

Supplementary Information

BacEffluxPred: A two-tier system to predict and categorize bacterial efflux mediated antibiotic resistance proteins

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Tier-I dataset

The complete dataset which is used in building of model for Tier-I which can discriminate bacterial antibiotic resistance efflux (ARE) from non-ARE proteins. Dataset is attached below in the form of protein sequences.

1. Bacterial antibiotic resistance efflux (ARE) : 210 protein sequences

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TLIPTLAVPVSLIGTFAVLLVLGFSANTISLFAMILAIGIVVDDAIVVVENVERVMAETGLPP
KEAAKQAMQEITAPIIAITLVLLSVFVPVAFIPGITGALYAQFALTVSVAMLISAINALTLSP
ALCGVFLKPHQGRKKSLYGRTMDKLSSGIEKISDGYAHIVRRLVRMAFLSIVLVAGLGAG
AYFLNTIVPTGFLPEEDQGLFFVQVNLPPAASQSRTAAVSEIEADITKMAGVADVTSVTG
FSFIDGLAVSNAGLMIVTLKPLEERLKDNTVFDVIAEVNRRRTAAIPSAVAITMNLPPILGLG
SSGGFQYQLEDQEGQSPQQLASVAQGLVMAANQNPKLSRVFTTFATDTPQLNLNIDRQK
ALSLGVSPNNIIQALQSTLGGYFVNNFNTLGRTWQVIIQGEQQDRKTVEDIYRINVRSSHG
DMVPLRSLVSVEERLGPLYITRYNNYRSASIQGNAAPGVSSGEALAAMAQVSKTTLPSGY
GYEWTGTALQELQAAGQTSMLALAVLFAYLFLVALYESWTIPVGVLLSVTAGLAGAML
ALWITGLSNDIYAQIGIVVLIALASKNGILIVEFAKERREEGVPLEQAAIIGARQRFPRVMM
TSFAFILGLVPLVIAVGAAAASRRVGTSVFGGMIAASAVGIFLIPMLYVVLERVREWGHA
RILRKPLYEEEEKQEKADGDASGPTVPPTQPEDRGLS

>Q8G2M7_RND

MTLNRTIRCFAAGAAFIIVFAAQPALAAQAPGGATPPPPQVFVVDIKPHDVPVITYEYAARINA
YRNVQVRARVGGILLHRNFVEGTQVKAGEVLFEIDPAPYQAELEKAQAQVAQAEQYQQ
SIRDAERAELVQQKVQSAAVRDSAFATRDLNKAAVAATAKAQLRTAELNLSYTKVTAPI
SGITSQEQVNEGSLIGTDASSSLTSTVQLDPVYVNFSTDTAAEIAKLRAERGATGEDAD
RLKIKILFGDGKAYDHEGTIDFTSSSLDTETGTLGVRAVVENPNHRLIPGQFVRAEILDIQV

KDAITVPKAALMQSAQQGFVYVVKNDNVVEVRPVTGARELKNDWLISQGLNSGDRVITE
GVIAVPGRPVPVVGVDKAAEAGKEQAADKK

>A0A0P7CXJ9_RND

MGFNLSAWALNRQIVLFLMILLAIGAMSYTKLGQSEDPPFTFKAMVIRTLWPGATAEE
VSRQVTERIEKKLMETGEYERIVSFSRPGESQVTFMARDSLHSDIPELWYQIRKKVADIR
HTLPPEIQGPFFNDEFGTTFGNIYALTGEGFDYAVLKDYADRIQIQLQRVKDVGKVELIGL
QDEKIWIELSNVKLATLGVPLEAVQQALQEQNAVSTAGFFETPSERLQLRVSGRFDSEVI
RQFPPIAERTFRIGDVAEVHRGFNDPPAPRMRFMGEDAIGLAVSMKDGGDILVLGKALES
EFERLARSPLAGMELRKVSDQPAAVKAGVGEFVQVLVEALVIVLLVSFFSLGLRTGLVVA
LAIPVLAMTFAAMHYFGIGLHKISLGALVLAIGLLVDDAIIAVEMMAIKMEQGYDRLKA
ASYAWSSTAFFPMLTGTTLTAAGFLPIATAASSTGEYTRSIFQVVTIALLTSWVAAVVFPYL
GERLLPDLAKLHASRHGKDGHAPDPYATPFYQVRVRVVEWCVRRRKTVILLTIAAFVGS
LLFRFVPQQFFPASGRPELMVDLKLAEGLASLANTAERVVKQLEALLKQQEGIDNYVAVVGT
GSPRFYPLDQQLPAASFAQFVVLAKSMEDRERLSWLSTMDQQFPDLRARVTRLNGP
PVGYPVQFRVTGEHIEKARALAREVADKVRQNPVNVHLDWEEPSKAVFLEIDQDRAR
ALGVSTAHLSSFLQSSLTGTTVSQQYREDNELIEILLRGRTRQERSELGNLGSALPTDNGQSV
ALSQVATLEYGFEEGIIWHRNRLPTVTVRADIYDKEQPATLVKQIEPTLRDIRAKLPDGYL
LEVGGTVEDSERGQKSVNAGMPLFVVVLSLLMIQLRSFSRTVMVFLTAPLGLIGVTLFLL
VFRQPFQFVAMLTIALAGMIMRNSVILVDQIEQDIAAGLDRWQAIIEATVRRFRPIVLTAL
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>W0HU59_RND

MNISRLFIFRPVATLLLTLAILLLGLLGYRLLPVAPLPQVDFPTIMVSASLSGASPETMAATV
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PTYRKANPSDAPIVMLALTSNTRASGELYDLASSTIQKIAQVQGVGQVSLLSALPAVRI
DLQPQMLNHLGISLDTVRSANSTTNLPKGMQLQGATTSFVVDGNGQLDKARDYRSLIIT
YINGTAIRLSDVATVTDSDVEDKYNIGFYNQTPSVMIGVTRQAGANMLETIDAINAALPALQ
AELPGDVELHKVVDSPITRASLYDTEETLLIAIFLVIAVVFIFLRNLQAVIIPALALPVSIG
TCAVMYLLDYSLDNLSLMALICTGFVVDDAIVVLENITRYIEEGLGPVRASIKGAQEVGF
TVLAMTSLVAVFIPILLMGSIVGRLREFAVTLTVSLLISMVVSLSLTPMLCSRLLRRKPPV
SKRPNRLYLLIESGLARLLAGYALALGWVMRHQRLTLFSLVLTIMLNFLYGVVQKGFFP
NQDTGLLMGMVRADQNISFQAMKPKVEAIAKLIQQDSAVDGVMSSIGGGAFGSRNSGTF
FVRLKDYDKRSDSATVVANRLTNKFRNEAGMQLFLMAAQDLHIGGRSANASYQYSLQA
DDLNLRLRVWTPKVKAALPELTSVDADSENGGQEIMLNIDRDKATRLGVNADMLDA
MLNNSFSQRQVATIKTLNQYHVIMGLNEAYTGDAEVLKCLFVVDNNGESIPLSAFITFSS
ANAALSVAHQGSATSTVAFNLADGVSLEQAQAAIKDAMVKIALPSTIQAGFQGTAKAF
AALAASMPWLILAALAAYIVLGVLYESYIHPLTILSTLPSAGLGALLMLVTGTQTLTVIA
LIGILLIGIVKKNAIMMIDFALAAERNQGLTPQQAITQACLMRFRPIMMTTLAAFFGALPL
ALSGGDADLRSPGLMAIAGGLALSQLLTLFTTPVVLYLDRLSRNSQRAWHRLRKTGT
A

>sp|Q65JB2|EBRB_BACLD Multidrug resistance protein EbrB OS=Bacillus licheniformis (strain
ATCC 14580 / DSM 13 / JCM 2505 / NBRC 12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson
46) OX=279010 GN=ebrB PE=3 SV=1

MKGMIFLAAAILSEVFGSTMLKLSEGFSAPLPAAGVIIGFAASFTFLSFLKTLPLSAAY
ATWAGTGALTAAIGHFIFQEPFNLKTLIGLTLIIGGVFLLNSKRTEAADQKAQLTIEI

>502347.3.peg.3992_SMR

MPFVFSIVTKVIVEIPLPPGKISVQLPALRDDLQTRLFIGDGPNSSEPDMSWIILVIAGLLEV
VWAVGVMTPTY

>56780.15.peg.233_SMR

MLSPFRALAAVACPPAISEQKTGASRIFPEIGLASSSSSSSRSLVFTISFRTQIGRYIMKGWFL
VIAIVGEVIATSALKSSEGFTKLAPSAVVIIGYGIAFYFLSLVLKSIPVGVAYAVWSGLGVVI

ITAIWLLHGQKLDWGFVGMGLIIAFLARSPSWKSLRRPTPW

>214092.21.peg.591_SMR

MAVFCYLGLAILPLIIEHDNVSRLSLCWLGRPSYASVFRGRPRLSEVVTMAWIILVIAGLLE
VIWAIGLKYSHGFSRLTPSIITLVAMAASVFLAYAMKSLPAGTAYAVWTGIGAVGTAILG
IVLLGESASLARILSLGLILAGIIGLKLAS

2. Non-antibiotic resistance efflux (Non-ARE) : 389 protein sequences

>tr|A0A1E7GHI5|A0A1E7GHI5_9DELTA Nickel/cobalt efflux system OS=Desulfobacterales
bacterium S3730MH5 OX=1869298 GN=BA861_05440 PE=3 SV=1
MQVNLIYYLTATLLGGLHALEPGHGKTVVAAYLIGSKGRKMDAVVLGLVVTLTHTLSVI
LLAIAAKVASTRITLTEEALHGYLEGIVAGLMILAVGIWMLVQRIRGREPFHFHSHDHGHGH
SHSHDPLQSHSHPHDHHHEEDHDHHHYHEGHHLEIHGDLHSHSHDHGDHSHGHSHDHD
HTYNHAHGHDLHRHSHDDSRGSPGVDVHHHDHYHEGHEVETDDSVHSHDHSHGSHD
HDHTHNDESSEGHSHPHDHSHEHDGEHNHREGHDLATHSSSTHVVHPHNHDHGNNPHSV
DMREGKRVSWQLFLLGVSGGLVPCPAIAILLAAVAGAGRLGEGTLTYILLFSLGLAAVLIA
IGIAVVSAGSFASRFLDAKRFARKVAIGGAALVTFIGCLTLVSSVRHLI

>tr|A0A1Q8SUR7|A0A1Q8SUR7_9GAMM Nickel/cobalt efflux system OS=Salinicola socius
OX=404433 GN=BTW07_05975 PE=3 SV=1
MPGLNATLRLFIPLALLGAIAAAGYSLGWVQHVAVQIVYWQGFYHALIEAVTALNRAP
SATTWSVLLGVSGYGVFHAAGPGHGKVVLTSTYLASQGGAWRRALGLSVLAALLQGVM
AIAIIGVLVFGGLWLRQAMGSIDQELASFVIVALVGLWLCVRSRLRLWRARHAVAHAH
APTATEPRVTPNFSSVSAWSAAPTSPQGALDGASPAQRHSPGASPGAHCPCGHDHHDPR
EVGDWRVALLTVLSIGIRPCSGAVLLLGAALLDQFGKGVAVLAMSGLTALTVSSLALL
SVLARDWVQRHLKPATGGGQWQAWVGLAGGALILMLGLSLTLAQWQRGPAAAPPMLG
APAAQQAQSPRGPFSGVPIQSATSKPTRGREIP

>tr|A0A1R3TVP2|A0A1R3TVP2_9RHIZ Nickel/cobalt efflux system OS=Agrobacterium sp.
DSM 25559 OX=1907666 GN=DSM25559_2797 PE=3 SV=1
MLRVVSAFCAQVSGSANGRPPLPCRASPPQVGRSARSAPLASSSTFETGKRVAAMKSPHL
WGRCPAGQRGVSPAHHQGLIGSSPTDMKQFTSARFLLILCAVFLATLSTAHAAQSPLGIGSAE
PSISIGGPLAPLFQWINVHQQSFYRALTGALKAMREDPWALTSLIGLSFAYGVFHAAGPGH
GKA VISSYMIANETQLRRGIVISFISAILQGAVALVGAAYLVLRGTSITMTKATQAMEIA
SFAMVALFGAWLLFRKLRLSLMVKVEPAPALELASPSPTVGPQRTGMGSGLRFGQKPVF
ADHAQSGTGDLCCTTCGNAHAPDPSMLRAKDFSLHEAWSAIIAVGLRPCSGAIIIVMSFSVL
NGLLMGGILSVLAMSIGTAITVSLLACLAVKAKDIAVRFAGTGSTKASRITHGIEIAGAVFV
LLMGLGLLGASLQV

>tr|A0A1V4MH18|A0A1V4MH18_9FIRM Nickel/cobalt efflux system OS=Firmicutes bacterium
ML8_F2 OX=1775675 GN=AVO34_06030 PE=3 SV=1
MMRLLLLHVLTALILVYPVMPSCPQSVAYAAATEMRSSQPPEWRRMYHKTQLQRLVHWQK
VLRAKLTRLTRDMRDDPWGASFWTFLAIAFLYGIVHAVGPGHGKAMVGSYFLNRSGLK
QGVLLGFLFAFTHVFSVAVLLLAGRAWLQTSARSLLASADHWLQKISAILLLVIGLLLTGR
TLWTCLPHRKKHLPNPKADLKSLCSIAAAAGLVPCPGAALILLFALSQQLLVPGLLAML
ALALGMALTVTLTSAVATIVTRGALLRVLPSTSRSMVVTGRILGVGGGLVITTLGALLLLSAT

>tr|A0A2E4Q009|A0A2E4Q009_9GAMM Nickel/cobalt efflux system OS=Cobetia sp.
OX=1873876 GN=CL809_07080 PE=3 SV=1
MSSEPKDTSGLGDIKSLKGMRDGLLKPASSRGRRLAGWLAVGCGLLVLMALWPGLVQ
GWGEALGWVFAEQSRFQSLGRSMSELAHPGTPWALIGLSFAYGVLHAAGPGHGKVV
STLLVSQPIVRRRALWLSLLAALLQGVSAVLVGLGAGLLDWAGRDVLGQVEKVTLTSH
LGVLVLGLLLLWRAARTLWRVARAQPVSSVGAPQAPAMQGLAFKPSPGHDHSHSHSHSH
SHGHDSHGHDCGCGHAHGVTAEQASGDWRTMGMAVLAIGLRPCSGAILVLLAALAN
MVGSGVLAVLAMSGLTALTVGSVAMATLIMKASGRLAAAGTRLGGPHSNGRRARRQWP
WAALVGLLGGGIITVFGALLVASSLKALDSPTGRGASPFDRSAPGTSLSQSPGPRSSGQSSG
DK

>tr|A0A2K1QDK0|A0A2K1QDK0_9GAMM Nickel/cobalt efflux system OS=Mixta theicola
OX=1458355 GN=COO59_04115 PE=3 SV=1
MLRRTLCLPGRQSLGVIATLLALLALFCWWNWNDFLAWSLATQITLHRYLVLHLLQINN
GQYSSGGLWLLFFTFLYGVLHAVGPGHGKFFVTTWLSTQQHSSPALRAVPLIGSLVQGLSA
ILFVFILAVGFNLMAGDLSLSRWVMEKISALLIAAFGGWMLLRGLRSFPHTEFAKRKAVTS
QHTSADAVHYAPLMAHTPVDAVSPHSTSHHDTHQPCGCGHHIPLVQPASRKELLGVIIAI
GLRPCSGAITVLLFSNAIGIVKWGMLAVMTMALGTGLSLLLLAIASRLRDTVAIIWLRES
PAATTTIIALVRIAGGVLLFFALILFLTVPVSPNGDFIAAGC

>tr|A0A351RRR3|A0A351RRR3_9BACT Nickel/cobalt efflux system OS=Nitrospinae bacterium
OX=2026769 GN=DCQ99_07715 PE=3 SV=1
MDSLFYISSAFLLGAFHALEPGHGMILMTYLISSKGRIIDAILLGIISTFTHTFSILILGIIATL
SSVLIIPETIERLTEIIGGILVLIVGVWMLISGFKNNHTHIEGHAHKKREGLIGLITIGISGGIVP
CPAALAVLSATIAGGRTADGFFLVLFSLGLGAVLISMGVLFVKASNFFEKYIGGIFGKKVR
MASAVLIIMLGLFLLLKNILPHLFLAP

>tr|C5B6Q0|C5B6Q0_METEA Nickel/cobalt efflux system OS=Methylobacterium extorquens
(strain ATCC 14718 / DSM 1338 / JCM 2805 / NCIMB 9133 / AM1) OX=272630
GN=MexAM1_p1METAp0026 PE=3 SV=1
MLLPMAMPSSTRTIPTFATAGPTTPIPTSSTPFTSAGQPCGRAERLPCLPGTSDRGKPTML
DLLTAVQRGLHTLLTDRIGGFAQTRNLAVLVSMPLPFGIAFGTVHALTPGHGKTVLSGYLV
GSRLTPLRSLAVSGALTVTHIGSAVLLAVAGAPILSRTEFGMFGRAPTLERASHLLIGLGL
WILVRAMRGRSHAHDQRDGVLVGVSAVLVPCPLTLFAMLMAIAKGVPEAGLIFALAMTG
GIGLTLGVVALAALAAGRWLQERLKENQTRLRSIGRALDIGSGAALVGLALYGMVQA

>tr|T0PGS6|T0PGS6_PHOTE Glutathione-regulated potassium-efflux system protein KefB
OS=Photobacterium temperata subsp. temperata M1021 OX=1221520 GN=kefB PE=3 SV=1
MEHSAQLNAGVLFLFAAVVAVPIAQKFRIGAVLGYLFAFIVLGPWGLSFIRDVDDILHFSE
LGIVFLMFIIGLELNPSKLWQLRRSIFGVGAAQVIFTAGVLAGLLYLTDFSWQAAVIGGIG
MAMSSTAMALQLMKEKGMNRNEGGQLGFSVLLFQDMAVIPALALIPLLAGETASSDWY
RIALKIAAFVAMLLGGRYLLRPLFRLVVRAGVREVFTAAALLVVLSSALFMEALGFMSAL
GTFIAGVLLADSEYRHELEISIEPFKGLLLGLFFYFGRYVPESGRATDTFVRCVTWRIGFGH
CERRCSLSYRMDCGLTGFIILAIFFRRSQGGGEFAFVLFSALGQNVLNQSGQMAALLLVVVTI
SMMTTPLVMQLIDAILARRYNAPDETEEQPFVEDNDPQVILVGFGRFGQVIGRLLMVNKI
HITVLERDVSVMSTMRRYGYKVYYGDAVELELLRAAGANKAKAIVITCNEPEDTMMIVH
LCQKHFPNLHIMARARGRLEAHELLQNGVENFTRETFSALGLGRKTLVGLGMHPHKAY
RAKHHFQRLDMRMLRELMPQIQGDVAQISRIKEARRELEELFEREMLNRLQPDGWNEH
QHMTSSGANNDSP

>tr|A0A1X7APD7|A0A1X7APD7_9GAMM Glutathione-regulated potassium-efflux system
protein KefC OS=Parencoccoccus haliclonae OX=1960125 GN=kefC_2 PE=3 SV=1
MDFGFFNQLLIIFSVSVFAIALFHRLRIPDTLAYLMVGIALGPTATGIIDTSFDITLLAEIGVV
FLLFSLGLEFSLANVLAMRRIVFGLGGLQVMICTLLIGFCGLMLGFSPVGTLMVMAAGLSLS
STAIVSKELTRRNELRSNHGQLAIGTLIFQDIAAVFFLILIPAMAGIGENSLAVSLLLSLGGK
LGFAVAFMVLFGRWVLPFHEIASTKSEELFVLSAIVVCLVAAWLTHLLDLSMALGGFVA
GMMLGESHYRHQIETDIRPFRDILLGLFFVSVGLMLNLDLFLENWSMILLASLGLILFKAT
MIAMLAWFIQNNKKHAIRTGICLAQSGEFCFALVALAGQYGLLEMSTSSMILSITIVSMAA
TPLLIRYSGPLASRITQQKQSKEPKKAVDVISEQTCVDRHILILGYGRVGVQVISRFLREDN
LPYVAIDDDPIHVREASRAGEPVFFGDCRRTTELLQAAGLERARMVVICIDSSRAAQAALLEG
IRSINKTIPILVRTRDDNKMELLKQGGATEVVPEVLESSLVIVSHVLTMLGQPEFSIRQRIQS
VRRERYDILHGGFFGQSETLRTQEGEDCELLQGITLADKAWAVGKTVAELPLDEAGIHLK
RITRDGEELDIDEQLRLTVGDALLIKGTQKQIEQGEILLRG

>tr|A3YEU4|A3YEU4_9GAMM Putative glutathione-regulated potassium-efflux system protein
OS=Marinomonas sp. MED121 OX=314277 GN=MED121_19614 PE=3 SV=1

MEFIWILFAFVCGLLVKLINLPPLIGFLIAGFALNAYGIQPSDSLNTIADLGITLMLFTIGLKL
HVKDLLKREIWAGTSLNMLLWSVLFIAMCLFGFALSPLYFTSLDWQTSALVGFALSFSST
VCIKLEESGELKTRHGQISLAILVMQDIVAVIFLVVATGTIPSIGALALFGLIFARPLFGIVL
NKAGHGEMLPLAGIFLALAGYELFYLFNVKGDGALIFGILLSSHPKASELTKSLMGFKDL
FLIAFFLSIGFTALPTLDMLVSAFLVSFALILKFALFFGLFILLRLRGRTAFLTALALSNYSEF
GLIVAQLSVDSGWLDKEFLVILALAVSISFVVTSLLYRRRAHDIYHTYQRIIRSFEKAEP
LAVDTFIQPAQADVLLVGLGRVGCFSFHSNLRIMPNSAVGMDADRLRIDRLKAEGHNVFFGD
GEDADLWEKFDVSHYKLVLLALPSIEDCSNITIQLRKAGFKGKVAIARYQDEREPLMAS
GIDNVNFYTEAGNGFAEESMQLLAKNNPSLDASPO

>tr|I0WDT1|I0WDT1_9FLAO KefB-and KefC-like glutathione-regulated potassium-efflux system protein OS=Imtechella halotolerans K1 OX=946077 GN=W5A_08452 PE=3 SV=1

MHFPLLQDIVVILGLSILIIIVAFQKLKLP SILGFLLAGIIAGPYAFNLISSSHEVELLSEIGIIFLL
FVIGIEFSLKELAAIKNKVFIGGGIQVFGTIGFTTALALLMDIPWNTAVFLGFLFSLSSSTAIVL
KLMQEKGEVKSHPGKLA VGILIFQDIIIVPMMMLFTPLLTGEADNILTITIGILT KVLVLFVI
YILAKYIAPIIFKL VVKTRNKELFLLTVTVFCFAVAWLTASVGLSLALGAFFAGLIISESEYS
HQATANVLPFREIFVSFFFVSVGTLLNLNFFFSHIGTIVLITLG VIVLKITVIALTAMFMHYPP
RTIFLTAFTLFQIGEFSLLSSTGVQNGLLEDAYYQYFLAVSILTMAATPFLMAAAPKLTDY
IIQAPIPKAVRRRLKAYKARHVQDTLITEENLHDHLIIIGYGINGKNIKAARNAPKIPY AIAE
LSPDAFKEAKKNEPVLFGDAAEDVILQHLHVQEARVIVIAISDPSATKKIVTIIRDYTKTA
CIIVRTRYVKEIDENLKIGADEVIPEEFETSIQIFTRVLKKYMPNDDIQGFINQLRSSDYEM
LTTVEGINTSLPTRQIRIPDKEVTSLYVESNTNKIVGKTVELSGIRKKYGVITLAIQRDKKYI
TEIKPDTLIMQGDLLFLFGNPDAINKLNKLFSV

>tr|A0A0U5NV43|A0A0U5NV43_9CLOT Manganese efflux pump MntP OS=Clostridium sp. C105KSO13 OX=1776045 GN=mntP_1 PE=3 SV=1

MHLISSLLFAISANIDSFIVGLSYGIKKANISLLKSTIISLVTLVGTVTAILLGAEISQFLPSSSS
QAIGCALLIGLGMYYIISLYTYLCIQIKKAEVKASESSSEPKDSSQTEDSLLTIKEGLFLGL
TLSINNVMGIGASITGLKLLPTAILSLIVSVTFLYAGNVIGKSKVPHISDRAADVLSGLILV
GLGIYELF

>tr|A0A110A6P6|A0A110A6P6_CLOPR Manganese efflux pump MntP OS=Anaerotignum propionicum DSM 1682 OX=991789 GN=mntP_1 PE=3 SV=1

MFFSLLLAFLSIDALGIGISYGLRRITFPAASKFLLALETFLMMEVFIMAGRGLALLLPSAT
GETLAPCFLLLFGLWLCLQGFRKAKEPPSPLASVHQPSVCDKASQTLDPKETLLLGFILSL
DSLGVGISAAASGMEIGKLPVFAAIFQVVFLSLGAFCGKCLTNTKIRENLWTTISGGILIFI
AILRLI

>tr|A0A1F5KFN0|A0A1F5KFN0_9BACT Putative manganese efflux pump MntP OS=Candidatus Daviesbacteria bacterium RIFCSPHIGHO2_02_FULL_43_12 OX=1797776 GN=mntP PE=3 SV=1

MDIFSLFVLAISLSLDTLSVGTAQGLHFHQHRLRNGLKLAITFGLFHL SMPILGWVIGQSLR
IFVSQIDHWIAFGLLSFIGIKMVKEALSSKKQVHRKHQKQTLTLLGIATSVDTLAIGITLAF
VEISIFLAGVIMGSVAFCLTMIGFMTGNKIGKMFSEKAELVGGIILIGLGIKILIEHLNGG

>tr|A0A1G6GJW3|A0A1G6GJW3_9BACI Mn2+ efflux pump MntP OS=Pelagihabdus alkalitolerans OX=1612202 GN=SAMN05421734_10198 PE=3 SV=1

MFYQFLLAIVLGLDAFSVCLAVGLNGFKIKQMVLM SGLIGFWHGLFPFIVGFLCGQVIVYY
VDDLIDLITGSLLVSLGVYLCLNSFTESVSIKWNKTKLIMMSLTVSLDSIPIGLTLVREPTA
WIYSIGLFFTMTMMMSMLGLLLAKRLTVSLHRMSDRLGGVILIGLGLHILVTM

>tr|A0A1M4XWE4|A0A1M4XWE4_9BACT Putative Mn2+ efflux pump MntP OS=Mariniphaga anaerophila OX=1484053 GN=SAMN05444274_103147 PE=3 SV=1

MSILTLILIAIAISLGILEISMSAGKALSRI RFWQAVKIAFILVLLQTPVFLIGWVSGNKFEDLI
HSYDRWVPLALLSALGIKMIFESLRHFNNKGKIRSLSVTMLPGVFLAILIDALLVGISFAFFS
QKLLLTLLVVGLLTFLATIAGILWGKAPQSKLSFHTKILGGFLLIGICVNLLKLPPIN

>tr|A0A1S8TB62|A0A1S8TB62_9CLOT Manganese efflux pump MntP OS=Clostridium puniceum OX=29367 GN=mntP_2 PE=3 SV=1
MLESLLLVSSICIDSFVASIAYGTSKIRIPPLSTIINLICITITLACSLFMGSIFKSFLPGNLPILG
FLLMIIIGIYRLFYIFKSSISKCSKSDKPLTFKIFDFQFVLQVYANEIKADFDNSKCLNIKES
FYLAIALSLDSLAVGFGSSLCNINYLEVLILCFIIGILSVSIGVFVGRKFAQKLHLELSWLSGV
LLIILAILRILK

>tr|A0A2N2D8K7|A0A2N2D8K7_9FIRM Putative manganese efflux pump MntP OS=Firmicutes bacterium HGW-Firmicutes-15 OX=2013776 GN=mntP PE=3 SV=1
MTMIEQLVTIMLVAVILGADSFSLAMGMGLKGVTRSYELKFALMVGFHILMPLIGLNLGI
VTGNLLGVWAGRLGAVVLAYIGGDMLWKAYCETRPQVFRFNQGGKQQFTSQVKLAEGWI
NLTVLTTSVSIDALTVGFSLGTLIQTPVFYTVVTIGLVAGAMTLLGFGKGGKLF SRVVGSYA
QMLGGLVLLLLAAKMAFY PN

>tr|A0A2S5D4E1|A0A2S5D4E1_LYSSH Manganese efflux pump MntP OS=Lysinibacillus sphaericus OX=1421 GN=mntP_1 PE=3 SV=1
MHWITIIFIGIAANLDNLGIGLAYGVKRVKIPILSNAVIAVMSMIVTFVAVTAGSTVIEYISP
HTANLLGSLLLCIIGIFTLFSNRFSKHSIAKNPEVDFEDKNHIISMREAMTLGFVLSANCLAG
GIAIGANGISAIWTVISIGTFSFITVGIGSHFGVLLSKTFIGKYSTAISGWLLIIGVFEVFAK

>tr|A0A377Z8H6|A0A377Z8H6_KLEPO Transcription regulator protein of MDR efflux pump cluster OS=Klebsiella pneumoniae subsp. ozaenae OX=574 GN=yofA_1 PE=3 SV=1
MDRIQAMQMFM RVAEAGSFVRAAETLSLPASTVTSTIKNLEKYLVKVRLLNRTTRRVSLTP
EGMQYLAQCREILALIEHSESTLSESVAR PQGRLRVD MARGHRAFRHAASAGLLPALSR
YLPDDRRQRSPGRSHSGRRRLRDTNGRAEQLQPGGPPSGPLSLGHLRVTGLSSGIWCAAV
TGGALSAPGGALFLRSGEAGR

>tr|A0A3D1K6X7|A0A3D1K6X7_9BACT Putative fluoride ion transporter CrcB OS=Lentisphaeria bacterium OX=2053569 GN=crcB PE=3 SV=1
MKQVILFSLYVGAGGLIGAVTRYLCTFLFLKYSFSPAGTFLSNVIGCLIIGIIIQIATGTELLS
PEARLFLATGFCGGLTTMSSFVYETSQFINDGEYFHASSYFFLTLTLSFAAFVSGCIIVKLIM
RYGGQYGT

>tr|A0A1V5K2D0|A0A1V5K2D0_9BACT Ferrous-iron efflux pump FieF OS=Candidatus Aminicenantes bacterium ADurb.Bin508 OX=1852832 GN=fieF PE=3 SV=1
MERQNNGNVESENDRIKQGERAGTVGVGVNLVLGTVKLATGLVVNSLAVVADGVNNLS
DSFSSLVTLFSFRWAGKPADREHPFGHGRVEYIAALTLSFLVMAVGLQFVKSSAARILHPV
PLKFSPWAILLMLLSVFAKLLLVGFYKRVASKIRSGTLQAAIDSFSDMAITSCVALSLVVP
RFTTFPADGIIIGMVVALFILYSSFRMIRATLTPLLGTSPDPLAKDIRRTILEHEPIQGVHDLI
VHTYGPEKHFA SAHA EVPAGLSTTELHEVIDHVERELEETLRVSVVIHMDPVNPDSEELRV
VREEVDRILEHHPSVLSMHDLRIVGQGDQKKLLFDIVLSCSCSLNRAAQEKL TQDIDKELK
RTHPFYTTHITVDREMA

>tr|A0A1W9UVF4|A0A1W9UVF4_9DELT Cation-efflux pump OS=Desulfobacteraceae bacterium 4572_35.2 OX=1971628 GN=B6I37_01455 PE=3 SV=1
MDSRARVRAAKIAITTAISLAIKMITAFATGSMALLSSATDSLLDIMMSFGNLLALRQANK
PADDDHPYGHGKFETAATLLQSLLIAASGLFILNESIHRLQHSDNKL AHLNIGIAVLAFSSIV
SWFLSRYLKQVGIKTDSSALQADALHYATDVYSNAVLLIGLIGVRLLGWNWVDPVLSIGV
GCYILYAAFELLKGSMNDFLDAGLPEEQRKQIVTCITNNESEITGYHNIRTRRSKGKFKMVD
FNLTFCRFKTIEEAHDSADKIEKEIKQCIDNADITIHL EPTKCTECPKHGQCARSKNIAKTSQ
QALQDRTSP

>tr|A0A257B5V2|A0A257B5V2_9BACT Cation-efflux pump OS=Chloracidobacterium sp. CP2_5A OX=2012633 GN=CFK52_04760 PE=3 SV=1
MAAEDTQAALASVAVRRVLWTLLVANLLVVA AKALVGWQAGSLAILGDAAHSLTDAV
NNLVGVWLIRAAAKPPDREHPYGHAKLEPIGAFVVAALMGLLSYEIGREAAALRLWSGTV
APVAPTPLTFAVMVGALIVNLWV VWHERRAGRRLGSAFL LADAQHTLSDVYVTLGVLA

GLVGMRLGWAWLDPVIALVVVAAGVGWYHVLMTAIDDLMDAAAVDGNALIALARQ
DLDVVDVLRVRSRGRGAYGFAELTLVFRHNDLRRAHATSDLLEERIRRAYGIAHVTHLE
PAEPAANAPNAGEVSV
>tr|A0A345WS00|A0A345WS00_9SPHN Cation-efflux pump OS=Sphingomonas sp. FARSPH
OX=2219696 GN=DM480_14115 PE=3 SV=1
MPASLAGSFLLPSADRSCSSICPARREGGVERGRDANRKPHCQLRAGHQLRQPPVTGAAA
AKPTNILKLAAGSILVSLVVLGLKYLAYALTGSVALYSDAIESIINVVTAVAAFFAIRISLRP
ADADHPYGHSKAEYFSAVLEGVLILVASLAILREAYGAFRDPHPLQAPALGLAVSAGASA
LNGLWSWLLIRTGRQRRSPALVADGKHLIDVYTSGGVIVGVLLVAVTGWEILDPIAAL
VALNILWAGWHLITESVGGLMDTALPPEDLAAVEATINAHMAGALEAHDLSRHAGRM
TFIDFHLIVPGSMTVAASHAICDRIEAAALKVEHPDSIISIHVEPEAKRKHGAMTIGSTA
>tr|A0A380NGG7|A0A380NGG7_9FIRM Ferrous-iron efflux pump FieF OS=Veillonella criceti
OX=103891 GN=fieF PE=3 SV=1
MQEQLIRWFVKDYDCIKAPAVRTRYGNLTSIVGIVTNLIISLGELIVGFLIGSIAMISDAIHD
LADAGGSTISLVSRFSAKKADQEHYPYGHGRIEYLLSIGFSILLFVVAIQLLIESVGRILHPEI
VEFSIWALVVMLCAMGLKVWLYSFFKSIGERINSPILKANGLEYLSDVWATLGITLGLVV
GGLFQIPVDGYLGAIVSVMIGRAGYHVLADAISRLGNEPSPEMVKDIANFVKSYPGVLGI
HDLMIHDYGPGHVFASIHVEVDKEDVIKSHSLIDRIERDAQKELYIQLTIHMDPLLVTKE
MALYDKIHTVVKAYDEKLSLHDLRAVKSSDKIHVLFDLVVPYSDRQRMDDIAKAIKKILE
AMDPTFEITITAEHSYTGDENIHDYN
>tr|D7JCG8|D7JCG8_9BACT Cation efflux family protein OS=Bacteroidetes oral taxon 274 str.
F0058 OX=575590 GN=HMPREF0156_00171 PE=3 SV=1
MPNNPAKSYFKFKTQRVIAIASLLIFIGKITAYLITSSVGILTDALESTVNVATGFISLYAVYI
SLKPKDSNHPFGHGKAEFLSASIEGFLILAAGAVIMFEAVRRLFSPTVIKQLDVGIVIVAVA
GLINYIIGWYSKKIGRQHNSVALVSGGRHLQSDTYSSIGLVVGLILLYFTGWQWLDSLIAIV
FGLIILVTGFRILSETTSNLMMDKADMKLIERFGRNLINENKKPQWIDIHNFKLVKYGDVFHIN
CDLVLPFDTSALADAHREGEELKAVMTANFSEDIVCNLHIDEFCVSYCKHCRKADCRLRRE
PFVEQLDFDIDIFVREKAETPPNQTS
>tr|K6YP35|K6YP35_9ALTE Ferrous-iron efflux pump FieF OS=Paraglaciecola mesophila KMM
241 OX=1128912 GN=fieF PE=3 SV=1
MNVKRVLLIEGCVNLFICCVKLFVVGISANSAAVIADAVHSFTDVVNNIMAWMATNIANS
ADKDHQYGHQKFEQLAVFGLASLLSIVAFEMLINAYNRFQGAVEQNYLGLIVLTGTLVVN
ILLTIWQRYWAKKLASDLLEADASHTLSVLTTIVVIVGWQLAAHGYYWLDTVFAILVSL
LIFYLAFKLFQRAIPILVDYSDVDPSAVSAEINRLDSVDSVVRVRSRKVPNGRVADLIVTVD
PQLTTADSHLIADEIERVLAKKFNIQDVLVHIEPRHRITDHET
>tr|M7N453|M7N453_9BACT Ferrous-iron efflux pump FieF OS=Cesiribacter andamanensis
AMV16 OX=1279009 GN=fieF PE=3 SV=1
MYVLGCKSRHSGPLPAITLAPASCWQQAQFQQNKKQGQGRIFWAKNRQLFSSFHFTFKP
YTRRIQRLTSGSLLQDKKKYQGLALLIGALLMLVKFAGWWITGSNAILSDALESIVNVAAS
GFALYSIGYAARPDLDHPYGHGKIEFLSAGLEGALIAIAGLAAMGKGVYNLFHPQPVS
LGLGIGLTLFTGGVNWALAHMLLKKGRSLNSISMQADGRHLMTDVVTSGGLVLGLGLIY
LTGQVWIDNVVAIVFGGIIILSGYRLLRDFVGGILDEADLSLVERVIVLLNRHRSKNWMDV
HHLRIQRFAGAGIHLDFHFTMPYYFTLEEAREIDEVTRLVQQNLPHEAEFSIHGDPCLPPHS
CGICKDDCPVRRQPLQRRIEWTMSNAYQNEKHSLOTPD
>tr|Q67QQ7|Q67QQ7_SYMTH Cation efflux system protein OS=Symbiobacterium thermophilum
(strain T / IAM 14863) OX=292459 GN=STH1001 PE=3 SV=1
MLSSASGDRRQRLIHRAGLLTIAVNCLCTVARAAAGFLAGSTAVLADAANSMTDILATLV
VMGGSRIAARPPDWNHPYGHDKAEPVAAKLVGILVTFAGLATAAGAVQALRAGGEPVG
LAAAVVTAVSIAAKEALARYLARLRRLRSQAVLADAANQRTDVLASATALAGALGGRF
GLPILDPLMGLLVSAIILRMGLGLYWQAVRDLMDRAPEPETVDAMRRAALSVPGVREVG

