMSLLGA
QLGADPATAYGLPGVGDLEVTGLSGRNKVYGVRLGRGEQPQEALAEMDRLEQTVEGVPAT
ALAVRFVEQIGGGLAERMPLLAAVNRLLNDAGVDPMTEVARAVLPVKPTL
>PFR_JS22-1_2190□PFR_JS22-1_2190□Transcriptional regulator□2481886:2482662 Forward
MEQQPATSRDVRIHDVLQVVTREGTIAVKELADELGVSSMTVYRDVAALETSGLIQRSHG
RVTAAPFSMAEASSLMRMGTELDAKQRIADAALPLLAPGSTIAMDDSTTCRHLFPGLGEL
APLTVVTNARFIADAVRDSAELELITLGGSYLRWADAYAGPMTEAMIDQVSPDVCIMSTT
AVTGGVCSHPDEAMAAVKGRLMRAARQRILLVDRTKFSRNALHRFLPLSEVDVVITEKSL
DPAHLATLRDQVERVITV
>PFR_JS22-1_2191□PFR_JS22-1_2191□DNA glycosylase□2483095:2484093 Forward
MAGARSGAAGSPAQRTVVGAAGRLDMALGRLAKGPADPTHRRVGAQHWWRATRTPDGPAL
LELFDYHADVVTRAWGEGADWALDQVPRLLGEQDDPSGFAALAADCDLLRRAHHDHPQWR
IGATDNLTEALAPAVIEQKVTGPEAFGGLRSLLAKYATPAPGPAATPDGPAHGMVVPPTA
EQWAHIPSFEFTRAGVDGRRAAALVRAMRRVPSLERALGRATDGAERSRLLQTQPGIGPW
TAAKVLQWAYGDPDAWSIGDYHAPALISLALTGQKGDDAFADEVLAPYAGHRYRVELLVT
PLVAHAARRGARRTLPSHVPGVGVNRRRSWRR
>PFR_JS22-1_2192□PFR_JS22-1_2192□Membrane protein mosC□2484093:2485352 Forward
MASGMESPETEHKASDKPAHKAGRVPTRLRLARLGVLLIFFVNGATFASLVPRYPEIIER
LHVSNTLWGLALGIGPIGGIALGWLAAPLMRRYRSRNVAALAQIASSGALVILALAGSIE
WVFVAMFAMSAFDAVTDTSMNYHGLRVQRLYRRSIFNSFHGWWCIGAVVGGFLGSAAAGA
AMAVPTQTYVTVGVLLCCVVASWAMMLPGEDREQVAGTEVATGRAWLRPRTLAVLVGLGL
LGALAGGIELGGSAWSPLYMTDQFAATPFVAGLGFVALMVFETLGRLTGDVIVDRLGLVR
TVIWGAVACLAGMALALAAPTPVTALIGFGASGWGIATMIPNAMNAADGLPSVPAGVGLT
ITTWVMRVGFVLFPIVIGALGDAVSLRLALLVIPLSAVLIMALSPLLRPRPAPQATATG
>PFR_JS22-1_2193□PFR_JS22-1_2193□ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein□2485381:2486808 Reverse
MIRPLRRAVLGRNGEPRTLQQRFAAMTAAVVALAVAVVGMIAYVSTSRSLYGQVDDELVS
VAGYMVTPIASDVTGMGGLNSSSLQAANVNIVLVKSDRSIVRVQGEKVSIQPDAPEVAVA
RMKFGKSTRTVSLGPDGQRYRLVAVPMEAKDNSSYALVLARPLEPLVDTLDQLRAILLWL
GIGFTIIAAAVGYTIGRRVMQPLRQLSDAVAHVTETDELVPIGSTRADELGDLSRAFDTM
MHSLASSRNRQKYLIADASHELRTPLTSMRTNVELLVADEKSGMLPEGARAEILGDVAAQ
LGEFTSLVGDLVQLSRDDVVLPSPEPLDFAEVVESAIVRAKRRGSSLNFDVSLEPFYVVG
EPDTLERAVTNLLDNAVKFSPRGGTVHVHLAGDTLTVSDEGPGIAQDDLPHIFDRFYRSN
KARNTPGTGLGLSIVAHTVKAHGGWVHADNAPGGGAMFTVRLPAAPPEVVAQMDH
>PFR_JS22-1_2194□PFR_JS22-1_2194□Response regulator MprA□2486805:2487500 Reverse
MAMQILVVDDDQAVRDSLARSLHYSGYEVETAEDGLEALAKLSTNLHPDAVVMDVMMPRL
DGLETTKMLRANGNDVPILVLTARDAVGDRVDGLDAGADDYMVKPFSLEELLARLRALTR
RSRPESQQANEVLSFADMTLDPQTREVTRGGRRISLTRTEFALLQTFMEHPGKVLDRSWL
LNEVWGFDFPATANSLEVYIGYLRRKTEQEGEPRLIHTVRGVGYVLRETAP
>PFR_JS22-1_2195□PFR_JS22-1_2195□Cyanophycinase□2487507:2488421 Reverse
MTLFLVGGGPSQATGPIYDSFVEQARGRGPRIALAILGAPEQAGASVGMYADPIRQRWPE
AQIEPIWLIDEDEGTVEWPTDPEQLGGLVVAGGWAPGYLDALTPLRDEIVRIVRGGVPYM
GFSAGAQIVAKHAIVGGWQSHGRAVGPEIAGDGSTEIVVRDGLGLIGSAVDVHIDSQHLL
ERAISALLDHDISSAIAIDEDTALVVDVASGRSDVVGSGAVHWLNNEGHEVRVRRTQGPQ
AQPVVEDDTESTSDAGSTGDTASPEDTASPEDTGSSEDTASTGADASADTASPGTESEPP
TNEK
>PFR_JS22-1_2196□PFR_JS22-1_2196□PtpA□2488477:2488941 Reverse
MSAFDLLFVCLGNICRSTMAEQVARAQAADRALGLRIDSAGVSDWERGNPLDPRAAKCLS
AHGYPVGDHRAHLVTDAELGSGLIIGMERSHLDDLASMGAPGDRLALITDFVPGDHADGL
PDPWYGDMSDFEFTLKVIEAAMPAILDDAASLRR
>PFR_JS22-1_2197□PFR_JS22-1_2197□Hypothetical protein□2488938:2489318 Reverse
MLWRTVVNAAAVGVATWLLPGISFIGNDTTGQRALTLAIVAIVIGLLNAFVKPVLTLVSS
CFVVITLGLFLWVINAAVLMFASWLCGAMGVGWHVAGWGSAFVGALIVSVVAMLLGGNRD
NYGGRN
>PFR_JS22-1_2198□PFR_JS22-1_2198□Ornithine carbamoyltransferase□2489457:2490461 Forward
MAVDLSGRNFLKEADFTPEQWAEFLRLAAELKAAKKSGTERPTMVGKNIALIFEKTSTRT
RCSFEVGAHDQGAHVTYLDPSGSQLGHKESVEDTARVLGRMFDGIEYRGFGQSRVQTLAD
YAGVPVWNGLTDEWHPTQMLADQLTMTERSTKPLREVSVAYVGDARFNEGNSHLVSGALS
GMDMRIIAPKELQNSAEVIATANEIAATTGARLTVTDDPNAVEGVDFVSTDVWVSMGEPK
EAWAERIDLLRPYQVNSALLARTGNPKVEVLHCLPAYHNLGTAIGREIYELTGMDALEIT
DDVFEANADVIFDEAENRMHTIKAVMVATSGERG
>PFR_JS22-1_2199□PFR_JS22-1_2199□TDG/mug DNA glycosylase family protein□2490465:2491064 Forward
MAKGFTRAELQAFRHQTVPDLLPEPLRLLFVGINPSLWSAGVGVHFAHPGNRFYPALAAA
GITSHVIDASHGYPPEGLSELERGGVGISNLAREATTKADELDNQQFVDGLARIREMVRR
YHPKVVAFLGIGAYRVATGDRHAKVGEQALRLDWGDGTGSSAHVFALPNPSGLNAHETVE
SLGRDYREAAEAAGVPLFH
>PFR_JS22-1_2200□PFR_JS22-1_2200□NADH oxidase□2491348:2492136 Forward
MSSNHASADILATRQATLADPLTLPSGAVIKNRILKGAMNEALGDRGAHPTEPLVNLYRH
WASGGTGLLLTGNVMVDPRQLGEPGNVAVEDETDMDMLRQWAQAGTENGAALWMQINHPG
KQSPRTINQHPVAPSAIGFGGKYERFFSMPRELSRGEIEAIVGRFARTAVIARDAGFTGV
EIHGAHGYLVNQFLSPLDNHRTDEYGGSLENRLFTDEGVAVVRPGAARRCRGEGRGLPMM
GVLTQPVRKTSTCLTLPSRALT
>PFR_JS22-1_2201□PFR_JS22-1_2201□Transposase of ISAar20, ISL3 family□2492103:2493458 Forward
MPDATFTRPDLTTFTRLDGLGLEVTGQLLEPDRSVLACRVVEPDDWCRRCGCQGVPRDTV
SRELAHEPFGWRPTTLVLTVRRYRCKECSHVWRQDTTAAAPPRAKISRAGLRWGLVGIVV
GHLSMARVAEGLGVAWNTANDAVLAEGRRLLIEDPTRLDGVKVVGVDEHVWRHTRRGDKY
VTVIIDLTPVRDGTGPSRLLDVVEGRSKKAFKDWLAERDQAWRDGIEVVAMDGFAGFKTA
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TTEELPDAVTVMDPFHVIRLAGDALDECRRRVQQELHGHRGRKGDPLYTARRTLHTGADL
LTDRQHERLDKLFAGDRHVHVECTWGIYQRMISAYRHPDRAAGRVEMSSVIDALAEGVPE
ALVELRKLGRTLTRRACDVLAYFDRPRTSNGPTEAVNGRLEHLRGLALGFRNLTNYIARA
LLEAGGFRPHLHPHLGRARSRFACRRGWCSR