DLRARVFGPGIYAECKVSVDAGLTVAEGHRIGKRVKEAVMRAVPGCRDVLVHVNPYPGL
EEEGDVLPLYPADELPAVEGAEDAWAGREGEGP

>tr|A0A376MJA9|A0A376MJA9_ECOLX p-hydroxybenzoic acid efflux pump subunit AaeB
OS=Escherichia coli OX=562 GN=aaeB_3 PE=3 SV=1

MCDYGGFALFSAIDQTRSGSRAGKFAGRAISINATLYQHGDGEVVDKAWGDLVRRTTAL
QGMRSNLNMESSRWARANRRLKAINTLSTLTITQSCETYLIQNTRPELITDTFREFFDTPVE
TAQDVHKQLKRLRRVIAWTGERETPVTIYSWVAAATRYQLLKRGVISNTKINATEEEILQ
GEPGSQSRVSRSTSSCDG

>tr|A0A011QEF5|A0A011QEF5_9PROT Potassium efflux system KefA OS=Candidatus
Accumulibacter sp. BA-93 OX=1454004 GN=kefA_3 PE=4 SV=1

MTEPCLARRGASERRFGESIKRLAFVSRFFLALLLALPVRAEVAPQPDLTRAIVAENAR
LVREIAAGTAALEQARSDLRQLRSRSELDQRMQRIERHAQVNALGQLFAQAVIEQLSRL
PSSEGFENDRRQRLDRLEAASDATLRAERALDELADMETATVMRFAASKPPLPDALWPQF
EAAARPLLGEQRTLLTGLDEQQGQLLQALQASDAAALELAQRTQAVRAELTRLLFWVPA
RPSLQTVGEFSRSWAWMTSLANWRAAAVSLAEELASRPFWPVLALLLAVTLLFARARLQ
AQLVVLAPADANS DRYWIGYTVTALAITLALALPGPLLMWTAATLLAASLDAEPFALAL
GAALAATGKLLLALSALAWLLDRRGVAGGHFGWDESLGFTRHALLRRFSLLFVPLLLV
TLNGLDHAPFANRESIGRMSFSFAMLVFAAFLVRLRLRRSPLIQRLYARAPRSWAVRLYA
LWFSAAVAVPLAIAGLSAAGYFVAAGYFFGHTLMSLFLILGAVALYGLIALWVQVERRRL
RRHQAREALRQAREAAAETGEDGSEVAEPAPARLDIAAISEQTRSLDLFITLLLLGGIWE
VWKGGLPALSVIGDYVLWTYHATVDGTATTPLTVGNLFMAIVVGVTTVAVRNVGAL
LDIVLLQRFEVQADATYAIKIITRYVLAAVGMVSALSIVGIGWADVHWLIAAMGVGLGFG
LQEIVANFVSGLIVLAERPIRIGDIVTVGEVTGTVARIRARATAVVDVFDGKEVIIPNKAFITG
SVVNWTLNQTTRLLLKVGVA YGSDIALVQRVLLEAVRANADV LADPSPSVFFMFGFGDS
SLDFEIRAFVGSFDKRLRVQHELVNAMEAVLREQGVEIPFPQRDLHVRSAPALVGLQESV
QGQGDGLPTAPAQAMPSASPSA

>tr|A0A024QBW8|A0A024QBW8_9BACI Efflux protein A OS=Virgibacillus massiliensis
OX=1462526 GN=efpA PE=4 SV=1

MSTHSQTLSPDPKRWKALFLLCFANFLVIMDASIIQIALPSIQESLGYTQESLQWVMSAFL
LIFGGFLLLGGKLADLYGNRRIFNLGVFILAVSSLFAGLAWNEISLNIFRGIQGLGSALIAPS
ALSMVMRLFNSTPEKEKALAFWGLSGAAGGAFGIVFGGLITGFFGWRWTLFIYVPLSILV
LILSPKLLQKSGQRLKGRIDYVGAALATASMLIVYGIVSAEHSGWTSSNNVISLIVGVVLF
LIFLIVESKMKEALLPLNIFKTPNLGIGNVG VFLTQAAWFPLIYMLILYLQQVLQYSPTAGA
MAVLPVPLFMAFFIIVVAEKVLAKLGKMTMVVG FVILGLGNILFSQFATVDGTYVISVLF
PSFVAALGNALAYLASTTASVSEVEPKKSGLASGLYNTNFQIGSAIGLAILVAIAGVATASS
TAGSQLVALNEGFFQQAFFWGGIIAFLGAVLALLFTRSPKQEESNR

>tr|A0A061BZ57|A0A061BZ57_LACDE Mechanosensitive ion channel OS=Lactobacillus
delbrueckii subsp. bulgaricus OX=1585 GN=AT236_01558 PE=4 SV=1

MKNLDFKIAGISVDVDNLFTSGVTILWKLLISTLVFYLVSHFGRKIIKRYLDKHNDKLVLS
KRSQTISALVNSLFHYTMVFFYVYSILTILGIPVGTLIASAGIFSLAIGLGAQGFMSDLVNGF
FILSEGQYDVGDNVEIGTEAGTVTQLGLRTTQIVTTDGTILIFIPNRQISIVRNLT HGGIGLNL
DLNLDANTDLKQLASLLDQADEDLLAWHDKLVSGPTQIGVVGGQGGQTITYRVHFQVKPG
FEGKIRQAYWQTYLQYLRVNQVKFGQEPVIINNSKKA

>tr|A0A077FNP1|A0A077FNP1_9RICK Putative amino-acid metabolite efflux pump
OS=Rickettsiales bacterium Ac37b OX=1528098 GN=eamA PE=4 SV=1

MRYIDIMKALLVAVLWGGSFVAAKLVLLEYFPPIFSMVIRSIIVISILLSFVGLPNISLKKVLC
MSFSYNIGHMVLLYLGKLG LPVSAAVIATQM QVPITSILSIILKEKMHLKQVIGMLISFIGI
VIIVGHP SIMDKIFPFMIVIIA AFFFALFNIQIKQVGNLNLISYILWSSILILPQLMILSYISEPIS
WSSIFIADV KLWLSIAYISMVNIIAFLWISLLKIYPVSLVMPFALCIPVFAILGSALILSEYIS
WHLIIGGTITLIGVAITIKFTNLTRYQST

>tr|A0A083ZVB9|A0A083ZVB9_9GAMM Putative amino-acid metabolite efflux pump
OS=Serratia sp. DD3 OX=1410619 GN=eamA PE=4 SV=1
MSTIWFIVAIGVPFIWGIQAVMLKFGIGQFPPIFMVSLRFLFMFILLMPFLSRLKGQFRLAAT
VGFTQGVAFHALLYIGFKYADVTSGMIVYQTNAIFTLLGSILLGEKMTKYAMSGTAICLI
GVSLILGMPQENTNITGLFIIACALMFALGNICVRKFGPFDPVGLNATVSLIAFPALLFISFL
TEKGQLESLRTASLEAWGALFYTAIFGGVLAFILWYKLLIKFSVDQISPFSLMPFFAMMG
SIIILDEKVTIVNWIGAVITIGGIIQYSNKLVTLKGRRSVIVTDQ

>tr|A0A086P4H5|A0A086P4H5_SPHHM Auxin efflux carrier OS=Sphingobium herbicidovorans
(strain ATCC 700291 / DSM 11019 / NBRC 16415 / MH) OX=1219045 GN=BV98_003876
PE=4 SV=1
MAMTIFGALMPVFGILIGYVCGRYDILGDRAFEVLNRFVIAITLPILTFRSIAHMDPANLA
VPGMFAAVTLGALLTYGIAFAVERHFGRHGSETNIAALCACFSNTGFIGLPALLAWGPEA
AAPVSVAMLIYSSIVFTVGLVMSEVTASEGHGPAAGLKLAAARSIVRNPLILLAVAGCLWSI
FRLPLTGPADILLATLAQATAPCALTAIGIFIALPRRSATPGPIGRVVALKLIGQPMITAIL
WMLPPIPLWAKVAILMAAMPSGASSFVLAGKAGRWAMELSAWAVMLTTTLASISLIGIL
WWLGA

>tr|A0A087C0A6|A0A087C0A6_9BIFI Cation efflux system protein OS=Bifidobacterium
mongoliense DSM 21395 OX=1437603 GN=BMON_0842 PE=4 SV=1
MMRWQRMNLIAKLVLLTFVLLSVGTRVYQFVDPNVPTAASSIDYFLNVNAFATPEICPFLI
VFCAGATRYEAFERVRVSAHHELGANVIWMVQCAAVALFGLLSWCGVEFLLSGRTWD
IPLGVSVAVFAQMLMNTFMELIVIGFVQFLPINAGVSWGKAMSAMLLFLLVCNWWFHNW
AEIIPETLFYFLPLVPPTFDGLASAKLPFVGAVVLLVHGQPVPL

>tr|A0A088MZ42|A0A088MZ42_9GAMM CO₂+/MG₂⁺ efflux protein ApaG protein
OS=Candidatus Baumannia cicadellinicola OX=186490 GN=IM45_1239 PE=4 SV=1
MMTNASRICIKVQRMKSQLEENRYVFTDTITLQIMGRYLLITNAYGQETEVQSKDVICEQL
LIIASGKFQYTSGGVLETPLTGMQRYEMLDYEGQSFRVALLIFRLAIPTIIN

>tr|A0A090JL79|A0A090JL79_9FIRM CHR family chromate ion efflux pump OS=Peptoniphilus
sp. ING2-D1G OX=1912856 GN=ING2D1G_0018 PE=4 SV=1
MFLKIGILAFGGGYASIPLIQRIVDDYHWLSMLEFLDLVSISQMTPGPIAINSATFVGQKV
AGLIGSIVATLGFVTPQFTLMMILGYFLFQKNKKFKLLDWMLNGIKAGIVSLIFITALQLFV
SSVFPEGFGSINIAAAICFIIGFIMYLKKYSIFQLVAVGATLGIINCAFKFL

>tr|A0A090QRC9|A0A090QRC9_9GAMM Magnesium and cobalt efflux protein CorC
OS=Photobacterium aphoticum OX=754436 GN=JCM19237_1051 PE=4 SV=1
MITAKQLLHYQQAAPHGDITPFISPVECIPEHWSGSQMLEHFRQTGASMVFVVDYGDYQ
GIVTPTDVLEALAGEFRHPDPDDLWSVEQDDGSWSIDALIPILVLQDLLDLKRLPDEQRGG
YHTLSGMMMWC LDGIPKEGDCMNWEGWQFEVITLAGNRIDKVWAHRLAGESSLTITDH
PSEEEQPADGPTPSMASTVHQPDHEDTENHPENAPKPRAKAGQK

>tr|A0A094ZQ85|A0A094ZQ85_9PROT Mechanosensitive ion channel protein MscS
OS=Acetobacter tropicalis OX=104102 GN=AtDm6_1231 PE=4 SV=1
MV MENQVHSIWSQLNGLLPVVLGYVSQFALALLVLFVGWKL VNAVTRAMGRMMEASH
IEPTLRGFLLSVVGFLKALLISVASMVGIATTSFVAVLGAAGLAVGMALQGSLANFAGG
VLILLFRPFKVGDSITAGGSSGTVTSIEMFRTVLRDANNEIIVPNGTSLNIVVNSSETDRL
LGSVTLIDYNDIDKARALLGLTEQDELVLKNPAPSVSFLPKAANIQVTLGFWCAPGNV
APLVAKYSEAAIKVLQKEGYRLGVTARTAA

>tr|A0A0A1W0B9|A0A0A1W0B9_MICAE Auxin efflux carrier OS=Microcystis aeruginosa
NIES-44 OX=449439 GN=N44_04073 PE=4 SV=1
MLAILSIVPVGFILIGVIAGKILTVEVHSLSQITVYILAPALVIDGLYHTTSLSDSNIGLIILGF
ALISLVMAIVVEIMAYCLSLDGDTRKSLMAAAVMPNNGNMGLPVASFALGAAGLERAIHY
MIGSSILLFGISPAYLQGKSFLSGFRLVFQLPLIWSIFIGISFQTFSFHLPLQLDKSISYLGQAAI

PLALIILGIQLSQQKLAIGKLELLGACLRLLVAPLLAFAIGNSLGLTGMDLKILILQSAMPTA
VNTVILVTEFGGSATLMARTVVVTTLASFLTIPFFLWLLKVYL
>tr|A0A0A8R1A8|A0A0A8R1A8_9ACTN Actinorhodin transporter OS=Propionibacterium
freudenreichii OX=1744 GN=PFCIRM512_08510 PE=4 SV=1
MTQTLTAVEPTTSSRLGRRLWAILAVVLIADAIDLMDSTIMNIAAPTIQREIGGEEGLIKWL
GASYALALGILLVVGGR LGDRFGRRLFLIGIAGFGVASVLCVAIDPAFLIAARLLQGAF
GALLIPQGIGILIA TFSREQFPTAASMFGPVLGGASIVGPILAGFLVGANIGGLTWRP MFLINI
VLCAAGLIAGWKLLPPDRDLQKVSIDGLGSALLAVGMLGVLFGLIQGSTNGWTAVPVICL
GLGVAGFIGFALRQRLATNPLIVPALFHNRGFTSGLLIGLGYFAVVNGFAYVVS LYFQIHL
GLSPVGAALAMMPMMVGIIASF GARPLIPKLGRNLVVAGLATTLAGIVALIAISIGAGDAT
NQWMLAPAILVLGLGMGASFSSIYDVAIGDLTTDLAGSASGSLSAVQQIASAIGSAVVTTI
YFQTSATADANRPFIASLIVVGAITVVCLIAAPLLPKRAPQDAH
>tr|A0A0B0EJD1|A0A0B0EJD1_9BACT Heavy metal efflux pump protein CzcC OS=Candidatus
Scalindua brodae OX=237368 GN=czcC_2 PE=4 SV=1
MDLKNIKNGLYFFSKLLLTGLFIVATFSGITIAEDRDDILRIRWVIDEALRSNP ELNSARLN
WDASKERVVPQVSALDDPDLGFTYYGEQTQTRVGEVQAGFMASQKIPFFGKLRLRGEIAEN
EANAIGERYRALERDIVAKAKSAFYELYWVHKSIRINEENRELLQRFVKIAEIKYASGKAT
QQDVLKAQVELSDIMNELITLEQLKETAIARINTLLNKH PETPLGIPEEVDITEFDVPIAELY
KEAKKISPEIETF KYRIERDKAAYKLSKKQYYPDFTLGFNYNLVNDLPSSVMMSPVGESRD
SYTGTL SINVPFQKRKYDAGVREANARLKSSEKAYRN MENKTLFEVKDFHFRTQTAERL
VKLYRGSIIPLAEQSLKAAEIGYQAGRVD FLNLIDSQRVLLNFNLAYYRAIADFGTNFSELE
RVVGVELSKKPQSKKP
>tr|A0A0B4XLV7|A0A0B4XLV7_9GAMM CzcA family heavy metal efflux pump
OS=Alcanivorax pacificus W11-5 OX=391936 GN=S7S_14210 PE=4 SV=1
MLTAPIVTRWNRSPAIRQDVDAAMIDGTLKCLRSMLMTMVT TTFELMPLLWKS NVGAD
MSARIMKPVVGRLWFCMSLTPLGTAGGLCHLVSLAVQRLRAPSR RPQSSD
>tr|A0A0C1NW99|A0A0C1NW99_9PSEU Arabinose efflux permease family protein
OS=Präuserella sp. Am3 OX=1515610 GN=HQ32_04585 PE=4 SV=1
MTTSPTPEVRRRSGTLVAVICCCAVIFDGYDLSVFGTTIPALLEYEAWNLD AARAGVIA SY
AFMGMLVGT LICGLATDLLGRRRMLITSMWFSVCMGACALAPNPEL FGLFRFLSGVGLG
GLLPTALALTA EFAPRGRRNLFNALVSSGFSVGTIAASLIGLV LIEPFGFRPMFAIGVLP LLT
LVPIAYAVLPESADFLRSKGKHDQAHRTALRYGLAENATPHGESDEDGRRAGLRDLLRRP
LLTTAIVFAFAGLIGQLFIYGLSTWLPEIMRSAGYPLGSALSFLATMSIGAIAGATVMSICAD
RIGPRTVAIWGFGIGVLSLVTMSLAPPTPVLYVAVALAGVGANGTAVILNGFIATWFPAAV
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RTLGAAREPQPAPVRGGQA
>tr|A0A0D6EC09|A0A0D6EC09_9GAMM Cation-efflux pump fieF OS=Halomonas sp. R57-5
OX=1610576 GN=HALO3634 PE=4 SV=1
MKSESSTLSFS AFMALLIGCAGIVATLASNSQAILLDGLFNLIYFSVALVTIKVSKLASRPDS
ESYPFGYSYFESLVNLCKGLLILGV SIFALVDAIAALLTGGREIAAGLAVLYALFATAACSL
TAWVMHRSQRHVSSPLVAADKLNWLVNSVISA AVLA AFCLV MLFERFGWQAILPYVDS
VLVIAVVVLCLGVPVRMASQALRELLNKTPDETIAEPVRQAVARG LADIDTVEVRV RMV
RPGRLLYVIVHVVLPEASDVSVTRQDSLVRIDDEVRRYYSPV VCDVVFTTNTRWAAPSC
GLLVEKHPA
>tr|A0A0E2UDU2|A0A0E2UDU2_9STRE Cation efflux family protein OS=Streptococcus
parauberis OX=1348 GN=SS13_contig00001-0180 PE=4 SV=1
MLPLYREKLKRG IHDQKKINNKSIERKALAVSTIVNFITAIAGIIIIYITGLNALLLDSVFSAIG
CASTLAGFYITKN SHRKTKNFPNGMYFLEPLFGILKSIATLMLLIIASLESATVAYAYFFKN
QGSPITIGPAFPYAIITGTMCLLLAYYNHKKNK SINNLSTMLQAEIKANFVDGIISYGIGLTL
LMLYFIAIDGKLGFLHYTG DFFITIMLV AISFKEPLMVLIHSFKEFAYSTVQDQEIKASIISVF

KAELPNHLENLDITIYKQGMQINVRVFIIGIDNTDTIEELALEKANLLNHLRKEFEQISLEFT
F

>tr|A0A0F6RC18|A0A0F6RC18_9GAMM Cation efflux protein OS=Kangiella geojedonensis
OX=914150 GN=TQ33_1072 PE=4 SV=1
MSTLKSAILLVAALLFSSVTNSQAETNGYGYTLESTLIMAIENDPWLRKSQFKELSLLSQA
ESQASLPDPKASINLANLPVDDFSFNSQPMTQFKLGFSQTFARGDSLCLKREINQLQASVEP
TMRINRKNQLIMVVGALWLDVHKAQQSIALINDKKYLFEELREAAEISYTSALSQTSQQVI
IRADLELAKLDDQVTVYSDKLHTSIRQLSEYIQLPQSYLSDREYGSVSFVSQSLPRMTLIEK
KDGFQQHPLIKSVDQSIKASQKVNNLKKQSYKPKQFTVNGSYAFREDAADGMQRPDFFSLG
VSFDIPLFTGNKQDLVDQSAVYDKEAKLEEKALLNHLMSAYNTELSRLNKLKERHKLYS
ESILPQVKHQGEASMNAYSNNEADFAELVRARIDEVNVQLTALDIAVEIEKTKLRANYYYQ
AKTPSELLAQISSSYKTTDVTDELSPSNPINSGDRHE

>tr|A0A0F7M318|A0A0F7M318_9GAMM Arabinose efflux permease family protein
OS=Spongiibacter sp. IMCC21906 OX=1620392 GN=IMCC21906_02232 PE=4 SV=1
MSISHTKDKPPAKVFFALYLAMMAVGMGQTVVFAIIPMLGRELALDKLVFQLPILDITLAP
KELTITSLSALAAVVFFFAAPFWGRLSDRVGRKPIITGLLGYALGSMVFNFAASYLGLAGIL
SGVALYFLLVISRGFHAMVMSGTHPGAAAYMVDITTVSGRTQGMGKLQAAANQLGVMFG
PVLAWFVSVSFLAPLFIQAVLATAAAILVWLWLPSIPPQPAADTRPRRMSYFDARYRLFIF
VGFVLFSLIAMIQQTGIFYFQDTLSVDGVRSAQLFSVAMVVSSAMMIFAQLGVVQRFGGA
PVTLLFAGMPFSLLSYLVLANADNLVMLLGGMALFGFGMGLTGPSFTACATLVVRAEEQ
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PSAVIKK

>tr|A0A0G0A4F2|A0A0G0A4F2_9BACT Auxin Efflux Carrier OS=Candidatus Roizmanbacteria
bacterium GW2011_GWA2_33_33 OX=1618476 GN=UR42_C0013G0004 PE=4 SV=1
MNFNNFQILLSVFLIFVGYISKAFKIIDEDFARKAIKFLFFLPLILVFLSFATTKLDISLGIYP
IISIIQSILIVISYFIGKLLKFDNKTIGTLIAASGITSTLVFALPFIQAFYGIENLKYLFMYDFGN
GLMAWTVVYLITGYLGNNKKQLGIKKGIISFVKNPIMFALFFGVIFGLLNKLPQFFTQFKTT
LSGFINPLLFSIGILLDFKYFLSKENLTKLFLSAGIIMGVSVLLAFMFTSLFDISGIGQKVILI
SAVSPAAALAVAFSVEHDLQKFASALVAFTMVLGIILVPLIILL

>tr|A0A0G1BLV0|A0A0G1BLV0_9BACT Arsenite efflux ATP-binding protein ArsA
OS=Parcubacteria group bacterium GW2011_GWA2_42_14 OX=1618820
GN=UV01_C0003G0005 PE=4 SV=1
MGKTSMSAATALGFAKEYAKRRKNDKVLIFTTDPAPSLADSFGQKIGNEPTQIEGAKNLF
AMEIDAKKVLEEFKKEYGEDILDILQEGTYLANEEAEELFSLDIPGLDEVMLKKITDFMD
SQEFGLYIVDTAPTGHTLRLLTPELLDDWIKFLASLRWKYHAMVRQFAREERVTKADQF
LLEMKKTVKKVRELLQDEKRTEFIVVTIAESMGVRETEDLISTLEKFHIPSRIIINNIFPKED
SDFAKFKRKNQEKEYINEIKKKFSNHAITEVLLQADEIQGIKSLES LGKQLFV

>tr|A0A0G1H920|A0A0G1H920_9BACT Auxin efflux carrier OS=Candidatus Wolfbacteria
bacterium GW2011_GWE2_44_13 OX=1619017 GN=UW32_C0003G0106 PE=4 SV=1
MLSTIFVSLPIFFIVFAGWLFQKMKIMQGDWVHQANAFAYYVALPALITVSLWGVNFRSP
EILSLLGVSAVSMVVFLALLFIVLSVWKVSRETKAALFLTAATGNTLYMGIALVEAGFGK
DHVPAGALVGNVYLIPLVLSMLVVNYWHTKEHSIKNELMEFLKNPLVLSMVLGVVLSFI
PEAGSAIIGSIKKTMTMLGSTSSPVALFALGGFLYGKFLKKDLHLVISIATIKMILFPLIVFGT
YIYFGKGGDVEIPVLLASMPVAVTTFVIAEKFKLNTALVGNAIVFATILSFITTPHILLR

>tr|A0A0G1NKG4|A0A0G1NKG4_9BACT Cadmium efflux system accessory protein
OS=Parcubacteria group bacterium GW2011_GWA2_45_14 OX=1618832
GN=UW94_C0005G0072 PE=4 SV=1
MLTKKQAEIHKNDVSKGSVQLAVMLNALSDTGRLKIFRLTKYEDLCVTDLANVLEVSVP
AASQGLRIMELSGLVKKERRGQMICYVVARDMPLVRALQRIVTGHVHTAKDSR

>tr|A0A0G3V367|A0A0G3V367_9ACTN Arabinose efflux permease family protein
OS=Actinobacteria bacterium IMCC26256 OX=1650658 GN=IMCC26256_111595 PE=4 SV=1
MTTTSSEPLDSKQGSNQLGGRGLRFWLPICVLAFAQFVMVLDSTVMAVSISAVVKDLGTTV
SKMQLAIACFSLVMAAFMLAGAGLGNRLGRKRAVIGLVYACGSFTTALAPTFGALFIG
WSVLEGLGAVLVIPAIAALTAANYSGKQRALAFGIIGGISGAAAAAGPVIIGGWVTSAYSW
RYIFASEVVICLAVVALSRFIKEGERPTVGKGFDFLGVALSALGFGLIVISLVQAGIWGWV
MPREAPFTVLGFSPTIPMVVLGIFVWIFLASQARLKESGGTPLLDPPELLRIPSLSGGLATLG
VQQFVIAGLFFVLPLYLQYVLGLDALESGLRILPLSVSLLVASFLGAALSSRFAARRLV
GLSITILGVVFCIAAVDVHLRSNLFALAMSITGAGIGIVASQLGNVTQSSVNVTRSNEVGGL
QGTAQNLGASLGTALIGAILLSGLNSAFVRTVGANPKVEPQTKVAVEAASKQGIAFVSED
QARAAAEASGLSSSEVDTVVNDYVTSQIDGLKAALGAVAILGLLGLVASRRIQNHPLAGD
DPEELDELENEEIVKNQ

>tr|A0A0J1IQ49|A0A0J1IQ49_9FIRM Threonine and homoserine efflux system
OS=Desulfosporosinus acididurans OX=476652 GN=DEAC_c14840 PE=4 SV=1
MNNVRGKGHGGGIAAIIISALGFAFYPIFGKFVFAGGANLATVLFVRFFIGAIAFWSLVILG
KSIKHLTKRDFRLLWLLGGVYAGQAGLYISAVKFISSMASLIFYVYPVLVTILALATKQ
ERLSISKVSGLLFSILGLILVLGVSFEGNLNLLGIFCSLGAAIYSIYILTSNRIINSVSPLLSSAII
TSAACVTYGITGLIQGFTWNIAAITWMDILGAILSTHAILTFFWGLQKVGPTTASIVSTLEP
VLTVGLAYIFLGEYLNFTQSIGAACVLLGAVLAAWPHKIMTISVKEAKL

>tr|A0A0J8DEE2|A0A0J8DEE2_CLOCY Auxin efflux carrier family protein OS=Clostridium
cylindrosporum DSM 605 OX=1121307 GN=CLCY_10c01100 PE=4 SV=1
MQYFNILNQIIVLFLIMGVGYVAARFKVISQEVNVGLSKILINITLPMFVIASFNFKFSQKML
SSGLILFALTIVHGVLAALVSLMLFRKCDSGKKSVLRFMTVFSNCGYMGYPLAHSVYGSE
GVFYTAIYNVFNIFLWTVGVMLFQKEKRKGLYKKVFKNPGMIAVFIGMIIFISIKLPFAV
SNTISLIGSMTAPLSMIIIGVSLYDVNLKTAFKGIEYYGASLMRLVITPLAIYAVLSLLGFTGI
ILGISVLLSAMPAAATTVTFAQIYEGDVESASKITVVTILSAVTLPLIMLLV

>tr|A0A0K1P877|A0A0K1P877_9DELT Magnesium and cobalt efflux protein CorC
OS=Vulgatibacter incomptus OX=1391653 GN=AKJ08_0028 PE=4 SV=1
MRDSRAERRRGGPPIGPPLLLLDRAHLTSSADFGLC SADGMTLQAPFPALALAAIVARFFFV
AAETALVAVSPERADELHAARGSLAARSLLALKRDVESSFATTRVGSISALALGAGLAGIA
CASWLGAESAVALSAAVGGGLAAALLCVLADTVARSLAIAAPEAWALRSAPPLRLASLVVA
PPARAAQAVLDRLLSPLGVRATFKGADPALEDIERILLSESHRDGPAPELVHSLFEFPSRTV
RDVMVPRTEVVAAPLGAPEALVRLVAEQGHSRLPIYDGRIDRIVGVLHTRDIVPLLAHPE
LIQLADAIRPPVFPWAMRIGRLLRQMQRDRIHLAMVADEHGGFMGIVTLEDILEELVGGI
RDVPSGTEVVEADGGHLVDAGIPVVAFNEHFGTALPEHGEFGTLAGFLNGLAGEIPEVGA
TLESHGLAFTVADRNRATRVLRVLVQAAVSAKRNSA

>tr|A0A0K1PPP6|A0A0K1PPP6_9DELT Putative transmembrane efflux protein OS=Labilithrix
luteola OX=1391654 GN=AKJ09_02162 PE=4 SV=1
MRSQPSLAPLYGAAAFVLAVDTAGVGHLLPGLEMATHAPPRGASWFISYMLGALLGAPLL
ARIATRRGRTTVLAASLAMFALASFVVGSSSYPLTLAARFVQGVAGSPVMPLGAAHLSA
LAPAGKKGRGLGLLSLSYSGGFLAGMAFVSLFLLVSFRLAYLFTGALASVACIAVARLPV
APTTSSSHDDAERPPPEVSTIAGWFVALALLALAINQVNVVDGAGAIAMARFAAVPALALF
AWRDRSVRAPLLPRDLFRSRVGLASASLALAAGVGQACVVLLPTCGMAELGVSAASGP
LLIPIVLGGLGTNLLASARLDRWGPKPFLAAGLLGMALGNLVTAWLGTNLLAFEVGALLL
GAGVSAMSSGALRYLATLYGAADDADANQAAISLLTNVGVLVGGSLWGAIVPSTSGIGV
AAVRVGIVVLTAALMPLSVGVLLVPSRR

>tr|A0A0K2Y7W2|A0A0K2Y7W2_HELHE Potassium efflux system KefA protein / Small-
conductance mechanosensitive channel OS=Helicobacter heilmannii OX=35817
GN=HHE01_07640 PE=4 SV=1

MRFLWALLVLFMGFLRADTHEGGDLIDLHLLLKQINQLNQVITRYQKDPTKHTEVSL
YSDQKNELMHAFALRLLNSQEKIGINIQENTKQQHALQKALLKSSKINDFYAYFSQTIQLK
NLEVEAQMYGFLEKIRTSTDLSQERDIKNITSTYLLKLEAFATRTYTIPEHLADIKKHELL
GALENYQIKLQTYTDVLRYYQKHPKDVLAKNVVFNNMQWVLERIAGAVNHIFPDMNGL
QNAKILLSLGLVLLLALRQIVTAIFVKALDYCVRFSRKNANINIQEKIRNSILAPISTFLFIY
SFDISIDILYYPHPAPPRFDMYLGVVVYVSLIAWLVLALFKAYGAAILATLASRKNGFRKEVI
NLILKIAFFIFVLTLGVLKQLGFNISTIIASLGIGGLAVALAVKDVLANFFASVILLDDNSF
GQGDWIVCGDVEGTVVEMGLRRTTIRGFDNALFFVPNSELASKSIRNWNRRKMGRRIKMI
VGLTYGSSSEALQKCVLGIRQMLEQHPQIAKASDLENITDHDHHDYIMERQNIVSFNDLM
GYKSNLFVYLDSEFGDSSINIFIYCFSSVWGEWLAIKEDVMLKIMKVVEDCGLSFAFPSQ
SVYIESMPHPS

>tr|A0A0K8PUF3|A0A0K8PUF3_STRAJ LysE type efflux protein OS=Streptomyces azureus
OX=146537 GN=SAZU_6288 PE=4 SV=1

MTVDLVGFLGVVLVAYVVP GPDFLVVVRSAAEAPSKGRAALGAQTGLCVHMLAAAA
GLSVIATRSPVVDYDGIKLLGAAYLVHLGVRALLTARQAARKQRHANEDAAGAPPQDSAH
PPGPPTPKAGVPVGRWQSGFTQGFLT NVLPKAALFFLSVLPQFVDGHGSMHAHQIFFLGIL
DILIGVVYWFGLVVVAARLRALLARPKIRHRWELTTGWLFIAGISAAAVA

>tr|A0A0M4DAA6|A0A0M4DAA6_STRPR Transmembrane efflux protein OS=Streptomyces
pristinaespiralis OX=38300 GN=SPRI_5798 PE=4 SV=1

MSTAPSAGRAGRSAHRNTGRDED RSAGRGDGTGESGPTGESAGRSPGRRVHRRITLAG
SVVGASVVALDGT VLTIVQPVMQRELHASFEQVQWTGTGYLIAVASLLVLAGRIGDRFG
HRQVFAVGTLGFGAASAGIGLAPDIGWVIALRVAQGVFGALLQPATLGMRLAAFPDRLG
MPIALRTSAIGAAAAAGPLVGGALAAELGWRSVFLLNVAPALVIGLLVLAVRDPEPVEAP
RTGLDPVGACLLAVTLVCLVHTLVGMPVSGRAAVTAAGCGAAVVAGAAFVRHVRRGR
DPLVPPEVLGSAAVASALGVLVCASAVLSGSLFAGVYFLQDVLGLDPFRSALQALPGAVA
VVLGAPVCAVALRRYGPRRATAVAMTLLVLGALALSRLERASGAVPVGGGFFLVGAGFG
AAMVAATAVVVRGAPAEHAGVAGGLQQTAMNIGPVLGVAVATALMTLAAPRGGPAGS
VVMVSATGPAMTVLA AVAAAGALLAAVLPGPSGAAPPRPTAP

>tr|A0A0M6ZSX5|A0A0M6ZSX5_9RHOB Homoserine/Threonine efflux protein OS=Labrenzia
alba OX=311410 GN=LA5096_03432 PE=4 SV=1

MTVLEYVLIGFLVGILTTAPVGPVNVMAIQHAVKNGFSHG VFVGLGAVVADTIFASAAIF
GVSAVTNFVDSRFGLIEIVGGALLIVFGIRIWNTHPHIEKDGN GREYSYLGDAAAFFMAIT
NPGTIFAFAAIFGVLDYRPAHDDHFGSLLMVAGVAGGATSWWLFVSATVSHFKSRIDDR
WLGRANHIAFGVLIVFGGLIYLNALDRLGHAAGIWGH

>tr|A0A0M7F1Q0|A0A0M7F1Q0_9BURK Efflux system membrane protein OS=Achromobacter
sp. OX=134375 GN=ERS369989_00840 PE=4 SV=1

MPAISM PNRSRSYPVLSEFAIAGIYVPPFFLYACATVPLYWLLRVVMARSGLLRRVWHPA
LFEFAVSLALVSLILTL

>tr|A0A0N0XLB5|A0A0N0XLB5_9NEIS Glutathione-regulated potassium-efflux system protein
KefB OS=Amantichitinum ursilacus OX=857265 GN=WG78_08825 PE=4 SV=1

MNFLNQALLILALPLV VWWPLRRVMPLVLSQILCGIAIGPSVLGHLAPTAF AQIFPSGTLG
ALGGISSLA VVCVGFIAGMELDIDELRHQARHVVRTGLASFAIPALGGAAFAGWALTQWP
ALAGAHATQGAFIAAGAI CFGVTALPVLVAILRELDLLGTAMGRVALSLAAINDMLLWV
GLAGLMLVISHKTQTLGNWWWVLVLLLTLVATLFAIRPKVSAWLADLDAGKELSTARF
TLVLIGLLACAIITDTLGLHAVIGAFVAGVLM PKALRPRITQLAGPFSNALLLPFFVVSAGLS
LDITAGPVWPFFIASV VIGSALKIISTAVPARAWGWRWAQALQLGALMQSRGLMEIIVLRV
LYDAGVISQSCL SALMLMALVCTGLAMPLARWLD RQSAAPATAATIANLPAAR

>tr|A0A0N8KBL8|A0A0N8KBL8_9GAMM Auxin efflux carrier (AEC) family transporter
OS=Idiomarinaceae bacterium HL-53 OX=1298881 GN=HLUCCO02_11535 PE=4 SV=1

MENLALILAYLAIGWFLQITRSLPEQSGHVLNQYVIYVAVPAMVLIHLPQLEVSRSVLAPL
FTPWAMFGLAIGLVLLFSRMLHWSKELTGAMLIVVPLGNTSFLGFPMVTALYGEQGLPFA
VLYDQAGSFLALILFTSVIAARYGQYQQNQGTNEPPSKRKQALKLLTFPPLLALITAILVGQ
ETYPGFVQPLLESQAQTLVPVVMIAVGLQLKILRADLVPFTIALGIKLIVLPLVTLAVFA
SLNLTDLAAQVTVLEAAMPMPMITAGALAMAAGLKPRLVAAIVGYGVLLGMITLPATAWL
TGVVLGTA

>tr|A0A0Q0TW72|A0A0Q0TW72_9CORY Leucine efflux protein OS=Corynebacterium oculi
OX=1544416 GN=leuE PE=4 SV=1

MDIALLSFWGLSILMTCIPGPDWGLILRHVIGSESRAAVNQAVAGIGAGYVLMASAVVAA
GVGVIVTQHPAVLTAISLGGAALLIYLGATLLWGLRPAARVAAGAQQQAQGNKASSPVW
EGMGVSLLNPKALMFFVAMLPQFVNTQAAWSVSTQMFTLGMAFTVSVVVVYTCLSLAA
RRVLRASNRAVVVMQGAGGVAMLVLAAMVGRW

>tr|A0A0Q9Z1S6|A0A0Q9Z1S6_9COXI Putative efflux system component YknX
OS=Candidatus Berkiella aquae OX=295108 GN=yknX PE=4 SV=1

MMQMSQALAQVTMQITNSKPLEKILYDGNLLAVNLLIEIQSPANGMLLKKHVFHFGDKVSQ
GQVLFEFASQELQAQLFEASMAVIENKEAYLKL RDWEQSYEMMQANSQMDKAYHELAR
TEVRFQQTKKLYQSGIVAKEECLDERFYKDSQQHYQNAKRQLAQIKEKANATALKLAE
LKLKQAQNKEAMLQNKIAALIVRSPMSGTVLAPHVEGTKQVFALYPQKPFQEREVIAWL
ADMSSLCISVKVDEFDVRQLQKGQQAQVLAASFTHSLAGKIMDISVQNNPANGTRQAM
VYDVKVALDVIPEEIQNKLLIGMTASIQLEERLPEGLWIDKTAIHYENDEPYVNVIHDTST
KQKVVLGDNVKNVRVIKGLAVGDRIVLHG