>PFR_JS22-1_2202	PFR_JS22-1_2202	Hypothetical protein	2493382:2493636 Reverse
MSVFDLAQTDPIEGAEPIPENPADAHQLSGDDPAGIAEAVTDWLTGQGWAIEHNQLGAGL
NGYTSPDDKRIVIGLFPDEGVGVV
>PFR_JS22-1_2203	PFR_JS22-1_2203	Ribonuclease BN	2493683:2494777 Reverse
MTSTAPSTPRNAPDPEASGKPDSPDDLHKRSWKYVLRKTIREFSSDQCTDIAASLTYYAV
LSLFPCLIAIFSLLGVVGQGKAASDAVLGIIEQVAPGDTVDTIRGPIEQIAESPGAGFAL
ITGILLAIWSASGYVGAFSRAMNRIYEIEEGRPFWKLKPAQLLVTVITIVLLVIAAIILV
VSGDVTKAIGDALGIGDVPQTIWSIAKWPLLIFIAVLVVAILYYATPNAKQPKFRWISMG
ALLAIIVLALATAAFGFYVGNFSNYDRTYGSLAGVIIFLLWLWIANLALLFGAEFDAELE
RGRQLQAGIAAEEDIQLPSRDTRKSDKAAEKERQDIEKGREIRQNADPDDTAKDATTPGP
AREH
>PFR_JS22-1_2204	PFR_JS22-1_2204	Hypothetical protein	2494840:2495403 Reverse
MSDSPDEIRADIERTRHDLGRDVDALADEVSPSKIVDRQVDKVRGAFTSVRERVMGAADD
AGSSLTDAGSHAGDLKDRAVAKAEGNPLAVGLIAFGAGLLAASLIPASSKEKDLAATVKE
QAQPLVDEVTDAAKEIGEHLKEPLQASVESVKSSAQDSVATVKDEAQGAASDVKDQAQHA
RDNISDS
>PFR_JS22-1_2205	PFR_JS22-1_2205	Hypothetical protein	2495400:2495558 Reverse
MPGVVVAVLWALIALILFLVGRSQIKQVKGVPQTVDTLKEIPETLKRNEENR
>PFR_JS22-1_2206	PFR_JS22-1_2206	Hypothetical protein	2495641:2496696 Forward
MDEILADLDDNQGGIGWWRGYVGWQVSAELGEYLLSACGGVSEALIKASLAIQEYRESSC
ARDHALTQAWRAIAKRGGSRDELIGAQQALGDAGQRREDRLDAWLEQTIVSLGQALDRVA
AVIVIVAGIKCDVIRTDWGELQKVAVKALKNGRGQGLRQGVLADVGTSGRERQNALLSDV
LKPEDHGPEDWLSWLIAQRNTMVHRAPRMSLIQMVGTRARPTGVINPLPSQPDWVGTRAM
IDAGKAGTMSSMFLVSTPQTVLEGLRGSMCTFLDQLLKETLGLWGARRSDPRLIVQPGDS
WQPVPKSGTLSFPGYGKPASMVTKEIAVHPSMGRRLRAARLMDYQVHLWEA
>PFR_JS22-1_2207	PFR_JS22-1_2207	Hypothetical protein	2496714:2497007 Reverse
MTSEEYQRALTGVHDVVASAVALPPADAGEALASMDMGIRAVTLSSGELGFWSRRDEVGR
AVVRGDLDTVRYSAFLEALGEHVVWPKADMQRNSVEG
>PFR_JS22-1_2208	PFR_JS22-1_2208	Hypothetical protein	2496964:2497386 Reverse
MPESLTQAEPIALSQAVSPLVLAMDIGSTSSRAAVHDALARPVVGHQTEAKHRFHEASDG
TSEIDADAMVAEISGLIGETVQGLPASSIAAVAMDTFASSLVCVDDHGGVDDPRPPQPSV
GPRGGADDIGGVSAGVDRGS
>PFR_JS22-1_2209	PFR_JS22-1_2209	SPFH/Band 7/PHB domain protein	2497500:2498264 Reverse
MALLIVVLAVVAVVLIVLLVSLRVIPEYQRGIAFRFGHLRPTLEPGIHFVFPLVDSLQRV
DLRVITLTIPPQEVITKDNVPARVNAVVLFKVLEPKDAILKVENYAIATSQISQTTLRSL
LGRVDLDTLLAHRDDLNIDLQGVIDARTKPWGIEVSTVEIKDVEIPEAMQRAMAREAEAE
RERRAKVISARGELEASDELRQAAETLSQSPASLQLRYLQTLLELGADQNSTVVFPLPLD
IIGPLLNKMGNALK
>PFR_JS22-1_2210	PFR_JS22-1_2210	Putative transposase	2498399:2499268 Reverse
MDAPLWGVDFVVWMFCAYALILVGVGYGLDLLAKRTSQQSSAKRNFGFHYHENQDAWLCS
EDQWLFPTAFDRDNRVMHYRASSIVCNTCQVKNTCTTSMMGREITREVDPWPYSESGRFH
RGIALAVAVSGLVLIAGVAILGHTAADIAVEVATAVAVVAASVPLARHLMRSPANFVEPT
HVKVVDADEIDAAVLADRFAQKWGNVSDERKRAAALERERVLADAAPATGWRGRGTRDTP
LHISSALAMKERLKRESRGAEVIHDGSAPIPGGPRPRDIGAGREETPDS
>PFR_JS22-1_2211	PFR_JS22-1_2211	Putative nitric oxide reductase, NorZ	2499273:2501687 Reverse
MPSKNQPTTEQVAKTKRRAETVSAYASKGWVQAVAFVMLLGFGIMAALAMRTYTDSMPQP
DRIVNEQGQEIISTEQISHGQALYQSRGLQEYGSVMGHGAYLGPDFTAEYLRLTTDAAVE
KYTADGVQDPRQAVEDEWRTNRYDENTGTLVWTDQQIAGYHQMVDYYTDFLGSPTTEHGM
FPNALEPGEEIEDTTAFFGWTAWASSTNRPGHDYSYSNNWPSEPNVGNGPTANLMIWSVL
SLIVLLGGIGILFAVYGRWSARIGWHGEEAPVLDFRQPDEVHLTPSQKVSGLFFVVIMVL
FFAQAMVGALTEHYRVELTGFFGIDIAQILPYTVSRTWHVQLSLLWTAAGFLAAGIFLAP
LITRKEPKKQGFLTGVLLVAVAIVVFGSLATEWLSQKGILPEGSLFSQQWEYLDLPRLFQ
IALTVGMFLWMFIVIRTLRSKLNSTKKTSLPWLFMFSGLAIPMFYAVGMLAGSETHFSVA
EFWRFWVVHLWVEDFLELFTTVMVAYVFVLLGVVRQKMAISIIMLDVILYSLGGVVGTMH
HLYFSGTSAETMAFGAVFSAAEVIPLTFLTVEAWGFMQLGSRQYTNRTKPFPHRWAVMFL
ISVGFWNFLGAGIFGFLINLPIVSYYEIGTALTANHAHGSMMGVYGMLALAFAVFVLRYI
IPEKEWPEKGVKWAFWATNIGLVWMVFISLLPLGVAQLYQSVGKGYYDARAIGYITDPGN
TLLDWLRMPGDVIFLSGIVPLLWLAWKALKSYFSKDSKPVVYELMDPPLYEALTDERIAE
MAAANKADAVPDQVSPYRSDRREE
>PFR_JS22-1_2212	PFR_JS22-1_2212	Hypothetical protein	2502417:2502614 Reverse
MAVKRGTTYCTFGTQVQTALAADATRTSLTLTNSQTRRSVAVTCAKGTTITTCTGDDGSV
VWLRG
>PFR_JS22-1_2213	PFR_JS22-1_2213	Hypothetical protein	2502663:2503007 Forward
MWRGLVALGEGVVMSTGNEKTRRQRRKFTAQYRHEAARMVIDSGRTIAEVSQELGLGPQL
LGRWVKAEKETMTPSTLSPDEREELKRLRKENADLRMDNEFLGKAAAFFAAKHQ
>PFR_JS22-1_2214	PFR_JS22-1_2214	Integrase, catalytic region	2503004:2503912 Forward
MSEKYTLMQAEKARYPIARMARLLKVSTSGYYAWVAAQQRDGDHLLPSLRARRRLDEAVR
RIWVDSRSTYGYLRVCAQLRREGVVVDRKTVAASMRRQGLAGISPRRFRPVTTIPGTRTH
SIPDRVKRHWDTGQVDRVWVTDITYLRTRAGWVYLCAIKDACYRKVIATAMSTTMTTDLV
EEALRRARILRPNAPRKVIIHSDRGTQFTSEQMYECCRELHLDQSMGRTGVCWDNAMIES
QWSVLKAEFYDRYEWDTPQQAIQGVEEWIYDFYNTKRLNSAIGYQTPVEFEAQHAAALTR
AA
>PFR_JS22-1_2215	PFR_JS22-1_2215	Hypothetical protein	2504197:2504505 Reverse
MRRRVQQDTLGRRGHAKDPLYRARRLLLTGANHLTEKMATKLDALLQEGDPNWEVTITWT
VYQKLIDAYQQSDSHDMVTLIDALKDLGVPPAWSEARGGADS
>PFR_JS22-1_2216	PFR_JS22-1_2216	Uma4 protein	2504542:2505849 Reverse
MSHPTFTTPCLTTFCGLDELGLEAVGQRLDPDRAVIECRVVEPDRWCRECGCEGAPRDTV
IRRLAHEPFGHRPTTLLIRVRRYKCCGCGRVWRQDTTAAAPVRAKISRGGLAWGLAGLVL
DHLSVTRVAAGLGVSWSAANDAILAEGRRRLIDDPARFEGVTTIGVDEHVWRHTRHGDTY
VTVIIDLTPVRDKTGPARLLDMVAGRSKAVFKTWLAARPKPWREGIEVVAMDGFTGFKTA
AAEELPDAAPVMDPFHVIRLAGDALENCRRRVQHDVFGRRGMKGDPLYQARRTLLTGAGL
LTDKQQARLDALFAEDRHVEVEATWGIYQDMITAYRDKDRGLGRFFLAHTIDKISASVPE
QLVEIRKLARTLTQRASDVLGYFDRPGTSNGPTEAINGRLEHLRGTALGFRNLSHYIARS
LLEAGGLRPALHPRS
>PFR_JS22-1_2217	PFR_JS22-1_2217	Transposase of ISAar20, ISL3 family	2505974:2507281 Reverse
MPDATFTRPDLTTFTRLDGLGLEVTGQLLEPDRSVLACRVVEPDDWCRRCGCQGVPRDTV
SRELAHEPFGWRPTTLVLTVRRYRCKECSHVWRQDTTAAAPPRAKISRAGLRWGLVGIVV
GHLSMARVAEGLGVAWNTANDAVLAEGRRLLIEDPTRLDGVKVVGVDEHVWRHTRRGDKY
VTVIIDLTPVRDGTGPSRLLDVVEGRSKKAFKDWLAERDQAWRDGIEVVAMDGFAGFKTA
TTEELPDAVTVMDPFHVIRLAGDALDECRRRVQQELHGHRGRKGDPLYTARRTLHTGADL
LTDRQHERLDKLFAGDRHVHVECTWGIYQRMISAYRHPDRAAGRVEMSSVIDALADSVPE
ALVELRKLGRTLTRSACDVLAYFDRPRTSNGPTEAVNGRLEHLRGLALGFRNLTNYIARA
LLEAGGFRPHLHPEL
>PFR_JS22-1_2218	PFR_JS22-1_2218	Hypothetical protein	2507526:2507699 Forward
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MTVRIGLIGAGGMGRAHVERIQNELAGGEVVAVADVNPDAAGYAESIAPATSPPGRN
>PFR_JS22-1_2219□PFR_JS22-1_2219□Inositol 2-dehydrogenase 2□2507714:2508535 Forward
MDAVIIATFGKVHAPDVIAAIRAGKPVLCEKPLATTAQDCLDILAAEQEAGRKLVTVGFM
RRFDKGYNEMRAQLTEGQHGYATMVHCRHRNPSVPGTLYTTRNMIDDTAIHEIDICRFLL
DEEITTVRVDTPRRSSNAPQGLQDPLVLVANTASGVRIDDEINVNIKFGYAIECELVMES
GTVRLADQDHTILRDIEGDRHAICRSHIDRFHDAFNAEVQQWIRAVERGEHAGSTSWDGY
AATCVVDAAIESLEHQGREVAVQMIDQPAFYAG
>PFR_JS22-1_2220□PFR_JS22-1_2220□IolH protein□2508754:2509620 Forward
MVDIALDPNMYYASMSTAQTLFKAAELGFDYVELSPNTEFHFWHRCPKADDDFVAGLNKA
QKDSGVTVRTLNPVFNWSSPDEQERAAQVRNWRRLLELADQINVREIVSEFSGNPNTPVR
CEEQWYKSIFELAPDFEKYGITLSMEAHPYDFVERHDDAYSIVRGTNLDWIGYEFCCPHT
FHLDDGVGDVERMITSCAPKLREVHVADTLNHRANDGNRYIVNPPGVDARVHQHSEIGKG
EVPFDKVFETLRAVGFDGVLSLCVFGFHEHADEINRRMLERVRSEFGA
>PFR_JS22-1_2221□PFR_JS22-1_2221□Transcriptional regulator□2509756:2510790 Forward
MAGGSRPTQADVARLAGVSRQTVSLVVLDDPRVSPRSRAAVTSAMAQLNYRPNVAARALV
SHHTGFLGIVFSDLANPFHAELAEALRAAADRLGFVPFISPVGQSADEEKVAINRFTEMA
VDGLILVSPLSDNTTLEALGAQVPTVIVTRNSGPANVDLVHADDRASAAQVTQHLLAAGY
DPVVFLGYERRIEGDSSLARIDGYRAAMRRAARPEQVQIVTQGGVPQIVGGLAASLTRGF
GLVCHNDLIALEAWAALAELGLEPGPDVGVAGFDDTGMARFPGVGLTSVNNGTTGFADTA
VEMISQRLAGRTARREVVLPTHLIVRRSTLRDQPDRPPRPAQQR
>PFR_JS22-1_2222□PFR_JS22-1_2222□S33 family lysophophospholipase□2511439:2512377 Forward
MAIQEVTFPSSNGRDTIYGWIYEPTQPARGVVQIVHGLGEHSRRYLHMITALLDAGFVVA
ADDHAGHGKTSTESGVWGDTGENGVTTVISDEYSLHKLVRDDHPDLPFFMFGHSWGSMIA
RGFASAHGATLSGLALCGVAAQIDGVETKLDRVGLDAALAAGPGTASGEEFVGQIFEDFV
SRYTDVRTPNDWIALDPDVVADHARDPFNNYYKPMSLRFVHDFVTLYDQVNAPDWYTSIR
ADLPVLVLAGDQDPVANYGEGAYHVANQLEASGHRDVRTHVYTGYRHEVHNEPQTRADVE
SELTVFIDGHLQ
>PFR_JS22-1_2223□PFR_JS22-1_2223□Glycerophosphodiester phosphodiesterase family protein□2512592:2513401 Forward
MLTAGNHTPDKEVTMAATRATQHVPTFNSTIFAHRGLPSRAPENTLAAFDLAADEGATWI
ETDVDIIADGTPIIIHDTALDRTTDHRGKLYDIATAEELAGIDAGSWFAPEFASERVITL
DALVDLLNRRKLNANIEIKANEQGAERTIVLVDAIASSLARLDDEREIIISSFSQPVLMT
FHARHPEYAIGVLYETAALYDDWLSVLELCGASYIHPEDAGLTRERVQAFRDAGYGVNVW
TVDARDRANELLNWGATGVFTNIADQLIR
>PFR_JS22-1_2224□PFR_JS22-1_2224□Transporter, major facilitator family protein□2513596:2514960 Forward
MATSTSSTRRFSLPVFLRKGRIGPFLAVVMSGQIIYSAFEAFKGSLMIPLQQMLGITQTQ
FGILMSYIGIAMFLYVPAGWINNRFKVRTIILWSLGWRLATYLVLFLLTPPFAVMSVIAV
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AGIAALTVYWSYINLMYTSAPYLTQVFGVSAGLAGAFGIFNTGLVGIFAGLLSGLLADYV
FKSSTKMMAISLGAVAVACVIVMALPVRSSMIWPIMIMLIVVAIATFLGKAVILAPVAEL
NLPEGISGSAMSVGSFLAYASVFWAYTLNGHLIDANAGNPQAGYRLIFVITAVVAVIGCV
AAGLLTVINRRVKAHQQVAAAEGGTDAAPAPRAE
>PFR_JS22-1_2225□PFR_JS22-1_2225□Transmembrane ATP-binding protein ABC transporter□2515328:2516044 Forward
MPRVQDFTLQVCATHEAGPYTRLRVRCPELLNPRKSDELLPTAWLRLLVPDGGRQHQRGY
TLVECDHGTGEASIYMLHHDPAGPGSRWARSARPGDRIGAQLLAGQLYLQPPPDAGALYV
GDLASAPAIAGAIAAAPASCDIAVVLQAEPGSWSPVPHTACTLTIVSPDAGEDALIEAVT
TIPGRDYAWLALEASAAQPLRAALIAAGLPRDAVQYQGYWRRGTPMGRTVETSARAAA
>PFR_JS22-1_2226□PFR_JS22-1_2226□AP endonuclease, family 2□2516192:2517220 Reverse
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IGSQTARDDYLATFEAHGMRLAGLNTSGNVLSPLPDQGPKHAYDLRRAIELAGKLGVGEI
VCMSGTPGTDPDGKYPAWVVNPWDGTQLEVLEYQKSVLDPFWREMDLRAQDAGVQLALEL
HRHNVVFTPVNFLEFADRIDAKNVGVNMDPSHLMWQGMDIVESIRLLGSHIKHVHAKDTK
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LKALVEIDPQMNINIEHEDAAFGQLEGVELGAKNLIAAADAR
>PFR_JS22-1_2227□PFR_JS22-1_2227□Oxidoreductase , NAD-binding Rossmann fold family protein□2517344:2518531 Reverse
MPENTLSVAVIGAGMAGRTHANAWRQVRTVFGTRGVPQVRLAAICDAYLPFATDAANSYG
YERATSDWHEIVEADDIDIVSIVVANKLHREIALALMAAGKHVLCEKPLSDNLDDAAAMA
AEAADASVVSGIGFGYRRHPAIAEIAELANSGALGEILHFDGRYWCDYGADPQVPIAWRY
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ATETVENDDIAEFNMHFASGAIGSISVSRVAFGMPNALCFDVFGTQGHASFDLARSGEIK
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GLPPVPSFAHGYRAMHIQDAVATSAGRGGASVEIK
>PFR_JS22-1_2228□PFR_JS22-1_2228□Periplasmic binding protein and sugar binding domain of the LacI family protein□2518663:2519706
Reverse
MAADPTQRDVARAAGVSRGLVSLALSGSSLVADDTRERIVQVAHELGYTRNLGAASLASK
RSPVVGVVLPDLRNPFFESVVDNLQHEADGLGLLPLVATSADDRSRETTVLQRFRELRAA