>tr|A0A0R2L2N1|A0A0R2L2N1_9LACO Efflux transporter, HAE3 family OS=Lactobacillus
pobuzihii OX=449659 GN=IV66_GL000910 PE=4 SV=1

MSKIFGKLSANIHQHAKWWIGIILAITIGLAFGLPNLEIKMGNDVFVSNNNSAISKDSNKYM
HHFGGDSYYIMQSGKQSDILSHDNMQELSKFDRKIRDVDNVRGTTDLVTVMNQELANAG
KGKSDSLSGQFDMNNSKLQKDLMNLSLSDKQKNKLQNQIQASLTDQQEQQVQKYVAGQL
SDQQQQKLQNEIQASLSNQQKQQVQSYVQNVLNDQQKQQAQAQSGSADPAQMQQ
MMQKALNQQQQVQVQKYTQSILTSKQQAMMQSALNDQQQDSLQYTMISILNGQQKNS
MVKTVVPMPLPKVQNMSTALLRDIFLSDNGKVPSEMEQMLPKNGKMNVLINTSEKASSM
DTDVQLNHDINKVIKNANFSDGIKVKLAGQPGILGQIRTEVLSSMITMFAIAIVIMIIVLALIF
PVRRLALLFVVP SLIWT FGLMGWFDLPITLATMATLP IIIIGLGTDFGVQFHNRYYYYEFRK
RKDAKKA AKESIHKMGPAVGVALIVMTFSFLTFLSRAPLMQQFGLTLAIGVISSYIVEFSL
MFGSLSLDSDKRKKNKNKNKQTKIKQPSILSKVLARYANFVTHHAGIVMLIGVVLGVF
GFSVEKNIDVETDITKFIPQNMTALKNTKALQNNIGSTTYITYLVDAGDL DVSQDNIQTID
KLGGKVDNKYSGVTDVQSISSQYKSAGGKLNASQSDIDQKILLPKALTSTMISDDHHYA
TMQFKVKEDLSSADQLILMNKITKTLKHGNGDLKISPAGAQSMMMLVAIDNISANHTLIELV
GLAVIFVILFLIYKNWRVALYPVVPILIVLGLSPLTLWLIGTPYNPLTITLSALVLGIGTEFTIL
ILERYREEYSKSHDTRKSIVQSVSSVGS AITVSGLT VVGFTAIMFSNFPILRQFGLITVLD
AYALISALTILPAFIYLLRDRKEEKKNQ RNE DTDKIE

>tr|A0A0S2W5M0|A0A0S2W5M0_9FIRM Putative efflux protein OS=Intestinimonas
butyriciproducens OX=1297617 GN=IB211_02262c PE=4 SV=1

MRHIRLAFYSAAHFWVDLSCALLLLGVVCPEADLVRCILLYNFSFAFAVQMPIGLLADRLN
RNHQVAAAGCGLVAAAWFLTKGAEAAVLAVGNALFHVGGGLDTMNRSGEKAGPLGV
FVSPGAAGLFLGAAARGAAEALALPVCGLVAAAVLILLWCRGPENPPAALPEGRGKWL
PALLCLLLVVVLR SWNGFLFRFPWKGALEAPLTCAVVVGKTAGGLAADRFGT SR TAAITL
GLSALCFLGSDWAPIGLLG VFLFQMTMPLTLWAAGRLLPSAKGLAFGVLT FGLFLGALPT
HLGWEPIMPGEVYAATALLSLPLLCYGLCTAQKRR

>tr|A0A0S4PTX6|A0A0S4PTX6_9HELI Magnesium and cobalt efflux protein CorC
OS=Helicobacter typhlonius OX=76936 GN=BN2458_PEG0883 PE=4 SV=1

MGLLITYFLFAICISFVCSVLEAVLFSVTPPFMESYPKIHHPKGGRILRYLKANIDNAIGAILIV
NLFANTVGAAGVGAQAVKIFGETWQGVVAFVMTISILYISEIVPKTIGATYWKSLILPASY
AIMVLYMITLPLVYVSRIITHLFRNNATNQMSRDEVLA VMELGEKSGSINELEGDILESIE
QKSLSVQDIMTPKERIFALNEEMSIKEANKAIRDHKYSRIPLYRGAEGNICS LIYRKKILQA
MLDKKKKKPLKHFASEIAFVDMNLT LFDLLKLFINKKEHLFVVIDKRKNLVGIVSLDDVIS
ATLGVVYVPEQQSETQGVAENVPLDSKNVETSIENFEIMTKDADYTETNDIGAMENTIEL
DSKDIKFSLAQKD

>tr|A0A0S7BEL4|A0A0S7BEL4_9CHLR Arabinose efflux permease OS=Longilinea arvoryzae
OX=360412 GN=LARV_00594 PE=4 SV=1

MHLPPSLRHRKFVLLWAGLFISIAGSQMQYWSLLWHIRELTDQPIAVSGIGLARFIPILAF
LIGGLFADRYDRRKIMLITQATMALVALALGLLTLSGQIRLGWIYLLTAVQAV AISFDLPA
RQSLISNLVPRDDLASAFSMSSIAADLGAIIGPGLSGLTIAALGLFSVYMINAVSFLAVIVAL
LMIGTVPQQAVKRAENNHFRGRVDAGLFDIREGWRFILHQPVMGSMILDDFFATFFSSANT
LLPFITRDVLHASVQQYGWLSAGQSIGAVSAALVISQSRMRMRQGSLLLGAVVIFGLATVF
FGLSHSFWLTLVALILIGAGDSVSTILRNTIRQLQTPDELGRMV SINQIFFQGGPQLGEVES
GIVAQAFGPAAAIIVSGGVGCVLAVGLVGGRWPQLRAYDGV EEAANA

>tr|A0A0T7CXI6|A0A0T7CXI6_9VIBR Putative threonine efflux protein OS=Vibrio crassostreae
OX=246167 GN=VCR19J5_1210175 PE=4 SV=1

MTKNKHLES DYIFNSALETGIRAVCILSVNLSNKFDIHQLLAFDHLVVHTGDIINAPPSLHP
ANLQRNGELLVRRPLIEDGLALMVHKKLIKKEFTRNGFYRATELACVFIESLTNR YIEEM
SERAKWAIYMYQDSGDKLFSEVFNNAFERWTKEFHLVEKSIEQNW N

>tr|A0A0T9LB39|A0A0T9LB39_YERKR Cysteine/O-acetylserine efflux protein OS=Yersinia
kristensenii OX=28152 GN=eamB_2 PE=4 SV=1

MLPGWLSKLRKVTRHRLQKVYQSVSGYNFIILYGITALSTFVLPYTKDALWVISVSVLLA
IIGTVGNVCWAAAGHLFQAIFRHYGRALNIVLSGLLFWVAIDMLI

>tr|A0A0U0K3N4|A0A0U0K3N4_STREE Cation efflux system protein OS=Streptococcus
pneumoniae OX=1313 GN=czcD_2 PE=4 SV=1

MKAKYAVVWAFFLNLT YAIVEFIAGGVFGSSAVLADSVHDLGDVIAIGISAFLETISNREE
DNQYTLGYKRFSLLGALVTAVILVTGSVLVILENVTKILHPQPVNDEGILWLGIIAITINLLA
SLVVGKKGKTKNESIXLISRPSGTASKKILSVDQKRERAFERIKKEMTRDKRGSRIYQSVNRR
TIAIRITATHPSVSSRKCR LRINSTMA

>tr|A0A0U1KPQ2|A0A0U1KPQ2_9BACI Glutathione-regulated potassium-efflux system protein
KefC OS=Paraliobacillus sp. PM-2 OX=1462524 GN=kefC PE=4 SV=1

MEAHPEVSSLVIVISAAFITPILMHRRLNVIPVVVAEII VGLIIGQSGFNIVEESNWLETST
LGFIFLMFLSGLEIDFSLFTRKKKKRSNDYDTGPNPVLIAILVFSGIILL SFGMSYLFVLAGFI
DNVFLMTLIISTISLGVVVPTLKEAHAMKSPVGQTILLIAVIADLVTMILLA VFVSIYGDGSG
NMWLLLILFAVGIVLYFVGRHFKNQSFLEAMSKGTIQIGTRAIFTLIIFLVALSES VGAENIL
GAFIAGALV SLLAPNQDLVQKLDSFGYGFLIPIFFVMIGVDINLWSLFGDPMVLM LIPLLLI
ALLSKLIPVAILKKWYDTRTVVGAGMILTSTLSLVIAAAAIGERIGVIDSQMESALILVAV
LTCIITPPFFKKLYIHEEEAIPKQIVSFIGSNQATLPVVRELDQELFESHLYHTRLDKIDEK ITR
SVFDIRELESYQINELQELGVFDS DIVVVSTGNEEINKDIACFAKHNGVERVIARAEISDIDK
QLKENGVEVFSLLSTKTLLKAMIESPNVVDILT NQESALYEIQMNNSVYDGIMLREFPFT
GDVIMVRIFREDDSI VPHGDTRLRLGDNLVVTGSTEYVEELQGLLEFS

>tr|A0A0U3EEF9|A0A0U3EEF9_EUBLI Chromate efflux transporter OS=Eubacterium limosum
OX=1736 GN=ACH52_0015 PE=4 SV=1

MDAKKLFKLFISTFSLSMFTFGGGYVIVPLMRKKFVKELGWIEEQEMLDLTAIAQSSPGA
MAVNASILVGYRVSGVLGAFVAIVGT VLPPLIILSVISLFYTAFRDNLYVGFL LKAMQAGV
SAVIVDVVIDMGGDIFKARKALPVVMMFVVFILSAFVKMNVII LICGLIGALVTFTAKRT
GKNLL

>tr|A0A0W0V7D1|A0A0W0V7D1_9GAMM Cation efflux transporter OS=Legionella israelensis
OX=454 GN=Lisr_2182 PE=4 SV=1

MKAHALSVEETREELAKDTQKYGPNELEEIETTRWYTMLARQFTNILILVLILATVLSFF
IGDVVDALAILAIIFNGLLGFBVQEWKAETAIKNLKKILSPKCYIIQDDEKKEVDVKDLKPG
DCVFLEAGNVVPADIRLSKSNLMINEASLTGESTSISKQTEAVSEQTPLANRKNMAYMGT
HVVNGHGRGFVVAIGMDTEFGRIAELTGEIEESKTQLQKQLSVLGRQFGILALAASAVITL
LGIMANRDILQMLMTGISLAVSAIPEGLPAVVTIALALGVRAMAKKKALMRRLQAAEAL
GVVSIICTDKTGTLTKNEMKVEKIWLPDRITIEITGVGYELEGGDFKENKKITIDPSSQSDLMAL
LNTGLKCNHAKINKEKDRFKVEGSPDEAALVAAAVKSGLNQEHKSNTSEFTFDSNRKRM
SVIEESKDERVVHVKGAPVILKLSSHVLIADKKEKLNEKLQKKIEKAYIDFAEQGLRTLA
LARKTLISKDEVIDIDKAETGLTFLGIAGLLDPPRKAVPDALKKAKAAGIKIIMITGDSPLTA
KAAGQIGLKIEKTLTSSDLQDLSDEQLASLLKKEVLFARTIPKDKFRIVKLLQAQGDVLA
MTGDGVNDTPALKQADIGIAMGIRGTDVARSVADIVLSDDNFASIIAAVEEGRRQYDNIR
KFVLFLLTSSNIGEMLAILINMIAGGPLILIPILWINLVTDSASAVSLSIEQAEKDIMERKPR
KPEQPIITRLSFFLLGLFGSYIGIMTFILYQFYLNQSQALANTVAFTALVFMSNLHALNFRNL
QNPIADIGWFSNKWLLAILVMLSLQVLAIIYLPWLQMILHTVPLSLFEWPVILAAALPLFLIP
EFYKWLRRKKDDTPTA

>tr|A0A0W0YSD8|A0A0W0YSD8_9GAMM p-hydroxybenzoic acid efflux pump subunit AaeB
OS=Legionella sainthelensi OX=28087 GN=aaeB PE=4 SV=1

MSSLTIENRAALRTALAAVTSLIIAFICHLDKPYWSGMTVVLVANLYTGDILVKALMRILG
TVIGALIGYFLSAFVVDSELLYFCLNFFIVAIAVYYYNCISKYAYAWLLGAIAAFIVISGVAIT
PEDVLSSTIWRPIEIALGVIVSSIAFFVLPNRITDKTVHDVNLIFATVDALFVNLDRLMEQ
DRSIIQDIKDQNSQLKNRARQSLQTIVLIRYEFELDETQLNQYRFLDTCLIFCRALNYFLSL
NTFAAISTLPIKETISAIRFDISNLQANFFNISPTTLLTESALNKFDQYQSWAVWATPNDFK
SAKAWRHFFYQTNRMILIGIQVSLQGSYKHSNLDICINTSQQLKHDYNVITHSIKAGLTTML
ALGLWLFMILPGGLNGIISIVISARRNLYDMQNTGTMRLGCLLGGGTGLYFIMTFTMSL
YLLLVIIFFTVWAFSLFSFRHINYAYLGMQANVAIILVMAEHGASVMTVLPPIERMAGIVIG
IAASFVVANLICRMSLTDMICRYLSKLQNLAHNVACLLAENDKKTKYLDLIDTFWTCRE
LLSNATQKYALVHTPRTQWTPRQWQIDRAIEMERLLNSIQVTLNNVRESMDRKRAIKSAS
TYGIDLSVLERKILELYCSKPSCSMLVPDHLIAQQAILEIMGVKGLSEPNHVELENCAY
VLALQLEVNNGRKMMLKIQEK

>tr|A0A100HWZ6|A0A100HWZ6_9RALS Transmembrane efflux transmembrane protein
OS=Ralstonia sp. NT80 OX=1218247 GN=RSp1417 PE=4 SV=1

MKKWIVLFSIGIYLLINLDLTIVNLALAEFSKDFNASIEQIQLVIVSYLAAAAAFFCLSGVL
ADRYGKKRVFMAGLLFVLSLYIGAFSAHSIEAIIVARFVQIGIFSATLGLALILIGKAFPPE
QKGLATGVAVTITGIGLAAGPPLGGFILQAFGWEMIFLINVPLGLLSLLLTAVFVDRDDAN
ELSARKLDVVGVPYLLGLGCLIVLSNALATLSWAQIGALTAVGAISTVLFVRRSLHVEAP
LINLSLLRNGTYLTVVGIRIIFNFVMASFLFVLPFLMQNILNYSKVRAGLWVLCMTACIFVV
GPITGKVIDRHGYKVPVLTGMTLLLVSAAFLTLRVELSIVLFVIGLVSFGLSNGALTATTI
NGATSQVSPKHTGTAGLFFTLMSVGMFGVAVSGLILSKVGEFELARHIASTAATFTPEQ
LHTLHGLVNASQNLVNVAGTFADHPIDTVRDLVNTSYVPAMRALMAFNALLAAIGIGLS
VALFKRKEARPADSTDPTKSRNEHLEGAV

>tr|A0A101F6V1|A0A101F6V1_9FIRM Auxin Efflux Carrier OS=Thermoanaerobacterales
bacterium 50_218 OX=1635288 GN=XD63_1202 PE=4 SV=1

MVVLQTVFPVFMIAIGYILGKITEIDIKPIAFLSIYVLAPALFFSSLVKTNLTAAEFFQIVGFI
ILLSSGTILLVKLWGKIEGWDPKTVKSVLLATLFPNCGYFGLPVLLFAFGEAGFERGIIYCV
FMNLLHNTLGVYLAQAQTHLSPRESLINVLKMPGLWAMSLGLGLTSLELTPPEMILKPLEM
MGEAVIPVMLVTLGVHLARVRVGANIWLAGKVTTLRLVVAPLIGLLILYLFDPSTSLTSKV
ALVESACPVAVASTMFSIQFNARPELVSTAALTSTIASIFTFALILHFLV

>tr|A0A101I8T7|A0A101I8T7_9BACT ABC-type Na⁺ efflux pump, permease component
OS=Thermotogales bacterium 46_20 OX=1635293 GN=XE05_1771 PE=4 SV=1
MLKDSFVIYRKELKNIMKDRRAIFSVFILPMILPIIFLTIGFVTSAAQQRTDAETLYVVNIIGD
EDGRFTEVLQNFLVFERDEARVPDYTRAMESENYIIVELEGTDSDLTQVGNTLDARIYYRS
TSRRSNFAAQQVRNALNQYSSMIMSERLRTLGLSLGDLNPVKTEMQDLAPEEARGTEFLA
IMLPYFVLIFIFAGSMNIGLDTTAGEKERGSLAPVLVNQVSRTSIALGKVFYVMTVAVLNS
LFTFVGLMVAFILGGSEAFGGGEIPVNLAGFGIGSLIALLLVLLVLGFAASLIILIGSFARNM
KEGAGYVMPFYLLAIFAGIATMNMESVHQIHFYALPLVNSVFVMKDILTLQFFWSRFVVM
LLSNLLYTSLLVLGVARLFNSEKVLNTGS

>tr|A0A124BR66|A0A124BR66_9DEIO Auxin efflux carrier family protein OS=Deinococcus
grandis OX=57498 GN=DEIGR_100262 PE=4 SV=1
MIQALSNVLLPVMLVAGLGALVSARFPIDQATIARVTLYLLSPALALNVLLTTRVQAGEV
LTLGAAYALTVAGSLLLGLWTGLRAPQAQRRSLTASVGIWNSGNMGLPIALFAFGQAGF
AHATLLFLMSFVGMVVIAPVVYTARVRRPDQPPPSAGGMLLNMVRLPAVWMVALGVTL
RALHLQPPEGLMRGVELLAQATLPMVLLSLGLQLGSGGWPRLDARVWLATAARLIGGPL
LGLAAGLACGLRGEVLAVLVLSASMPTAVNALLIAREYGGDADTVARTAFSTVLSVPTI
AAVVALLPRLTG

>tr|A0A132BZ71|A0A132BZ71_9RHOB Cation efflux family protein OS=Tritonibacter
horizontis OX=1768241 GN=TRIHO_15060 PE=4 SV=1
MSASKWRDTDDKVTNSRRELIEYIRGYRIMSKQKNDRQTNLTRGIRVEIASLVYNLIEVVV
SVTVGLLTGSAALVSWGFDSTVEATSAGTLIWRLKAEKDGGDKRTVLHRNKVALYVVA
CAFWIVVAAILYEAVSAFISQEAPGFNWWGIAILFVSLVVNPLLAWGKYRYGKRLDSPAL
KYDAKDTMICEYQTIVVLGIGLTQWMGWWWADPVAALLIVPYVAWEAFEATKDARS
VGPGEAEATADA

>tr|A0A133SJG7|A0A133SJG7_9FIRM Transporter, auxin efflux carrier family protein
OS=Megasphaera sp. MJR8396C OX=1603888 GN=HMPREF3201_00634 PE=4 SV=1
MEITIKAAILVSFILCGYILKQLRFLGRSTFQTISTIVFNITLPAVIIANLNGIHFEVRYLFISLL
AIVFNLLMVGLGYGVGRTKDEKAFYMLNLNGYNIGNFALPFVSYFFDSAAVLIVCLFDAG
NSLMCLGGGYGLARYVRGEKGDNIFYILAKTIFSSLPVLSYMLMIILALGGLALPQVVIDW
VKVPASANTFLSMLMIGVALGLSLKKEYLHLYSDIGLRL LISAVFAVFVYVGLDYSMDIK
RVLMLVLFAP IAGMACYYTARLKLKIEVAACISSLYILISIVVMSTLIVILETI

>tr|A0A133Z478|A0A133Z478_9CORY AEC family transporter OS=Corynebacterium
kroppenstedtii OX=161879 GN=CJ202_00285 PE=4 SV=1
MPQVLSGFATIAIVIAIGFFVGKANLLGKHAQFTLQMYVYFLATPALLLDKLYVTDPLDVL
GPQLAVASGSALTIGLIYFLWARTALHRPIHESAVGGGLASSYCNASNLGIPVAAHVVG DST
VVVPTLLFQIAFYGPIVLAILDVVTAKEAHADGRAGRVNTRSLFITPFKNPMLLGALTGLVI
SILHAHAGVSVPHPLVEPVHLIGQSAVPVALIAFGMSLAGQKVLPSTSPRLEVGVASATK
ILGQPLAAFLIAHFVFGMTGHALFAACVVATLPTAQNVYTYATRYGRGLTLARDAGVITT
AASFVMIMLLALVFT

>tr|A0A136KTM2|A0A136KTM2_9BACT Arabinose efflux permease OS=Armatimonadetes
bacterium OLB18 OX=1617424 GN=UZ18_ATM001002104 PE=4 SV=1
MSRSEWPLLA AVFLEMTGFGMAFPDIQLRAEVFGAPGQIIGAVLAS YFVVQLLVSPA WGR
LSDRVGRKPVLLVCTALSAGSMVIYALAHTVETILLSRVVAGLAAANVVAAQAYIADVN
RGVQLERSMGRMSAAMLAGLVAGPAIGGFLATVGGNQLMGFAAAGCSLASLVWILFGV
RSVPVVASATSEAPRLRRRSWALLQDTPGLMRFVAIAVAGWFLACLEGTYGRLIKHNL
GMGQFEFGLIFSYESLLGAAVGWTLGWLATRLGSSWMLKGGYLLQAIGLLAMPFAPGFG
VLLLASTFYAFGIGVTNPTINSVCSKMTSNERQGELFGVLQAARSVGFVAGPILGGALFDV
LPGLPYYYVAAGVAGVAALMVVVPQDGTVPESAPVDAA

>tr|A0A137SMF1|A0A137SMF1_9GAMM Potassium efflux system KefA protein / Small-conductance mechanosensitive channel OS=Moritella sp. JT01 OX=756698 GN=AKG98_3020 PE=4 SV=1

MMTKHYVVLILFSLFMTVPVYAELSYGEAQLNNTLSQLEELESTPSVKLQIKYYQQALKD
LTEDTNARQTAVRYQKIIDDYPVTSQTLKAKITDYISAKFADPSDWSLNKVEQAIAKQNSN
LTDLKQQQQARSSSELTIGIRISSFQTDIERLRRLKLTHTQKESDKLISAGYSSLNSEQEAIRIS
LQIKESSLSTQIQMLELEQLSASNRSELAQLNRRLIQREQKDVSKNLTTLTDLRNSILRKET
EDAIARSKQINDSSLISSPFLQLQLEINQELSKELATVSAKSEIIQRKQQAQVTTQQVDALTTTL
TNFNEQVEWLKISSAFGENLRAQVSSLPSEPPLAKLENEIVESRLARFRYKKMLTQLDSLPL
ATKTLTPVEHESLLRFIELRRLLSQLISSLDNHIYEQTKLKVSYSKMNSTLVQIKQQADEH
LFWVPSSPFVNTQTISELLASMLWITSIDNSITIPQAILSVPLATLSLALLFILGLTYLHAPLN
KYFTKHIAEIPKVGKVTDKFSYTLRNLAYSFADALLPLSLFIITELLISAWFEPFAVNIG
HALQDSLFLLVIIYLFMRNLTRYKGLLQIHLKIDKKLIAKIWGYQVLFYIYWPSYIIQVLCN
QYPEQAYDGSGLRLAFIIACCALTQFYRRLYREKLPLTYKKKNNDKPHIVHHSIWTVFIMA
PIASAIIALMGYLYTAQVLLKQMESSLLMGVFFLLTYYLIRRGMHLLQKRRLAFERAKAKRI
DIIAQRMEKEVEKGEQNTSQESHFDIEEPEIDLQISAQSLGLLRLLTLLFVALNALFWSEIQ
SAFTFLDTITLWDAANTLNGVEYIDPITLKSGLLAITIFALTLVLVRNLSGALELLILQHLDL
SPGTGFAITTLAKYMTISIGFVVGFNFLGVDWAKTQWLVAALTVGLGFGLQEIFANFVSGL
IILFEKPIRIGDTVITRELTGSISKIQTRATTIVDWRKEIIVPNKAFITEQFINWSLSDSITRVII
NIGVEFNSDIELVTKLLLDCAEENSLLENPGPEVFFIEFGQHSLCFEVRVCYVAEMGHRLTM
THALNIRINQVFKEHHIRIALQQLDLNVKHGKIVSDSGHVMMSMKKGLSR

>tr|A0A139T2R5|A0A139T2R5_9FIRM Transporter, auxin efflux carrier family protein
OS=Candidatus Stoquefichus sp. KLE1796 OX=1574263 GN=HMPREF3037_02910 PE=4 SV=1
MNKIRDVKVKEEFMTALSTLFPVLFMVLLGLISRIKGFITPEQKEGANTIVFNVLFPIIFNI
LLTSKIESSAIFIVVYVFIASFAMVIGKLLGKFTGQHFSHISHFMLTTCEGGNVALPLYTSI
VGVAAYASNTVIFDLAGTLIAFVVIPLVAQKSAGETTFKELMKTIFTNSFVIAVMLGLILNLT
GVYDMLSQSALIDVYTNTVSTATAPIMGMILFVIGYNLKNLATIGSILKLLVVRVIFYIVVI
AGFFILFPHLMAEKTYLMAVLIYFMCPTGFALPMQISPLYKSDEDANFTSAFISLNMIIITLIV
YAVVVIFIA

>tr|A0A142YFN9|A0A142YFN9_9PLAN Magnesium and cobalt efflux protein CorC
OS=Planctomyces sp. SH-PL62 OX=1636152 GN=corC_3 PE=4 SV=1
MDGSPRTDLDCRMISIVVLVLGILALLAASLFSLLHASEAAQIQHLREQAAKGDRGAKA
ALRRAGDPESAATAARLGAIFALILAGALAGAAASDGRGGLDWLPGLAAVLGIAAAATIL
ADVAPRVLAASRPEWFAARLARTVGPATAAIEPLARRLRAGGFLAARLGARNAERASG
VEQRIKDLMNAGAESGGFDPSKHAIFKRVRFRCDRRARALMTPRDQVVWLDVRDTPPEIA
RKIVLSPHASLPVCDETLDNLLGMVQMKSLARGAEGQPTRFKGLLTLPDFIYEGTRGPQI
LDVLRKAATGAAVVLDEYGSVVGVTADVRDALLGTMIEKPEEESPRAVQRPDGSWLL
DGRFPIDEFVDLFIQIPRAQGEFDTLGGVLVTKLGRIPRVGEGFQDLGLRFEVVDMDANRV
DHVLRPLDLAR

>tr|A0A143WJC1|A0A143WJC1_KOMXY p-hydroxybenzoic acid efflux pump subunit AaeB
OS=Komagataeibacter xylinus OX=28448 GN=aaeB_4 PE=4 SV=1
MTVHVFPFLYVPVHRAPPISRPLPHPAWGRALVKYLSRLYDIFRNDGQWRSFMATAAFSA
RVLVSMSIALFLAFSFQLQSPMSSVTTVMIVANPTVGALVSKSIWRMIGTVLGAIISVALM
ATFVQSPILYIMGLSVTVGLACMAATFLRLFRAYAAVLTGYTIVIIAAPAFGDPDGIFLSAL
SRLSAVVVGIVTTAAVFLVTSPRRSDPLLEQIRTVFCDTIRYVLSRHDGGASTTTDGAFAHA
QRAGMLARIASLSDAVEYAATDNYDISVRHREIRAGLARLSGIVASYHPHAVIALGAVPVS
ASQDAPPADGRIAELMRTLLQTMENVPLSEGCPPACRHIANREALLEQAEHSPSPRQLLF
LDDARDLLSRLEHALCDLAHRGGNDRSLRLRPYMEWPTALRNGARGALTLLAGLAWY
VLHWTGGPMMMLYVVAASSLLSTAPSASRASGLLASGTALGVPAGLLCHLFILPRIDGYP
LLCLSLGLFLLPGIWLQFNPRLGIAAFGYSVFSTIMLQVNNPIHYNDIPLMNEWVAILMGC

CMLVLSFRVILPPNHRDLGARLVASLSRVSRLALARASFQGGQWIVWEHLQLQKVARLA
MRLSFCAPAEVTNLYVDAALAAISLGRLLVERLHRLADRADISLPERQQLAALGAFETLTR
DPLATARTLHNICTRSGAGQALTTLSPRRMEALACMEQAEQIIVDIPAFDRNGPIQWSDD
YPRAREFLRAAYSGGAMSG

>tr|A0A143YSR6|A0A143YSR6_9LACT Auxin efflux carrier OS=Trichococcus flocculiformis
OX=82803 GN=TFLO_2047 PE=4 SV=1

MISILLVRKIAQLFLIMILGYLLVKLRILKTEESIVLSKLSLYLVMPAVILSAFQVDFKPEIQA
GLMLAFVAAVAIHILLIIGHISGNLFHFEEIDIASIIYSNAGNLIPIVTAVLGTEWVIYSTAF
LSVQLIFLWTHCKLMFSKEKKPHFRKIILNVNMIAIFIGVLSMLWGSRLPAIILLKLSNAA
SLVNNGTEILLITFLATVTPAASTVTQFAQVHDKNAAYAGAINIMTTLLCIVTMPIFVILYYI

>tr|A0A160P4M2|A0A160P4M2_STRLU Transmembrane efflux protein OS=Streptomyces
laurentii OX=39478 GN=SLA_4646 PE=4 SV=1

MGVQAGLARLQLDEVEDLGLAAEDQVVEAQQHPRARTDGGGGPGDLGGTSGICLGDV
LGRGLGQVRQLVPGEGGVGGTAGADDPRVSRATSSGVTTSAASRAPAGAGAAGLVPA
ARSAPEGVVAAVEVPGSA

>tr|A0A171EY59|A0A171EY59_ACIBA Homoserine/Threonine efflux protein OS=Acinetobacter
baumannii Naval-82 OX=903921 GN=ACINNAV82_1605 PE=4 SV=1

MWQLYGHEFLTALIHFMVILPGPDFVITVRQSVRYGYLIGCLTAIGIGVGISVHVFTLV
GIGFLIQQSEWLMSLIRTAGAAYLVYLGWQCLRSQPNPNIEINGQTDSDTPSLLKAFTMGF
LTNALNPKATIFFLAIFTTIVSTTTPMKVQVFYGVWCMVNAIWMVSVLFAQPIVRKR
FLEFGVYFERVMGVLLIGIALRLIWSLFV

>tr|A0A174BMS8|A0A174BMS8_9FIRM Probable amino-acid metabolite efflux pump
OS=Catenibacterium mitsuokai OX=100886 GN=eamA PE=4 SV=1

MVGFIVLKKESTYICATCRKCMNAMKNYTYHLVAVLTVGIWGLTFISTKVLIGHGLSPQEI
FLLRFLIAYMGIWLISPRKLFADNWKDEFWMFLGGMTGGSFYFFTENTALEITLATNVFSI
VCTAPLLTTILSLWVYKKEKATRGLMAGSLLALVGVALVVYNGSFVLKISPLGDFLTLLA
AFSWAFYSLMRKMSNCYGITFITRKIFFYGVLTILPAFLIHPWNFDIARLLEPAIFNLLFLG
VLASLICFVVWNVILKQLGTIRASNYIYLNPLFTLIGSAFLGERLTMVALMGAVLILGGV
YWAGKR

>tr|A0A174MNE8|A0A174MNE8_9ACTN Magnesium/cobalt efflux protein CorC
OS=Collinsella aerofaciens OX=74426 GN=ERS852514_01841 PE=4 SV=1

MDITISLITTLVLTILINGYFSMSEMALTAKRAVLEHEAEEDGDKRAERAIKLAADSQLLA
TIQVAITLVGFASSAVASTSLSDPLATWLMSFGIAPLSAIARGLAPVIITVAVAFVSIVIGELV
PKRIGLSNAEGVSKQVVGTLSTFFQKIARPLVWLTGACSDGLARILRIKSADDRQNVSEEEIK
YMVSEQDDLLDEEKRMIEIFDLGDTVAREVMVPRVDTTMCEDDETADVLTSTMRQTGF
SRIPVYHEDPDNVAGIAHIKDLIQPALDGKGDQPIAGFLRDATFVPDTKDILPLLSEMQTSH
DQIVVVVDEYGGTAGIITIEDIVEEIVGEIEDEFDPDNKYLTRLSRREWLVDRFSCDDAIEL
GWPLEESDDYETIAGWILELCDSVPDIGEVEVAGYKFKVQSMRGQRISLIRVIAPAETDK
KDESSVDEPTTSGAGSANPHDGD

>tr|A0A180F7C7|A0A180F7C7_9BACT Macrolide-specific efflux protein macA
OS=Bacteroidales bacterium Barb4 OX=1633200 GN=macA PE=4 SV=1

MINDSTPNKVSNLVRGKQFIIKNQMTRKSCFIGIMGIMGIVAAGLVSCGNGKDGFDATGTF
EATEILVSSEASGKIMALDIKEGERLEAGAFAGYIDTTQLYLKKRQLSAGLRSDIRKPDIR
KQIAALEQQIATAKTEQQRMENLVQAKAGNQLDDITNNIKLLQRQLDAQYSTLDKTA
GASDAEAESLQYQIMQLDDLMEKSRIVNPRGTGLVKYAEQGEVTAPGKPLYKIADTELL
YLRA YITAGQLSRLKQGQEVKVYADFGSDSREYAGTVAWVSDKSEFTPKGIQTKDERAN
MVYAIKAAVRNDGYLKIGQYGEIVFEP

>tr|A0A1B1FV78|A0A1B1FV78_9BACT Cation efflux system protein CzcC OS=Flammeovirga
sp. MY04 OX=1191459 GN=MY04_2659 PE=4 SV=1

MSLTLPQGEEIFLEKNLTLVAERHNIDIAKAEIIQAKAWPNPELGVEIAMYDNEDNKWFRT
DSEAQRVVEIHQLIEMGGKRKKRTNIAQKEAEIAEYEFYTTMRELRTSLMVELHYLQ
EKSNSYLNVEIPLERLIEVYKEQSDKGNIAKSEVVRLKALLDARKGWL DIEQEATDVSSQ
LKLILNLQPQVDLTITLPTFNYSQNVVDPELWVSEAQEHMRMDFKIEQLRLQQVAESLAEK
AENVPDIELGTMYDRRGHAHQADYWALQIAFDLPVWNRNKGGIQAAKIAQEQQQVKVTQ
AENQLQIDVYNAAQKLNQITKVYDALDPELSEEMRAVMESVTKSYQKQEISLIEFIDFFES
YKENLGQLFDTEYALFSALELINYTVGKDIYPIQ
>tr|A0A1B2FNM4|A0A1B2FNM4_9ACTN Na/H efflux pump OS=Streptomyces sp. CB02366
OX=1703935 GN=AMK24_28920 PE=4 SV=1
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LGPTLLGQIAPGLSGRLFPADMSQAHLLDAFCQFGILLVAIAGAQFDPLILRRRGGLAAR
VSLAGLLVPLGLGIATGYLVPASLLTDSGERGVFALFLGVAMCVTALPVIKTLADLNT
HRNVGQLLIAAAVFDDAVGWLLLALVTALASGGAGGPVVLTTMAWTAVFIAAACAVGG
PIGRRMSRTGGGRVPVSAITVGVAVVVLYGALTAAGMEALFGAFVAGATLLRHIDPAR
LAPLRTLVMVAFAPVFLGSLVGLRMDLTALAEPVLLTGVVVLFVATLGKFAGAYVAARS
GGMSRYEGLALGAGMNSRGMIEVVIALVGLRIGVLDTVTFTIIVLIALITSVSAPPLLRWAS
SRIAFESDEQEREERLAGWSTEPAFSGGPPPKSARQEKTADTS
>tr|A0A1C0U3B1|A0A1C0U3B1_9GAMM Leucine efflux protein OS=Photorhabdus australis
OX=286156 GN=leuE PE=4 SV=1
MNTVTLLTYLITCVVSAATPGPGTMSVIAYS AFLGW RKTLPVIFGIQVGMLAMALLAFSG
VTAALSASPLLFNLLQYIGALYIAYLGVLSLKYARKGIGTDGAAYDKGAFRNFNHGALVT
FASPKTLLFFTSIFPIFLDASRSVLPQMVFLLTLLLGCTFFVHHIYAFCKMYFSRLLKEHSVIF
NITVGIIIFLGLALYMALQVELYVI
>tr|A0A1C3GW61|A0A1C3GW61_9PSED Putative amino-acid metabolite efflux pump
OS=Pseudomonas sp. 1 R 17 OX=1844091 GN=eamA_4 PE=4 SV=1
MNPIADKSYEVRLTSPLPIVFILLWSSGYIGGAYGVRYGEPFTMTFYRFALAALVFLGVAL
AIKAQWPKRLAPYFHAATVGLLLQALQFGGLYAGISQGVPAQAALIVGLMPVVFVIGA
YFCLGEQLSWRDLPGSILGVGGVAIVVASSFFGSEASVGGYGAVGLALLGITLGTLYQKRF
LGGVNLWVGCFIQMVTASLVMLLLAYTTETMQVTEWVPFVASVAWITLMNSVGALTLL
YLMIRRGEASKATNLFHVIPAVTQIMASLVLGEVPSGVAILGFVVSGAGVYWMNHVRAK
>tr|A0A1C4GVH3|A0A1C4GVH3_9GAMM Regulator RcnB of Ni and Co efflux
OS=Acinetobacter albensis OX=1673609 GN=GA0116959_10817 PE=4 SV=1
MKKILTILAISFSALMASSVSTAAPHDKQDRSRGWDHPRHQESNKNRDFREDDDDERMQ
DKRRGREERGKRLQQHKWQTGYVMPQHYRGNGYKVDYKNLDLPKPSRNQQWYKINN
DYILVDSDSHNIVQIKGF
>tr|A0A1C5RPS5|A0A1C5RPS5_9FIRM Magnesium/cobalt efflux protein CorC OS=uncultured
Blautia sp. OX=765821 GN=ytfL PE=4 SV=1
MESGSSMPLAGFVILLLLLWLNIGIFYGFSAAVHNLSENEVEKRAQEGDKKAVFLLSLINNP
VSFVNAIPLIVMASGVCFGAFIVPWATETFHPIYIKHLAALILVLALVILLASLGILTFRRIGT
YHPEKYAYRYMKIVGFFTRILYPFTMCVTFIAKLAARPFGVAFNQSEDPVTEEEIISIVDEA
HEQGVIEENEAEMIQNIMEFTDTEAKDIMTHRKNVIAFDEEDNLQTIVDTMLEEGNSRYPV
FRETIDNIVGIIHYKDALKFLTRNSWAKFKPLKDLPLGLIREASFIPTRGISDLFKSMQMKKI
HMAVVVDEYGQTSIGVSMEDILEEIVGDILDEYDEDDSTFRTQKDNSVIIDALAYLEDVAE
ELGIDFGKVEFETLNGYLTNLLGHIPTEDDLDEIVVNGYRFRILSLGNKTIGKVRAEKIKK
EPKGEDKKCQDIQNSQT
>tr|A0A1C5UCE9|A0A1C5UCE9_9ACTN Spectinomycin tetracycline efflux pump
OS=uncultured Collinsella sp. OX=165190 GN=stp_4 PE=4 SV=1
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QASQSAPTPHAVPAPRPTAGKWVVLFTVVAMTFMSTLDSSIVNVALPAMQRELGVGASDI
QWVSSIYLLACCVTVLVFGRLGDRYGKVRFFQVGVALFTAGSALCGLATTLPVLIGARVV