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IVAVSFVSGLGEVWVAHRHRALARAAAAAGMPLERVEVPRGEALAPQLGGVLAAQADQRV
AVVTHNDLTAADVLAFVRARGLRPGHDLAVIGFDDTHMARRPEFDITSVSQNTGELARLA
MVALQGRAEWMGARALRRHPDAAEGDDEPLRGREFIVAPALSVRSSS
>PFR_JS22-1_2229□PFR_JS22-1_2229□Thiosulfate sulfurtransferase□2519733:2520551 Reverse
MTLIDPATLRAKLASDNPPVVLDARWSGPAATVDEGHKDFETGHIPGSLWVSMNKEMSNP
DVPGGRHPLPDPGAFEADMRRKGLNEDSSVVVLDGGNSLAAGRLWWLLTDGGLTDVQVLN
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>PFR_JS22-1_2230□PFR_JS22-1_2230□Glutamate decarboxylase□2521035:2522375 Forward
MFARPAEATEFSKFRLPASESLPETAYQVVHDEAMLDGNARLNLATFVGTWMDDYANRLY
AESADKNMIDKDEYPKTAEIETRCWMMLADLWHAPDPDNTIGTSTIGSSEACMLGGLALK
RRWQHARKAAGKPTDHPNMVMSSAVQVCWEKFCNYWDIEPRYVPISEDHKVLDGTNLADY
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MRAEVAYLDALPAPMPSQHKQSGFHH
>PFR_JS22-1_2231□PFR_JS22-1_2231□Amino acid/polyamine transporter, family I□2522568:2523965 Forward
MAMLTLVTVASLRSLPAMAEYGLASVALFIIPAVLFLVPTALVAAELATGWKGGIYTWVR
EAFGNRWGFVAIWLQWIQNVVWYPMQLAFIAVCLTYVFGVNIGNNGFYVAALIIVFYWAS
TLLSLAGKGLFAKVGSWSGIVGTIFPAVLLIVLGALWLTTGAPVQTDMHASAMLPPWTGI
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VAVVVVVLGVPPLILYALRRPGWDVRSDEEKADDQAILVNPAPKD
>PFR_JS22-1_2232□PFR_JS22-1_2232□Hypothetical protein□2524260:2526293 Forward
MQRTVRRDYLLWLTAITSDMLSRSVWSLALPFVIFGLTRSTATAGVVQSVGQAAYLCVML
LGGALVDRINRRTGMVVRGITGMVLWIGLGLLLYAHALSLWLLVAIFVAAQLCDGLFGMA
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NESALTFHDVPRGTFVI
>PFR_JS22-1_2233□PFR_JS22-1_2233□Hypothetical protein□2526110:2526547 Reverse
MTLPGVTAERMQAAIVQVTEQVPAEVDGGWEVPAESNAVIRFEPPSDNGLLRVAVVSPVK
IAQKDYPTVLMVFNEFNMKSTDATLYMTKVPRGTSWNVSADSFIMTADGLDEGQLIAAMR
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>PFR_JS22-1_2234□PFR_JS22-1_2234□Hypothetical protein□2526558:2528132 Reverse
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LTLIPLGVIAIVFVARAPGIVAGIEGLIVFASFAWLVAAMREAATAATRTDPDGGPLH
>PFR_JS22-1_2237□PFR_JS22-1_2237□Choline transport system ATP-binding protein□2529766:2530686 Forward
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VNRLAAPTSGSVLIDGDDVSGTNPVQLRRHIGYVMQDPGLLPHRRVIDNIATVPRLLGRH
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PIVRAELQRDLVTLQRSLGKTVLFVTHDISEAFKLGDHIVLLDTGARIVQQGRPADFITH
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GQERPS
>PFR_JS22-1_2238□PFR_JS22-1_2238□Choline transport system permease protein opuBD□2530683:2531330 Forward
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PSLPLLVVLPLVIGTGVRDRLNVIAALSIYGFALMIRAATDALDAVPRSAEVASIAMGYG
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AGIVATVVVALALDGLLVLTGRLLMPWARPERSRP
>PFR_JS22-1_2239□PFR_JS22-1_2239□Choline transport system permease protein□2531327:2532007 Forward
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LVVGFSGAARALPAIGLLTMVALIAGIGLIGPLVALVVLAVPSVIAGAYSGIDSIEPVTR
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>PFR_JS22-1_2240□PFR_JS22-1_2240□Aminotransferase class I and II□2532111:2533298 Reverse
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ATTWGAQNFREALADKYSPTIGRTIDPASEIVVTCGGTEAMMAAVMTVCDPGDKVIVFSP
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EPVNRFIRLHFARADEVLTESLKRLEKLAALLPAA
>PFR_JS22-1_2241□PFR_JS22-1_2241□Hypothetical protein□2533483:2534265 Forward
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DDNDNELMARLHKEFFDYPDDIETLAADYYGNDPEPTDAPKLPSSGEELAMDIDEITYII
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YQNNVDLQAAAQEQLKAATN
>PFR_JS22-1_2242□PFR_JS22-1_2242□Hypothetical protein□2534279:2534569 Forward
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GLQRAAEAVLGERFGYRARVLVRRVDELAAIIAACP
>PFR_JS22-1_2243□PFR_JS22-1_2243□Hypothetical protein□2534597:2534875 Forward
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TTDSAFGKQQNRGPAVRRPTVRNLQTLQRMVG
>PFR_JS22-1_2244□PFR_JS22-1_2244□MFS permease (Fragment)□2535032:2535931 Reverse
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FGLGTLAVAKVSLQVMWPIALISGIAWILSLTTLNVAMQLTLPEWVRARGLSVYLLVFMG
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>PFR_JS22-1_2280□PFR_JS22-1_2280□Putative membrane protein□2577298:2579142 Forward
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GV
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LAAGAISDVAGRPLAFAVGAVFLALSSLVALRMPGGRPDHSAGSVASADPDALLSED
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VLAQGIDPASPVRQATVRQGAPTQLTVVSVQTTLGDGGPAPAPDQDLVHRVGRLQSEQLV
RAAAYGTSVHLVTGGDAARAELAAATGRVRVPLQELLKKQTTPVALQTGNTDEISAPGSL
TGAESTAQTQLGFYKALTGEDAGIDTELLITRVWSGSFADADAAETYLNTAMATVSAALQ
SGGVEVHMSEKLIVPSKSTSLPISLTNSMSIPVRVRVHFDSDNSSRIDIDDTDVIRLDPG
ESATVRITPHASGSGTVQMDAMVMTAGDQAHQLGDSVRFTVQANNVGNIGWIIIIASGVV
LLGATALRVRQVRHERAQQHTPADDDPDVPFDPSPLDD
>PFR_JS22-1_2312	PFR_JS22-1_2312	Hypothetical protein	2618777:2620828 Forward
MSAESQPELPGARPYPRNLIAGDLVANRYQLETQLNQWDAGVTWRAIDRTLSRRVVVHLF
NPHSPETARALEAARRAAVAVDSRFVRVLDAMDGDQPFIVTEFATGITLRSLLAHGPVTA
LESAHIVRELADALAPMHAEGLFHRRLNPDTVVVTRTGNVKIMGFLLEAALAGATISSSD
NWARQEAEDVRALGKILYACLVARWPIDPSLAQTSQWGLPAAPMSEPGPDGPHWAPPSSV
DPRVPPTVNAICIQSFDPRPDSVPLRTADEIVIALGRVLGTAEADEVLGRRIRALPADEA
GENAHIGLHAPGIDELPQRAATPDDDGPATQRMAPVTGHDDPNWPGGDDPNWPFGADDSS
PLGTTDTGTRTPLTGAQAAAAGSAAPRPPAPVGTVQTFITALPEPEDGGAPHPDRRDSDR
GDLDHRHSDLRDFDPDRTDPRLRRLRQSDADAFDDDDDPDDDLTIDVSGKLVGPLPDRDA
EPRRLATHARAYRLARWLIPLGVVLMLVIALTGMVRSCQATSAAKAAQAKVVAPASVVEF
DPTADGGEAAESPGEVALATDGDPSTAWHTQEYGGSAAFGGVKPGSGLLLDLGRAHELSS
VTLTLIGAPTGVQLLVPHDDANPSMSTVKDWTVASRADAAGQSVTLTPDKATSIRHLVVY
LTSLPQLTNGRYQGAIAEISVNS
>PFR_JS22-1_2313	PFR_JS22-1_2313	Phosphoglycerate mutase family protein	2620904:2621623 Forward
MKLLLIRHGQSANNALSGANHPVSSQYPDPTLTDLGRQQAETLAHAFTDGLLPRPSVLLS
SPMTRAVQTAAPLADELDMPIELETQAHEVGGIFQSVQGEPGSFQGASRAELADISDRLI
FNEDIHDEGWYRLGSHVETPAEGQGRGKRLYRSILERYGNQDGVVALVCHEWITNYVLRA
ALGLSDPEGEPDPWFSLPNTSSTFIQTGLPLPGPYEGGGTAMIWWVGRFDHLPDEQVSR
>PFR_JS22-1_2314	PFR_JS22-1_2314	Extracellular solute-binding protein family 1 (Precursor)	2621752:2623071 Reverse
MRLQRRGLLAWAGAAAAAATLSACGGKSSSSSTLSSACTPSPTPTWQDAKSHGSGRLNML
SALYQDQASQDSYANNMLTGFFAGTGYSLAATYTSLDKLPDKVITSLAAGKLADVLMPGQ
GWVPVLERQNALAEMPADITDGLNLDQRLMTGCYWGDKLFALPYALDLTVIGYRTDVLAD
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DGTGVKALDYIIGLVKDGTADPAKIPTDGAQPLFIQQKTAMSPMSSTLWPALRRSHLDDE
GHLGFFPLPPDQASKDPVVLQTGTQLAVSRQSQFKEVAFQFCQYALQSQPLLSAVSMLPA
VPPRSDVIAGSQLAGNRVMSAGLANVRYATASLGGCPAWLDLEPVIEGQLMAAIRGQQSS
DMTVGNLAKVVSDSLSRGA
>PFR_JS22-1_2315	PFR_JS22-1_2315	Thioredoxin-disulfide reductase	2623490:2624467 Forward
MNDEIRDVIIVGSGPAGYTAAIYTGRAGMRPIVLEGSVTAGGALMTTTEVENYPGFPDGV
LGPVLMSDMRAQAEKFDAELIADDATKIELGGDIKKVTDSEGNVYRARAVILAMGSAYRH
LNLPEEEEFSGRGVSWCATCDGFFFRGKEIAVVGGGDSAIEEATFLTRFADKVTLIHRRD
AFRASNIMAKRALDNPKIEIAWNSEVVGMSGDGTLNALRLRDTQTGEERELAVAGLFEAI
GNVPRSELVKGQVELNPDGYVKVAGDSTLTDAPGVFACGDLVDHVYQQAITAAGTGCRAA
LDAEHYLSALMDENSDQATEALANA
>PFR_JS22-1_2316	PFR_JS22-1_2316	Thioredoxin	2624641:2624964 Forward
MAQPKDVTDATFSDEVLKADKPTVVDYWADWCGPCKQLSPILDQLAEEYGDKINFVKVDA
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DANTKVATDQGILGLPTVQIYQNGEVVKQFQGGKPKSVIVKMLQEFV
>PFR_JS22-1_2317□PFR_JS22-1_2317□Putative redox protein, regulator of disulfide bond formation□2624964:2625410 Forward
MSGEQTKTSRVGVNLKRVSPVHYEVTNGRGSTISVGHGDDVFSPVELLLAAVGACSSIDV
DVVTTRRADPEKFDVSIAGDVEKGPEGNRVKDVDLNFSLSFPDTDEGRTAQSLVARLVKL
SHDKDCTVGRTVMLPTELHSAVDGEVVA
>PFR_JS22-1_2318□PFR_JS22-1_2318□Chromosome partitioning protein ParB□2625705:2626688 Reverse
MSARPGGLGRGLGELFQRTDIQAAEEPREPASDQMADGSYYAELPVAQITPNPKQPRQVF
DEDDLQELTESIKEVGLLQPIVVRKLDATHYELIMGERRLRAHQEAGIAQIPAIVRATDD
ESMLTDALLENLHRVQLNPLEEAAAYEQLMGDFGITQDELARRLKRSRPHISNTIRLLKL
PVTVQRRVAAAVLSAGHARALLALDDPLAQERLAQRIVAEGLSVRATEEIVALGGDEKPK
QRMARPKEHDPRAEQLATSLSDRFDTRVKVNMGRKKGRITIDFAGEDDLQRIVEMLKGVS
ADSGAAPRPSNQADPWDFLIPPHGHTK
>PFR_JS22-1_2319□PFR_JS22-1_2319□Chromosome partitioning protein□2626685:2628220 Reverse
MSEPLGYPVKDHRKTTRPLGYPSELEITAEEHREVPRHTIDGRDIETLEVGATRPVGDDH
DDASGEDDAGDGDPDSHRPGSMGEPNVSRETSADEQAGMSGKDSGQTPADSSPSIQPAAP
IGVVPGNDVPLVSRETLSAVGDGQSSAGAHHSDIEPRGSRDAVGSGMASDEEKHDVSRET
SEEGEALTGSDDPAAPRPLRNPAARHPAPRPPEEPRHRPERALYEEPLSLETMNVSRETR
VKTVPLPHLDAPRRIVIANQKGGVGKTTTSVNLAVALAQGGLNVLVVDVDPQGNASTALG
IPHQEGVRGSYELLLDEVPVADLVVDSPEAKGLKVVPATIDLAGAELELVSKVAREQRLS
RAIRDYEADHDVDFVIFDCPPSLGLLTVNALVAASDILIPIQSEYYALEGVQQLMRTISL
VKRQLNSDLELWAVLVTMYDARTRLSAQVAEEVMAHFPKETLHTMIPRSVRISEAPSYGQ
SVLNYDPNSVGSNAYRKVAQELSQRAMKEQE
>PFR_JS22-1_2320□PFR_JS22-1_2320□Hypothetical protein□2628480:2629094 Reverse
MRWGLFARSAELEPPGRLAGDVKGPPGAGQFERVVHSGTAGARFAALVQRSESMRGWGDA
HVSGPLGSCWGVGAAHLSGCKGAAGSGDGSRERASEPPRPGRFIRSAEQVPSGFRRRVGV
SPRGASTLRPARTAGGAGWGSGTFTGGSVWRQDSTSRRSISIGSASPWIPSESWHRRWRC
PPECPGEALARAWRAGPAWERSDR
>PFR_JS22-1_2321□PFR_JS22-1_2321□Ribosomal RNA small subunit methyltransferase G 1□2629233:2630003 Reverse
MDDPMDDARHGAARRDDGRVERTGGPSDDAPHGVHASRERRVAQARDDDAGREQQAAQGA
RALFGDQFESMSGYVDILVGQGVEWGLLGPREPERIWSRHIMNCAALLEVIGEGVDVLDV
GSGAGLPGLVIAIARPDLNVTLLEPLLRRFNFLKEAVDELGLDGQVLVERGRAEDLKQHF
DVVTCRAVARLPKLLGWTMPLFLPDGELLALKGESIDEELADSADIIARNGLSAQVMQVR
ATPEVDVAHILRVQAG
>PFR_JS22-1_2322□PFR_JS22-1_2322□Hypothetical protein□2630026:2630991 Reverse
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PDESPVAQQVDSEVAADQAAAADEVAEGGPVQPDDSPVARKVTALEDEDEEAVEDEISEG
GPVSADEDADDDAEDDSDDEDEDDTEGEDDDSDEEKPAGPVARERSSSSAEDSLIEEADA
AADYLEELLDIADLDGDIDTYSEGDRAHVSVVTDSEVLVGRDGEVLEALQELSRLAVLTT
TGHRSRLMLDVAGHREKRRKELQLLAQDAINDVNETGEPVRLAPMNPFERKIVHDAVKAA
GLFSESEGEEPRRRVIVQPAK
>PFR_JS22-1_2323□PFR_JS22-1_2323□Membrane protein OxaA□2631043:2632134 Reverse
MNAGLLTLMGIGDSLGKIGSAIMQPLYWAVSGLIVLFHKLFSFFMNPDSGLTWTLAIVLL
TCFIRLLMMPLYAKQLNSSRAMQSIQPKVEELQKKYGSDRERLGQETMKLYNEEGVNPAS
SCLPLLIQLPIFWALFRVLSSAASDRNVHGYWLQRSPEITASLSHADLFGAKLSGTFWPL