QALGAASATANNMGIVTEVFPASQRGRALGITSTFVSLGLMCGPTIGGMLVAVYPWESIF
LINVPVGIVAFVLVGLKTLPRDAPRTEADRSARSGFDIAGSLLLAPAIFFTFSSLTNLANGATP
LLMGLLAAGLALLVVFVLVERRVEAPLVRLDLFGNAVFSANLAAMLLCFLAVGATEYLL
PFFLQDACGYESNVAGFILTAIPLGMAIMGPLGGALSDRIGSFWPCLVGLVIYAAGIWFVG
GLSDDAGVVVIVLLMAAMAAGTGLFQSPNNALVMGSVEAEDLGFAAGSLVSLVRYMGMS
AGVTGGTVLLYGQMSSLAGHAVTGYVEGRPELFLAGFSFTFDVLAVLVLLGAVLLVVGA
VLKRGR

>tr|A0A1C5WDA2|A0A1C5WDA2_9CLOT Potassium efflux system KefA OS=uncultured
Clostridium sp. OX=59620 GN=kefA PE=4 SV=1

MIIGKIINSVIVLISYILIKLIQYLLHRLFEFTNFDVRYENTLSSVLSSITYYIVFVICVILVLRE
FGIVDATKFGSLVTGASIVGLIAGFASQSILKDIFNGFFILFEKQLQVGDFVIINEEFRTVEE
IGIRSTSLRDWDLRRITLPNGSINSIKNYSKDKMRVVVHVKVSYEEDPNKVISSLQEVCEIM
NNQYSDYLYKDINSNKNKGFCVYGVTDIDKSSIGAQYTTITGMVKSRYRYSALKESKLQILI
VFNKNNIKIAYPRHINIISHENKDMNSLD

>tr|A0A1C6A3R7|A0A1C6A3R7_9FIRM Arabinose efflux permease OS=uncultured
Flavonifractor sp. OX=1193534 GN=SAMEA3545394_00572 PE=4 SV=1

MRIASHAPSRASAGLRAWVVCGLGCLALFTVMGLGVNAFTVYQPYLLRVHGFNTAQQGSWI
TTVRSLFALLSILTVDRLCRRLGLRNTMVLGMACFVGSYLLFGFARGFSAYCGGAVLSGL
AYGYGGMIPLTLVISRWFPTRGRGFALGMAAAGSGISTIFAPPLITGAIQALGLSAAFLWEA
AAGVLLTLLVLLLVRDSSDCPELQRAGDSAPGGRGEGLSRPLLGMVLLSAFLTGGPCGPG
FSHLTVLYTSAGFSSGTAALLMSYLGVLVIAAKVLYGWLSDDLGRMANRLIFGVFLAGF
ALCCLAYTQSLPLAAAIITLTGLGMPLSSVTLSVWAGDLSAPEDYDRLVKWLSSAYMLG
SLVTGPVPGLLADRFGGSYVPAYGLFLFLLISMLLIQTVYRRTGVGGRPQR

>tr|A0A1C6HNM7|A0A1C6HNM7_9CLOT Auxin efflux carrier OS=uncultured Clostridium sp.
OX=59620 GN=SAMEA3545404_01813 PE=4 SV=1

MTDIGMILGQVAILFIIMLVGVIAARKTKILSDAGLGAMSQLALFVTVPCMVLVVSFQSEFSQ
QLLLDMGHAVAWSLGVHIVMWLLGKKIFNRFALHQRKPLQFAAIFSNAAFMGYPVLQAI
FGETGLLLGSMYTAIFNIFLWTVGMSIFSGSEKEDRKAAIKRVLLNPGTIATVLGLVMFVFS
IKLPDMPMQALSMLGNMTTPLSMLIVGARLADVRIKEAFAGAGVYLACALRLVVIPLILM
GLMKLCRVPLAMGVVTIQAAMPIAANTAMFAEMFGGDAPFASRLVFLSTLLSIITIPFML
LVA

>tr|A0A1C6RZP3|A0A1C6RZP3_9ACTN Threonine/homoserine/homoserine lactone efflux
protein OS=Micromonospora aurantiaca OX=47850 GN=GA0070615_0179 PE=4 SV=1

MSDIQIVSFVAASLLIIVPGVDFALVTRQTVRYGRRAGFVVLAGLFAAALVHASLATAGL
SALLVSSPALYTVLRVAGALYLLYLGGTILWATRPRRAAAPAAQPVTVGAGGPGPDADT
GPVAAPETVAADPHVARRSFVMGVTSQLLNVKVVVVFYVSFVPQFVKPGDGAAARTAVL
AATFIGLAVLWWACYILLIDRLQPWLTRPSVLLVIERLTGLILIVLAVRIALSH

>tr|A0A1D8AZ91|A0A1D8AZ91_9BACT Sugar efflux transporter A OS=Lacunisphaera
limnophila OX=1838286 GN=setA PE=4 SV=1

MKALLAPWRRLLGHREFGIMALSNLVLGMAYSFVAPFYSMFGTLEVGMTNWVFGVFMT
VTSLSGIVITTFLSRWSDTRISRRAILLACVCGVAGYAGYAYVRDVIWLTVIGSLALGVSS
ITFAQLFAYQREFLTRHGVPDAEAPLYMNIFRLLFSLAWTIGPAIAAWVMIKYSYEGIFLTC
AAMFGLLFVIVWRYIPARPPTAAAMANKVPLSQVLRRPYLLCYFAAFVLVFICVTMGMM
NLPLLILQTLGGTAEQVGIAFSVAPVFELPLMFWFGLLASRSHPGRLIRIGMIIAVAYYALL
FFVTQPWHIYPLQILSAAMIAVVSGIAITFFQSYIPDQPGTATNLYTTANRIGSTIGYLSFGSL
AGSFGYRAIFLVCAVLCSA AFLLLWLSREKHEQAVAPA

>tr|A0A1E1F3G7|A0A1E1F3G7_9SPHN CDF-family cation efflux system protein
OS=Sphingobium cloacae OX=120107 GN=SCLO_1020190 PE=4 SV=1

MTMHGDHEQGHGHHHHHHGHHDGPERHAHSGHGHNGHGDGQDDGRGGRDRFPFPRAD
AEISHYFDHIYLSAGHDRNAKRTVWVWLTAATMVVEIVFGWITGSMALLADGFHMAT

HAGALAVAAAAYGYARRHARNPRFTFGTGKVGDLSGFASALLLGVTALFIAVESGMRLF
EPVDVRFGEATLVAVIGLAVNLLSALLLGHHDHGHGGHDGHDGHDHGHGAGQDCHKHSDN
NLRAAYVHVLTDALTSVLAIVALMAGRYLDWWWMDPAVGLLGAVVIARWAWGLMKD
TAAILLDTAEPALMARVRDLTEAEGAVIRDLHVWRVGPAAHAAIISIAPGADSAAVRARV
SALPRMEHVTVETV

>tr|A0A1G5ZL72|A0A1G5ZL72_9RHIZ Threonine/homoserine efflux transporter RhtA
OS=Sinorhizobium sp. NFACC03 OX=1566295 GN=SAMN03159448_05462 PE=4 SV=1
MEDDQNKWLGTLIIIGSAIAYSLSGYFTRLITLDVWTVLFWRGIFGGLFIGAYVWVRYRK
DLWVAIRAMGMAGFWVMILSTVATICFINALRLAPVADVMTIHAAIPFMTATLALVFAGE
REEWATWAASFTALVGVMIIVNPQASSDYLAGYAFATTMALSYAAMIVIIRKNRHASMLP
AASLSAFLCAFVALPFAQPMQLAAPVMLDLVLFGTQVQFGLGLLLMTIGTRLISATRSALIG
SMENPLAPLWVWLAFFGEFPAWATWAGGGLVMGAVIFDVLTCKSKRRQKSVEALAQG

>tr|A0A1G6CIV7|A0A1G6CIV7_EUBOX Threonine/homoserine efflux transporter RhtA
OS=Eubacterium oxidoreducens OX=1732 GN=SAMN02910417_02434 PE=4 SV=1
MVCFLTITFFLSSIVKQKKIKGMVSKNMKKFAIFMPLLAGICWGLTGLFVRNLGDHGLSN
VSILGGRTVFAVLILLIGILIYNKERLKRHLKDLVFIILAGFVGSFALNVCYNYTISVMTMS
LAAILLCLAPIFTLILAAIFFREKITTKKVLCMVFAIFGCVLASGIVGDNSSVNVTLTGVFGL
LSAFFYGVYSICKVVTNDGYTSLTITFYVQVILACIPFTNWNVSVLHYMASDPFPHSAILII
HALLSSAVPYLLLVSFFHHMDTGLATIIASGAEPVTAAVLGMFFYQEIPTVIIIGILVITIVA
LCILLKPDAPPKEEPSQVPS

>tr|A0A1G6KNG8|A0A1G6KNG8_9ACTN Threonine/homoserine efflux transporter RhtA
OS=Olsenella umbonata OX=604330 GN=SAMN04487824_10923 PE=4 SV=1
MGNASGAGIGAGWTQRRADLMIAVIACAWGSSYLMMQVGLSSIPPFGMVALRFGIAFVA
VAIIFRKRLRELTAASVARGAVLGFLLCVFFGLLMYGLKTTASTAGFLTSKAVIFVPLIVA
VATHRAPSRATLAGIGICVAGLALLTLGSPVSLGGAGLCLAGSAVYALQIVATDTFSRSD
DALLLGICQLGFAAVFGAFAFNLAFFGPVLPQSPAEWGAVLGLALVCSAFGFAMQPVAQS
RTTATHAGLLFSLESVSSAVLSFVFLGEVMAPOCYLGCALILAAVLLSSLADGKADAAEG
AADARAFSASTHGGLARGLATARVHAKRAQE

>tr|A0A1G6W2J5|A0A1G6W2J5_9GAMM Regulator RcnB of Ni and Co efflux OS=Aquimonas
voraii OX=265719 GN=SAMN04488509_10486 PE=4 SV=1
MRTQLSGRFLSHATLLIGLALAAGSAHAERPDRGADYGGRGSDSGVERGDSKKGHDG
WGERGGGRGEREQSWQAGSQDRRDSWQERGSSRSEGWRGESRGESSQMQRAGWQGG
HREPEHRGGREPQWQGDWRWGQDRRDHWNSTGTRRDDARHWQSDRDWREEHRGRGDWR
RDDFRNRDWRHDDRHRGDWRGDWRHPEWRRHWQHGWWGGHRYRAEVRYVYPRGYRA
QSWRIGYRLPPVFLVNDWYVDWRYRLAAPPWGCRWLRVDGDLILLVDERSGEIVDVLY
GFFYY

>tr|A0A1G7EKG7|A0A1G7EKG7_9BURK Cu and Ag efflux protein CusF OS=Massilia sp.
PDC64 OX=1881046 GN=SAMN05428966_109297 PE=4 SV=1
MIRFSSLFGTLFVSAGLALAAADASAQMOMQMPMDHHDQHSAMAATSQEDTNALSEGEI
KKVDKDTGKLTIKHGPLTNLGMPGMTMAFKVQNPAMLDQVKVGDHVRFRVERINDTFTI
TKLEASI

>tr|A0A1G7Z4I9|A0A1G7Z4I9_CHIFI Outer membrane protein, cobalt-zinc-cadmium efflux
system OS=Chitinophaga filiformis OX=104663 GN=SAMN04488121_108121 PE=4 SV=1
MHACAYGSLQRLTINLYVPVLLISHKLFNTNFIINDSNMSSKDLHVASIYRILTCCLLLAA
GISAKAQDTHINLPDAEKQFLDRNLQLLAEKYNVSIKAKQIIQARLYNNPNLTLSGNLN
PDQKKFFDISNQTGQYEIGIQQMISLAGKRKNQVKLARTNAEMAENAFFDLLRRTLRLS
DFYQAYYLQSSMKAYEAQIATLEKMDATYKELQKGLVTLKDAVRLRSLLYSLRAERTN
MQNQVNDLEAELQLLLQNNHWSFAPEVQDNALAGIPEVRQTSLSLVDSAYANRQDLLL
AQNSLLYNQQNYSLQKAMAVPDLTLGASFDRKGSFVNNASFLNLGIDLPFFNRNQGNIKA

AKFSVDQNKLLVQQQTQVVENEVQTAYVKAMNTDKMLESVDPAFRGQFEQLLQSITDNF
MKKNISLLELTDFYDSYKENILQLNQLQNDRMQAIETLNFAIGKTLFNK

>tr|A0A1G9P3W2|A0A1G9P3W2_9RHOB Threonine/homoserine/homoserine lactone efflux
protein OS=Paracoccus chinensis OX=525640 GN=SAMN04487971_1442 PE=4 SV=1

MEAAALLTYMATLGALTAPGPLVAVLVARSSSQDRAGACALAIGMCVGDVLVILAICA
GLGFWLQAHPEIFTVGKYAGVGLLLWMAFRMWSASAAPAAHPAPTTCGISSALVGLALC
LSSPQTVVMYLVLPRVIDLTGVRAQETMLIAATILALLGVFLLVIFCADLTQRLLRSSVG
VVLWARGTALAVATSAAGVFFW

>tr|A0A1G9SGW9|A0A1G9SGW9_9RHOB O-acetylserine/cysteine efflux transporter
OS=Maricaulis salignorans OX=144026 GN=SAMN04488568_10983 PE=4 SV=1

MRIRDLLALIAVCAVWGVNFVVAKFSITGSPGWVPGFEGSPPLFFAFLRFALLFIILSPWLM
PRPGDMKAMFGIALTMGALQYALMFLGLQWATPSGMAITLQMGVPFATLLSVVMLKER
LGLPRITGIVIAFAGIILVVARPGIGGLSFGLLLGIGAAFSGALGMILVKRMPLDSMRMQSW
IGLISWPPLLVLVSLVFERDQISSVMAGGWPFMLTVIFTVLLVNVFGHGVFYKMLQRYDAT
MIAPITLLAPLIGVISGIVITGDEAGWRLFVGGGLALLGVGIIALRPNRALPEAGLAREKTL

>tr|A0A1H0R2I3|A0A1H0R2I3_9ACTN Arsenite efflux ATP-binding protein ArsA

OS=Nakamurella panacisegetis OX=1090615 GN=SAMN04515671_3368 PE=4 SV=1

MSDTIERPAVRPATRTRIVLHTGKGGVGKTTMSAATALAAARAGHRTLSTDPAHSIGD
VLDLEIGSDAAPVNGVDGLFAAQVDTRGRFEEAWADIRGYLVGVLAARGVSELQAEELT
VLPGADEIIALLEVHRRALEGQFDVIVVDCAPSGESLRLALPETIRFYADRLMGAPARLM
RSLAAGFAGLTGGRASSGPSAAQVSDALTGLLDDLADARAMLADPAVTRIRVVVTPERV
VINEARRLLTGLALHGFVAVESVLVNRMLPEIAVGGEFMAAWYAAQQACRPLIEESFGRLP
LRQVRLSAVEPIGLSMLLEDVAAQLFDELDPIPEAAPAPSLRTDGSDGRYRLIDLPLAERSA
VGLSRAGDDLVTIGPLRRRISLPSTLQRCRTVGASFSGDTLVVEFVPDLDRWPAALSEPLT
RRSTSPTDHPWSEGRPASQSRSGEPRTGVTADLAGAS

>tr|A0A1H2Q6E4|A0A1H2Q6E4_9BACT Cobalt-zinc-cadmium efflux system protein

OS=Hydrobacter penzbergensis OX=1235997 GN=SAMN05444410_10152 PE=4 SV=1

MAKVRKLLALAAGLNTIIFVGEMLGGAEGHSTSLIMDGVHNFSDALVCLFLAYLLPVT
MSRNFQRLANALNSIGLISISVFLIWQSVNNIHPVPTIGYIPLIAGLLAAIANWGVARILYSI
KDRNAAIRLTYIHIVGDVYVSLAPVVAGLLVLLTGKYIFDPIIILVGVWLIWATIKEIAHS
HDELIWPEHVADQ

>tr|A0A1H3V967|A0A1H3V967_9PSED Threonine/homoserine/homoserine lactone efflux
protein OS=Pseudomonas sp. PDC86 OX=1882759 GN=SAMN05444743_13944 PE=4 SV=1

MMRFIQEVVLGSGAHCLIIVFGEQVSARQCERPNIHAAVDDPYVRDCIQHNFLFASGSL
NLRAFPVDGPSMIDLATLAVFSGAVVLLLLSPGPNMAFVISHGMTHGWRGGAASALGIGV
ADLLLTALTAMGV TALVASWPPSFDLIRYAGVIYLLWLVSRTLQAKPRGAATQVERVRL
GRVCVQAMLNSLLNPKALLFFVVFPLPQFVRPEAGPIATQLWVLGGVLTFAAVFHLVLGV
FGGAASRFFSGRPGTATLQKWGLATVLTVLAVRLALMARPT

>tr|A0A1H6F5S4|A0A1H6F5S4_9GAMM Cation efflux family protein OS=Thiotrichales
bacterium HS_08 OX=1899563 GN=MBHS_00593 PE=4 SV=1

MGGAILADVHILVACDLTVSEGHQISEVVHQTLKASHDICDVIVHIDPEDDEEQPRNSDL
PLRDTVLTQLQKQWQHIPAAKHIIHINLHYLAGKISMDIHLSDIVENFAQARHIAEQFSSS
AKDLVYIKQIRVYIDPYPGLSDNK

>tr|A0A1H6Q8U1|A0A1H6Q8U1_9GAMM Homoserine/homoserine lactone efflux protein

OS=Pseudospirillum japonicum OX=64971 GN=SAMN05421831_10110 PE=4 SV=1

MVFEIWVTFLLAICVVSLSPGAGAVAAMSTGLNFGFPAALWTLAGLQCALILQVCLVALG
LGIILNTSMIIFEIKYLGILYLVFLAAQNWFITPRSLNQQQPTQAYNAHKLFKAMLINLSN
PKAIIIFMLAVLPQFIQLQDPLLQYLVMLTMSVDLLVMGAYATFAYRVNLNLLKKPSHQT
LLNRSFSCMFLLAASALFWFEPSS

>tr|A0A1H6Z3I2|A0A1H6Z3I2_9DEIO Threonine/homoserine efflux transporter RhtA
 OS=Deinococcus reticulitermitis OX=856736 GN=SAMN04488058_10841 PE=4 SV=1
 MSPHSLGLLLLVLVTLLWGSTFAVVKEELGELPPAVLIAWRFLIATLALLPALWLWRPRS
 AGAAPAQRGPAPRLWRDGLILGAWLIAGYGTQTIALQTTTANRAAFFTALSVVVLVPLWLT
 VAQRRRLSPALWLALPLAVGGLGLLSWEGGALVVGDFWALACAVTYAGFIVALERMAS
 RHEALRFTVAQLLTVTALAWVWALLTPVGQLWPPAGAWGPLLYLGLAATALTLLQTV
 GQRHVSAAEASLIYALEPVTASVFSFLLIGERVGPRGALGGALVVVATILSSRAEGHAHPE
 LPAPATAEPPG

>tr|A0A1H7W950|A0A1H7W950_9BURK Glutathione-regulated potassium-efflux system
 ancillary protein KefF OS=Variovorax sp. YR750 OX=1884384 GN=SAMN05518845_117176
 PE=4 SV=1
 MLVAGAFLPGETPASVLLRYVRGMTTTTSTGTPADRPDGGSGGIYVLAAPHWRDSRVN
 RRMLAAARAVPGVDVNDLYGSYPDFADVEAEQARLARASLVLLHPIHWYSMPALQKL
 WLDDVLSYGWAYGPGGTALQGKDLWLVTGTSPEASYHPQNYHRYFFDAFLPPYEQT
 ALCGMRFLPPLIFYGARSASEVDVKSHVETFAQRLGSYPDWPEIEEIDVCVSCPVPESDRPA
 DNDDVAKVVSNAFQAAMSHGLATATAIASADDNGRKAP

>tr|A0A1H8NKT1|A0A1H8NKT1_9RHOB Threonine/homoserine efflux transporter RhtA
 OS=Salinibacterium flavidus OX=569882 GN=SAMN04490248_103232 PE=4 SV=1
 MRTESRPTTSSATLSMGPVEWAMLLLLSVLWGGSFVVGAVVRDLPTLTIMVLRVGLAA
 LVLWGVIKRLPRNPRAWIAFLGMGVNLLIPFGLIVWGQQTIASGLASILNATTPLF
 TVAVAGFLLSDERINGRKLGMIAAGFAGVVVMIGPGALSGLGTDVAAQFACLGGAVS
 YAFAGVFGRRFKRLGVDPVVVAAGQVTGSTLVLAAPLALVIDRPWALAMPAPSTWAAIVGLA
 VLSTALAYILYFQILQRAGATNLLVTFLIPISAIAGVLLLGEHLGLEIAGMVLIGAGLLA
 IDGRVLNIGKRRSATSQATIRR

>tr|A0A1H8UWU5|A0A1H8UWU5_9ACTN Threonine/homoserine/homoserine lactone efflux
 protein OS=Streptomyces rubidus OX=310780 GN=SAMN05216267_10907 PE=4 SV=1
 MPAAVAFLAVLPAFLGACVLIAASPGPSTMLIIRQSLRSRRAGFLTVLGNETGVFVWGV
 VAACGLTALLAASQAAYDAMRIVGAVVLVGFGLQTLKAARAGRHADGDPVPGAPPLDG
 SDPDAVRPGAANSAAAPGSGPGDRDPRHEGLRAYRSGLLLLNLNPKAAVFALSFLPQFVP
 AGEPSLPAMIALAAVWAVFEVGYGYLYVWFVARMRAVISRAGVRRRLEQISGGVLLLLG
 LRLAVEG

>tr|A0A1H8XV75|A0A1H8XV75_9PROT Threonine/homoserine efflux transporter RhtA
 OS=Rhodospirillales bacterium URHD0017 OX=1380357 GN=SAMN02990966_06235 PE=4
 SV=1

MDRVSPKVLALLALLTAVWGTNWPLFKIALDELPVLTFRSITMVTAFILLTAILVVRRESF
 AVPKGKWPALIAASAMNILVWNIATSLAVLYIPSGHASVLSYTMPLWVALIGFVAFGQRL
 TGRLLAAILIGAAVLALMLPNFASYERAPAGLFWGLFAGFCWAVGTIVKRTAWPGMG
 LSLTFWQIVISLPPVLLGALVIDGVPDHWPSAKALTATIYTGAIPMALGTATWFALVKLLP
 AQVAALSSIAPIVAIVSGVLLLNEPLSTLQTIAIGSTVVALWLALVPKRER

>tr|A0A1H9FT58|A0A1H9FT58_9ACTN Amino acid efflux transporter OS=Friedmanniella flava
 OX=1036181 GN=SAMN05421756_103374 PE=4 SV=1

MTRITARAAAPGLHPDRVTESRVGTVRGTALFVAAIVGPGILTLPALAAGEAGPASLVTLG
 VLLTVSAPIAFTFAALNAAAPAAKGVAGYATVAFGPLAGRLVSAWFRSGVPVIGVPALGLI
 GGGYVAEATGGGKATAVTVAAGICAVAVVASVLHRPGSGVLTLLLSAALTVLIVGTAVV
 ALPHGHTASLRPFAPGGGLAAVAASALVLTWVLTGWEAVTNFTDVLDPRTLPRTVTGAT
 LVVVALLYAAVAVPEILVLGPTAGGTQAPVAAMLRIATGSAGAVLAAVIAVVIATGNSIA
 YVGS LAEMGTTTRPTRGARAARTGRASALVVPVVIAGGLAAAALTSVSTGELVSVCA
 GSVQVPVYVAGLAAGIKVLPTWSRSWWSSVVATAAVALLVPAGRYLLIPAVVALGVVARY
 AYQCRSPGVRTAGPPRSRAEQDA

>tr|A0A1H9IMA2|A0A1H9IMA2_9GAMM Outer membrane protein, cobalt-zinc-cadmium efflux system OS=Solimonas aquatica OX=489703 GN=SAMN04488038_11098 PE=4 SV=1
MSSLSKAGRSLALLALACQTLLYAQPPEAPPEPAQLSLPAAAQLALRFNPPELAKFGYDR
QALQGRQTQAGLRPNPELGFEDNFAGSGAAREITLRLSQAIEIGGKRDARLNQSQRLDR
LDAEQSLAQLEVLAEETTRRFIDVVETQQQLRLAERGVDYAQQSLAAARRRVAVGAASSL
EINRAQIAQERALLEREHQEHLSTLRRKLSEQWGRSEAQFEAAQAQLLELPEVPDYSELL
ARLRRSPDFARFDLERRLREADLRLAQAKAHGDPVLSAGLRRTDSAGDVAMVASLLMPL
PFANRNQGAIAEARALRERVDTQQAAQVRSEVVLVDMLQELRHARTVVESLQTTLLPQ
AEEALTLTRRGYANGRYSQDLIDAQRTRLELERELIANAADYHRYLAAVERMTALAPA
AAP

>tr|A0A1I0BDJ2|A0A1I0BDJ2_MYXFU Outer membrane protein, cobalt-zinc-cadmium efflux system OS=Myxococcus fulvus OX=33 GN=SAMN05443572_101955 PE=4 SV=1
MDSVTPVAVVLARNLLESLWVGVGTRLALGQGMSLVSVSLVLTSPSEAWSLERVVS
ESLARSPEVAAAQAEEQGAEGVRATDGRWPRANPSVELALVTDALTGDTGEQRTLVLS
QALEVAGQSGLRVERASAALSAARARRHAVMLSASAGAVESAVELERREARATLARES
ELTREMEAATVRRFAAGDVSELDRNAAALERARAEARAAQALAEVVAARAELNRRLGR
SMDSALRVSLVDTATQPLPSSLEGEPPSLVAARAEVAASGSEVDLLRRERIPSPTVSLGYER
ERRPESHGAFSDVHTEHLIARLSVPLPLWDRNQPELAEARARRKVRESEQVARERDVSA
EQSVARATFDAARSAHEALMAVRPSVDRNLELVRRAYEAGELGLDALFLARDRAFAAAA
EGVDAAAALVRARVALLRSVGRLPTGQVPE

>tr|A0A1I0WMV6|A0A1I0WMV6_9CELL O-acetylserine/cysteine efflux transporter OS=Cellulomonas marina OX=988821 GN=SAMN05421867_10371 PE=4 SV=1
MPPRDRLTALLVALCWGVNFPPIHLTLEQFPFLAGSLRFVAVLAVPAVLLVPRPQVPLRW
LLGYGLGFGTLQFAFLYLAMDGGMPTGLASVLQSSAPFTTVVLGALLRERVTRRQAVGI
AVAVLGLTGIAVLRAGAHGAGGLVPVLLTLCGGLGWALGNLASRRAQAPDPVRFTLWM
STVPVLPLLALALVVDGRDAVVRSTTLGTATGAWALAGLAFTVLVATLLGTGRWTALM
ARHPSSVVAPWSLLVPVVGIGTSWWWFGERPAGGELALAAALVVGGVLLGSTARPAPPPQ
PVPPSLSAAPSRDAARSQPAVAVPAGATGTTRAIPAIPATPSPLPVRPRPSVVVAETETGAPT
AADSAAASASARRGPSRGRLPTTCTTTTLPTA

>tr|A0A1I1U4N8|A0A1I1U4N8_9BURK Cobalt-zinc-cadmium efflux system protein OS=Acidovorax konjaci OX=32040 GN=SAMN04489710_104106 PE=4 SV=1
MQSRTTTAVLLGLAQTALWASSYYLPKYLKFNERKAMSAGHSHALQAEGKERSIWWA
LGLTSAFMIAEVVGGGLVTGSLALISDAAHMFTDTAALAIAVAIRVAKRPADALRTYGYH
RFEILAAAFNALLLFGVAIYILFEAYQRFQSPPAIQTGAMIVIAALGLVINLMSMRLLSGGK
DDSLNVKGAYLEVWSDMLGSIGVIAGAVLIRYTGWWVDPLIAVAIGLWVLPRTWVLLK
ESLNILLEGVPQGVKIPDVMVMAAVPGVQSVHDLHVWALTSGKAALTAHVVYQPGVE
SESLRPLQEMLAKRFQVLHTTLQMEATMCEHTEDGCNFVAHPSASAGDHIHSH

>tr|A0A1I1XPA7|A0A1I1XPA7_9DELT Outer membrane protein, cobalt-zinc-cadmium efflux system OS=Nannocystis exedens OX=54 GN=SAMN02745121_02988 PE=4 SV=1
MPLLSALLSAALLASPPPPAGCQGPLGRAAVVTCALAEHPSIRAAEAGRAAAEGRKLGAR
TLLPSNPHEVTAGRRVGLWNGERDINVYGRVSQELEIAGQRRKRMAMADA EVAQADR
QIELSRDVA AAAALSAYFEWIAAREQRAMIERIARTSDTLVDLARTSERTGLGSGLNADV
VVATSVRVRQQIEADRRIAAARAVLAGLLGRDGAGLEVEGDLAPLAVPQELSALLTAAL
TKRAEIELAKAEREVFVRQVEVFRRLRAPNPSVVLYAQRDGFAEQVLGGGLAFPIVLPAPL
GRTYKGEIAESQALARRAEAEVERWRRVVQAEVEVALREVEARKAELALFEAERLQRAE
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R

>tr|A0A1I2P9G5|A0A1I2P9G5_9BURK Threonine/homoserine efflux transporter RhtA OS=Duganella sp. CF458 OX=1884368 GN=SAMN05518865_108122 PE=4 SV=1

MNGLARTLPLVSLVTLVIWASVPTVAKAALAHVSLVTYLMRLRYTLAGLFMLPYLKQSM
 AGASRLSWWSWAVLISSCMIIYVQTWAIQQVTASWYIVVFSSCPVLIALLLRYRFTVRAI
 GLLATVGGALALYLQDSHAAGTPFQLGALLGVLTGMLAWVAYTVIITRFHKVYDDTQIT
 AICSYIGAIFSLVLFLAAGDYSVQQANWQVAAAIVVSGALMPLSLWCYSYSMRKAEALTI
 FGQYLEPLIGLFIAFLVFGAELTAVACGAVALILGGTIAVTRYSVKPANS
 >tr|A0A1I3HGY4|A0A1I3HGY4_9BACL Threonine/homoserine efflux transporter RhtA
 OS=Paenibacillus sp. UNC496MF OX=1502753 GN=SAMN02799624_00514 PE=4 SV=1
 MKFDMKYAIAVFLGAVSYGILSTIVVKAYGRGYELGEVVGSQLLVGFVLSWLLAAATKR
 TAIRKRRNAVGLGEGGRSAAPARPALSWKQRLLLMAAGMPTALTGLL YYQSLRYIPNSL
 AIILLFQFTWMGVLDALRRRKPSNLMLITLAVLFGGTLMAAGILDHGLANFDALGAAL
 GLSAAVSYTMFVLFSGKAVPSAEPAYRSAWMITGGLILVFVLFPPAFLFNGLIWGPLLLFG
 FLLGLFGAFIPPVLF AAGVPHVGEGBMAAVLGASELPVAVMLS AVVLHESVSVLQWAGVV
 LVLLGVAMPEVVRRRLPHSRPKGAAHRA
 >tr|A0A1I3KU14|A0A1I3KU14_9FLAO Threonine/homoserine/homoserine lactone efflux protein
 OS=Myroides guanoni OX=1150112 GN=SAMN04487893_10156 PE=4 SV=1
 MSTEVLYAFFATCLLLILTPGPDILFVISQSITRGRKLGFVALGQVGGLVFHLSLFAFGVS
 ALIVSSDWIYKGIKILGGVYLLWLAYSAYTSETKIKLNEVEITSSSFGSFMWKGLLMNVLN
 PKVMLFFLALFPGFISEQAGNVKEQIFILGLIFTVLTIVFSIICGVAARFTDVLNNRVFSLII
 KWMQVILFTVLGLYILL
 >tr|A0A1I4VWZ1|A0A1I4VWZ1_9GAMM Outer membrane protein, cobalt-zinc-cadmium efflux
 system OS=Dokdonella immobilis OX=578942 GN=SAMN05216289_103143 PE=4 SV=1
 MVLMTMLAACASVSRREGADRVQALVGQRVPDAGFWSQAPQVPA AIESRVNELLAAPL
 TPVSAQKVALLKNPDLAASFALGLIAQADVVEASRIGNPGFSASALRDGGPSKITMGLSLP
 LSDLLLSSKRRFAEGEYERAQQLIAAEIVTLCADVARAWYEAAGARQVAAMRDAVSRA
 AAASSDLAQRYEAGNISALALKLEQASASQARIAASMARAESTRARLALNARMGLNGD
 MAGRWQLDVPLAAPAETEDLETALALARENRLDLLAARREVDQLGEALGVVRRWRLI
 GNIDLGVERERE PDGGKLSGPSLALAIPLFNQQAIAARAQAQLEIGRANLARLELQIDND
 VVLGRDRVAAMRSIVEDYRSALVPQREAIARQQERTDFMLSGAFDLLLLSRQQEFDAYA
 AYLDAVRDYWVARTELGRAVGTVLPSDASISTRVIDVEALLAPTEVSAPHEMHGGSAD
 AMPGMDHSGHGVPA MEAGPADDQAPAGGEGRTMDHSGHGSPPIGPAPTGTHGAKERHE
 KAQDTSDAMHDGYEGSK
 >tr|A0A1I5VZW6|A0A1I5VZW6_9FIRM Threonine/homoserine efflux transporter RhtA
 OS=Lachnospiraceae bacterium XBB1006 OX=1520827 GN=SAMN02910358_00784 PE=4
 SV=1
 MNKKLFGSICGIMTGVCWGVSGVFGQFLFETRGVESFWLVPIRMLSAGIFLLLYGTITDLP
 NTKRLLHNRRDFLQAILTGVC GTMMFQLSFFLAVQHSNAGTATVLQYLCPVITMLYVCLR
 DRHAPKKVELLCIFLALAGIFLISTHGNVGS LVITPAALLWGVATAFFMFLNTVIEGIYKR
 YPSTVVIGWAFLFGGIALCLIFRPWNYSVQIDFAVVISMLFIVLGGSVFAYLFYGNAIKRIGP
 AKSSLFAASEPVAAAALSIIWLKTSFSVIDILGFVLIISTLFILSSTNA
 >tr|A0A1I6J1X9|A0A1I6J1X9_9BURK Outer membrane protein, cobalt-zinc-cadmium efflux
 system OS=Mitsuaria sp. PDC51 OX=1881035 GN=SAMN05428960_0692 PE=4 SV=1
 MKRLIFISPRREGAGSTAETTSQRRRPTSRDRTLVLAAALMAGFPMTYASTAATNAATAT
 ATATATATAVATTAPIASNSSKLPSTLVVTAPTDPDANTDTTGVPFAAYLEAVERFSNAIAA
 QREAVAAARAGVPMAGLRPDPSLSLGVGPAELGREVRPKPRLAQSIGLSYTIETGDKRER
 RVAAARSQVSADEAALAGAGRQAAADAAAFAIEACRTREALQRQEVSLAALGDIVRMN
 ERRHGAGDLGGLELLQSRNERDQFLATVVRARADARTAMEALAAPLGRRWREAFGDAS
 PLCTFRDQGAPGLDGVGIEGTGGSVGIQESHEDEALDVARALDQRDDVRIARA AVD
 SARAAADLVANRWVDPSVLSYGYTPQGRRGVAADGSAVDPSPRSNTVSVSVSVPIPLS
 RLDRSDLVQAESAVTQALLALRQTELQAQADV RATHAQYRAALENLTRYRDATLG DAR
 RVVEGLRLSYRHGAASLLELLSAQRAADDTLAYLQARSELAAATVRLQLSLGRAPAP

>tr|A0A1I7B382|A0A1I7B382_9FLAO Threonine/homoserine/homoserine lactone efflux protein
OS=Lishizhenia tianjinensis OX=477690 GN=SAMN05216474_2511 PE=4 SV=1
MSGIIKGIVTGLILSIMLGPAFFLLIETSIRKGVKAALSFDAGVLVSDIIVIVYALYQEV
GFADGENNAVIKLIGGIVFLGFGVVLFLKKVKSQKSDNSGKMVHDSKDYIMLFTKGLVLN
MANPLVIFYWFSVLAFFGGEGNNKVSLEPLDVFIYVAVILLTFFTIDVLKILGAKQLRPFITN
AVLKSLNRITGILFAFGIFLVVQSCYLIMFK

>tr|A0A1I7FXR2|A0A1I7FXR2_9FIRM Threonine/homoserine efflux transporter RhtA
OS=Eubacterium pyruvativorans OX=155865 GN=SAMN05216508_1042 PE=4 SV=1
MKKGYFYIAVTTIFFSLMEIMLKSMGNAFNPVQVTFTRFLIGGLVLLPLAVRHLRKKNLHF
TGGDIRRFALLGLIGVAVSMTFYQLAVVYTQASVVAVLFSSNSIFVMVFAFLLLGEPYRR
NLVSLSLDIVGILFVINVLQMKLSLAGVIFTMLATVTFALYGVGGKKPTEKFGGLVNTCMS
FLLGSLEMILLALLTYIPGVSAAMNHAGLTMFSTRPLFSGYSLSVLPAFLFVCVGVGTGIGYA
CYFQAMETVSVNTVSLVFFFKPVLAPILALLVLGDPMPVTKIVGICFILAGSLANILPPMLA
ARQKAEPLAASLDEEAAGVERILTEEADAAERVLKEVNE