TGGFGATQGFALALAILMTGLMFVQQLHMLKRNMPPAAQTGPMAQQQKMMLYMFPLMYLF
GGMAMPIGVLLYWLATNIWTMAQQYVIIRNYPTPGTPAYIEWEERMKEQGKDPREIERAR
QNRGRKHPRASNKTAQAKTDENGRTVVSRQSTQRTTVRRDDSDRQTVVRRQPSRQTRATR
KKK
>PFR_JS22-1_2324□PFR_JS22-1_2324□Putative membrane protein insertion efficiency factor□2632145:2632495 Reverse
MKFLLIGFVKAWRKFISPLYGDVCKYYPSCSAYGLEALQLHGAVRGSWLIMRRLARCHPW
SMGGVDPVPGSPLEARIAAGEQVGGHDHNLKNHDHEGSRPQRSAAGTSAVTGNAAL
>PFR_JS22-1_2325□PFR_JS22-1_2325□Ribonuclease P protein component□2632492:2632920 Reverse
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GNAVTRNRVKRRLRHMARARVVASTADVPLPGALRVVVRALPAAATEPKRLAGDFDSAWD
RALARLTPAPSAAGTSPSGGAR
>PFR_JS22-1_2326□PFR_JS22-1_2326□Hypothetical protein□2632926:2633063 Reverse
MSKRTYQPSNRRRARTHGFRARMSSRAGRAILAARRRKGRSELSA
>PFR_JS22-PH_1□PFR_JS22-PH_1□Exonuclease VIII□3:557 Reverse
MMPITKPCAVKDMPEGEYHSDPCVEPSLSSTMAKTIVSGEAGPARLREIMSHGQEHKAVF
DFGSAAHEKVLGRGAGVEVLDFPAWTTKASREARQAVWDAGGTPVLAKDSAQVDAMAEAI
LSNPVAGELFTRGAGSPELSMFTIDEETGRWQRGRLDFLADRKTIVDFKTSGQSVELPDW
IKHSW
>PFR_JS22-PH_2□PFR_JS22-PH_2□Hypothetical protein□554:1195 Reverse
MNRTYFKAVRADGTDFYTGKVRWLPDDGAPIPAGGWVVEHPTSERVGDDARTYLSVSTVE
TDCAGMGWPCRLLRVVPDGRQVSIPEPVGLPSTRASIRWRVIEELPAWQALGPQGREIEA
LLGQVESLTEDQTLEMSAARGFARGFARDVARFAALVASRGGALNAAQGGALGTALNAVR
DAVLGWLVKDFISDEEFRTLVGPWEQVMGRVIA
>PFR_JS22-PH_3□PFR_JS22-PH_3□Hypothetical protein□1192:1938 Reverse
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GEVGSWDAAFYLSASSVETDCTGFQWPALLLSVEPVGAMWTPRPDKFPRKRAAHAWRVIE
ELPAWRLFGPQGRTVLDIIEQTAHLTKRQIAALNRALDAARDTVWDVAWNAAWHAARVAA
RVAARGAARGAARYAAWDAARGAAWYATWVAARGAALGWLVKDLISVEDFRTLTGPWEQV
MGPIEVAA
>PFR_JS22-PH_4□PFR_JS22-PH_4□Hypothetical protein□2162:2377 Reverse
MKVDDFDDVRPLTQKDVAELLHASVGYVRSCRLATKPKGRVFPMPGWKTDGKRYLLPAWR
FREWVESLPDA
>PFR_JS22-PH_5□PFR_JS22-PH_5□Hypothetical protein□2364:2456 Reverse
MTSTLTGNIIALLIVAGVIVLAMGVRREGR
>PFR_JS22-PH_6□PFR_JS22-PH_6□BRO family protein□2453:3256 Reverse
MSILPFDYHGQEVRFITDESGEPQVVASDLAKALNYRNAPDMMRSIDLEERGTRPVRTPG
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>PFR_JS22-PH_7□PFR_JS22-PH_7□Hypothetical protein□3319:3522 Reverse
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LTSEAAA
>PFR_JS22-PH_8□PFR_JS22-PH_8□Hypothetical protein□3652:3906 Forward
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FELARVLDFEPGVFMDAAQARYQR
>PFR_JS22-PH_9□PFR_JS22-PH_9□Hypothetical protein□4178:4630 Forward
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GADVGSAKYTVHCDVTGTDQAPVVSNFQAW
>PFR_JS22-PH_10□PFR_JS22-PH_10□Integrase family protein□4703:6124 Reverse
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AYDGWQANGNRRRRWVYGRTQAECKRKLRDLKREIWSDTQQMNVNPRETVKSWTASWLDD
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VDLDKGTITIDRQLQRIKPDAALPPGYKVTRLEGSHCLVAPKSRSGIRRVPIVPWMGQAL
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SLLLAAGVPESVVIAIVGHASFAATEHYAHTDLEAARAALMKVQDRLGLELES
>PFR_JS22-PH_11□PFR_JS22-PH_11□Hypothetical protein□6483:6932 Forward
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VDVESSEDEAPYDLAVRSIIGDQPFTWIR
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IIADATQAGMTADTVSQLPGGDITIALQDFTPDGTDSADLLSARDKASQLSACATIAMEH
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GRTWQGNPPVWAIAWLPAPGGGTMIQLLGRLGDYPPGFADVDGPLVEILSILIRPESDLD
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>PFR_JS22-PH_14□PFR_JS22-PH_14□Hypothetical protein□8530:8868 Reverse
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DFTAGVPTTAKGLEATTVGKTDTTPVTPPARVAEEVPAGFVPDTAPDPVPTV
>PFR_JS22-PH_15□PFR_JS22-PH_15□Putative 1 N-acetylmuramoyl-L-alanine amidase (Family 2) with peptidoglycan binding domain□8886:9779
Reverse
MCGAFSFLKDLETFMDWTNLNADVTKLMGVHFTPGREGRTIDKIVIHHNGGNLSIDQIWN
VWQTREASAHYQVEAGGRIGQLVNDLDTAWHAGDWDANLTSIGIEHADDSTDPWHVSDAA
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>PFR_JS22-PH_16□PFR_JS22-PH_16□Hypothetical protein□9788:10063 Reverse
MNDFQTWITVLGGAGFLGALVTLIKGLVGWRTGKSGRKMRAAHDAIDSLNLAGLWAEAYW
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>PFR_JS22-PH_17□PFR_JS22-PH_17□Hypothetical protein□10060:10488 Reverse
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VCGLIGCPWGQWWIERAGLVAIGAAFAVHLSFVVAISPPDGPWEVASALGLLLLVATRWI
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>PFR_JS22-PH_18□PFR_JS22-PH_18□Hypothetical protein□10503:12194 Reverse
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>PFR_JS22-PH_19□PFR_JS22-PH_19□Hypothetical protein□12194:12805 Reverse
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PKGTVVVSAELNAIWVKTSDTLDEWATIIQHSDEVATVSVVSTQSDQVTTVQKFTIPESG
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>PFR_JS22-PH_20□PFR_JS22-PH_20□Hypothetical protein□12848:13078 Reverse
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LLRLSGGEWVLIGALA
>PFR_JS22-PH_21□PFR_JS22-PH_21□Hypothetical protein□13075:14250 Reverse