>tr|A0A1K1MVV9|A0A1K1MVV9_DESDE Threonine/homoserine/homoserine lactone efflux
protein OS=Desulfovibrio desulfuricans OX=876 GN=SAMN02910291_00649 PE=4 SV=1
MISLENLLLFPMAALLVMLPGPDFALIAKISLLNGRPQGQAAACGVALGIGVHTTAAML
GISAIIAQSVLWFSILKYVGAAAYLIWLGIQALRHGRQASAAVVRVAPQADDLKEHALAHG
LMKKPAAAPRLTGRQWWSFFRQGGFLTNALNPKAVIIFLTFLPQFMNPHAPLGPQFLELGGI
LSALCLLWYVPLAYILGRVRHIFENSRLFQLWLQRFTGFIFIAFGLKLAAAQSR

>tr|A0A1L8QRL7|A0A1L8QRL7_9ENTE Arabinose efflux permease-like protein
OS=Enterococcus aquimarinus OX=328396 GN=RU93_GL000336 PE=4 SV=1
MPNLGVGLLWAMNMTLIPMLVATFNVSNSKAALLITMGSFTGIFVQYLSGLLSDRSNFK
MGRRKPFMIMGSAVTTIAMCAMPFAGSYWTLFVVAFFFFYFSLNFYQGPYYSLIPETVDDS
QLGLANGFSKVSVVLGGAFIFVIGPRLWASESVLNKNHALPFFVSALLGIFTVILTIVFIKEK
KVPKADTKQKIAFDYKFPSAMKFLGIFFIYMGYGGITPFFVKYCVQYLNLSGTAASFLL
LLTITGALFAYPLGVLSKIERKKVLVFGTLLFVVALFFGIFVKETMGLYLMMSVIGIGFIAI
QVTSYSILAEVPPERLGEFMGIFNFFVSSSQFISGNLMGLLLDRVGYQVFFPLSIVWLTIAS
VILYFSRIEKIGLQATPVTK

>tr|A0A1M4DZK2|A0A1M4DZK2_9ACTN Putative transmembrane efflux protein
OS=Nonomuraea gerenzanensis OX=93944 GN=BN4615_P1504 PE=4 SV=1
MKKSLLVPIVLMVSVFVVGTSYELIAGLLPQVAADLDVSVSTAGQAVTAYALGVVVGGP
LVTILTVRLPRKGLALGLLLLFAAGNAVCAAAGSYEVLIIVGRVVASLSHAAFLTLALMVT
TRVVEPQVRVGTAAIAVGSFVSATLLGVPLGVLMGESAGWRTPFVAVLAGLALAVTALLA
VVLPRQEAATSVREEVATVLRRLVVIATTAVGLAATSTVFTYLAPTLTEITGFGAAA
VSTLLLVIYGVGSLIGGLVAGRLADRSLAATVRGTFTVGLAVVLAVFPFAVPWAGSAVVAV
LVFGLLTSATTPVLQSLVLRHAGRPTLAVSVNVCAFNIGIAGGSALGGGLVAVDGLRWL
GLAAAVLSLAALAISSYAAVPRRESRESPESPELTGSPA

>tr|A0A1M5C8J2|A0A1M5C8J2_9FLAO Threonine/homoserine efflux transporter RhtA
OS=Chryseobacterium sp. OV279 OX=1500285 GN=SAMN02787100_2197 PE=4 SV=1
MRIAASLLAAILFIYHNEVSGYFNYYVVTLQAVKKIMKKKNILKGVLFVGIGASIYGMLAT
FVKMAYHDGFTTSEVTTAQFVMGLVGLLFLNFMQTITSKQKLSSPSAKEVRMLMIAGTSL
GCTSLFYIYAVQYINVSIAIVLLMQSVWFSVVESIIAKKLPNARKVVSVIIVLVGITLATNL
INMDIELDWHGVFWGLMAAASYTMTMFTSNTLATHLPVFRKSIIMLSGGAIVIFGFLFFAQ
IGPMYFDGLKSLYLNFTENTEHHSFNYSIFWTYGFVLALFGTIVPPILFNVGFPNAGLGLGS
IVSSLELPVSVTMAFVLLGEKVLLVQWGGIILILFAIVLMNLPAKKELKTIEVA

>tr|A0A1M5FHI9|A0A1M5FHI9_9BACE Threonine/homoserine efflux transporter RhtA
OS=Bacteroides faecichinchillae OX=871325 GN=SAMN05444349_14515 PE=4 SV=1
MIESKNIEDKNRSCYESYKRHIVCSGIFLYFWVSSVFSITLLLAGFSSFEVLSYRWGVAAITL
TIIGLLSGCNFRLSRRDFIVVFCLSLFRAATSFSLIVAYQNIASGVASTIHFMYPPLAVALVM

MFFFGEKKSMWVIIAVLMSLFGASMLSSGELNVENGNTTIGLIGACVSVFSYAGYIIGVRK
 TRAVQINSTVLTCYVMGIGTIFYLIGCGCTTGLRMVTDEYTWLIILGLALPATAISNITLVQ
 AIKYAGPTLTSILGAMEPLTAVVIGVWAFHELFTMNSAVGILLILLAVSIVVFRERRIKG
 >tr|A0A1M5NRD9|A0A1M5NRD9_9FIRM Threonine/homoserine efflux transporter RhtA
 OS=Asaccharospora irregularis DSM 2635 OX=1121321 GN=SAMN04488530_11153 PE=4
 SV=1
 MEKKKGYIFICIAGLLWSTLGLFGNVLMGYNLTPEQVAFTRLFLGFLVLTIIYSIVKNPSALK
 ISKKGIIYSIMIGIVCQGLFNLCYFKAINSVCISAVLLYTSPLFLT VFSKV FYKENINIQKIV
 SLGFCFLGAVLA VTGGKLDVDKLNGLGLILGISAAITYALMPIISKNILKECSSITILIYGFLF
 GSIFMLPLAKPLEMLKYSLNPKILVWMLVLGIVPAALAYIFYVEGVAKGVLSIAGVIASV
 ELISSVLIGWTVLGENFSIVKLIGLGMVVSALIAVKASKQEEPLLEDIEQNTLHEAL
 >tr|A0A1M5RW70|A0A1M5RW70_9GAMM Potassium efflux system protein OS=Ferrimonas
 marina OX=299255 GN=SAMN02745129_1778 PE=4 SV=1
 MTLWRSMGLTALLFWLVCWPAAANMPVTEQLKQQLEEVKGAADADPQLVQSYETLLA
 TIDANEKATQANQTLRDFMTAYNGQMSALQQQLDQVPEDPLFGPPPSEEPDDVELALTAL
 DSAEADWRRQLSRNKQAMQQVERLPEVLPGE LSDLRQLRELTPVEPNEATPV PYWQFL
 ANTKKLNLAIEGRQLQLQSYDKKKNALELEQQLLSQLSAAQTQRERLQGM LSQTKQTV
 AQDLLRQSSALVGLAPEQDAQAKKTAEQLKRLARELSELVSSNDDQARRRQQL EQQTRQ
 LTSERELIANNIQLWQKSTAFGATLRAKLRLALPEQAPNDDL VGQIAQAHVRQFSLRQLPPI
 VDPRTL VNESEVEADPSEPA SEPSGAANRIQGEADNDSVLPWDPEQSAAF WQQAESLQQQ
 LVQQLDEEYEQFIITLTHLQTVREQYHLELTSSLSYLKQQQLWTRSHPLWQWPEGFN RFT
 LLGIEQPLD TLAQLRLQQPRQFALALVAVLAFGFALSRSRQHRRALAALPTIKQSF KPFR
 AKLFASLTGAVLMALMVVAMSKLLTAFWPQPEPLDIQALLTLAVVITLLMATLFTLGSPG
 GVL RDHLDWPKDYCN TLQRQAIASGLPSV LLLLAMMLGTLLAGAHGSELVRWLQLAVQ
 ALLLVLF LRMVAPRSLERVLPTVLRRPWFLKGLQLVVLTTQAVAFLLTVLGYYYAGLSVT
 LYLSTTMMVIVLFFIAGQLGRGWLLAEQHEL RQQRLREEWLEQQAAARQSEEGSAPA EPM
 PEIDEEQIELDEVNQQS FALLKGALLIGLGAALLGIWGS AVEQVQWFNDVVLWQVIEQTE
 SGATLVNISLRSVLIAIGLLLLTLFAVQNLPGMLELLVLRRLDLQPGSGYAITTILRYLVILT
 GVMTAFAMVGFQWSKLQWLVA AVGVGLGFLQEIFANFVSGLIILFERPIRIGDIVTINNL
 SGTVSRINTRATTIIDWDMKEIVVPNKAFITDQLINWSLTDPMTRVVISVG VAYGSDIDKAE
 ELLHEVAR DHPTVLDDPAPQVFFLSFGASSLDFELRLYIPAIESRNFVIHAINKAIDRRFREA
 NIEIAFPQLDLHVREL PKAPPEDKGNAPND
 >tr|A0A1M6HVG6|A0A1M6HVG6_9GAMM Threonine/homoserine efflux transporter RhtA
 OS=Cycloclasticus sp. DSM 27168 OX=1884353 GN=SAMN05519226_1788 PE=4 SV=1
 MKNETLKAVVLLNIAGLLWGGNMILGRYLADFLGPWSIVSTRLVIGGFIFILLIQTGELKK
 IKHITNWWTFIALAIFGVIFFQSLLYYGLRLTTSTNAGLINSLTPLLTA FMAAAFLKEK LNY
 HHWVAAAVTIFGLLFILGEGDLTNLLLLNFNVGDLLVLGAVISWVIYSLIAKNAMIGMSPL
 LLTALGVLLSLVVVIPLGIYEAKVIQTPHLTVNAFWALMFISVGPTVLSLLFWNKGMKVIG
 PSRASLFLNTVPVYIIINAVFLEEMPYQYQIIGMVLIFMGSFYAGLKAHKPKLRD
 >tr|A0A1M6R7L7|A0A1M6R7L7_9CLOT ABC-type Na⁺ efflux pump, permease component
 OS=Clostridium cavendishii DSM 21758 OX=1121302 GN=SAMN02745163_03561 PE=4 SV=1
 MSSLIKFEFKKLAKKRTNIITVVTTILTIIFFSLPAINFECLDAKGFKAISLARDNIKNISIKM
 TEEQVTDKDIKEIQSLYADPKNVT KDEKGEKWFNNDVYDKFINPRRDYLSMISENYANPKE
 FLWISGLVDIKLKDGA KFYETRDSKVSKLLNQNHGGNYSEQEKFWLDKNSKIDKPYTY
 GYYHGWGDGILGIFGSLIFMLLAICITVAPVFAGEYQCGADAVILSSKYGKTKVIRAKIGAVF
 IFVTMVYFVNAIFAVGMPLLTFGVDGWNLP IQICNTIIPYNLTFA SCTLISVGIFYLVMLGIV
 SFTLFISAKCKSPFTVLIVDVLILFVPLFLGDGADNGLYQHIIYLLPYQKSMIHLFSAYISYSF
 GGLTSLISMRMLAYIVMTIAFLPFIGNAFRKHQVQ

>tr|A0A1M7RTD2|A0A1M7RTD2_9FIRM Threonine/homoserine efflux transporter RhtA
OS=Desulfitobacterium chlororespirans DSM 11544 OX=1121395 GN=SAMN02745215_00070
PE=4 SV=1
MSDRNQGYLLIILSAVFYSTLGILGKFIYNTGIEMSLVIVLRLFATVILLGLFLLITRKEPLLT
FSRAVLFGQIFFVATAITFFLAVKYLSAGLATVILFTHPALVAVLAVIFYHEKIGAAQIAGLI
LALLGLFFISGLCIESSTALSPLGLILSVLSAVVYGIYALLGQRVVKTDGIWTITFTISLMGLV
ISALIFPYNLSALLSITPYQLFLGFAMAFLGTILPVVLFLKGVQKIGSLVGTLSIIEIPFALILA
YLLLGEVLTSMQVVGTLLILIATTMAVTIKHQKENDGRN

>tr|A0A1N6EST4|A0A1N6EST4_9BACT Glutathione-regulated potassium-efflux system
ancillary protein KefG OS=Fibrobacter sp. UWB11 OX=1896202 GN=SAMN05720758_0280
PE=4 SV=1
MNNQITILLSHPNISNSMFNKHLLVDINRKNPNFVFHHLDKNRVNGYFDLEAEKKLLKESK
AIVWQFPYIYWNPSASLRDWQDQVMSPIVYSADNFLKGMPPVRVFTAGAAAEHYTHEGL
NRYTAEEMLIPFEMTANAAGMKWFKPLGFYGCSPDTTKATLDKAAQEYEESSLELL

>tr|A0A1N6N677|A0A1N6N677_9GAMM O-acetylserine/cysteine efflux transporter
OS=Lysobacter tolerans OX=1604334 GN=SAMN05421546_0115 PE=4 SV=1
MGVPAALSRRDFALLLFVCVWALNFLMSALGLREIPPFTTLLRFVVLALLALAAFMRVP
PRDQWPRLAIVSLLVGCVHFGLSFLALRLSGDLSSPAIVMQSYIPMTTLLAWWWLGERFK
WWTGLAIAVSFMGMVMVIGFDPHVLSRPAALITMLISALALAIGTILMKGLRGIDMPNQQG
WMAAASVVPLLGISLWLEPGALATLPGVSATAWAGVAYAAALASSLLGHGLYYSLVQRY
PVALMMPWLLLVPVIAVALGIVFWGDRPGTRIWIGGAMVLGGVLIHIALRQRFKSRTQQPV
TEVVAEYPQG

>tr|A0A1N6ZG85|A0A1N6ZG85_9BACL Threonine/homoserine efflux transporter RhtA
OS=Paenibacillus sp. RU4X OX=1907395 GN=SAMN05880555_3299 PE=4 SV=1
MGRRARGSYWTAVLFVLLGASSYGVMSPLIKHVYGFYTFSSQVHVHQLAAGSAMLWIA
AGAARKRSSASLSPRLSLGQWAGLALIGTAGLAMTTVLNQLQGLKASFAIVLLFQFTW
ITIALDSIWNRRRLPGWGRGCVAVIVAGTVLALGIGGVSGPHAAALPLLCGLGAAFTYSLY
LAGTGRFRSDLPAAASAIMVTFGFILVLALFGRGAWAGEAEPRLILWAAVLALLGQVIPT
LLFTIGIPRIGSSLAALLGAMELPVAAAAAWLIGGETLSALQLGGIAAILAGIALAQKVPK
ESPASLEE

>tr|A0A1N7E5P8|A0A1N7E5P8_9SPHI Threonine/homoserine efflux transporter RhtA
OS=Mucilaginibacter lappiensis OX=354630 GN=SAMN05421821_11341 PE=4 SV=1
MFMVFAGACSYGILSTFVKLAYQAGYTIEELSVTQASIGFIVLTTLTIQGYKKPEAMSIP
VSAWLYLLLTGACIGMTSYVYYLSVKYIPASVAIVLLMQFTWIGILLEWLFNKKPAIQF
IIIGIWIATIIASGVQGTQNSHLPAMGICYGLLSAVFYAVFILINSRLKYAVSSLMKSSVMIM
GSAISLIIFTGHQLLAVHHFNIQLLKWGMFLALFGTIIPPLLFASGIPKTGHFKSSVLMTVEFP
VAMCCSWFFLGEHISLLQWIGVIAMLMMAIVGIKRKSA

>tr|A0A1N7M5T6|A0A1N7M5T6_9RHOB Threonine/homoserine efflux transporter RhtA
OS=Rhodobacter aestuarii OX=453582 GN=SAMN05421580_105129 PE=4 SV=1
MKTDGTGGPNAAPHSIAPADLAGADMPPAPPLPEPEKSLIGKGIGLLLIALLFFTLMDVAAKK
LGQSYAPAMVIWARFAVNALVSLIFRGSFLKHARSRQPGLQLLRGAFQMATVALFFLAI
RSIGLAEAAALTDLNPVLITLGAALFLGEKIGPRRVAGIFVSFLGALIILRPGAGVMDPAAL
FALAAFTYAGGALMTRVVRHDSTATSVIWSAGVGTALSSLALPFFWQEVAPVDLPLFIA
VGALGAAGQAALIVAFRHAPAGVLAPYGYLGLVLSSLWGWIFFAQLPDLYTVAGAAVIV
LAGIWWVNAERRAALNAAAR

>tr|A0A1R4GLE3|A0A1R4GLE3_9MICO Putative transmembrane efflux protein
OS=Gulosibacter sp. 10 OX=1255570 GN=FM112_13745 PE=4 SV=1
MVARNEGSGERMRENVSRIPIGGGARRGALLVAVLAAVFAVPLSVSGTAVADIAAASLG
ESAAGQQWALNGFNITFAASTLAWGSLADRVGRRPSFQAGAILFIAGSVLSVLAESYVVL
DAARILAGLGAGAVFSVGSALLSVVYAGEGRARVFSLLGAMAGLALAFGPTLCGIIAQTW

TWRAIFGVQGGLLVVSFALMQAARPLLRRDEPRSTAPFDWPAAILFFAAIASLVAALVTGSE
 AGWASAPTLGLALIAAFAFAALLRRERRAEHPLLDLALIRQPRFLGVTLVVAVASFTFAAG
 AVVSAWLLVPAMVMLGAGFGLHAGLVDNEGLAAAPDEDAGMAAGWINTMRVGTEAV
 AVSLFGAVFIPALGGGGEPGAGLRRDRARRGSRRARPGGDLDPRHAPPMSARASWRLRY
 SCSTTGPRRCRSKRPGCRWSPWPSATPRRCGKRSRTPACIDTSAERPHRSGS
 >tr|A0A1R4IUK9|A0A1R4IUK9_9GAMM Potassium efflux system KefA protein / Small-
 conductance mechanosensitive channel OS=Pseudoalteromonas sp. JB197 OX=1434839
 GN=CZ797_03395 PE=4 SV=1
 MKLIENIPLFKQMEIINRLGFFKEFSLNERQILLESFGLLYLVRENSFLFKQHDNDKRLFIVL
 SGALIVFKHNHLELGTIRPGEFIGEGAFINNRRARSISARAKTDAIVLAITS DALTRLPNVIRE
 KIKDRIIEGMSLRIAKLSEHIENHG
 >tr|A0A1S6RZ73|A0A1S6RZ73_STRHY Transmembrane efflux protein OS=Streptomyces
 hygroscopicus OX=1912 GN=SHXM_09667 PE=4 SV=1
 MCLSRAAIRLETACWLIPSSSAAAWNWPVSATATNVRSTSTSTLPPYFHNCWLCLAWRRV
 V
 >tr|A0A1S7U895|A0A1S7U895_9RHIZ Arabinose efflux permease family protein
 OS=Agrobacterium deltaense NCPPB 1641 OX=1183425 GN=AGR7A_pAt20117 PE=4 SV=1
 MIAGRLKQTSWWLVLSVQFVTVAVPLAVLPFLSLHLQRLSGAGTTDIALWAAVIAAAPAI
 GAILSTPLWARLASSYPLGRMLGSLCLNALSALLQAQSGTVEVFALGRSIQGLTGVGVL
 LLAVEHSRTTRGSGYSGLQQALAAGCIAGPLLGGWAFDNDALQGLLTGFAVLLVALSVF
 CGYVFHDARPVKDEEQSSGFAGLLPPTPTRMLVLSGLLATAGASGFMPFFAGWALEQESA
 VLTASLIGLLHAGSWAAIVVLPLWGRWIDAGRERAVMRLSTAGSLFALVSLLAGSTVVL
 ISLSRIVHGAFNSGLAPSLFSVLGRSRHRVANLAAGRMATTLGQAIGPAICGLAVFAAGNN
 GALFAAALLTLLASILLYLQPEARSHDVE
 >tr|A0A1T4K5B8|A0A1T4K5B8_9FUSO Threonine/homoserine/homoserine lactone efflux
 protein OS=Cetobacterium ceti OX=180163 GN=SAMN02745174_00309 PE=4 SV=1
 MDMIFFKGVATGLFLSLPFGPIGIYCMKTLVKGEKEGYISALGMVTVDIYGLLAYLFINQ
 IGHILQYQSFVKVLVGCFLILIGYKKIKANIEIKDISHENKSLLQDYLGTLVICLFNISGILAI
 AGIYATLNVGLTGDHAGFFTPFKLASGILTGGASLWFLTTFILYNFKKKITNMLIKISKLA
 GFFILIFGIFAIIFAFYK
 >tr|A0A1T4XQZ9|A0A1T4XQZ9_9FIRM Threonine/homoserine efflux transporter RhtA
 OS=Gemmiger formicilis OX=745368 GN=SAMN02745178_02185 PE=4 SV=1
 MKQKETAAVLMVLLAAACWGANGIFINILTAYGVNGTQMTLVRMASMAILTGIWLAAK
 NPAALKIDLRDLVWFVPAGALGLFMFGLFYTYSIQLVGMGTAAVLIYLMPSLVMLFSVVF
 LHEKFTPGKGLCLVLSLLGCALVSGVAGGVTLTDAGGVAYGLGAALCYTLQNILLATKLLK
 KYSPMTNLFYMFSLFSAASLVFTAAAGELPGVAYILTPGALAANLGLGLVCSLAAQWL
 YTAALKTIPASRASIAATFEPVAAALFGLVLFGQKMDGFGVAGIVCEVAALVLLQLPAPA
 KRKG
 >tr|A0A1T5EIX1|A0A1T5EIX1_9MICC Arabinose efflux permease OS=Arthrobacter sp.
 31Cvi3.1E OX=1279032 GN=SAMN05660916_02894 PE=4 SV=1
 MTGHGNHAKRAALWLCLGAGFITLLDQSMFVLAVPAMSASLHVDSGSVQWILAGYSLA
 FGVALVPAGRLGDIVGRRTLFIAGIAVFGASSLVGGLATDPSLVIIARLLQGLGAGTLNPQV
 LGLLQDIYSGHDRAKALGAYAAAGGSAAVCGPLLGLVLSLGDPSIGWRILFLANVPLVL
 VLVPLAFRLLPRPAGKHPENGTTKTSIDVLGALLGGVVIASLVPTIYGAGIIAVTSLAIGA
 GALLAFAGWEILYHRRGRTPLLSASLVKSRGYTLGTVVALCQFGVGAGMAAVTAFYFLS
 GTGMAPLAAAAILAPQAAGMLLASSFSWRFVARYGRAGIVYALVGSCLACLIAKDLFVQM
 LDGGTAALAVAAVGLAQGVATGLVVAPNQTLTAHAPAGTAGVAAGFYQLSQRFAAAL
 CSAAAAGMFLQAQGAATGQASKDAFHQGIVMCCVLLGVALLAGGLDWFREARDRNA
 RAAVVTSGKETATAAVALTSERPTAAGAQRSEATESVDA

>tr|A0A1U7GES1|A0A1U7GES1_9BACT Efflux transporter periplasmic adaptor subunit
OS=Planctomycetales bacterium 71-10 OX=1895807 GN=BGO49_24950 PE=4 SV=1
MFMLKSMLRWAAVAIAA VIGIGAWLYYDARERAKLPPGIVSGNGRVESVQVDVAAKY
PGRVLRIFAHEGDLVRAGQVLAQMDVAEAELEAAGKAKIAEGNETEAKIKADILSREAA
VRYEDQQFIRNRELFSSRRYISREEMEQTQTKVDIARTQLDAVKAQLLANERSIEAATADVQ
NTQAKIVDSTLVSPVTGRVLYRLAEEREVLGAGGKVLTLVNLDDVYMEIFLPSDEAARVD
VGSEARIVLDAYPQYAGRARVSFISPEAQFTPKQVETRSDKLMFRVKLKVPQEKLLPYI
EKIKTGVRGVGYVKVDPNAPWPEKLEHPFPPPAAMGIKPAEGAKPEEKPESPKAEPEAAK
PSGAEKPTNP

>tr|A0A1U7PNZ4|A0A1U7PNZ4_9BACI Threonine/homoserine efflux transporter RhtA
OS=Edaphobacillus lindanitolerans OX=550447 GN=SAMN05428946_2298 PE=4 SV=1
MAMKQYLGDVLLITAVVWGSFVVTALAEHLTAYQVMAGRFLATLILCVLFHRKLR
TLRSVLWKGA VLG TILFVAFALQTVGLEYYTPSKNAFITAVNVVIVPVIA YLVFKRRIDR
HEGLGSVLALAGIGFMSLQGSMTINIGDFLTLLCAVGFAFDIFYTNLFVKKEDALSLTIVQF
ATASILSVGAVLV LG EVPAGLNGAAIWPVVYLA VFSTTIA YVCQNI AFRTTPTKAAVILS
LESFFGTAMSVLFLHEVLTGRMVLGAVLILTALIAELKPAFKFRPKIRPEH

>tr|A0A1V4X8C4|A0A1V4X8C4_9DELTA Magnesium and cobalt efflux protein CorC
OS=Syntrophaceae bacterium PtaB.Bin038 OX=1811716 GN=corC_2 PE=4 SV=1
MSDLLLLPIAVCLALEGLFSGGEIALISADVHRIRQRAEAGSKSAAIALRLLDNPEWFLAT
CLMGTDLCVITATALATSLISVFGPARGEWVSVAVMIPTILIFGEIVPKSYFRHRAERKAV
FIAPFIWAASWVFYFPFVFMISKIARGAVYTLAGERGKLSLPYITKDGLKHLHHEALGTDV
KHMEKEMVDRIFDFSETSVGQVMVPVSNVAALEENATFGDASKLINETGFSRFPVFQGNV
INVVGVVNAFDILKTMPASASRPVREILRQPLFVPVSKPAGDLLLEMQRRGEPMAVVVDE
YGGAVGIVTIEDILEEIVGDIRDEYDKRERDVRKLA PG RYLVTARIAIERLQEILPLGIPEGP
YETLAGYLLHQMGRI PR MEQFRAGGIQYVIEDADLKSIRQVQVILPADPAAVKKEEGPPE
PQRPVGGL

>tr|A0A1V5CXS7|A0A1V5CXS7_9DELTA Toluene efflux pump outer membrane protein TtgI
OS=Syntrophorhabdus sp. PtaU1.Bin153 OX=1811705 GN=ttgI PE=4 SV=1
MILTRWRGAKAWARKYVPAMACFLLVFLAVPVFCGTMSPTTPAPPVTPKAGEQFTLPA
VIDYALKNNPRARISARDVETETYGIDAAKAERMPRIDFGSGAARYRYPMLTPPVISGPF
GSGLEIPEYDRNIYDAGGSFRLPLFRGGRLYRGVVRVAEIRKAMAEDNLA STRQELVYNLSS
VFYKIAQLDKLLAANEANVRQLEAHKQDVEFLKAGSVPQLDLLKTDVELSHAVENRLL
VRNNLESTYELLKTLMGIDDMTKEISILHQT VSGGPLPPLEESVSKALSQRPEYRAVEKKK
RIYEERVKIAQGGKRLPDVYAAGEYVGKAGDAQSYKENWYAGVRLSIPVFDGGLIAAEVN
KEKVELQKVREEERSLKL SITREVKDAYLAVANAVERIDVGTKAIESARENVRVERLKYQ
SGAGTATDYLD AQTAYLRAETDYCQALYDRETALAFLRKAVGEHWPNGAAGDQGMPE
K

>tr|A0A1V5FPK6|A0A1V5FPK6_9BACT Magnesium and cobalt efflux protein CorC
OS=candidate division BRC1 bacterium ADurb.BinA292 OX=1852824 GN=corC_2 PE=4 SV=1
MTLALILTAIALCMALSFYFSGAEVAIVSANRYRLRSMEEQGDASAGRLVELLEDSSQRLLV
MALVGTNLANVLTALFFKLFLQRGWPELAATEALGVILWSEVL SLLILTPILIVFAEILPKA
LFRAHADALIHRLHFSRLCLVLLKPVIWSIERVAQLILSPWSESHRATMRQLTREDVITLL
SPEPAAAADSTTADAVEETIAHDAERERHEPFGEAIAREHDGEEERLSESADQRRMIQNII
ELHETLAREIMTPLVDLVAVDLKRYDLNMLKSLAQSGFSRFPVYRDRIVNLIGYVDIFRV
LREDDGTRKLED FIERAHFVPETKRVDLL EFLQMRIKNAIVVNEYGGCSGWISREDML
EEIVGELEDELDEPGDEIVEQAEGVYLADGRTEIDHLNDVLGA EFDDQEWETIAGLFLSEF
GHIPQVND SV CV D GWRLTVVRMDGLAIDTIRLEREKN

>tr|A0A1V5HIJ7|A0A1V5HIJ7_9BACT Magnesium and cobalt efflux protein CorC
OS=Lentisphaerae bacterium ADurb.BinA184 OX=1852901 GN=corC_2 PE=4 SV=1

MMTFLLMVAILACLLAMGFFSGTETALTSDPLFIHAQEQRGDRNAPRVRQLLSRMEMV
LVTTLVGTNLMHVSSATLAELLHRHVPQGWEALVNTLLMTPIILVFCEMVPKATGRTHA
NRLSLLVARPLRAVELAFLPIVALNVVLSTGAARLFGGPRRRRGAVTRDDLQVITDMAAE
EGTLPEGAVGMVQTVFELRDRPVSSVMIPLMQMAAVREEAMVEDALRLSAVTGFSRFPV
YRGHIREVVGILDVRAVLRYLPAENLRQSSAPPRAPVRNFMQADFARVPEHRPVGELLHE
LHFHKTPMAAVINRGGAVIGFVTTEDLIEEVVGDIRDERETDAHTAADAAR

>tr|A0A1V5IRA0|A0A1V5IRA0_9ACTN Threonine and homoserine efflux system

OS=Actinobacteria bacterium ADurb.BinA094 OX=1852790 GN=BWY94_00760 PE=4 SV=1
MTSSGSGRPLGATTTAGARRSRGYLMVGSTAVMFGATGVWVGMTDLPVSTVLVMRMG
LAAVMVALLGGGRRWLRQALRPGVLRLLLLGVIDALQLYTFMLALRRLDVALAVFLSY
MSPIYIALIAPRLKQRTEPVVVVALVLAVSGIAAMLAPGLFEPGLRAAPDGIALGLVSGL
VLAVFFLLAKALSADVDGSTLLISDAAVVAAMVPLGLVQWAATGFAFSSTDWLAVLGL
AVFSTAVSGTVFLHGMRYIPVQHTSIVGLLEPATAPVFAFVFLAERPSVWTLGGLLILVG
AVLVVVFGAAEEGLAGSPEEAVGEAGAAEGRGPL

>tr|A0A1V5L5E7|A0A1V5L5E7_9BACT Magnesium and cobalt efflux protein CorC

OS=Verrucomicrobia bacterium ADurb.Bin474 OX=1852931 GN=corC_1 PE=4 SV=1
MNAPDNLAKLLVVVWATGSFMLFLLNGTRAALIDMRYRSMRAPIDEERKRWNTLIQWV
RSSHPHHLRFLLHPVFALVNSAAGWIVAFVVRWGFNNSITWFSGLLTFILAMAGLALH
LWMLELLPRTLAVRFPAPFLFLSQALMPMAAWLVHPALKLADSMGLMRKALIRSQHPL
VEPLDHELQISALDIDDPDMTPVTEKIVAHALGLNDLTVYDVLLPRNQVQYFDLNDLSKD
NLELSRTTGHTRFPLCEGDLDACIGIVHIKDIYRFRGAPEKLDLRKIRRDIIRFDLMDPLDTA
LQTLLSKRIHMALAQDEFGGVAGIITLERILEELVGDIHDEFDRGEERMIIRIKKDFFRVSGI
APIHELEEVLGIDIDNDDVSTLGGGLVVAELGRIPEPGETLGMGRMVITVQEADEKRVLSCT
LKLLPPLSEPID

>tr|A0A1V5M1A0|A0A1V5M1A0_9BACT Drug efflux system protein MdtG OS=bacterium

ADurb.Bin429 OX=1866930 GN=BWY76_00703 PE=4 SV=1
MSASLTHPTTPPPVETQPRNPLAAAFGILFAYPVLIPGLVTLFAQLTYSGVNNVTMHQYI
KILGATSRNDGIILGWVGAMFLLSETFLRVPGWLSDRFGRKAMVILAMLLSAPSFFISSTV
THYSWLFPLRWWDGMMAAALWPSVFALIGDTPPARARANAMGAINMMYMLALFTGG
ALAGILLDRSGSPRTFFVVGSAVMLLGGLTALTFFRTCPQLDAPHPEVHIEDEERAALSPLR
HLPLLITFVQNFAILILAQLLFDYVRHDLGFTLKQIGLLVGAPVVAIALFALPLSRVGMV
GKIAVVRVAFTAVAIALWAFANKTIGLSIITAIIGIAFAMGIPAWLAITSLSGRKSRGVTF
AAYGTVQGLAAVCGPIAGGYIWNLTGHSAIFMASAAISLGALLAWTTLPHEPKSSS

>tr|A0A1V5NUY2|A0A1V5NUY2_9BACT Magnesium and cobalt efflux protein CorC

OS=bacterium ADurb.Bin374 OX=1866937 GN=corC_1 PE=4 SV=1
MTLLDGLVFLLLLCGSAFFSGSETALTSDVGLASLSDKGDRAKMAISLIASRGTVIGA
LLIGNNIVNTLLAVYAATVFDSMILNSPLPAWMAVVAASVLSITVLLIGGEVLPKNIAIRFN
ERISLWVAYPCHYLVKMLTPILAVLNLVNRLVLLVIGTPKDRTGPSADELLAMVRMSQKA
GIIDPMERELIGRSMFLNETMAREIMIHRTQMCAIAETASMNEVKDIYTKELYTRLVPYRE
SLDQIVGILNIKEVFRFDHLRETFRIPDMMSQPIFFPETARIGVIFDKMRQSRTHLAVVDEF
GTTSGIITLEDIVEQIFGEISDEYDQGAARIRWVSPRVFEAEGRTSISEIQAELASKKLPQLSE
EACEDVETLAGIALRQTGRIPASGEAFVFEGFRFQVRKATGQKIQVMSVRVPDPEPERDRE
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>tr|A0A1V5QAE7|A0A1V5QAE7_9CHLR Magnesium and cobalt efflux protein CorC

OS=Chloroflexi bacterium ADurb.Bin344 OX=1852860 GN=corC_2 PE=4 SV=1
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EQVNVIWLAAKINAVIVSIFAFILINDSFCLYRSQWLLLLSIILIPLVLYFLEALISGIAARNAD
SWIKYFHGIARLTVFFFKPLYSVYESFKPDNIRNDYTFNEVEAHLREWNNAPDNAALKE
DERKMVRSILHFSDTLIREIMIPRIDMTAVDVETSLEEATSIVLASGHSRLPVYEDDIDNIIG
VLYAKDLLKIYTENPENRALRDYLRPALFVPESKKAGDLLSEMQTSGIHMOVIVVDEYGGT

AGIVSMEDIVEEIVGEIRDEYDDSEEKLINEISENEYSLGRIDLEDVNEILGTHITRESADTL
AGFLYSQIGKVPVGDDEEIEVEGWIFRIEELSGNRIRRVHVKKLEEDSPNKEGEQDEE
>tr|A0A1V5RTH8|A0A1V5RTH8_9SPIR Magnesium and cobalt efflux protein CorC
OS=Spirochaetes bacterium ADurb.Bin315 OX=1852912 GN=corC_1 PE=4 SV=1
MNISLAVVFALLVLSALFSATETAYTSLSFFQLKTLENRKSRA GKLAYALSQDKDHLITTV
LIGNNIVNLSASALVTTITIKYFSSALVGYTTGILTFMILVFGEIVPKRLALVHNVRIAILMA
YPIKTLMLLLFPLAWLLQVLSSAITRLFGTKKEEPVITTEGVMHVVDAAEDVGLVDQYESDL
MQRAIHFSSTTVRTIMTHRTEVFTLPSDLTIEEAFPKIIKSGFSRIPIYQDNQENIVGILLLRDV
LRAQQKQVVNKTLASLSRKPIYVVEQMHLDLDFYLFKKNKLQQAIVIDEYGGFSGVVTM
EDVAEQFLGELFDEHESRFPDRVVQHKDKPGTFVVMADAPFQQVVDDLWYEGDRVS
TVAAAYLLQEAGSIPVEGEVITTDLGTWQILLMKG NKVEVVEFTPNPASVD
>tr|A0A1V5UPG1|A0A1V5UPG1_9BACT Putative amino-acid metabolite efflux pump
OS=bacterium ADurb.Bin243 OX=1866936 GN=eamA_1 PE=4 SV=1
MLNFSITLILFSLLEVSSKPLMFFLDPVVLT FYRFLGLLTMI AFAYHKNILSDIKKISYSDFK
ILSFLGIINIALAMSSLQLAVKYSNAATAAVIFCSNPFFVFIFSI LSKSEKFNLCFSGVVLGI
AGVVLVMSRHGFHISHGALFAVMASMLFAFYIIVNKKVSANCRPVIVNIVSFFAGLAVTA
AYLLISAKGLYLPSEIFTSYKYIMILLFLGIAVSGFGYITFINTIKKYTPISASVIFLLKPALATI
FSLVFLGEKLGALFY YGLLLIMSGSWLILSSKY YKTN
>tr|A0A1V5Y0V2|A0A1V5Y0V2_9BACT Magnesium and cobalt efflux protein CorC
OS=candidate division BRC1 bacterium ADurb.Bin183 OX=1852823 GN=corC_2 PE=4 SV=1
MSELVLLALAILVCSAMTAFFAGSETGAISANRHRLRN LQKSGDERADDTIVLLSDSQKIL
TITLVGTNIF SILGVLF AKNFFEIILESLNVHEAEG IADIVSLLTMT PFLLIAGEIIPKRLFRKYP
DQLMLAFRKPLKFFSIIFMPAVSFFNSITYILLRPLGIKKGITQSNLTREDLQNLVESVEPAPS
HGHRMPAPNGEADMIQSIINLEKTLVREIMKPLVDIIAIPINAATRETIIDTALRTGYTRIPVY
TNYIFNMVGYIDVYDILRGDATAWKDLKSEIKDAC YVPETKRIDDLLQEMLGK HISVAFAI
DEYGGCSGFVTLEDILEEIVGEIDDEFDKSTFTFSEQKPGVYIVDPRMDLDDLNEKIGISLPK
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>tr|A0A1V6DIS4|A0A1V6DIS4_9BACT Magnesium and cobalt efflux protein CorC
OS=Verrucomicrobia bacterium ADurb.Bin118 OX=1852928 GN=corC PE=4 SV=1
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IETCVSAIQLGMTFCGLATGAMVQPVFRALLAPLFALLEVESVIARQTTELIVGFV VSTVLL
VVVGELVPKAVAIRQTLPTALWTAQPLAWFSRLAYPVVWLLNYLSQAFLRLLGIRPLSES
EVPHTEEELRLLVGAAQERAGATRLGRNIVLNALDLRHRIVRDV MRPRQEIVALDIEADIA
ACLEVVEQTNYSRFPLCEEGLNDRTRGVIIHKDLYALRNKARSGADLLPAARALIYVPETG
RLEKLLTLFLERKLHMAIVVDEF GTTVGMVTLE NVLEELVGQIQDEFDQEKPLL VRLSER
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GLRVSRLKVTRTVESPPATPAPD
>tr|A0A1V6F7R1|A0A1V6F7R1_9BACT Magnesium and cobalt efflux protein CorC
OS=Candidatus Cloacimonetes bacterium ADurb.Bin088 OX=1852835 GN=corC PE=4 SV=1
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LGTTLLGTNITTVLLAAISTYL VHRINSPPFNPKY TALIVGGVALIFGEVFPKAYFRSHADTL
VPKVFPMLRAISYILSPFVLVVTWLN RGVRLKLLKISGEQDFNYLTKDDLAYLLSITSTDAK
DEPQLEMIEDALDFTEQEAHNVMVPRTDVIAIQESATIAE AIEIAREEGFTRYPVYRQNLDD
IVGILIIYDVLKREFTPQTPVSKLMLEPYFTPENTDL DVLLREM QKQHR SMAIVVDSYGGTS
GIVTMEDILEEIVGDIEDEYDVEDEAPDVQQVSPNTWLASADVEIDTLAEDHGIDLPEGDY
ETLAGLILDRLERIPLRGQVIELEPWRIQVLQATEKKILKVKLHKMNKRGEST
>tr|A0A1W2GLI0|A0A1W2GLI0_9BACI Threonine/homoserine/homoserine lactone efflux
protein OS=Bacillus sp. JKS001846 OX=1938743 GN=SAMN06272738_2729 PE=4 SV=1
MLARSNVKSRRAVVLF AEPEEKEKGFDYYNTY NRRIFMIITLFTYILLGLSLAIPAGAMTV
QMTKQGM RNGFVHGW FVGIGGMTVDLSLIVLIYLGFS SVLTNPWVETVMWLLGFIFLMFI

GIESIKEAKSEVNIDGEDPNKSLLSAYLSGFMIAISPANIVFWIGVFGPVLVSSLGNASTSTFI
LIAVGILLGIFMMDMILLSFVHFTRRFLNPTFIKRVSIFAAIVLFGFSGYFGYEFIKQVMTFIS
KA

>tr|A0A1X6XA45|A0A1X6XA45_9CORY Magnesium and cobalt efflux protein CorC

OS=Corynebacterium xerosis OX=1725 GN=FM103_01800 PE=4 SV=1

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TQLSGAQLGITVTNLGIGFLAEPAAIALIGPALVDLGLGTVAARSVSVTIALVLATAMTMIF
GELVPKNMAIAQPLRTAKAVVGFQRIFFTIFALPIRLFNGNANAVVRALGVEPQEELGSAR
SAEELSALVKRSADEGALAAETASLVQRTLAFGDRRAHDAMVPRGRMDSLDDVDDTVED
LLELARTTGHSRFPVLTDENEIAGVAHIRHGLAVPFEARPTTLVDTVMGTATFVPDTPVPLD
DLMDTLRSGGLQMAVVVDEFDGHAGLITLEDLVEEIVGEVRDEHDEETDDTPEPDGSDW
LDARMRPDEATERLGVTVPHEHEDYDTLGGLVTMELGRLAEVGEIVVATDPAPGEGPAQ
LRIEVTVDGLRIETVHVKVEPLADEHEDAEDTDGQEDRSTRREREKAERRERSERRDSEK
AERRAAKDREESEAR

>tr|A0A1Y6B841|A0A1Y6B841_9PROT Threonine/homoserine efflux transporter RhtA

OS=Tistlia consotensis USBA 355 OX=560819 GN=SAMN05428998_101593 PE=4 SV=1

MSGDGRDGRGLGYLLASITLFWGVNWPAILKLSVGVLSVWDFRLLSAGVGGGLLLTIARL
GRERLAVPRSQVGPLLLCALFNWVGWHLCSAFGVLLMPAGRAAILAFTMPLWASLFAVPI
LGERLTATRVYGLLLGLAGLAVLVGPDLVVFRTAPLGAGFMVLAASVWGLGTVLLKRFR
WTIATTTLAGWQQLAGALAIAGLAGLAAGGLDPWPADIAPVNLAIAIYAVSVPMIYCFWA
FMYTVRLLPAPVAAIGTLAVPVVGVFSGALLLGEVPVGLREVGALLLICSALAVVLVLP
AWRGRRA

>tr|A0A1Y6CAI3|A0A1Y6CAI3_9PROT Threonine/homoserine efflux transporter RhtA

OS=Pseudobacteriovorax antillogorgiicola OX=1513793 GN=SAMN06296036_113137 PE=4
SV=1

MMTVKPNLSLRYGLLAIFLWSTVASAFALTLELVSVYQLLCLSSLTSLLALALAMLVTRK
WTKLLELRISQWLQLIGLSLLNPILYYICLFSAYDRPKPQIAQSINFSWPLFLALGSTLIGGQ
GKNRSSLMFMIPIPSFLGLLITSQGSFSGITSNGAGILFAFLSAIIWASYWIISSQINIDALVKL
FAVFLVATPILALISWLDAPSALWLNYPKAILGSLYIGLFEMGLTFFLWLKALEHSNDKVM
LSNLSFLSPTLSLIWIQVILGESISLFTWVGFAILICGNGAPQISSSIRRKMTSQS

>tr|A0A212RT41|A0A212RT41_9PROT Predicted Co/Zn/Cd cation transporter, cation efflux
family OS=Arboricoccus pini OX=1963835 GN=SAMN07250955_1148 PE=4 SV=1

MTAADATATTNAALEQRLLRISALATLAIGCVGIATGLLIGSRAIVFDGFIYSLTDLVLMTCV
SMLVARLVALGASRHFQFGFWHLEPMLVAFNSSVLLACGYAFLDGLSTFLVGGRTVAF
GAGAAYALGVGLASLGIAAYAKRASRNHSSLVEIDIRAYVLGGFLSLGLFASFVLGAVL
TSQRATDLAPYVDPVILMLLTLVLAPVPIASLIRALAEVFQLAPADLDAEVDALMRALVAE
LGFKAFKAHVAQAGRAEFIEIDVIVDPAPFVSSVADLDAYRQRIADGLKPSAATRWTIAF
TTDPRWT

>tr|A0A221K649|A0A221K649_9RHOB Glutathione-regulated potassium-efflux system ancillary
protein Keff OS=Sulfitobacter pseudonitzschiae OX=1402135 GN=kefF PE=4 SV=1

MHTHIVHVPETASYNGALTRTAEHALRTAGGMVTVTDLYRAGFDPVERFGHYANRVE
ADRFAALGEQRNAWATDTLPGDVVDEIDNLERADLVILQFPLWWHGPPAMLKGWMDR
VFISGGLYTRKMRYDAGYFRGRRALISVTTGAPRAAFGQGSRGGDFDTLLWPVQYSMHY
MGFSVLRPFVSYGVQGHGYSYEGEGRRLRDLRSRNLDWSSCLSLDEVEPLSVPSWADW
NEDGSAIASRQN

>tr|A0A238WXH7|A0A238WXH7_9ACTN Threonine/homoserine efflux transporter RhtA

OS=Actinomadura mexicana OX=134959 GN=SAMN06265355_103433 PE=4 SV=1

MSPLKQDGQGGLTAVMSRLGMFMGFGAMIVVVISQGSGLALGSALKSFQGSFSIVLVGT
VIVTIVTVLKNMARMHLSVAAVSTPEVWREGLRSLRWSLFTRGQRDAIFSLAVTSAL
INLGGVVAVRELGNVNAAFSTAGALAAAGALLRFAPQWLLRFAVLTAVVFAAIGTGQG

NLSLLGLVAALCAASHMWNLPKRVVRLGDKSDEGLTWANLISAPVVLIGTFWWDHSQG
VSWEWGGKEIFGAVCAGLLVMVIPVFLQNWAGSRGVSEQDMGALSSLSPLHAVVGVV
LAPVTLALTGKEPVLPTFNQWGFFIIVAAVAIIAPQLPKDNRWKIQQAGPGVAVREDDEAC
EQPPVPHGDLDEQPQAPLVEPKNPWVPRQRGEEQSTSRDVEHPVESGVGGSAYETPAW
AVAQGANLDPDEGKLILTPRGRTVLTEEGVHYPGGCSLTyrKGNLSVEVEFVDEGTFDVG
AFVGLRATGITVVIGGTEMRYPDAEKFSVDLRTGRFHVTKPGDVLFGGRAAE

>tr|A0A239W504|A0A239W504_9ACTN Arabinose efflux permease OS=Cutibacterium
granulosum OX=33011 GN=SAMEA4412665_00314 PE=4 SV=1

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SAPWRGSMDDRGLRRTMIPSIVVMTAVYAVAPWLGYYPPLLVLALGYLWNYPIYTIPRQ
VLIATVPLRKRRRAALSLDAVSIEICYMFGPMVSIHASSVGTRATMIGCAVLAALGATGLTV
LDPPIAETSGAASEGQTPSSSSPDGNPSPDPRSATEPVAPTQSSATETLAVEGTTHSDSPTI
DVPTAHPSTTPALAWVNRFTVAILIGCLAAGYTLGGIELTTVGAMREMGSTQAIGWVLAF
SGLGSALGGTIYGALNRSVPMALLTLMGLTAAATTLATSPLQAGLILLIGGLFVSPTLTAS
IDQLTNLTTPSRRGSVIGWQGSFLNAGVAISAPTIGAVIDGVGWHQAFILSGAIAAVIGLAV
GAVMRTRGS

>tr|A0A250JAW3|A0A250JAW3_9DELTA Macrolide-efflux protein OS=Cystobacter fuscus
OX=43 GN=CYFUS_006164 PE=4 SV=1

MIRGAMQPSHSASSLLGSNRNYRNLFIAHTLSVLGDWFNQFSLLAIVYLKTGSSAYVGLTL
VSSALPALLLGPFIGALVDRSDCRRVMIISDVARVLLAATFILTVDWVWSIYPLLALMSLFE
TAFSTARNAIMPSVVDKPLPIANVLMNVARGMMASVGAALGPIISGLIGQNGAFWLNSA
SFALSALLISRIVLNAPAQAHSRRWSREDLLAGYRYVLSNPIVLGVFITGVAWSLLGGAYY
VLLTVYGAGVLKGGSSGIGVMYGAQGFGSVVGGLLVLRFLVHDEVRAIRLFSWGKIAQV
LVFFGFLFAGELWTGAALILLMRTIGGLTPYDTTLIQAYTPHELLGKVFAARSTFVEFAT
QLCTFVFGIWLFSFYNEPRITGAVFGLGSLVLA VTGFVILNSRASRDMAAQRLEPG

>tr|A0A257N9K4|A0A257N9K4_9GAMM Potassium efflux system protein KefA
OS=Methylococcaceae bacterium NSP1-2 OX=1917481 GN=CG439_295 PE=4 SV=1

MKIIAFSIVPSLFWWAKKPAYPTLLLLLITLCSGNVFAESPTTPPPPEPTNYNASQDITKDSL
QAKIDALTARKGLDEALKSRIIAAYQSAQDELNNIKAFNEREIAFKTAIQQAPDLTKKLQK
DIDQASEKPPKPNEEDFVKIPVEELTQRLVIEQDKVKQLDEQISKLSNELIEEQTNRPNLIRQ
ERLNAKQELDEANKAIQDAIANADSDSDAKLAQDAQKIYLTQIDAKTAKLNMLDAETL
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VIQETRENIQYSQQQLQTINGKISHYNEEKATADKQISDIDANFSSAAKKIDLASLSPPLGKIL
HEQRRNLLSQDKFVSQSESIQTETATTNLGQLAIEEKLKLLDDFDGYLQHKMELNVDDKKL
SRQDRMKIQAELRVLLNYQVELLNKLSVAYNSYLRTLGDGDFVRQQRHNVKVEKFALYLD
ERLLWVRSSSELAFTDNVSEVYRSTLWLLSPTNWNLSILKNVANLPAKNPFLTLFALLNITI
LLAKNWAKRRLKITSKVGKIYTDNFHYTLEALGYTLILVAPLPLTVTYIGWLLSNVSDS
NFTQAVGLGLNRVAIAWFFLQFFYRLFEPGIMRNHFQWQEDPATLMRTQLAWIRFVILP
CGFIIRVTLASGVPAYSNGLRLALNISLLAVVLFLTKLLHPRHGLLQHIVIGDALEWTRFV
RYFCYLAASFPLIIGFSVTGYYSALQLQQQLMVTALIFIIHILYEIALRWLTLANRQLVIK
NLQQKRKSSADGQKHVSVTGSEDPVLPIDDEQVDIPEVNAQTKTILNVLCFSLVVSFWMI
WKNIFPAFSFLERIELWQNKTIINNKEVYQSITLVNLFAGIYSFITVVSVRNFSGVTELLIFR
RVSMEAGSRYAVNQLAKYTLTTIGFFCFANELGFNWSQVQWLVAALSVGLGFGGLQEIFA
NFVSGIILLFERPIRVGDTVIGNVSGKVSRIHMRATTLIDFDQKELIVPNKTFITTQLVNW
LSDAITRVVITVGIPYGSDELAKHVMMLDAVCATPLVLKDPEPSVMLIEFSDSALTFSVRVF
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>tr|A0A259BET7|A0A259BET7_9GAMM Magnesium/cobalt efflux protein OS=Halothiobacillus
sp. 24-54-40 OX=1970385 GN=B7Y07_02160 PE=4 SV=1

MNDIHLGALFTALIALVLLSAFFSSSETALISLNRYRLRHLAKRGHGGAIRAQKLLLEKPDQL
LGLILFGNTFANILVSSLATIIGLRLFGDSGIAIATGALTILLIFGEVAPKTAAATAPEPIAWP

AAYIYSFVMPLVLPLVRLIGLLANGLLKILGFNTNRHRSHGLTAAELQTLVRESSQHLPEQ
 NVNLLSVLELEQAQVEDIMIPRAEIVGIDLDEPWDHVLAQIKSASYSRMPVFNGSVENTV
 GVINVRRLFGPLMDNTLTLSKFKRLLREPYVPEGTALTQTLLNFQTENRRSALVVDEYG
 DVQGLVTLEDILEEIVGDFTTSPDPNTDIINEEDGSFILRGNMPIREINRELAIDLPTTDAST
 LNGLIIEALETLPQTGARITIENVQIDVLSVQNHAVDTARLKFIDEDNEPNTKSQTHGAG
 >tr|A0A285PGC9|A0A285PGC9_9RHIZ Threonine/homoserine/homoserine lactone efflux
 protein OS=Cohaesibacter gelatinilyticus OX=372072 GN=SAMN06265368_3872 PE=4 SV=1
 MISQLATAILPMALFSLTTSISPGPVNFIALSLGTQKHKRQAFVSGATIGFTVLLALLGLG
 MEQLTTYQPLLTIFNLLGSLFIAYLGYKIFTSQSPISTNQNNGGGFMHGFLQWLNPKAW
 GSCLAGHAAFQTSNAPELLALFTLIYLIVCFVGVGSWAVAGTQISHLLSNQRTLCLFNRM
 GGALILLALFLALQPYL
 >tr|A0A286DJW1|A0A286DJW1_9ACTN Arsenite efflux ATP-binding protein ArsA
 OS=Streptomyces zhaozhouensis OX=1300267 GN=SAMN06297387_101313 PE=4 SV=1
 MSGAPRTLLVTGPGGDGVSTVAAATALASARSGRLTLLSREPADRLGALLGVPADALA
 GARPVEVAPGLWAGRIVSGPPFRAAVLAAQRQARTALAAALGSATLEEDELTELPGAEQW
 ATLAALRAAQADERWARVVVDLPPAVDAVRLALPGQLRRYLRRLLPQERRAARALRPL
 LAQLANVPLPAEALLGAAVDWDASLSEAEGLLADPGLAVRLVFEPTARSVALLGTAHAG
 LALHGIGVEEVLANRLVQGRSPDRLVRALAARQDALISGFAQSVGRSEAPRRVPHMGDP
 DAATLAGLLPAPADRAIPRPEPVLEDRLAEDGRLVWRLPLPGAVKHDLDLVRRGDEL VVT
 TGPFRRLVPLPSAPRRRCVVDGAFAHAGELAVRFTPDPERWPRDAEGGSEGRATAASAGPT
 APTTPAGSEGAERGEAQRAGGGERGEAERDGVFERGGESAG
 >tr|A0A286G4D3|A0A286G4D3_9PROT Threonine/homoserine/homoserine lactone efflux
 protein OS=Caenispirillum bisanense OX=414052 GN=SAMN05421508_101521 PE=4 SV=1
 MTLHTVAALLATCFLAAVLPGPGTVALSARVMAQGVRRSLVFVAGMLSGDVVWIAFAV
 TGLTVIAKTLGPLFLAVKIAGGLYLWVLGKLLRTRHDDAADNGPTVPVTEPSAWRTYLS
 GLALMIGNPKVMLFYVSVLPTVIDLHSLSLPLGIATVGVIGVGVGGGLVPWIVTASRLRGL
 MRSAVARRRIDRGAGVVMVGAGAAVAAT
 >tr|A0A286RKK6|A0A286RKK6_9PLAN Cobalt-zinc-cadmium resistance protein CzcA, Cation
 efflux system protein CusA OS=Thermogutta terrifontis OX=1331910 GN=THTE_3895 PE=4
 SV=1
 MTAARGARIGSFIVFADDWGRHPSSCQHIFRHLLEDFPVMWVNTIGMRPPRLDLFTLRRG
 LEKVGQWLKIFDARPSAILPRPNICEKTPRVNPVMPWRLRQGWERAFAFRMLLKWQLA
 AEVRRYPRPRILVSTVPVAAILVSALQVDRWLYYCVDDFRNWPEMDKEGIGDLERSLVEV
 ADVIVAANEQLKKHIEEYGKTAVVITHGINWEIWSSPACQATPEPVSDWLQRYERPWIVF
 WGSINWQVDANAVAAISERLKRGSILLVGPVNTHDPKLKESARVTMPGPIPVMLPVLAC
 YADVLIMPYRRGPGVDESEPLKLREYLATDRPVVVCDDIPATRRWADALDIAATPEEFAAC
 VDFRVKTGVDPRQLEARRRVRGESWAEKARQFVEVAFDSL
 >tr|A0A2A9HFD0|A0A2A9HFD0_9CHLR Threonine/homoserine efflux transporter RhtA
 OS=Thermoflexus hugenholtzii OX=1495650 GN=A9A59_1261 PE=4 SV=1
 MTTRHILTLALLSVVWGASFLFIKVQLDAGLDPLGVASVRTLLGAAALAPFAAAAVRRAR
 PAPRDAVLLAALGVTNFAVPWTIALAEHHISSGMASIANSTAPLWAAVLAVFLREERV
 NRTKGVGLVLGFSGIVILAGPASLVHLSSDAAGVALVLASTLSYAASAIIRRALGHLSPA
 VIAFGQVAAAAAALFPAAAATGAFAGVDWSPHVVASAATLGILGSGLAVVAYMGLIQQI
 GAVRSVLVTYLIPPWGVLFGWAFLEAISWNLLAGLVILAGVLLVQGVRLRLPGARPPES
 AGSAALGK
 >tr|A0A2D3WPN8|A0A2D3WPN8_9PROT Efflux transporter periplasmic adaptor subunit
 OS=Sulfurovum sp. UBA12169 OX=2015906 GN=CFH81_00865 PE=4 SV=1
 MKKIIKIVLYVLAVAGVAFYAAYNAINPKIPENFAYGNGRIEAAQINLAPKVSRLLEI
 YVEEGDIVEKGQMLARLDTTELEARWEVASAQIKQAEQKNRTMAIVEQKKSELALAE
 NHKRGESLYQSKSISLLQYQQYETAYKIALANLKSADVEASHAAIEAARAQAQAIRVTI

DDSTLYAPKKGRVLYKLLQPGEVVAGGQRVLVILDLLDTFMTIFLPTAQAGVINYDSEARI
VLDAFPRIAIPAKVTFISPQAQFTPKQIETQNEREKL MFRVKVAIDSDLLKEHIDKIKTGLPG
VAYIRIDQTIPWPEQLRNVPKSYREDSR

>tr|A0A2E1JZC7|A0A2E1JZC7_9GAMM Magnesium/cobalt efflux protein OS=Legionellales
bacterium OX=2026754 GN=CMF43_00545 PE=4 SV=1

MSSGKTPSSIIDKIASILGYLRQPSNKMFRDYCNQAISQKVIDSYEGQQLIRILDLEQKAAE
DIMITRSAVDVIQDSDSL DHIKKLRKSGHSRFPVVDKDNKKVLGILLAKDLVVSRSKKSA
LDLVRKALFIPENKKLNNLLAEFQRKHQHMAIVINEYGDFTGVITIEDVIEQITGEIEDEHDP
QHIGKNIVKENNGYYAVEGITPIEAFNQHFQCQLMDDDDIDTIGGLVLKYLGYIPSKGEKLT
IKQFEFIIRSASERQIKWLLVKKLKKSETNQSENT

>tr|A0A2E3QK85|A0A2E3QK85_9GAMM Lysine efflux permease OS=Gammaproteobacteria
bacterium OX=1913989 GN=CMQ39_03630 PE=4 SV=1

MEWLGSLSCSVGSVINVISHPFITGLLVGFSLIIAFAQAQNFVLNHGLMRLYVFPVILFCSLA
DFTLIWLGIAGIDYFEDSLELYKAEILAFAXWLLFYAIXKLKSAAVGNILRENSGPGYASL
SQTFTGLLXVTFGNPHVYLDTVLLIGTISMQFSAVEKAYYGLGACLASLTFFFSGLGYLGVF
LGRFLXTAWIWRLIDIGIAIIXLXISLSMLEGGGWIKV

>tr|A0A2E9BKE1|A0A2E9BKE1_9BURK Bcr/CflA family drug resistance efflux transporter
OS=Variovorax sp. OX=1871043 GN=CMO32_06805 PE=4 SV=1

MKTGTAAVAAMGPALVVGVTSTAVQPLGTDLYLAALPAIRNEYAARVGVVQLTLAV
LVFSFGLSPLLWGPASDRFGRRPVLAAGFLLYAAGATVGAMAPNIEVLIAARAAQGLGIA
ACMVCGRAIVRDLFEQQHGHVMTVAMSVLACLTMLIPVTGALLAQTGLGWRATLWSMA
LCGLAGALLVLARVPETARSLKPDALRLGPLLAGYARIARDPAFQSWTLLNAFGYAAANFG
FFSSSAYLFIETFGVSRVGFGLVIGGASVTYLAGTMLCRRWIAAHGIVTSVRRAGFLSLLA
ALVLVVPQFAGAHTAGTLTAGLWMLLAYGIHQPCGHVGMATPFPLQAGAASALGGFIF
AGAAFLCGGWMGLMYRSGSAAVLSLTGVLAAAAGTIALTLVQRHGRPVPARPAVP

>tr|A0A2G7QIN9|A0A2G7QIN9_ACHLA Drug efflux system protein MdtG OS=Acholeplasma
laidlawii OX=2148 GN=NCTC10116_00553 PE=4 SV=1

MKKFMLFYLIIFYVQGIVTNLHHPMPYYVEAIGVPNFMFGFFFFSFMNLGMMFGGPFWGN
LADHNKKKISLIIGILIYCLMQILFGLGHVFDMWTLTSAFRLISGFGMASALTILTGEMIITSD
KDKRAKNIAFGAAAVGLGGAIGQFLGGFIHTNSFFIKAFRTDIFFNAFLQGISVGFFAVLIA
IWFKPKKTIVDPNKKRVQFWEGFKEVRNIKPELLYFLVALTLITIASTNVEKYLDVYFKDL
GFLAKELGNFKMIAGVVSLLSGIIIVPLFMNIKHRLKLISVFQIISAVLIFTVFRSSSSSLFLILL
YTMYMAYIAIKAIFTPLEQDHISKFSGNHNVATTLGIRQSFYSVGTIIGPIFGAFLYDYSRL
LFDTSVIFFLISLVLIFISNHYRKKDFIQNSINSNI

>tr|A0A2H1IG72|A0A2H1IG72_9MICO Threonine/homoserine efflux transporter RhtA
OS=Brevibacterium antiquum OX=234835 GN=BANT10_00850 PE=4 SV=1

MTVAPRVVPEPNPSTALAAMVVLGALCLSSAILVKLAGVDAATTAVLRCAIAVIALVPL
ALFERRRRGGLSRAGVLWAIAGVALGIDYIAWTASIYLVGAGVATVLVNVQVIVLPLLA
LVIDRERV SARFLISLPLMLIGVGLVGGIVSFAEVGEHAVLGTGLALIAIGIGYGVYMFTRR
GTRRKAEGTIQPLAWATASAAVTAIIAQFTGGIGFTGIGPSSWMYLIALALLGQVVAWLL
INRRSVRLVPSMTASLLLIQPVLAALILGETLTVGQALGAGLVVAVAVANGVWQ
MRSRRRRQVLRGPDSAPR

>tr|A0A2H5VHM1|A0A2H5VHM1_9BACT Magnesium and cobalt efflux protein CorC
OS=bacterium HR07 OX=2035402 GN=corC PE=4 SV=1

MSIAVGVVTLAILTVLSFFFSVSEMAIASVSRLRLKTMIQEHPRQARALQALSENPTALITAL
AIVNNFVNLFASSIATVLTFLQLPALSGSETALVATLLITIYLLIFGEITPKHLGKNNNAERLTP
LVIGPLYWLSKILYPLTVAFQAIAQGLRLLLPEHYRQREP VHVSEDQIKLLIEMSEERGMLQ
EEEGEMIRIRIFVYDDL VVRQVMVPRTHVVAIEINTPLAEVREIIAREGHSRYPVYERSLDNI
RGILHAKDLLRFGYAEKQKLDEYKKKLQDELPRRMKEATTPEELKKLTEEKAFYEAEIRR
LRELLSNARLEHIIRPAFFTAPNKPIRKLLRDFQKNKKHMAIVVDEYGGMMGVVTLEDILE

EIVGEIRDEYDEPEEKKAALQIKQLSPTVYLV DGETPLDELNARLSLELP ISEAVTIGGLLLH
RLAEIPKVGTTLVVDGARITVAEATEKEVRKVRLEVLAMSKV

>tr|A0A2H6JPM3|A0A2H6JPM3_9BACT Antibiotic efflux pump outer membrane protein ArpC
OS=bacterium BMS3Bbin14 OX=2005737 GN=arpC PE=4 SV=1

MVKIGFTRLVSLCLLTWVLAAGLVLGSSLKTARAAGILTLDEAIRAALANSPQIKENQAV
VRGAVSGTKAVRAGLFPQVNGYARYDRFSDPVSVVPIQGLNLPPLFSRDQYQAGLSFRV
PLYEGGRLRGGIRAAARDEGIARAGLAYSRENLIAAVTDTFNRLYLKALRRAKEKTLAAI
EETRKEAALRLKLGRIAPLDLMEIDTQVASERVDLVRTRETLKRAGQQLCLLLGRSPATGI
ETRGSLEKNGKEEADLVASLTGPSGRRLKACIGKRPDIIRAGKMVEKADELLRIARGRL
PNVDLVGDYGRHAGAGLDGEEGRWSAGIHVSLNIFNSGLIAAKVAGAMAKRAAAAEAL
KGLVLKAESQVYAALSSLREAGARITLAGQARLTAAEAYKVETLRYKKGTGTVDLLQA
QAAWWTAKALYIRALFDRQQA VTALRLATAVTPWAGPSGGQQ

>tr|A0A2I0BL97|A0A2I0BL97_9MICO ACR3 family arsenite efflux pump ArsB OS=Microcella
sp. HL-107 OX=2035245 GN=CLT70_1307 PE=4 SV=1

MTTVPRPEGVGPVLGWPAQHPVPIILVGVGGGFALGTLAPGLATVPDAVVATVVAVAI
TLLPVPLASLGRAVVERRFLLAVIGLNIVVSPVLAYILSRVVFRDPDLQLGLLLVLAPGVG
IVAIFVRRAGGAVESLLSTAPIMLVIAVSLPALMVLFTFADGFLTDL SRLPLAMLF GIVL
PAVVVTVIQLIASRAPRLQRLTRQGGALAVPATALAAAFVAAVWLPRATERSDLLSAVAP
LFGVYLILMTPIGILVGTAAGLTLSQVRALTFSGGARNGVLVPLAMAFEEGFELVPLVVV
LGIGIEMIGLFIYRLLVPSVVQQSRGPLAQE

>tr|A0A2I6QNNQ6|A0A2I6QNNQ6_9BACT Magnesium and cobalt efflux protein CorC
OS=uncultured bacterium OX=77133 PE=4 SV=1

MTSATAITVKLLAVVLLVAANGFFVAAEFALVGVRRSSRIETLVAQGSRS AKRLMELLQNL
NAYLSACQLGITLASLALGWIGEPVA AALLAQPLSGLSETLRHGIAFAIAFSIITSLHIVIGEQ
APKLMGLAMAERVALAVALPMQLFYRIFSLPIRALDWASARAVGLVGIKATAEHASTYT
EEELRKLIDISRESGHLRAEERRLIHRVFEFSDTV VREAMVPRTEMAAIPNTCNLEQITKAF
DQHRY SRLPVYRESFDDVCGFIH SKDVMPYLLHPEKFKLEDVLQPPLYVVD TARLEHVLR
QMQQAKMHFGFVVDEHGGLEGITLEDLLEEIVGDISDEHDEEVNEQITEIDKHTFVLDGG
LAVRDLNRRLKLSVPESEGYTTIGGFLMTEAGHVLPGEVVQHDGLVFKVERVEKRRVM
RVKLEIQQT DGEGEIEDELDRARSSTGNTGLAR

>tr|A0A2K8SXP6|A0A2K8SXP6_9NOSO Cobalt-zinc-cadmium resistance protein CzcA, Cation
efflux system protein CusA OS=Nostoc flagelliforme CCNUN1 OX=2038116
GN=COO91_05519 PE=4 SV=1

MSNSNIEQFGNLVQDAQRDDEYINATKWCKHFGSRLDNWKQLPETKARSKHLKITESNT
EPWIVERVGKTWVTWVHPIMAVHLASYLDPAFANYVAEIFIRYAEADPTLAADIASRQNT
VEGLDIINEAVQKQYSLIFARDWLCETSKIRFDFLDKDPWLRHELSESNLVFLLNNKFGLP
CKGLVVIHLNEELLEDFLKDKYPNIYQSACRIVQLPSGQHLDISMADETALFSYFFREIND
WVKEKGGTDCSFLK

>tr|A0A2N0UUU1|A0A2N0UUU1_9FIRM Magnesium and cobalt efflux protein CorC
OS=Ruminococcus bromii OX=40518 GN=corC PE=4 SV=1

MTSDIIMGVVILVLILLSAFFSAIETAFS FVNKVRVQRYKDDGNK KAAAALYIIEHFDNALT
TILICNNVNLSCSSIATVLCMNLF GDAGSAIATGATTFLVLT FGEIVPKCLAKEHCDAFSL
KTAGLLRGLMTLLTPLVWIFTRFKMIALKIAGSSGDAPSVTENELKYIVESIEEEGVLEESE
SEMVR SALDFDETTAE EILTPRVDITFISIDDSPEKIKNIIENRYSRIPVYEGTVDHVVGILHT
RDYLERLADGKAPDVKELMQPPYFVFKTQQLSKILNAFKRTKIHLAVVTDEYGGTLGIVT
MEDLLEEIVGEIWD EDEEIEHNYKIGKGEFLVNGDMELEDMLGLFDMDEDSLECD SVTV
GGYILEHAGTIPHKRDNIEADGFKFTVMEVKDQ RILRVVVKKSDTSEENESDEKSENKKSE

>tr|A0A2N2RWX2|A0A2N2RWX2_9PROT Bcr/CflA family drug resistance efflux transporter
OS=Betaproteobacteria bacterium HGW-Betaproteobacteria-4 OX=2013716 GN=CVU31_08275
PE=4 SV=1

MLASLASLGPFSIDAYLPSFPEIAEKLNATQLEVQQTLSIYLLSFAVMTLWHGAIADRFGR
NVILVAVGLFAVASAGCTLATRIEHLWFWRAMQGITAGAGIVIGRAIVRDLYDGAAAQRL
MSQITMMFALAPAIAPVIGGWLQSWFGWRSVFAFLVVSTAALWLACWKLLACAAVSLN
FGGFFIYVLSAPVFLMTHLGVFETGFLWLFGPAMAGMICGAGLSGRLAGRISPSRTVLIGY
LVMGCAAAFNLTNLALPPGLPWSVMPVIFVYTTGMSLAMPSTLTFALDPFPEQRGLAASC
QTFQSGFNSISAALIVPVLWGSTLSMALGMAGLLALGGLAALLHQRWRHKPA

>tr|A0A2N5NC54|A0A2N5NC54_9BACL Potassium efflux system KefA protein

OS=Paenibacillus pasadenensis OX=217090 GN=B8V81_0068 PE=4 SV=1

MNFLHQPLAAANPAASPPPSASPGPSASPEPSVAPLPTDLEGMKEEVANKTSAYWDAMTS
YFDSQFWINATHICIKVAFILLVGQLIIFVVGKGIDKVMERETRVRQQRTRRVVTMGRLLKN
VTNYVVYFITGMLVLSMLSVNVAPLLAGAGVLGLAIGFGAQLVKDVITGFFIVLEDQFA
VGDIVQTGTYKGTVELIGLRTTRLKTWTGEVHIIPNGTISQVTNYSLNNSLAVVDVDPND
VPIETAERIRDMLEKIDNPVLVKVPDLLGVTSMTTAEYKLRIVAECMPNTEATVSRQINR
ELQLLLRSGEQPQEA

>tr|A0A2N7R3E7|A0A2N7R3E7_9PSED Glutathione-regulated potassium-efflux system ancillary protein KefF OS=Pseudomonas sp. AD21 OX=396378 GN=kefF_2 PE=4 SV=1

MHALIVVAHHQPRSLTHSVATQIAEGLTQAEPANTCEIADLYAQGFQPVFGAADFAVHHR
EALPPADVQAEHARIDRADALVLFPVYWWSPALLKGWIDRVFSNGWAFDYGSDQKH
IKKLQRLRVHLVGLGGADAGAFQRHGYAAAMKAQIEHGIFDYSGATVQSSTLLLESESSD
PQGHQTAYKIGVRIFPVPGGSEPAREGTRAVELIAS

>tr|A0A2N9KFR9|A0A2N9KFR9_9LACT Cation efflux family protein OS=Leuconostoc
suonicum OX=1511761 GN=LES9216_01595 PE=4 SV=1

MNQKNIEQRSLIIGCLWLFLMGISALTAYFATHLEALFVDAYFTLITLTALLSIVISKISTK
VSTRFPNGLFVLEPLYAFFQSLTIIILLTVSLITVGGKAYQYFVYGHGHLNIAPIVPIEIM
VILSLTSLSYFYKHQNKKIHTSTLLSAETKSAMIDGIMSAGIGAAFFILFISKNSPLSFLLYT
GDSFITVIIVLFIRVPLRIMKNALIEISGGLTQDQGIKSFIEGSIRSHLSNDFAINDCVKYKVG
MSFKACIAISSKTHMIDTEKLAIFYKNNILNDLSQKLAFINIVFVYSNVGKNEKS

>tr|A0A2P7QRI3|A0A2P7QRI3_9SPHN Efflux transporter periplasmic adaptor subunit
OS=Sphingosinicella sp. GL-C-18 OX=2116704 GN=C7I55_09660 PE=4 SV=1

MQTGDSPLSWRPRAVPAALGAALLLAGAGLYTAGAASGSDPAAPLNRPAASADATS
LLPLDAHVEPRTATLVTAQQGGQIAHIRAADGSMVAHGAPLAEIANPQFVLAVASQEAEL
SRLGDLQAQNLGLQRGRRAADSQEIAAAELALHEAEDELRRQTRLFEAGVVTAARIKPLEA
RAAFHRDKVAALRAAAATEHEAAASQQHRLAKAERQLDANLGTVRATLDTLVLRAPAA
GRLTNFRLRPGQPVAAGDTLGQVDGDDGYKLYALVDEAHLGRVAAGQAARARIAGAAV
PLVVARVDPQVAEGRFKIELHFRGPTPATLRRGQVRVRAELALAPAETG

>tr|A0A2P8D480|A0A2P8D480_9BACT Threonine/homoserine/homoserine lactone efflux
protein OS=Taibaiella chishuiensis OX=1434707 GN=B0I18_104110 PE=4 SV=1

MNFSEAVIKGVLLGLFMAISVGPTLFAVIRYSMHHSYKAGIAFIFGVFSFSDIYVTLANIATN
WLNFLAHQKTVGYIGSVLFIGMGLLSLLRKYKPKRPSQGKALDISAGAYFKIWGTGFLM
NALNPAVILLWVGSASVAGAALPPRIVFFGVCLGIVLGFILDKVFLADKIRRRRLTLRRIMY
LNRISAVCILVFGFILLAKVYFNIELSH

>tr|A0A2S6HQ54|A0A2S6HQ54_9BACE Threonine/homoserine/homoserine lactone efflux
protein OS=Bacteroides xylanolyticus OX=384636 GN=BXY41_109192 PE=4 SV=1

MILKGLRFGMLLQLAVGPICLMVFHTSTTYGVIYGLHLVLAIALVDTLYIALSCVGVAAII
KKGKINEVIKVGCLVLVLFGANTIAGVFNLFSMPHIPFSNVSGKNLFFVQGLLLTASNPLTI
VFWSGMFSTQMVENQWNKKQLFFFASGCIMATVIFLTAVAFVGSALGGFLPQIIMQVMN
VGVGIVVFFGKPLLIYLRHLT

>tr|A0A2S6S8F6|A0A2S6S8F6_9PROT Cysteine/O-acetylserine efflux protein

OS=Alphaproteobacteria bacterium MarineAlpha5_Bin12 OX=2013087 GN=eamB_1 PE=4 SV=1

MIDYIPQLIIYVFIAAITPGPNNTIAFYTSYNFGIKNSLHIPIAATIGVSLIQLLCCIGLGSILLKF
PIIQSILKVFGCIYLIYLAQISKFKISKNNQNVKKINFFECFLFQFMNPKLYVFASTTSVIFT
NYNYNFLLETFAIVSIMGGMTIIAISIWIFLGNFLLKLFNNDVQRKIINYTLISLFLATAIWIF
TS

>tr|A0A2S9XIX3|A0A2S9XIX3_9DELTA Magnesium and cobalt efflux protein CorC

OS=Enhygromyxa salina OX=215803 GN=corC_2 PE=4 SV=1

MLAKLIWTAVFVFLNGIFVAAEFALVKTRPARMQALAEQGDARAKRLLAMIDELDLYS
ACQLGITIASLVGLYLAEPFAALIELGAESVGIDTHGSTTLHVVSFGLALTIVTLLHMLVGL
EQWPKIWAHTAERTSLRSLPLKIFTMMFKPLIIVNVLSNGLLRVGVSGGHGEHNADV
RELKGIIGAAASAGNISARQRIFAENILDLVELEVRHVMLPRTSVAFLDLSAPTKDNLRLR
SLGHSRWPLCNKNLDEVVGIVLARDVLDLTLGAGGEVELEAIARPTQFVPDTPQLSRFIVGS
QQTGHQGAIVQDEHGTTVGMVFLDALVGLPLHDERDELQEPFEKGEDGVIMDMGAL
DLPAASALLGVELEDSDHTIGGYIIATLGRLPRQGDKLVVGAFDAEVTRVGRRRSVARVC
FTPREDAES

>tr|A0A2T0QLI2|A0A2T0QLI2_9BURK Cu/Ag efflux protein CusF OS=Paraburkholderia sp.