MIEVSKRWASSVGAGARWSVMVSWSSDGGQTWHDVVPTACSVDESTGQQVRWKLSCTLRK
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PFNIPGIASLAGGGGYVGYAGGTLNAAAGTAWVGENGPELVDFGGGESVYNRSQIDGLED
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>PFR_JS22-PH_24□PFR_JS22-PH_24□Hypothetical protein□19188:19556 Reverse
MSLFQLLATHWEELEGDFQEAYRVDLRDLWRGRLSPARCWVLLTQLPPGSRLWRMLGGPM
AWGMVERAVREEGWRLASQNAGKELPRPEPPAPGWRDKQDDLRRREERRLARFMQRHAER
NN
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>PFR_JS22-PH_25	PFR_JS22-PH_25	Hypothetical protein	19556:19909 Reverse
MAEAKKISAAEKARRETQSAKDTGTITDTTVQIGDIELTVPAAVFEDDWEFQEAILMAND
PDATDEDRARASMTLFRRLVGNRHREVLDQLRDESGRVPVSKVTETVKKVMDAVNPN
>PFR_JS22-PH_26	PFR_JS22-PH_26	Hypothetical protein	20007:20870 Reverse
MAVNSVNVHVFGSDDDVLYLGPSGLNLGNISLETAIPKEMIDTGWLTDDGVTLGMKDSVK
AIQGHQGHANVLQFMDSSDTTLEATLMESQLQTFLWNLDADAEDIDGVTKITAASSRKVL
NLCAIWDTFDTQHSGIHWRYVFPSLTLGERDDIPFKVGEASAYKYSLGVLEKFFVFTNAA
AMKAGGASAKTVTGVKITTTDGATVGLPSSLKVGEKVSLAAEISYSDGTKAVKQTNAVGL
TWTSSDKAKATIDGGVVTGVSAGKADITASIDGKTSEALSLTINTAA
>PFR_JS22-PH_27	PFR_JS22-PH_27	Hypothetical protein	20880:21248 Reverse
MKPPDLHTLVAHHLAELLDVPVVSTRPEGETAPSKFVRIISTGGAGRYGRVFQGIQLTIG
SYAGSAATARDLAMQVDEAMNGLPVSPLPVSKVTGNTPSDDPDPDTQQARHTATYQLTTL
IS
>PFR_JS22-PH_28	PFR_JS22-PH_28	Hypothetical protein	21245:21493 Reverse
MANFRFEPNTKAFTEWAQRDCDAHLIAGITASMGAKAGEGFSTMVSNNGDRTRGYLATAS
TKGRMRQAQGHVIERVIGSSGV
>PFR_JS22-PH_29	PFR_JS22-PH_29	Hypothetical protein	21486:21827 Reverse
MKRSWPTPVERLREGPPEIDRDGDPIAGSGVITKDPLPDALFAPGGSQILVAPGVAAVVD
EPTLYWRGSEVIDVVATDKVRIAGRVWTPEGNPARWPKGVVLKLKAQEAKNRG
>PFR_JS22-PH_30	PFR_JS22-PH_30	Hypothetical protein	21824:22204 Reverse
MVAPDPELPFATVSDMESRWRSLSKDEHTRAEALLDDASGLIVDTCPRWEQASPATLRRV
TCSVVRRAMAADDEDIGATSLMDTTGPFTTQRAYSSPAGDLFLTKAEKAALGGVTGAFET
SLLGLT
>PFR_JS22-PH_31	PFR_JS22-PH_31	Hypothetical protein	22191:22391 Reverse
MKVTSTIPNLTVLDLDIQFVDGQADVDPHLAERLRRLEPLGVRVPTASRKPPTRSRRKQG
VSHGRT
>PFR_JS22-PH_32	PFR_JS22-PH_32	Putative phage major head protein	22417:23397 Reverse
MPGITGQGTTYNLPNYVGELFAASPEDTPLLSAIGGLTGGESVGARQFEWQGYDLRDADG
SRQRLEGANAPDGEERTRYSASNVVEIHQESVEVSYTKQAANRERATNGAATVQLAGSVL
PADELTWQIDQQLKQVARDVEKSFIAGTYQLPTDNAKPRRTRGLLEATTTNVAASTHTAK
ELTVEEILDLFQKVWENGGIQEAETRTVIVGAALKRTLTRLFITDVKYQEESRNVGGVNL
QTFETDFGKANIMLDRFMPSDTLVVASLEDLKPAFLDIPGKGHFFAEPLAKTGAADKVQI
YGEVGLQYGNQRKHGKLTVAPATPAK
>PFR_JS22-PH_33	PFR_JS22-PH_33	Hypothetical protein	23414:24046 Reverse
MHKKLMPWVRLIEAVETPAGAAPTPAIDPKDPAANPTTEPKPADATSEKPLGEAGKVALD
REREARRSADKRASELEARVHQLEDAGKTEAQKQADELKRTQSELETLRGEKARLEVASA
TGVPVDLLAGPGDDLDAYAQALNAWRDKQSEKPAAPAVDTPSPSPSGVTGQPVQPNRTVD
ELIAAAEKNGDLATAKQLKLMKLDALRRTS
>PFR_JS22-PH_34	PFR_JS22-PH_34	Hypothetical protein	24376:25140 Reverse
MTDRDDLNHFHEANDAIQRRAINDLNKFWARLAKSDPKAVRAAMDLFVPQLIASYGELAA
EAAARWYEELRPADKKNFQAELADPVSDDIIEADVAEALGTSGAWDTEAVRGSLADAIRR
QIFYMARATVARNIAHDPKRPRFARVPRGAVTCAFCTMLASRGWVYYTAKTAGITRPWHR
KCDCQIVPEWKRGNIHFAGYDPDKMFEQYAESVDAVGSSFDTKAILADMRRRHPEALTDG
VVNMSEGQGPVTSD
>PFR_JS22-PH_35	PFR_JS22-PH_35	Phage portal , SPP1 Gp6-like family protein	25127:26638 Reverse
MSLLVNPYASPSFFSSPSVVGLGADEQELLDELVALWARKKPRNVLRGLYLDGKQQIKNL
NIAVPDEIADSLQIVVGWPEKAVFGLSNLCMWDGVVTPTGDENPFGLDDLLSANRFDVEI
NETITSAMANSVAFLTVSAGNVSIGEPPVVIMPFSAEWASALWDRRTRSIKAGLTIGDID
YLGRPTSLSLFTRTATITCVGSRLGWMIEDRAEHGLNRVPMEPVPFRPTLDRPFGRSRIS
RQVMTIVDRAMRAALRMDISSELFTAPGLLLNGITPEQWAEIQKWTWKLGTVRGLTRDED
GETASVETIPQQSMEPFIAQLRELAEEFASATSMPLSALGVVQDNPSSADAIYAAKEDLV
IEATNANRITGYALSRVFQDAVMMRDGLTEMPDELGGVAAKWRNPAMPSIVSQSDAMVKQ
ISAIPGLAATDVAFEQLGYSAADIVRIRTQMRRAQAADGLTSLLAKPATSSTPGAEPSQS
ASPTEPAASTPLPDLEGAPGDRS
>PFR_JS22-PH_36	PFR_JS22-PH_36	Gp8 domain protein	26635:28089 Reverse
MVPSPQTKHGDRKLSEVAKHLILPEGIVSTGWPAVRDRCGEWGVVFDRWQDGMGRVILSK
RGSGLFAAGVGGVGMSIPRQTGKTFTVGMIILGLCSLSEELTVLWTSHHSKTTTKTFESL
RGMAQRKKVAPLIRQVRTGNGDQQIIFSNGSRIYFGAREQGFGRGFDDVDIEIFDEAQIL
SEQALSDMVPAANVSTNPLIIFMGTPPRPSDPSEAFANRRAEALAGDAPDAAWIEFGADE
HADPTSRAQWRKANPSFPHRTSETSILRMKKMLGPESFKREGLGIWDETASVRAIPAEGW
RVLTVKEPPADAIQSFGIKFAIDGSAVALAAALKPKDGPIYVEGIEQRSASDGIEWLADY
LTPLWRNTAQIVIDGKSGAGALVDALRRGGVAAKVILTPSVADVITAHSLTLEAIKTGGL
SHLADPELDRQVRIATKRKIGAAGGFGWQAPEGDTVALLDAITLAHWAALTTKRHPGRKA
VALA
>PFR_JS22-PH_37	PFR_JS22-PH_37	Hypothetical protein	28043:28339 Reverse
MAAQVRAVDPDERPPARKRAKTITQAAKSGTEVELLEALQARVARAVQDRDTPPRDLAAL
TKRLMDITRELEAARVKDQEAGSDGAVTADETWRPQAL
>PFR_JS22-PH_38	PFR_JS22-PH_38	Hypothetical protein	28355:28729 Reverse
MRSRTAWVRCDGKRPITLAGAPASSTDPGTWSGWSQVRRATAGDGFGTMLGDGLGCWDLD
HFDDQGARAFIDRIDKPIIFAERSVSGHGFHIFVRTDEAPGRRTGNIEFYSRHRFIRVTG
DQFV
>PFR_JS22-PH_39	PFR_JS22-PH_39	Hypothetical protein	28859:29107 Reverse
MISTAWGGIPPTPGFLAPTSHSDISPGFSTGCPPRASLSSSQRTLNARQHSRRSEQPRSE
CVGPVWIAHEFRNKPLATARFR
>PFR_JS22-PH_40	PFR_JS22-PH_40	HNH endonuclease domain protein	29104:29442 Reverse
MSTSRTGTATWLRHAAQAKREAQARGLARCPLCGVWMDYEVGKRPNSAEADHIRPHSLGG