BL25I1N1 OX=1938804 GN=B0G73_110223 PE=4 SV=1

MVDVDGRGLAVWTVFNVGACEMKNWLASMAMGCMVMISASAYAAGEASESQMSASA
DAQTAMSHGEVRKVDAAAGKLTIKHGPLENLGMDAMTMVFKVKDPAMLAQVKPGDTI
DFVADEVAGVLTVVKLEKR

>tr|A0A2T1AK18|A0A2T1AK18_9RHOB Threonine/homoserine efflux transporter RhtA

OS=Epibacterium scottomollicae OX=483013 GN=CLV89_103218 PE=4 SV=1

MSTSSAAQSLSDTDRPLLGLALMLGFCALIPLGDAVAKILSTRIPVGQIVLARFAAQGLILAP
VALMLGISLRLPSRVMPKVILRTLLQMAGITAMFMALRYLPLADAVAIAFVMPFIMLLLG
KYVLKEEVGLRRLACVVGFAAGTLLVIQPSFAEVGLNALWPLAVAVIFSVMVTRTLAR
DTDPIAIQAVSGGIACLLMAGFFALGYGFSIEELNTTLPATPELKLLALAGVLGTIAHLLMT
WSLRYAPTSTLASMQYLEIPVAVFVGWLVFSELNSIAACGIALTVAAGLYAVLRERQVN
RAAREVNPAATTESGLPASPE

>tr|A0A2T4ZPP7|A0A2T4ZPP7_9RHOB Threonine/homoserine/homoserine lactone efflux
protein OS=Oceanicaulis sp. PT13A OX=2135616 GN=C7969_0950 PE=4 SV=1

MSLITLAAFAGAIFILFLTPGPGNIAMVGRITLDAGPSHGVTYGLGILTGDVFWLTLAVFGL
AAAADAASEYAEFFWIAKIIAGILLWFAWGAFQGWRRHPAPAHAPMAKISKRGLAMTYA
AGVAMPLTNPKPIIFYLTFLPAFFDLTTVGPLSYLAMIGVMGAMFLLFALVYVGLAHKAR
GWLREKGVKRWADLVTAIVMTAVAVLLLTR

>tr|A0A2T5X788|A0A2T5X788_9MICO Threonine/homoserine efflux transporter RhtA

OS=Microbacteriaceae bacterium MWH-Ta3 OX=207608 GN=C8A06_0667 PE=4 SV=1

MSRKGLFYFLATGVVWGIPYYFIAIANQAFSTVSIVWLRVVMGAIILPIAIKRGVLIQAFRQ
WRWVLVFAVLEMVFPWWFITEAERSISTSFVGLMMTTIPFISALIMGILGEKAAWHPLTIL
GLVLGFTGVVSLIGIDALSGHIEVLPVLMLAGAALGYAIAPIIAAQKMAHTSTLAVIALSM
VIVAVIYTPAVVVQLPVDIAAGITAEQWWAVIILGVVCSALAFVLYFELFKLIGPRRGSIT
YVNLLVASILGIWLLNEPITPGIIVGFPLVVAGSYLAGKLHKPWSRKGQAEPAN

>tr|A0A2T5ZVU0|A0A2T5ZVU0_9ACTN Threonine/homoserine/homoserine lactone efflux
protein OS=Nocardioides sp. CF167 OX=2135685 GN=C8K06_12351 PE=4 SV=1

MTVLTALAFTAAAAVIVVVPDPDQALLQLSAAAGRPAAVRAAAGILLGIALWGVASIAAG
LSAVLVDGSAAFRVTVLSAAYLAWLGVRLHAARWPALPEQEVVNGSSGRFFLRGLL
MNCLNPKIGLFYLSILPQFVPSSATSTVGAELVLSAIYLAVSALWLFGFAFVAARLHPLLVR
PQVRRPLELMVGLIFLVGLIAALVSL

>tr|A0A2U1DG33|A0A2U1DG33_PANAN Threonine/homoserine/homoserine lactone efflux
protein OS=Pantoea ananas OX=553 GN=C7427_10298 PE=4 SV=1

MGVCWLYRQKTACYSERMFTGDTLMTASLLSFLLAIIILTLTPGFDLTALILRSAAAQGWQ
RASATALGVATGCLLWGIAVGLGLGALLASEMAYNLLKWAGAAAYLLYLGIKLLWHPR

AQSVSMHAEAAAQQRHLACFTRGLLGNLLNPKVGVFYVTFPLPQFIPQGASVPIWCSLMAL
 THMLVGLAWSTVLIGSSHYFAEQLKRPRIVKIMDRLTGCVFIGFAAKLALSRR
 >tr|A0A2U3KC48|A0A2U3KC48_9FIRM Putative efflux system component YhbJ
 OS=Candidatus Desulfosporosinus infrequens OX=2043169 GN=SBF1_1790002 PE=4 SV=1
 MAEADSKKKKLPRALIGGIVALLIAVGAGYYLYMMRYVSTDDAQISVAEGNSVPITVAFP
 GRLSTWKVNLNDDVNQGEVIGTESNQSVLSANPLLLPMVTADQLLAGRLIEMENIRSPISG
 KVLQTNAAAGQGQVQPGQVLAVIANANQLQVTANIQETDISKIRVGGQIVDLDLGLPGQQL
 HGLVSRIDDVTESVFSIVPNVTAASGSYTNVEQRPVVIQITDKNLAKKTLVPGMSAHVQIH
 VQ
 >tr|A0A2V2ZP82|A0A2V2ZP82_9BACI Potassium efflux system protein OS=Bacillus
 oceanisediminis OX=665099 GN=DF073_11427 PE=4 SV=1
 MEELNVSILLIKNVTIQEAALFLFFTGVILAAKWMINTVLNKTGKKKSIQNERILQGVASLV
 NWAIFYGIIILFLFYFSKEKWSYILFTAGEVDVTLKLLIVAFLTVSLAHRLVQVLTKEYLLT
 SVYEFYGVDRGLGYSFNRMVYYTVMIAALGISLTTVGLDLSAAAAILGVLGIGIGFGMRN
 VAGNFISGIIILFERPVEIGEMIEINNKGKIESIRLRSTIIRTAKEGTLIVPNQYFIEQIIKNRTGS
 EMLAQVLISVAYGTDTEKVEELLHEVVVREIPNADGVLLKPPDIRFVDFRNKAMDFLIEV
 PVAHFEAKQNFESRLRHGIAETFYKNGIELASPQGYPAD
 >tr|A0A2V3VLX0|A0A2V3VLX0_9SPHN O-acetylserine/cysteine efflux transporter
 OS=Blastomonas natatoria OX=34015 GN=C7451_10483 PE=4 SV=1
 MQPDSQLQDLPDRGFNRLDWAVAVMMMLLWGFNIIAMKSAVDSAGALPGAFLRQAIVA
 VVCLPFLRIVPGRMKLICITLGVLSGGIFYVAVGLSLKVTNNVSALAIAGQLGVPFSLILAVI
 FLKEKIGIPRLIGIVLALFGVLLLVPDPAAGKELPAIAISAVGSLIWATATLIQRNLGGIGVLN
 ISGWLGLIGSLVILPFALLLEPDGMALLPHLSAETYAWTAYAAIGSSIGGHGAMVWLLQR
 HSVSTVSPLTIPTPVISVAFATWWFGTPLTWLMIAGGLIALLGVSVIVAVRNAQKARELAEA
 RLMKEGTRS
 >tr|A0A2V4W4W2|A0A2V4W4W2_9GAMM Threonine/homoserine efflux transporter RhtA
 OS=Shewanella chilikensis OX=558541 GN=C8J23_11131 PE=4 SV=1
 MSAKGQARTGLTELHLAVLLFGGTALFSRLIPLSALNITLLRCVIAAIVLALLVKLSRQRLR
 LLRGKDYLIALLLGIVVSLHWVTYFAAMQLSSVAIGMIAFFTYPMVTVLVEPWFTGSRLH
 LRDLVSGLAVLLGVILLIPEPSLGNVTLGILVGIISAILFTARNLLHKRYFTAYSGQQAMF
 YQTAVAVLV LAPWHSLDAGDISNQTWGLLLLLGVVFTAAPHALFTSALRYLSAKTVGLV
 SCLQPFYGAMLAWLLLDESMLTTAIGGTLVVATALFETSQSHKSQAPKKNLG
 >tr|A0A2V5EIA3|A0A2V5EIA3_9BURK Threonine/homoserine efflux transporter RhtA
 OS=Acidovorax sp. OV235 OX=2135489 GN=C7505_12242 PE=4 SV=1
 MNDVATQGLSSRRLFLLVACLTAVWGNTWVLFPIAVREVS VWTFRAICLLGSGALVLLIA
 RLQGMQLAVPRGEWRPLVTAGLTYLVIWNVASTYAAVLLPSGQAAILGFTMPVWATVLS
 WIFLKQRPSARLLTSVVLASCGVGLLAYAAREAFSSAPLGFLVGLTAGLGWAAGTLILKR
 ANITTPAMVSTGWQLVIAGVPIACVALLNGSHQLFMPSVATILVIGYITIIPMALGNLAWFS
 IVKVLPASVSGLSTVMVPIVAMLTGAVVRGEPLGTLEITAMCFCASAMAIVLLK RTE
 >tr|A0A2W7NGJ0|A0A2W7NGJ0_9BURK Threonine/homoserine/homoserine lactone efflux
 protein OS=Paraburkholderia tropica OX=92647 GN=C7399_10389 PE=4 SV=1
 MSLSTWFKPAFIAGFFLLRPNRSMTGQMPARDRLWTRAHWHNRRFAYFFLTSAVAMN
 LHTWWLFLATVFVCAIPGNMMLIMSHGAQYGLRRTSATMGGCLSALVLM LAVSAAGL
 GVFLQAWPTMFNVLRFIGAAYLVYLG VKAWGAPVEEHAASNAEAETLAARPARSPATLF
 RNGFLVASSNP KAILFAAALLPQFIDASRP TLPQFGVLVATFAVCEVSWYLVYAGFGTRIG
 ATLSRRVAKAFNRVTGGVFVFGGAMMALMRQ
 >tr|A0A2X1BPW2|A0A2X1BPW2_BREVE p-hydroxybenzoic acid efflux subunit AaeB
 OS=Brevundimonas vesicularis OX=41276 GN=NCTC11166_01125 PE=4 SV=1
 MARALSPRRAAEVRAALQMAVGAMAALYLATWLNLPHPYWSVISAIVVIQASVGGGV
 TVARDRAIGTATGALAGAVFAFIRPPGLESMALSIAISAGLLAFFATGRPWLKVAPVTATIV

IAGGTGAEGPASLALDRVMEILVGSGVGVLAAILALFPRHAGQSFKLQAREAAGEAAGLLA
LVSKAAPEDAEEISRRHADLKRRLDALGQAAKNVIDLPGPQRETADRAALVRAFWRVRS
DIVILGRGFQAEGAGARLDPWSQDAERA VEQLRALSEGRAAQPMGAIDQSLALSMAVEG
DDVALGAAAIGVAHMRDLDDLAARFADLKL

>tr|A0A2X2IQ09|A0A2X2IQ09_SPHMU Arabinose efflux permease OS=Sphingobacterium
multivorum OX=28454 GN=NCTC11343_00842 PE=4 SV=1
MMMPFGSAFAVNNLKVSHQLPMLFMISGLIASLIIMPVIGKLSDRYDKFKIFAFASLWLMV
VVFYITNLGVTPFYIVVILNLMAGILSRMTTPSSALITAVPEMKDRGAFMSISSSLQQLAG
GVAASLAGVIVQETKESPLEHYPTLGMSVILLSIIGIFMIYRVSSMIKKRKANS

>tr|A0A2X3B7J9|A0A2X3B7J9_9CLOT Arabinose efflux permease OS=Clostridium
paraputrificum OX=29363 GN=NCTC11861_02027 PE=4 SV=1
MAALSLTAAAVLAGTSARSTARVVGAGGRRGASDGMADAPAPRPGRLPLATVLRNRGAA
ALIGISLLRTAGFMGALAVVA AVYAERHGLTGAGFTLVWTVSGAPFFAGNWFSGRLLSV
RDADAALMAGGIVASLAGVALVFAASPFTLMVTGTAVLAVGHAMIAAGVTTGLARLAD
PARSAALAVNGVAQAAGTVAGAALAGAGYALAGWPGVAWALAAVTVPCAALLVMTR
AGRN

>tr|A0A2X3K0F8|A0A2X3K0F8_9FUSO AEC family transporter OS=Fusobacterium
necrophorum subsp. necrophorum OX=143388 GN=EO219_06115 PE=4 SV=1
MWIIIQKMLLLLCVSALGYWICKAKLITLEHNRGYSILISNVTVPCMVIFSIFSQPPIQNYGEI
FSIFGVGFLFFGFFTLCSLFLPILFRAKNEEIGIYRFMTVFNNNSFMGFPPIQSVFGNKYLFYA
AILNIVNALYLYTYGMHCITKDVEDYHFDWKKLCNPGMVVSVISLALYLLHFSLEFFLEI
SRQVGNITTPSLMLVIGVNLSPMFREVFSETKLYLFSFFRLLVFPLILWFLKGFMANITDFL
IVVLVTAAMPGAAMMVNLATEYKGNVYFASKYLVSTLLSVIIVPVVIYVLQNYV

>tr|A0A2X4NAE1|A0A2X4NAE1_9BACL Threonine and homoserine efflux system
OS=Gemella morbillorum OX=29391 GN=NCTC11323_00051 PE=4 SV=1
MRRFVSELILIGVVIIWGLAFIWQNIASKVLGPLTVVGLRSLIAVIFITLVAILVPSLYKSQAP
KLIGEASSSKKLWLIGMCGVVLFFAMYIQQIGIGMTTAGKAGFITVLYICIVPFIGVFLGNK
LNKFFIIGLILAVIGFYLLSVKEEFTLELGDVIVFISAIFFGVHIIVIDYSALRVNSMFLSIIQLV
VVAIFSLGLAMIKETIILADILGVAAPLLALGILSSGLGYTGQIIAQREIPHTTSLIMSLESV
AAIGGVILILNEHIGLREGIGMAIVLVGIIISQLREKKSPKLEQK

>tr|A0A2Z6IGJ1|A0A2Z6IGJ1_9PROT Cation efflux system protein CusC OS=Acidithiobacillus
ferridurans OX=1232575 GN=AFERRID_06470 PE=4 SV=1
MRKRTLTPWRIPARHPGSTRWVLACWMMIGILPGACAGSLTQNDADGAGLGSALMNALP
ASPETVAPGLLPPAQAQARRAVKKRSPVGSTPTTPAPIRTPAALSHVVPSTTVALALSSGH
GVTKVRNSAADAGTHPADHAAAVTIMAPRASAPALPDLHATAHSSAAPVGAVAAGGGS
KLHELLATALANNSDIRLADQSLREAQAESLDAFGQFLPHLNFQAQTQLYGNQTNHPAVS
LIGSTIVVTQGNYSNYLSVMASLNLFEFGGQGANLAASRQGVHAGHEQVSERRRRRTALN
VLAGEEELQSLQWQLRAIQRSVFMQRDLALAEQRMQRQGNESRIDLNQMRSQVANLEA
QRQDTKKRLVKAQTNLALLTGKTGAFDLLQSGVHDSIPTPPEFDVATVEGA AVENLPSVQ
VARAALRKARDRVDAVRGSFLPNVNLQTGYNWIGTSSQGFGRAIGSTSPSNYTVGISITQT
LAPFTGHMAKLDTAEARSEAALIRYQRALQEGRQELRVNQEEVRAGTARLA ALESYARA
RQNQKLMEELYAHGRISKTD RHAAQIKTMNAEDACRDARAQLQVARWMLYAMVDPRH
VADSLQKTQAGEADNAAPSSSGAGAEHA

>tr|A0A315ZCA4|A0A315ZCA4_9BACT Threonine/homoserine/homoserine lactone efflux
protein OS=Sedimentimix flava OX=379075 GN=BC781_102754 PE=4 SV=1
MNQALLLPFLSYAIVTTITPGPNITATSAGIQLSYKKTVPYLLGISVGFFVIMLIAGSFTSYF
TSQNDNLFSVIKWFAGAVYILYLAFIPFINVKNKKNKSLNKNYSFITGFLQLINPKVILYGV
TIYSSFTQLIGGSNIRVVSSAIFLSALAFVCTSIWAILGTTLSSYFENKTFSLVFNSILALLIYI
ATTIILI

>tr|A0A316AT94|A0A316AT94_9ACTN Arsenite efflux ATP-binding protein ArsA
OS=Quadrifera granulorum OX=317664 GN=BXY45_113116 PE=4 SV=1
MSTAWDWDALLDDPSVEVIVCAGSGGVGKTTTAAIALRAAERGRRAVLTVDPARRLA
QALGTDGTPGDAADDAEAGAEAGADEGDAPGPDEPRGVPGVDTRRGGSLDALVLDAR
RTLDDGLVDAALPPARAAQVKANPVYVSLATSFSGTQEYMAMERLGQLRAGRDTAAGWD
LVVVDTPPSRSALDFLDAPTRLASFLDGRFARLLMAPVRFAGSARTSTGLRAAGGRVVGA
LAGGVAAMVMDRVLGGRLLRDVQALVEGLDEVFGGFRERAEVTSALRDGRTAFVVVTA
PEAEPLAEAVFLTERLRSALRPAAVVNNRAARAATGLDAATARQAEEALRTGTTGGAA
RGGKTSAAAEKAARVLDLQVELLERVERERRLVAERLADSGAPTALVPALDGDVADLDG
LRAVGDALGRNR

>tr|A0A316CHN7|A0A316CHN7_9THEM Threonine/homoserine efflux transporter RhtA
OS=Oceanotoga teriensis OX=515440 GN=C7380_11555 PE=4 SV=1
MVSSQLKGWVYLLITVFFFSTIEVVTKPFAGVFDPLQITFLRFFFGGLVLLIFLLISGKMKTY
KLTVKSLVLMGLIGSLNSVLSMSLLQLSVKFSNASTAAILISANPIFVVILASLILKEKITLRK
VVSMAVGALGIIILMSNSSGDSTLGLLYGVLATISFALYTVLVKKYVKEIPSIIFVTFSSLLS
SIIFYIVLLIFKIPVTFEIESFNVIWMLAYISIFVTGIAIYITFFKAFEVLDASKGSFSYLLKPVIS
MIMAYLFLNEIPNNMKLIGTVFIILSVAIIALKGKKNKI

>tr|A0A318J4V9|A0A318J4V9_9BURK Threonine/homoserine/homoserine lactone efflux protein
OS=Undibacterium pigrum OX=401470 GN=DFR42_105357 PE=4 SV=1
MPELANLLSFILAAACFVIIVPGPATLLVAELASLSVQGAIAVAGIVMGDIVLIAALSAAGFA
VLMQSLPWLLPGLRMLGAAYLLYLGINLLRSAGTMTQLQPRPASVSFARGLLITISNPKPIL
FFSTFFPLYLSPAHDAAVQGFVTLGAMFEVINVLVYFILLCSILRWTAKRLAHSKGRQGWLQ
KAGVHKICCVGLILCSLAMAWN

>tr|A0A318TYH1|A0A318TYH1_9BACI Tetracycline resistance efflux pump OS=Lysinibacillus
chungkukjangi OX=1202712 GN=BJ095_101161 PE=4 SV=1
MEGTIFSLIPPIVTIALIITKRLFLSLGVGIVLGALLYNQWHIFDSVSNIFNIGVEVLVGDGKI
LIFVLLIGILSSLLYLSGGINAFSQQWGTKVAKTRAQSQMATIFLGFFTWFDDAFSCLFRGT
MRSVTDKYNVSHSKLSYLIHSSAPVALLIPVSALSAFIISIIDGVLSNNIAEYQALEAFL
AIPSNFYTITITIVLVIIVAYTGINLGQMQRDEKRAIEKNILFDTKHKGIPGADESKLPSRNDG
KMMDLLLPVLALILVTITAVTIGSAGEGSNSPIELLKNTDIITSLLYGGICANIIILVRLIHKKT
SAGHLSSTIFSGIKTTLPSTILFLALVTAQIISSLGVGQYLASLIQGNMSIAWLPVIFVFVFAA
FISYSIGSTLGTAGIMIPIGAEIVATIDITFLIAIIGAVLAGTVFGEHSSPLSDTTILASIGSSVHP
IDHMMTQLPYAVLSSIASIIGFLVLGFTNSILIGLVSLVAVVIGIFFLKSRQAKLKST

>tr|A0A327TDZ3|A0A327TDZ3_9ACTN Threonine/homoserine/homoserine lactone efflux
protein OS=Kitasatospora sp. SolWspMP-SS2h OX=1305729 GN=K353_04281 PE=4 SV=1
MTSSAFAVAASPAFLASCAAVVCSPGPDSSLVRLVSRARHRRPVLAAGGMMLLAGAGY
AALAVTGSMVAVTALDPRLFLWRVAVGALVAVTGARALWEAVRPGPPGGAPEPGPAR
DRVGRHLLLGFLCTAGNPKVGLFLTVPFLPQFLPADAAASALPLLAAYVLSIGALWLLVL
TEVGVRVVTARGADGRAAFPPLAGRIGGGVVGAVLLLLAASLLFR

>tr|A0A327WX07|A0A327WX07_9GAMM Putative Co/Zn/Cd cation transporter (Cation efflux
family) OS=Aliidiomarina maris OX=531312 GN=B0I24_10884 PE=4 SV=1
MLRSFSSDRLILVSALMALGFAVGGAIGTWLQSSIIIFDGLFSFISLGLSLISLVAGRYVRS
VNESKYPFGKSIIPITLVFKYLAIFILCTLSLFEIGIQTLGGGRALNFEQAFVYSVVTLCL
LAFKFLQRRTPPEHSDLLVAEQREWLMGTGLSLMLTLGFALAIVGQWLGFDRFALMVDP
LMLIIAALFFMRIPTRGILDAGKEVLGLKVAEAEADVRVHVVEDIVLSYDFKDYLRQLQKV
GSTVYLEVDFIVHANQVSLSILEQDKIRSALYKQIRVFPYRWWYTISFTADEQWAR

>tr|A0A328X155|A0A328X155_9BURK Cation efflux family protein OS=Paraburkholderia
unamae OX=219649 GN=C7401_13360 PE=4 SV=1
MQVTCVAVLVNVVLMAMQFVTGWISGSDALLADGAHTLVDAALGDGVVAGAIYFDQAM
RAGRPHKLTTPVAIVLANLLIAATGAELLSAGMLPNAVQGAGARPAALAAFAVSVASVA

AKAGLFLYLRAAAARVKPHDGDLSALNAGAWHACADSVSSVVAAGATGVLLGLPA
LDRSATALIGALILMAGLQRNASALRSLFRRLARMGRTRRAHAHAGQPEPTSSQA
>tr|A0A330PD81|A0A330PD81_9BACT Arabinose efflux permease family protein OS=Mesotoga
infera OX=1236046 GN=MESINF_1359 PE=4 SV=1
MKDLGRNFWLYAIGRLVSLIGSGVQSLAIPLYILDLTGSGTIMGTFMVITMLPRILFGPIAG
VLGDRFNRKMIMIIYMDFARGAAILAMAGANSLTITVLFIFQLLISTFDISFDPATAAML
PDIIDSDKLLRGNSILGAINSLSYIIGPVLGGILYGMFGIEAVLILNGASYIASAISEIFIRYQQT
TEKGKISLKS VFKDIVEGVGYMRKINGLILVMVFAMLSNFLSPFFSVVFPFFARTIVGFTS
EQYGFLQSGWVVGVLIGNVILGTLLSKKRQGNLFAMGLTAETLILFLLTVFFFPYFIDLFG
WASWRYFAALGLPILVTGIFNAFVNTPLNTLFQKIVPTNYRSRIFSVISILTQIATPLGAAIY
GFAVDRVPVHYLILVSSICNALLTLVFLKGMTKLFDGKTPDSEGLVEKSVEAVKEGASL
>tr|A0A335EIV4|A0A335EIV4_ACIBA Glutathione-regulated potassium-efflux system protein
OS=Acinetobacter baumannii OX=470 GN=SAMEA104305308_05530 PE=4 SV=1
MTHEFPLAKLLVRSYDREHSLHLVKQKVDYMIREFESAIFKGGVILQELGVDEDEVERIT
EEIRDLNERNFETEIAADDVYAGADMQYTHAHHPRPTAPLIRPKQEGRILNKDDASDNEN
MDG
>tr|A0A344PLI0|A0A344PLI0_9RHOB HlyD family efflux transporter periplasmic adaptor
subunit OS=Paracoccus sp. SC2-6 OX=2259340 GN=DRW48_11485 PE=4 SV=1
MTAPDTPDLPLDLGRDTGDAAAPARRRRWFRKRYLLVLLIPVFMFSGAVIGLYYQPPGLQ
NFYALTGLQPGGGADNPALPPEIDLPEEMAETLLPSDVVGLARLMRPGDVAIVAAPYGA
GDARVAEILVSVGDRVSRGDMLARLDNMQALES AVLTAETLAVRQATLAQTRSAVAA
SRAEAQATLDQARATAREAQANLARTEGLAERGVATEATLDAARTAAEEAGLAVVRAE
ATLARFTGTALDDQPDVVVAARNVDAAQAELARARADMAQAEVRAPVDGTILEVNATP
GQRPPAEGIMEMGDTSAMMAEVEVWQDRVA AVAPGQPVELAAPALGQGVRGTVESIGL
TVGRQGLISDDAAANS DARVIRVLVALDPASSRLAARYVGLEAVARIDTGAPARVGQ
>tr|A0A346NMC3|A0A346NMC3_9ALTE Chromate efflux transporter OS=Salinimonas sp.
N102 OX=2303538 GN=chrA PE=4 SV=1
MHEPSTSSAPPSSGSNQITRDATAGNLNAFGHYITFGEAVRVWLRVAILSFGGPAGQIAVM
HRILVDEKQWVSESRFLHALNYCMVLPGPAAQQLATYIGWLLHGIKGGVLVAGALFVLPGF
LSILVLSLLYAGYQEASLVQALFFGIKAAVLAIVIQAVIRIGKRVLKNAYMYALAVAAAFVA
IFFFAVPFPIVITAGLIGLLGRHVDPERFVVIKGHDTPEDAGRAIDAMMEGGAASHTRASR
GRALKVLAVWLPLWFAPLVALLVTLGYEDVFTQIGLFFSKLAVVTFGGAYSVLAYMAQE
AVQNYGWLAPGEMLDGLGMAETTPGPLIQVVQFVGFMGAFRAPGTLDPTAGILASVLA
TWVTFVPCFLWIFLGAPYVETLRGNQAVSAALSAVTA AVVGVMNLAIWFAVHVAFNEV
ETVRAYGMLLLIPAWGSIHIVSVALAAGAFIAMLRFKVGMLPMILVSALLGIVYHLLFAGA
PAA
>tr|A0A366EKV6|A0A366EKV6_9BACI Threonine/homoserine efflux transporter RhtA
OS=Bacillus aquimaris OX=189382 GN=DET59_11161 PE=4 SV=1
MKEKVNGKPVYLYMGLLFCVICWGSNFIFGAILVHYFKPMEIAFLRLIFITLFLLVFYKSIR
QFSSLKSMVIPLFIGFIGVTNLNHSFYASLTASPVTAAALILATAPICTSLINSVVFKERKSP
FFWMWSLFSFFGVLLVIMKKGAIVIGMGEGYIFLTMLTFSVMILVERYARHLSSILLTFYS
TMVGLILMTVFLPFSVDVTLRSVPFSIWMLLFFTAIIMHGICPLIWNHCISEIGSTNTSLLLNI
EPFVAMVVGVIYVLKESVSTMQMIGAITILISVTMALHSNRMGQRDRHLVPTNSNTL
>tr|A0A367PMV5|A0A367PMV5_CUPNE HlyD family efflux transporter periplasmic adaptor
subunit OS=Cupriavidus necator OX=106590 GN=DDK22_09775 PE=4 SV=1
MKDDARQGGLKPLSEALDHSAEGIGLLSAEPSRLGLLTIVTTFALVLCGLVWSFVGHAD
VIVTAQGT LAPSEVRRFYAPVDGELADLYVAEGQPVSKDDVLARLNARGAIEAAANAL
EAQLKLEDSEREWKFQPDKKALMERRAAALKQQIDVATRQHETRIAEGTTRLAEQQRAQ
LQEARSNLENARRAREFARQEQDRYARLLALPGGGGVSSQSQVDAKRAAAQDAENNLRV
AQSR LAELDARLGRELTAASSQLESSGQDLAGLRVQYDAALREIANTEDKLRLQVQTARL

VADAAARIRFENIDKDNFLLILAPVSGVITDVTSTQRGDKVQANTPLGGIAPKDARPVVKI
VIAERDRAFLREGLPVKLKFSAPFYQRYGIIEGTLEFISPA TKPGGPD KQPVYEGRVRLARD
YYAVADNKYPLRYGMTATAEIVVRERRLIDLGLDPFREVAG
>tr|A0A369ACI5|A0A369ACI5_9BURK Threonine/homoserine/homoserine lactone efflux
protein OS=Extensimonas vulgaris OX=1031594 GN=DFR45_1193 PE=4 SV=1
MNATEFTLLLFCAAMTFSPGPNTTLSTALAA NLGLRRALRFCLAVPTGWSLILLASGLGL
ATLIARVPALRWAITLLGVAYMLWLAYRLSTSARLAQADEARPGACRTLGVESENAPQR
GQFLPDSPPHSGAMGQEAGKKWAAGAHSQPTIPKPDRLLGLGFWQGV ALQFVNIKAWM
LALTLSAGWVNTAEQSAIPAERLAIVSAVMLAFAFASNFTYALLGVLLRRWLAQQQR
LLWFNRALALVLVATAVWMLRL
>tr|A0A369XW18|A0A369XW18_9FUSO HlyD family efflux transporter periplasmic adaptor
subunit OS=Psychrobacter sp. S5 OX=2283384 GN=DV867_13815 PE=4 SV=1
MSKKMMTIKEYELTTDYFFRKELRLMIFYIYFLTSLIILLTWSYFFNIDILVKSRGVVRPIK
KISSILNQFEGNLTKVNYQDGKKVKKDDLYSIDTFILENNYLKNSDLLRKEEKEIYFLATL
KESLVAKKSFFKDKDNEYYYLYQKQKYKDKRLEAILRAAKMEYLKYKALGSDYVSEMD
LEKYRRAYEEALYNYKMSDAELLSEINN KIFTLKEKTENI KENIDLKNQIEKGSVKAPITG
TIQCSKVFNKGDIYIPKDQKVLDIVPQGSKLKMIVDIANKDISKIKVGQLIKYRIDSLLYKEY
GISKGKVVKISPSSNKGSFRMEGTIDREILENNQGDRESLKIGMTSDIRIVTTQKSILRVILE
KLNFMNE
>tr|A0A370F3S2|A0A370F3S2_9NOCA Threonine/homoserine efflux transporter RhtA
OS=Rhodococcus sp. AG1013 OX=2183996 GN=DEU38_12462 PE=4 SV=1
MSRGPAAVNAGSRSLGTGAWAAGLASAAAYGLTPVVAVLAYRDGVSPSVLVTLRGLC
GSAVLLLIAAGTGRLRGISRRPAAALLFLCGPLFGVQILAYFAAVQATGAQVALALVHIYP
LFVLLLVCLARRQRVNVWTVALCVP MVCGIGLVAGGGAASSSITVIGVGAALLSASGYA
VYLVLGEEWGRSVGVVNAALLVTVGATITTGIVAVATRQSFAPQGVWNVAVVQGLL
NPVGIGCAFYAMRRLGSVAMSMIGLLEPIFGIVSAALVLGEHLDPVQWLGVGFILSLGGLL
PWTMSALRRRPVASSGAVQAHQEVNRAGVVDGHESQ
>tr|A0A374DUW3|A0A374DUW3_9FIRM HlyD family efflux transporter periplasmic adaptor
subunit OS=Ruminococcus sp. AM36-2AA OX=2293210 GN=DW846_02595 PE=4 SV=1
MQDEISQLDESIQEYQDSDEENVIESSVSGRVKKINVSAGSDLS DIMVSDGALMVLSLDGK
MAVSLSGVSGVSAGDSVTVTLS SGTQVTGTVD SASGEDCVVTLTDNGTTYGDTVIVTDSS
GQELGSGELTIHEPLEITGSGTVSAVNVS ENASVSEGTLLTLEGSANETQYQELLAKREA
RTATLKKLIQLKADPEIKAEISGTVQSVNVSAGSSTTTDSSSGSSSGSSSGSGSGKTVSQ
MSYVVS GSDTTAGNAVQLISLGSTTSIAAIEANVNASVVRCSDTGA AVSSDSVTNIADSNL
NSQETGETEEIISLQTDTEQQAE AVALASSD TDFSSDVGGE GDSSGENTSETSTTLQFAIAT
EGTSTASSLVIAAPVTGQTPVTSVSATDGSYTGTVAWNPGDDSFQEKTVYQAVVTLTAGD
GYVFQAGSVSGITLGT VSGICVSQDGKSMSFQITFPETA AETEDIKKDDSGDGKTS DSTDN
GKNADDNKDNDADQITDRAAGQTGNNSGQNGTGSTSSNGK DSSDNGTNSTSETNGNSTQ
SGNDQSGNGAGTSANNISGSSSGASQTEDTQETDSSASTSGTELSTSEYSTDVALFTISPDD
TMTLEVSVDEL DINSVEIGQEA AVTFDAIEDKEFTGEVTEIGN TASVNGGVAKYTVSVSVP
KDEEMKQGMNASATIT IENRENVITIPVNALQEKGNKV FVYTEKDEDGNLSGETEVT TGL
SDGTTVEITEGLSEGD TVYYNKSGNTDSGSGNDSGMPDGMGDFGDMSGGPGGNSDSGNS
GGPGGNGGGPGGSGSSGGNGGGT PPNM
>tr|A0A375AJ90|A0A375AJ90_9SPIO Threonine/homoserine/homoserine lactone efflux protein
OS=Sphaerochaeta dissipatitropha OX=1945881 GN=SAMN06298221_10394 PE=4 SV=1
MQIDMLATLTFALITTFPGPNTISSQAMGLNYGYRRSLPYFFGIATGFFSIMLLSAVLAAA
LTQLIPSVVTYLT IAGSLYILYLAYHVFTSSYSFSQTIVKPLGYSNGLLLQLLNPKV IILGLTV
YSTFLRDMARTPFNLAASALCFTLMSFSALSTWALFGMGISRLLRTEHTRKV VNAALALL
LVYTAVRMVWSL FSA

>tr|A0A376BGI6|A0A376BGI6_ALCFA Copper efflux oxidase OS=Alcaligenes faecalis subsp. faecalis OX=32001 GN=cueO PE=4 SV=1
MKRRDFFKLTGASLLSSLPMRSWGQGMGMHGHGSMSEGMPGHGMSTRPSLMPIEKMPA
GQALQALPVLKNSSQKKGLFQAKITAAAHQRVLADGKSTELWLYNGQAPGPLIELYEGD
QVEIEFENQLDQATTIHWHLVPVSDQDGNPQDAVMMPGQSRYYRFTLPEGCAGTYWYHP
HPHGKSQGEQVAHGLGGTIIVRSPKDPLKDYTEQHWASDLRLDINGHIPTNTGPDWMNGR
EGQFVLLNGQRQPLIQAATAERIRVWNSSCARYLKLHIPGARLVQVGTGGLLEQALAAA
ESILMAPAERVEFFIQTDKDLSSQLALYYDRQKMMVQESPETLTLATLKIRHQEIPLKQ
LRTIPAIPAAASTAKVVFSEVMPMNHDMQSGHSGMTNSSGMNHQGMAGMDNDMMMPG
MAAMRSMFRINNQVYDMDRIDLCPTGQWQYWDVINDSHMDHPFHLHGTQFQVLAHQ
TGMQSVPEAFRAWRDVTNLRPNETVRLAQRQELPGLRMFCHILEHEDLGMMMAQLMVE