SDDIDNIRVICRRCNQSRGNGLKRPGRQRQRPIKRIELAQPARSGAFPAPPA
>PFR_JS22-PH_41	PFR_JS22-PH_41	Hypothetical protein	29439:29732 Reverse
MKQPGPHQRMRATFKADRGWRVACPRCAWHATSTHLAWLMDQASTHTCAPLLLSPTPPDV
ELAPAGDGLSVLWPEVDGDVQFTCIHTSTATCRQDAP
>PFR_JS22-PH_42	PFR_JS22-PH_42	Hypothetical protein	29875:30090 Reverse
MALALRLPKRVELTSDRQLLIDGELFKWPIEEDGTTISPGKLKDVSRLTLTVLLHPSCAI
IVDPQDCPDGG
>PFR_JS22-PH_43	PFR_JS22-PH_43	Hypothetical protein	30195:30911 Reverse
MEPSDTLDRLRQIPDMAAELWASGRATGDTGDPKPGQVRPHRAKPSTPIDLGRHDILRTD
EHGLLSEMSQAVRAVWEDNPGVALSNPPTWAGECGWLLANVELWDLDPFLSAFVSDAAWL
VWRTLDRALHHPAPARLTCPVCGGRLAESAGGWITCRDCASQFPGRERIATQMIHKRDMT
TDEIAAEFQIDPARIYKWRERGLIKPTNPGCKPATWRPWDVLAVLHPDIVEAIDEKAC
>PFR_JS22-PH_44	PFR_JS22-PH_44	Hypothetical protein	30945:31175 Reverse
MSNPEYLDPQATQGPQNRAQRSVQWIAIDPKAGMTLDEMAGLVQDAMRADIDGSTPIRVT
VGFRSQIRVATIGGVR
>PFR_JS22-PH_45	PFR_JS22-PH_45	Hypothetical protein	31237:31704 Reverse
MTTPITVVGNLTDDPTLRFTPSGKAVASFQVAVNRRRKDQSGNWVDDGADWHSVQAWGTL
AENVAESLTKGTRVVVTGRLESREWQDREGNRRTSWEITAQGVGVDLSFATATVTRSGPK
RPPQQAQGSQFAATPPQGEPPADPWAAAKTDEPPF
>PFR_JS22-PH_46	PFR_JS22-PH_46	Hypothetical protein	31701:32048 Reverse
MIQTEIERVALAVHGLRPDWPATSLRTFIENNLAGKAYQDVAVAFAWIACDPTTNTPKRI
LGAGPWWNATRAGVQHITDLPPRFTPEPTPKRDPAFRRELIDQFKQDLHQTKETK
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>PFR_JS22-PH_47	PFR_JS22-PH_47	Hypothetical protein	32045:32257 Reverse
MSKQTGKQTGKQVLTELGKQNDQKRQALSKQTGKPIVTPYPYPYPYICSYVSTKSKFSTV
RAILDLEVER
>PFR_JS22-PH_48	PFR_JS22-PH_48	Hypothetical protein	32238:32603 Reverse
MAWFKVDDQFWSHPKVIRCSDKAIALWVRAGSWSSQQLTNGEVPVEALAMFKANRQTAEE
LVGTGLWKRNGTGFQFHDWSTYQPAGSEVEELRVKRAEAGRRGGKKSAQTRWGDRREQAN
G
>PFR_JS22-PH_49	PFR_JS22-PH_49	Hypothetical protein	32603:32983 Reverse
MSRSRRSARTAGTRFETSVADYLARHVDDGIERRARNGSKDRGDISGLRHMAGRVVVECK
DYGGQFKAAQWVGEADVERGNDDALAGVVVAKRRGTQAPQDQWVLMTLGELVALINGNRD
HYEKGE
>PFR_JS22-PH_50	PFR_JS22-PH_50	Hypothetical protein	33225:35324 Reverse
MSTPTIGSLFSGYGGLDMGVQSVTGGRVSWVSDVEPGPCTILDTHHPDIPNLGDVTAIDW
KAVEPVDVICGGSPCFVAGTSVLTHDGLRPIEDVQVGDLVWTHAARWQRVTHTMRRTSET
VQFRSGSYCTPEHRLWLRAPQRRWNNTIHHYRRHLDAPEWVEAKDAHNLFAASPVSVTHE
GVSKPDTLTWWQIGRFVADGYVNKQVNVYIRKGKESDADNFPGWTHHQQKTALCLTMPKS
AAERDWLTEHFGKLAHGKTIPAFLLAETEENRRAFLDGYWSGDGWKPEGRKFTESTSVSA
CLTTGIELLAKSLGYTCTVSQYQVAPTTVIEGRTVNQRQWWMVRATPDDGRFTETDADWH
WFKLRRAPKAGEVTTVYDLTVERDHSFIAAGIVVHNCQDLSMAGRRAGMRPGTRSGLWES
MMTAITTIRPRLVVWENVRGALSADAFTLCDLESESRHLGDRPAGPSLRALGRVLGDLAN
IGYDAGWCCLRASDVGAPHRRERVFVVAHPQGQPWGSGDGEYGVAANADGATIGQQSPES
PREETGPYPGDRPGHHGRERPAEEWRETSNPEASLTLLPTPIAERPDGHKSAAFTAGHTT
FRDVIDRNRWGEFAPAIARWESTLGRPAPEPSEPGREGRRLSARFVEWMMGLPDGWVTDV
DISRTAQLRALGNGVVPQQAAAALKTLLMEADTSQVMVA
>PFR_JS22-PH_51	PFR_JS22-PH_51	Hypothetical protein	35321:35572 Reverse
MNTLRDDSIVWDAKDIRSACHALWQTAYIYRRVKVPDPTTADAVRLLRRWEANADHLDKL
IHGLEGLQRQQVQPRIKLTTEDA
>PFR_JS22-PH_52	PFR_JS22-PH_52	Hypothetical protein	35617:35910 Reverse
MSTPGSLRAALDQLDEIGIADHVQSLEWDRAGARTTAWLETCGDFAAACQWGDAAGEWVT
WDITDVAEADVSPRLRVKHMHLRARPCADAPAKAVAA
>PFR_JS22-PH_53	PFR_JS22-PH_53	Hypothetical protein	35907:36437 Reverse
MKATQYAKSTDPEVIATIEENELSRRAWIDDTKAWFGKTIRTGIPGAKLFLFSTRTAIRL
LGIVTSDEKKPAGWKFCWRSRSRFEPRKNNPLRATWDARRWQAASIPGLPVVLTSSVSGE
LQSWLRMYPCPFISSGAAWLDLEHMPDPDSPHFGPQWTEVRASQAMAAKEALKDAS
>PFR_JS22-PH_54	PFR_JS22-PH_54	Hypothetical protein	36440:36679 Reverse
MITTTQLGEADRWGRGLQVRSILCNGCGIALATDIGLRGDATALQVQSDLHARARTAGWT
HPAWRVDLCPQCTTTTKGA
>PFR_JS22-PH_55	PFR_JS22-PH_55	Hypothetical protein	36676:36909 Reverse
MIFKDTTIGPLETRFTWSMRCDRCGTPLDWLVAASCKTERSEVIAVKFLRERARDGGGLR
EWGELDLCPSCFSVMDA
>PFR_JS22-PH_56	PFR_JS22-PH_56	Hypothetical protein	36906:37130 Reverse
MSANRSRRATYNHTGIFVHLREAAEPSEQPPSDQTCPALHVIAGLTPWADHQPRHALGVD
GRCRHCHTTIKGNP
>PFR_JS22-PH_57	PFR_JS22-PH_57	Hypothetical protein	37127:37687 Reverse
MSAPLTKAQKVAAVVEQLLRGGADTSTLLEATGADRPGRLRDTLRRAGRDDLAARIITTD
RAAQRRREVIEAVEKLVWVDRADEIAAELGYSSRYGLQQSLRGWGRRDLADQIVLTRETH
RDRVIADVEWIAGTRGPEDVARATGYRNAAALQAALTGWGRKDLADRIVGASRNDTGRFR
FTWRAA
>PFR_JS22-PH_58	PFR_JS22-PH_58	Hypothetical protein	37684:38016 Reverse
MSWPEEHHDVWAGVEDAIPEWVSDKVACSVRSDADWNADEDSRKAVAAVRICERCALTEQ
CLDWALAHHEAGIWGGLTASDRERIERGAPVRRVREIRRRRTAVRQVQES
>PFR_JS22-PH_59	PFR_JS22-PH_59	Hypothetical protein	38013:38177 Reverse
MSTLPADAAERWQQWDGLARTILALHLGLTDLEMVELVGGLIGAGWHQDGPVES
>PFR_JS22-PH_60	PFR_JS22-PH_60	Enterohemolysin 1	38174:39013 Reverse
MTETTPSTDIETTAPTPSGSIAAVGSETAGLTLQQKLDYASALADSELLPAAYKGKPANV
LVAMEYGGELGIGTLVAVNQITVINGGVSMEAKLMMTLARRAGHIVRLSGDDKQATCIII
RADDPGHESVVTWDEAKAKTAGLWGKGHWQKNPGLMLKYRAASENIRLTCPEVLAGIVYT
PEELDERTERAGRSTMRVHQVVAEPEKTAAYFMKALHLNGGQFKEFAQRVLGHPLKSWES
LAKADKQRVLGALASWENSGADPTTGEVLDAEPVEGGAA
>PFR_JS22-PH_61	PFR_JS22-PH_61	Hypothetical protein	39015:39308 Reverse
FGYHIQAAAYMDQAISLDLVDEDAIFLHVVQETKPPFLLAIYQVSADQLAEGRRQMRRAL
DLWDRCLTLDEWPAIPAVIQLSKLPDWVHTTDDEKDS
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