>tr|A0A377TD10|A0A377TD10_9GAMM p-hydroxybenzoic acid efflux pump subunit AaeB
OS=Ewingella americana OX=41202 GN=aaeB_3 PE=4 SV=1
MKWFSKSAVLFSLKTCFAAFLALYIALALNLDKPAWSIASVFASQLYSASTLSKSVFRL
GTMLGGLFILLIYPATVQLPLLFSLCVSAWVALCLYLSLHDRTPRSYVFMLAGYSAAIMGF
PDVTSPQAITYTVLSRIEEIGVAIVCSSLIHSLILPVSMNILEKSITDWYDSAKKLCNALLTA
PTPEKSPDHENILIQMAGYPANVEVLITHCIFEGNAARKLIRLVTVQYQHLSYLVPTLTSIEL
RLNMLAQRQIAFPENVQQTFRHFLWLNNNDKAEDSATIQQNAQTQTELQQAHSNAM
NVEDSLLLNGLLDRLGDFVRIAEANFSVGKRVDFNDNKAKRSTAHWHIDKGMLLLSSF
TAFLVTFLCCLFWIGSGWKDGATAPMMAAILCSFFAAMDNPVAPMKVFLTGVVVATAISI
FYVSMLIPLTTTFEALVICLFPGLFVLGVLIANPATNLLGLIATQIPGLISLGHFFKPDPLAT
LNGAISSLVGVVIGVVVTAIIRSKRPSWTARRALLRGIKELIQFLAEIKLHRASLNTRQRFVA
RMLDKVNVILPRKKNDTTEELASGGDLITEVWLGANYYDFHMKNQELLADHIHATDRIF
YELKGYLKARLKSFQASPHPKLLREIDLILLIKLEAQSSKDARYYAPMLSFLNIRLVLFSSRH
WPSFE

>tr|A0A378MET9|A0A378MET9_LISGR Macrolide-specific efflux protein macA OS=Listeria
grayi OX=1641 GN=macA PE=4 SV=1
MKKWIKWLITIIIVVVGGIGLFFAMNKKDDASGTSKLVTTKVQKQDMKINATGTGAISP
ENQQLPDYDKLQVAQMDELDPDIKKDQKVKISVAAIPNKTYTGKVKEIAKQGQVQNG
VSSFKVTISLDKKDKLKAGMTADASILVHENKHAIYVPIEAVQKNDDDKYYVVPKKNK
DGKTKQVKKFVETGLHNEDNIEITKGLEKGDTVILPTVDTGNNSDF

>tr|A0A378QSD6|A0A378QSD6_9GAMM Probable amino-acid metabolite efflux pump
OS=Moraxella equi OX=60442 GN=eamA PE=4 SV=1
MHTKDYLVLFSVLIWGVNFLAMKIGLNDVPTLILGMVRFLILLPAVFFFKKPNAPWIYL
ILYGLTISFGQFSLMFLALSWHFPTGLSALILQAQVFLTVLFSCILLKESVKPNHLVGMITAG
VGLTLIGVGQYQGGFSLIGMLPVLGAAFSWAIGNVIVKKIGQVNPLSLVIWDNISAFMAFT
IFSVMFYGVGGVMSHLANFSTLGILSVMFLSYVASCVGYTGWGYLLAQHSASKVTPFIML
VPVIALVVGYYALKERLILWHYVGILTVLFGVHLLDGGQWFDKKF

>tr|A0A378Y7T8|A0A378Y7T8_9NOCA Potassium efflux system KefA OS=Nocardia
otitidiscaviarum OX=1823 GN=kefA PE=4 SV=1
MEDVLRPLIVFGGTLAVSIMAGLLIDRVLRYSANRHPGSSVATLLRRIQLPLQALLASAGL
HFTYPLAQLELQQDQTVIRNVLATLAILATAWLAMRAADTVAGNTLDKYANRTADTARVR
RLHTQLGMVRRIVTTVLVTTAAVAMLILFPNLRTLGTSLLASAGVIGIAGVAAQSTLGN
LMAGLQIAFGDSVKIGDTVVEGEWGTVEEITLAFLTVRIWDDRRLTMPISYFNSKPYEN
WSKGGPQITGTVFLYLDHSTPPELRQHLHEFLRGRKDWGRKWNLLVTDSTPTAIVVR
ASMSARNADDVWDLRCAVREELGWLARYHPYALPKIPTAMVSGGTPAMAE

>tr|A0A379TGA1|A0A379TGA1_SALER Potassium efflux system KefA protein OS=Salmonella
enterica subsp. arizonae OX=59203 GN=NCTC8297_03919 PE=4 SV=1
MRWTLFIFFCLLGAPAHSAIPSVTTGTSTSQQTATAPEPNTTEQKKSGLRSPG

>tr|A0A380C4K7|A0A380C4K7_SPHMU Probable efflux pump outer membrane protein ttgC
OS=Sphingobacterium multivorum OX=28454 GN=ttgC PE=4 SV=1
MKRVYIYSTLCFLLSYAKAGAAQTEQRLTERVAGTATIAAVDDKQITKRSLAECIQLAIKA
NPTLLQNELDVRRAEVNLAQAKANRLPDVDASLQHSLSGRSQDNSTLQYISSNNSTGNF
SLGASLPFRGFRFLFHDIRMRAKTAGKLTFTDQINALKLDVITAYIQSLTAQDILRQSEM
QTEVTREQVRRRAESMHKEGAINPGDYFDLKGQLANDVNTIENNRQLLYSSRVKLAALLN
MDENQLGELDNLGIKESGQRLDAKQLYEMAVDQLPDIQALDYRIKVAERDIKIAKSYYP
SLSLSAGLGSNYSKLGIGQTYWSQMRNNVGKYISLNLSPIFNHLQVYNNVRLAKLDLQT
ARFQKEIQQNVLSATSNAVFNLQNASNMITQLRSQNENYAESFRIAKVVFELGNSNSVIF
LTAKNKFDNSQIQLVVKQYEWLLQKYINDYYAGSLNL

>tr|A0A380KFS5|A0A380KFS5_9STRE Lantibiotic efflux protein OS=Streptococcus
hyointestinalis OX=1337 GN=NCTC12224_02243 PE=4 SV=1
MTDNKDAEGVKGEFDRWLSSLSLAVKELTSVPPELRLSMIIVPVNSIFVVLPSLLVLMMSQ
DRAFMLGNASITLAAVNIAMTVGMIVGSILVMNLLKKMSILSLLRMGTLGVFLMFFSLFL
RQPYFLLVFLALTGIATGAINPKYNALIYNRLPEEQLATIEGGLMTYFQLGTVFSRLLVSTLI
LVLTVNQLVLLFLLAAFFLLLYSLKRVPLMTVDEDNKNL

>tr|A0A380W1C0|A0A380W1C0_ALCFA Potassium efflux system KefA OS=Alcaligenes
faecalis subsp. faecalis OX=32001 GN=kefA_2 PE=4 SV=1
MKTLRLGVQVLLLFLALLGAWPQAQAQALSEVEQEREMIRELQQAQDEIRLMQYRLEGN
QVSIRPERSYEEDQKLVRTQELSGRVVQSLERRSRLKARLQELGEDSGDEAEQLIVHNER
MQLRRADAALRADLRVARLVQVEAQARQLLREATVRYEKAKRWRRNASLVLESPE
LAQAWPADRSKLSDFAAQQWRGTWSNSSWQQSSASLWMAAAVLLVMLALFRVMPLWVS
RYLPAGRLRRSSLIANFFLWFIATWVVVDQLVELVFQRPGLSPTQFELLAYLKVGAWAA
AVALACLKSMVVQPRASWRLIPVSTQTQHRLRYFAPAFFLLVYADITSSFFRGSIGLSDAF
QSMADGVSSLLYLILYGYGLWVLRDELNFRTDVAGQGASRTGRSWARLAFKGGVLIYIL
VLGLFIGGWQGLSDDLMSHFITMPLILGLLAYVCMVWLQDIADSLTYLRNRSHDPEAAPI
RVQSQFIVVFFAIARMSVLLLAIWVMSGDWLTEPKQMLESGLDVSREALRLGAVQWRLD
LWLIALGVMLVGAVLIHFLRTWLRQHYPNTTLEPGLQNAIVGMVGYVAYFVLLVICLS
MLGVPIESVTWIFTALTVGLGFLRGIVQNIASGLMLMVERPVKVGDWVEVEGSEGNVR
QIRLRATYVERFDRTMVMVPNSQMMGRQVRNLTYPSTSLGAIESRLLFPLDVDADAVMQ
ILREAVQSEPEILTEPAPILSCDGIFGDGVAFSTRCFINTMRVQRRVRSNMLDILRRLRQQG
ISLHPAQRWVQEAMDKDRAEDPDL

>tr|A0A381ILF1|A0A381ILF1_9BURK Spectinomycin tetracycline efflux pump
OS=Burkholderia oklahomensis OX=342113 GN=stp_4 PE=4 SV=1
MDTHTPHPALSRAALVRIVSTVSAGFVITQLDVTIVNVALARIGIDLRTGVAGLQWIVDAY
TLALAGLMLSAGALGDRFGARRLFAAGLALFAVASFVCGIAANATTLIAARALQGFAAA
AMLPSNLALLNRACAHDPRLRARAVGWWTASGAISIAAGPVIGGVLIAQFGWRSIFFVNL
PLCAAGLAATLRWIDKDETSAAASGKGAASASRFADSTANTEASRPAAVRAADIRPRGID
LPGQCLAVALTLFTGAVIDWHPTLVAVALAAAAAFVFVESRSAHPMMPLALFKQRTFS
VAVLFGVCMNLSYYGIIFVLSLYLQVRHDTPLAAGLAFLPLTGGFLLSNVASGWATAHY
GARRPMIVGALIGATGFALLSMTRADTPVAALVVPFLLIPGGMGLAVPAMTTTVLASVER
ARAATASAVLNTARQAGGAIGVAGFGALASGALPAQIVSGLRASALVSAALFVAAAAIAT
AVRGVPHRASSAARTKHANPAGADAR

>tr|A0A383TXY0|A0A383TXY0_9FLAO Homoserine/Threonine efflux protein OS=Candidatus
Ornithobacterium hominis OX=2497989 GN=SAMEA104719789_00671 PE=4 SV=1
MFEMILYAIMLGVSLSLILIGPAFFLLIETSLTKGWSAIALDAGVIVADLICIAFAFFGSKDL
IHYYIETHRSLYIIGGFIIIMYGCYMFVSKPTLHINNEALVNKNYIKTFFNGFLMNILNIGIVIF
WVFWVGWVILNYKKSIEIALFMGVALSVFFCIDLAKIFLARKFQRKMSDELVYKIRKALG
VVLAIFGLVILLKGFISFAPADHIFKKSQNIHNINTTSDENP

>tr|A0A385ZKQ6|A0A385ZKQ6_9ACTN Glutathione-regulated potassium-efflux system protein KefC OS=Streptomyces griseorubiginosus OX=67304 GN=kefC PE=4 SV=1
MLASPPVRTGQVRLLSVRGVLGISWEFTGASGPGRGTTRPGEAVFSLVGSVPNQGPV
GDAAHMMVVCDDGLAHLAAELRGVYGEQVTLVVPASERSVRPPVVVRTRAASALLD
RVVTAAVGLTGNGTAGGNGGAGATGGHGSAPAHSSGTGGDPRGGIRLMEAAEPSEAAALAE
AGVERADALALVYDDDETNIIRAALTARRLNPRRLVLRLYNRRLGQHIEALLDQAAALA
AGSADGDSADGSGFDASTTVLSADTAAPALAATALTGTSKVLQTGGLLLRAVERPPAG
AGVSAAPGLATLALLSPTDPTDTTGPGGDQGPTLLPDAAAVRDGGERTTVVLEQVSYAGP
ALPDGRGVMPWFASLFSRRLRWSLAGMVGCVVALAVALWLVTGIHPLRAFYLTLLDLFA
IDDPAGQSVGRQILQLLSGLAGLLLLPVLLAAVLEALGTFRTVSSLRKPPRGLGGHVLL
GLGKIGTRVLTRLRELNIPVVCVESDPEARGLATARRLRVPVVLGDVTQEGVLEAAKIHR
AHALLAVTSADTTNLEAVLYARAVRPDLRVVLRLYDDDFATAVYRTLRAAHPGASTRSR
SVSHLAAPAFAGAMMGRQILGAFPVERRVLLFAAVEVGGHPQLEGKTVGQAFRAGSWR
VLAREESGDAPGLTWDLPDTYVLQPSDRVLAATRRGLAELLGRRGRVGT

>tr|A0A391NQJ0|A0A391NQJ0_9PSED Cation efflux system protein CusF OS=Pseudomonas sp.
SCT OX=412955 GN=cusF_1 PE=4 SV=1
MKAVSLALLAVLWLSGPASAEDLLKPSTTPPPVDDVSAGNALEAEPTHEGEGVIRAIDVQ
QGSVTIAHGPVPDLKWPAMIMPFKASAAQLRGLAIGDAVEFRFTDGEMDPQIVSIRRR

>tr|A0A396CAP8|A0A396CAP8_9DELT HlyD family efflux transporter periplasmic adaptor
subunit OS=Desulfovibrio sp. AM18-2 OX=2292040 GN=DW219_08870 PE=4 SV=1
MLRARTLCRAASRRVLSFVRVPAVFLLAALLSAQPLTAPLAAPSVSAAEAQPSIGNGATI
LTGKVVTTVTRAVPVPFNAVVDQVLVKPGDAVHKGAPLLRYHLQEEAERVLQREVTG
AGTEDLKGGQALDLERRLAETSAQRNKTRQLVASGLGSRQALSRLDDVHSLQRRIELLRT
TISKTESNFAARLKELGGYFGAPIREGELPATLTLTAPIEGYVLSLDTTLNAGTLLPAGSAP
IRVGQLDPVLIQVPVYEAESAIEGDAVEVEIPSLNNKKFLGKVNEISWVSSDMSVANPSY
YTVELTVPNPGLELKPGFKAVVRFKGSR

>tr|A0A397L164|A0A397L164_9RHIZ Threonine/homoserine efflux transporter RhtA
OS=Ochrobactrum haematophilum OX=419474 GN=BCF22_2514 PE=4 SV=1
MGQGKTGAQALGRASFDGLAVSLVVFIMFSWGLNQVAIKIGSRGFNPMLMAAARSALGG
VCVFLWCYWRRIPFLSHDGTLPKGLLAGLLFGTEFVLIFLAMDLTSVSRVTLMMNVMPF
WVAIGSHFLLGERMSVRAFIGMCVAFLGVFVVFSDHVSRRPGPYAFYGDLLALLSGILWGL
TTLLIKRSRLAHAVPEKILLYQLAVAALVPLPLIGLSGPLLRDPGLIPVISLLFQSFFVVAFTY
PLWFWMISRYPASKLSNFAFLTPAFGVLLSGVVLGEALSWKIFAALFLIGLGLIIINRPAKA
TTAR

>tr|A0A3A4NGD1|A0A3A4NGD1_9BACT HlyD family efflux transporter periplasmic adaptor
subunit OS=Candidatus Abyssobacterium bacterium SURF_5 OX=2093360 GN=C4520_15735
PE=4 SV=1
MIHAYKGIPLALLIPVMTVGYLSFDHWVQRESLPEGLIQANGRIEGDFVTIASKAAGRVQ
KLMVYEGDSVTAGQVLAQMDDIQVRAKVEQAKQGVAALDAQVRAERTALSCLKKEVP
LNIEIAQAALSHAHSVLSEAKAKEERANRDAQRFRLADEGIADKHSNEQADTAWTIARY
EVDSASAALTQAERQLSQTKLGWNQVEAKEQELAALAEQRMRAVLTAEESIVADMTI
LAPTSGVITTRMVNVGEVTPAGAPLLIVVDLDHLYLKAYVPEFQIGKLRLGLPARIHTDAF
PDKPFEATVQYISSRAEFTPKQVQTSDEVRVCLVYATKLYLKENPDHSLTPGLPADAIIRWK
EGVPWENPRW

>tr|A0A3A4PE42|A0A3A4PE42_9BACT HlyD family efflux transporter periplasmic adaptor
subunit OS=Candidatus Omnitrophica bacterium OX=2035772 GN=C4527_08925 PE=4 SV=1
MRGARLYGHVHFVHSGVSKNFTGRRTVSRRSSTCAGYVPRYFSSRRVAEGAAIMKRLIPLC
LVFIGFALWWWIREGENNRPFQSGTIEAKDVSASKIGGRTVSVEVEEGDVVKQGDILVQ
LDRESIEARLRETESELRRARERQRELENGSRPQEIEHANALLEAARQQWQLLKNGPRED
IRAARANTEAARAEVQLASITEKRQKELFASKNTTAENLDRAQKELSVANSRLRAAEAL

EQLLAGFRQEDIQASYAQVLAASAALALTMEGPRQEIQAAQADTARLASVLDVRVIDLQ
ETRITAPSDGVVETSTLEPGDLLAPNQSAMTLILDKPLTVRIFVPESRLGDASIGREIELSVA
SFPDKRFQGRIVQTNRRAEFTPRNVQTPETRDDL VFGVKIEIDDPGHQLRPGMVADVFLPL
VKQ

>tr|A0A3A4VTU6|A0A3A4VTU6_9CHLR HlyD family efflux transporter periplasmic adaptor
subunit OS=Dehalococcoidia bacterium OX=2026734 GN=C4555_03815 PE=4 SV=1
MRIPRIWLALLLGVWGLALAGCGSGGASAVGGQLRTVERGDLKISVTGVGNLALSDKRD
LAFEMDGTVLEVLVEEAQSVEAGQVLVRLSASDWQEQLVALEDKVTAAERNVTAKGRA
VTSAERTLAAKEQAVIQAERNVAAKELAVLQAQANLNNAAQLSLEQTQAATTDPLQVEIK
RLQVQVAQGNLEAARQALEDARTIDIDNARQAVEDARAQVGDAELAVQDAQKALSEAR
SNLDEARNKSPEITAPFAGFITRVNVSSGGDEVKKGTVA VVLADPAKFEADIPVSELDILQIK
LGGTAEVQVDAVSGVTLPARVTRISPTATISQGVVNYKVKVVELLSTSLAQAQASASTPVP
AASDNVTGASGSFLGRGNYGDDGFTQEELSAMLAQRQSGQLRQSAAQLLADLQLKEGLT
VTVSIVTDSKANVLLVPNSAITTRGGQAFVQVPGADGALEQRAIQTGISDYQYTEVTGGL
NEGEQVMVTTGTTATTTSGQTGQRQGGTFVPGGGVILR

>tr|A0A3A8ZYF0|A0A3A8ZYF0_9BACT HlyD family efflux transporter periplasmic adaptor
subunit OS=bacterium 0.1xD8-71 OX=2320099 GN=D7V83_15155 PE=4 SV=1
MSQISENKTEEAKVTDVNDTKENKKEKKAKKEKKPMDKAKKKKIRRRIAVLVIVVLVA
GFFVRNSIMAKNTLPTVFTMEVTIEDVEQTLRTNGTVKSMETKSYFAAVMVPVSEVKVA
VGDKVKKGDVLLKFDEAALSEARQEAEKLASSQGDYSSSLYKNNKYLADLSEANTNLP
VLEQQISDHETYLKGLQKTIEDKKAWYANQGALLQVSLLEWEKTISDEKKALEERNAYE
AESQDMDDKEKREKRERDDAAKNQIAQDEETLLSLQEQVQYNSYEQNNQEIRDLEREA
AEIEKIIADAKELKAKMESQKEASEDAMMDTGSKEKLEADTALQKLTNGGTLESIQEVES
GITADFAGVVTEINAVEGATPAENGKLVVLESTDKVVIHANVSKYDLEKLAVGQSAEIDIA
GNMYEGKVDKIEGMATTNNNGAAVVGVDIGIEKPDENIFLGVEAKVVVHTAKAEGVTTI
PMELVNSDRDGDGFVYVEENGLVAKRRITVGISNESLCEVKEGLSVGDKVIMSMGQEFEEG
MAVTAVPQG

>tr|A0A3A9UN94|A0A3A9UN94_9ALTE HlyD family efflux transporter periplasmic adaptor
subunit OS=Alteromonas sp. BL110 OX=1714845 GN=D7031_01095 PE=4 SV=1
MRTGLFRKEVIDEQSNTVEGSFLMTPKPAYLALAGLLVWVAVAVYLNMESYARKAS
VSGWLEPSHG VF KLYSDARRGKILDVIASEGQLVEKGAPLLKISYSSKDALGHRVSTQLLA
ELESKQNRTRQSIERLRTLHLAQQQRLEEQLSQAHNSTALHDIITLTQSQWLLASTQWEK
AQTLMDEGHISRTDFETYTLQRLNAEQKLALAKKDWSNEQANIAAISHELATLPEKHANE
LANIKNTYSDLTQQIVTHKSNAEEHYPAPRSGVISGLHVRTGYTVDSSRPLLTLLPQNADIQ
ARIAVPVRSAGFLREGQALHIRYDAFPYQKFGVQFGEIVNISPSLVLPGLTDPVPISEPAY
LVTATLNTNEVLAYGNSISLKAGMTFSADVQLSQRTLMEWLMEPLYSIKGL

>tr|A0A3B0IW16|A0A3B0IW16_9RICK Magnesium and cobalt efflux protein CorC
OS=Wolbachia endosymbiont of Aleurodicus dispersus OX=1288877 GN=corC PE=4 SV=1
MDWLLISVLSAIFLLILSFLFSGAEIGLTSISRSRVNKLKLDGNKRAKIIDRLLNTKELTIGTI
LLCNTIINITCSALFTAIFINFFESEGIFFSTAMMTFCILLFCEVLPKTYAMQNPEKFTLLSAYF
MLFFVNILSPLTLGIQFIVNLILKLCGLHKNREVISADAMRNMITLHRSEGTMLQQDLDM
LNSILDLAETEISQIMTHRRNLFSLDIDQNKEDLIREILTSRHSRVPLWQKEPDNIVGVVHV
KNLINALREKDNKIEVVKVMSKPWFIPSTPLSVQLHNFRKNRKHAFVIDEY GALQGIVT
LEDILEEIVGEIADEHDLITENFIKKISDSVYHIEGKSTIRNINRQLHWNLPDDEATTLAGMI
VNEIERIPEENEFEFSMYGFYFKILKKDKNIITMIEVQVKT DNTV VAIN

>tr|A0A3B6Y8V6|A0A3B6Y8V6_PSEO7 HlyD family efflux transporter periplasmic adaptor
subunit OS=Pseudoalteromonas piscicida OX=43662 GN=D0N37_23260 PE=4 SV=1
MRKKILAI VVPLWLLGCQEAP EQPTQLLYTVESKPFSITVDAEGELEAASETVISAPTSARG
AQTLAWIMPEYTQVKKGDVIARFDGSQLERRKRFSEFDK GKVAQDITVTDSDLTTRKSHL
DSDKVIVSEEKHFAETFSIDDERIRSKLDILDQM QNVEYLNAKEAYFGWQTEQFSSSALGE

MELLKLQSKQHESKIAMYNANLEGLEVIAPHDGLLTLNADWRGEKPKPGQALWPGQKIG
GLPDISSLQAKLFFVHEKEALSIAIGQKVEFTLLSNSDERFGGKVTKVSPYPQSIRRGDPQKY
YEVIANLDETPAYFKPGNKVLATLFFVQENKQALLVPKHSIINDNNAFFVQVKDGSQFKRV
KVELGQSNLSHTEVLGLSPNQQIALVPNKEL

>tr|A0A3D5PVS0|A0A3D5PVS0_9FIRM Efflux transporter periplasmic adaptor subunit

OS=Dialister sp. OX=1955814 GN=DGT53_06770 PE=4 SV=1

MAVMNHHGEDFMQLSWLHSSKAKIIIWTVILVFLLCGIYAYTHRSRVSVGKTSAHPLVKV
EKMERKDMMKRVVLSGDTVPRESDISPKEYAGRLEKVYVDLGDKVTKGDILISQDTKDIS
FSIAQNRAGSHEAAADAVESRASDAGTLKAQSDYDNALSTFNRYDTLTFQEGAVSRQER
DDKYQAMMEAKAALQSLTGQDVEGVPAVIASKEAAAEKAAAYTVDSLESQKGDMTMYA
PVSGTIGYRDAEAGEWASAGQKLLTIVDNSALYLDCAVAEQDIGVLREGMDMDVSDSL
GETVKGGQIIYISPDLDASTHSYXDVSIDSLGEKVKGRIIYISPDLDSSTHSYKVRILLDGDGK
NLRGGMFGRSTVMALERKNALYLPKEGVLENNGKKWAFLIDSSHKVKKVEVTTGLYND
DSIEILTGISEGDRAAVTNISKLKDGMTVDVEGTV

>tr|A0A3E0GZB4|A0A3E0GZB4_9PSEU Glutathione-regulated potassium-efflux system

ancillary protein KefG OS=Kutzneria buriramensis OX=1045776 GN=BCF44_118152 PE=4
SV=1

MGESGTPDLWRSRPDLGDHCERGRPNFGGMDALVLLDHPDLRSRINATLAEAVRELPA
VTLHDLRAEYPDRVIDVAREQRLVRVHSLIVFQFPFHWHYAVPSMLKQWMDVLVKGFA
YDGALPLLTGKTLQVVTSTGGVEEAYREGGFHRYPMSSALLAPLENTAHRVGMAYAPPLV
LHDVRGVTPLELAEHVERYRDLLASSGACLT

>tr|A0A3E0LZX1|A0A3E0LZX1_9CHRO HlyD family efflux transporter periplasmic adaptor
subunit OS=Microcystis wesenbergii TW10 OX=2060474 GN=DWQ51_08780 PE=4 SV=1

MPMPLSNCLREDLLVTRKIDRQTSKRYFIQDPISQETFEFGEEYFLCQLMDGVTSVPEIL
ASFQERFNISLTEEDYQKFAGQIDSFGLLEPHQNQLPSSQSEEGNGHKNSSPTKKKSKQHSL
RFIWKHPNPDAVFTSLARWTHPCHRWLRWSTWLLLPLLPIALLTFWNNRTVLWYDVGRF
VDGLPFVLSYLVLDILNLNLCGRIIQGTVFVAAAYGGRSSVFGMTLALGFKPHFQVDLREYQSV
PRKAQLWIYGTPLIMRLFISFGMIFWYAQRSSGTAHIWLLLLAHAALVTFVLMACPLWP
LYGYYFLIAFFRLPDNFMSQSFRWGMVIGRNLPSFLSTREKLMLVGFGGLGSILFCLLMI
YLIVTNFAKGLYTLFPEIFGAESAIIVSVLVFIGFRKQISRLFFRGRNSQGTSGLPSNLTEETK
NSKKPSSRSRQGFQSWLKKNLKFFILAGLVALLFLPYRTMPGGPLQLLTPAEVAIQAEVDG
KSKITRVMFPGGNEQLIRKGTVIAQMEDVDIEDTETLQSQIAKALGDVKIKQSYLAKLLA
TPRKEDVEVARNQVKIAREEVDKAKKEVAVDKQNLEVIKKQIESALTQADFYFREASRL
EGYKEGAIALNLVEDAQRNAQTKKIEAEKQALLQQQQVIEQARSQQLASKQRVLETSES
QLKLLLAGPYPDEIEAARQDVEVARAELERLRKQEQQERDKLKLTTLVMPLDGYLVTPYL
DTKVGSYLDQGETFATAQDATKILAEVQVPEYDVGGQFSIGKNVQIKLNAYPTETIMGKVV
SITPAAGNSTTTADLSSEPVVKVLVEIPYGKHLFKTGMTGYAKIEGPMKPFIVAFSSPIVRFF
QIEIWSWLP

>tr|A0A3E0PTY9|A0A3E0PTY9_9BACT HlyD family efflux transporter periplasmic adaptor
subunit OS=Planctomycetes bacterium OX=2026780 GN=DWQ41_26960 PE=4 SV=1

MKTVLQCALLVFCVLLGNLLVEPWGWSVWEMISPAPDDAPPPPAEPDERSRELRLVGRLT
PTHGIINLSATPGDRLKSLNVSEGDQVQAGTQLATLESETLRQLEVEAAEEQLAQATALRD
AEIKAAEARLRASEKALEQAQAKNPQLEQQKRQVELAALNLAQAEADLKRVQELRADLV
AVQEQEQLELLVEKARIEKTAETALDQLQQADEFLQTARSEYEVALAGLDQVKTLRRI
EPYEA KLKLAQYQHDQTILTAPSDGTILAIPTRPGESVTPEPILQMA DTSEM SCIAEVHKS
VDSL SVGQ RVRIESDAFEGRQVAGEIVRIGNQVDPPQLRNL DPLAPQNRHVVEVLINIDEG
VANVS NLIDLQVDVVILPRESHDGETGDDAQ

>tr|A0A3E4LNH7|A0A3E4LNH7_9FIRM HlyD family efflux transporter periplasmic adaptor
subunit OS=[Eubacterium] rectale OX=39491 GN=DXD13_14930 PE=4 SV=1

MRSLLNSSRLILWMLKQPHNFDYEKRKIMKPIIVDLKDISDSTEVDYDSKPNRFVPYTIYIICA
ILAIALIWMYLFMRDIVVKADSVFRGDDDDSTAVSCAVTGKITKMSVKDGQYVSEGDELYE
IDIENLGSTIEDYKSKLDSVQQRLDILNAYQKSLDGDNSEFDAMSDNQYYSEFKDRKELLN
TSIDAGKEKNKTGEVYDENITVINDSIDKYNEKINKLKDVKQCIVSRNNTFDQNDTYYYYS
MVNSYISSYDYTALQYDNKKDETTMDSSQLAEVDTEKNQALSNLESNEISTIEQQIETANE
QIESLKSNISSVELQKKQTENSNNDDSDIKILTEKGNVSAEILTYEDKKQEYEAAYLKDYDI
KNNNCTIKAGTSGYFYTNQEISNGTYIQEGDSIGQIYPKEQSGYYAQVYVENS DIAKIKPD
QEVKFEMASYPSEYGYFTGTVKEIAKDVTVDQNTGNAYYVVKVECKNMEIKNKDGEK
GNLKSMAAQAKIVVDDDSVLHFLVDKINLVD

>tr|A0NKH3|A0NKH3_OENOE ABC-type Na⁺ efflux pump, permease component

OS=Oenococcus oeni ATCC BAA-1163 OX=379360 GN=OENOO_63060 PE=4 SV=1

MNKTWIVAKHVFLKNLKSPSYWMLLAPFVFLIGIGASFLINKAVSGNQPTIGIVGQPQQ
VSLKLTALKSKASVKSESSLKAAKNALSNEKIDAYVKTNAGYTKTEIVANSKSSANFDSSS
ISQIISSLKTESAVAKLGLSAKQVKSITAPASVKTKYVSVENKKVSQNSNNGGRSVRYLFA
QGATIIIFMFLAIYIYQMTGSEIGTEKGSRILESILAAVPARQHFTGKIIAIVGLFIFQLIAYIFIAL
IAFALAKPFNYSKYLNLDWSQLGTSFIVLTALITLGAIIIYIILAAVFASMVSRQEDVAKST
SVVMWIAMVLYFLSFVASSANAPVFKVLSFIPLLSQSIMPIRMAVSSATTFDALIALALQI
LIILLVKFASSYARNSLDYGDGKPLKLLKYFQSKNS

>tr|A0YH94|A0YH94_9GAMM Putative transmembrane efflux protein OS=marine gamma
proteobacterium HTCC2143 OX=247633 GN=GP2143_06938 PE=4 SV=1

MTFAKHLTLSSPAFVQNSRSVLWVLLVGMLATGFPFTILAVALKLIAQELKVSEALASWS
VSAPMLISAVCMPFLGKLGDLYGHRRIFLIGIVGSTMFALLCYFATNIWWLVGLRILSMAF
AGATTPSAMALIFHVFDQDKRTQAISWWAMGGPASAALGLIIGGPLIDAMGWRSIFIFQAI
TGVLAFAFALALRSLPETGQRTAKFDHQGNILLIVSFCMLLFAVGSITDTSIAGSLKWLSVLG
VVGILIFYKIETKVDEPIPPSLLQKSFMAPVATSFICQAAYLGGFVVTPIVLIDQFEFSIAL
AALFMLARTLSLTIASPIGGRLSVAFSERAVVLLGLLIQAGGLVVVGLGVLTSNIVLLGIGL
VLQGIGHGFALPPLTSVISYCVPPQLFGTASGVSRLATQIGASLGLSFFSALLIMDRNDFGL
AEIFYLGAGITLLGLLPAVAITGKTTTQVVLDS

>tr|A1R0X5|A1R0X5_PAEAT Putative arsenite efflux pump OS=Paenarthrobacter aureus
(strain TC1) OX=290340 GN=AAur_0057 PE=4 SV=1

MLEATNTPSKTEEPAPVNPALAAEAKIARIAVTVFPLLVVVAGVLGFLIPDLFKPMGVAV
PYLLGVIMFCMGLTLTPPDFASVARRPWAVALGIVAHYVIMPGAGWLIALLQLPPELAV
GLILVGCAPSGTASNVMFLAKGDVALSVAVASVSTLIPIVTPTLTLFLAGSFLHIDAGA
MVMDIVKTVLLPVIAGLLARLFLSKLVAKVLPALPWASAVVISLIVAIVVAGSASKIVAAG
AIVFLAVVLHNGFGLGLGYLAGKLGRLLDDKARRALAFEVGMQNSGLAATLATAHFSPLA
ALPSAVFSLWHNISGAIVAAWLARRPLKD

>tr|A3CLU3|A3CLU3_STRSV P-type ATPase-metal cation transport (Calcium efflux), putative
OS=Streptococcus sanguinis (strain SK36) OX=388919 GN=ctpE PE=4 SV=1

MNKKELIGLNQTQVDEKISQGLTNDFTSDTSTSNWQIVKRNVTFLNALNFVIALALVSVQ
AWSNLVFFAVISFNAVGTIITELRAKHMDKLNLSRELVTVIRDGQEIKIQPEEIVLGDLIK
LSAGEQIPSDARVVEGVAEANEAMLTGESDLVLKEEGAELLSGSFLASGQIYAEVHHVGA
DNYANKLMTEAKTLKPINSRILYNLAKISRFTGKIIPFGLALFFEALVIKGLPVKNSVITSST
ALLGMLPKGIALLTVTSLTAVIKLGMKVVLVQEMYSVETLARVDTLCLDKTGTITQGKM
TVEALHSLSDKFSDETGVQILAAIYQTSEDNNPTAQAIKRGYGHLDHAYTSDNVIPFSSDR
KWGAMHLSSVGTIFLGAPEMLLDSNPAAVGEAQKRGSRLVLAHSDQVLDKHSIQLPED
MTALAVLEITDPIREGAAETLDYLRSDVDLKIISGDNPVTVSHIASQAGFANYESYIDCSK
ISDQELVEQAEETAIFGRVSPHQKLLIQLTKAAGRTTAMTGDGVNDILALREADCSIVMA
EGDPATRQIANLVLLNSDFNDVPEILFEGRRVVNNIGRIAPIFFIKTIYSFILAIICISSILLGKS
EYLLIFPIPIQITLIDQFVEGFPPFVLTFERNIKPVEKHFLKRSLLQALPSSLMIVFSVLVRI

WGSSHGWSDIEMATLTYYLLGSISFLSVIRACLPLNLWRSLLIIFSVFGFYLSAFVLQHLEI
ATLTAATLPVYLILMVVFGLVVFVACTIKQKYRFD
>tr|A4CXI1|A4CXI1_SYNPV Putative efflux transporter family protein OS=Synechococcus sp.
(strain WH7805) OX=59931 GN=WH7805_00330 PE=4 SV=1
MDPSTSGHGPNWNLSSLLDFSRPAHAAWTDAMRGAGITTLLGWIALTLNAPRALLPLTLGS
VFTAIAETGQGRDHPWRTMAWTTTWLMVAAGFGAAIGENTPLAVFASGAMGFICASAAS
RDKRTAVTSLTLLVFTIYVGYPGPIVPALQDMGLILLGGVIQTLVCSVVRAFQQVKHERL
CIPPIWRHLRTFRTSDAHVRHGRILAITLMVATAISESTGLPHQYWLPMSVAWMSRAQLNS
TCQRVLHRLGLTLLGLGFIALVVRWIGPQGAHWLPLSLLGAGILAIYVWVHYAAAVVGV
TIWIIAFAFALVGDVIDTLWNRMLDTTIAAIVLMAVWIDPRASES
>tr|A7HZG4|A7HZG4_CAMHC Transporter, auxin efflux carrier (AEC) family
OS=Campylobacter hominis (strain ATCC BAA-381 / LMG 19568 / NCTC 13146 / CH001A)
OX=360107 GN=CHAB381_0033 PE=4 SV=1
MIYQSLFTIFILLAGGYISKLIKVLKQKQSRSLFDFVVFALPCLIFDKIYHLNFNFSILLIFA
GFISTSLAGIISVIIGRVFKFSKPTILSMFVLSAFGNTLFVGMPPVSNVFGEEFVGEVIMYDSL
AGAIPISILVPLILAMNNGEKVTIVKNIKTIIYFPPFIGLVGLLALKGFEIPEFVFAPIRMFGGS
ATPVALFAIGLSLGFNAIKSSYKSTVIVLFMKMILAPAIFILILQCFGAADFCKSTLIAVLESSM
PTATIVCVMVMKAKLDSNLAASSVAFGLVLSVITLPIILLNLTGLSTF
>tr|A9ED99|A9ED99_9RHOB Cation efflux system protein OS=Sulfitobacter indolifex HEL-45
OX=391624 GN=OIHEL45_16441 PE=4 SV=1
MIDPPALAGWTVVILGGVALVVDTLTALLTYSMQKGSVNIRALFLHNLSDALASVAVIFG
GTLIIFYDLRWVDHTTASGSYISAMRMLRLATFCLLLILAAVGSALILPHVSLAMTTGAA
VYALHYDGIGPILGAILTASAASATVSKGVWLLAIGAVGRCLHQVAGGVMLVMGIGMMT
GQLSAFS
>tr|A9M0F3|A9M0F3_NEIM0 Efflux transporter membrane protein AgrA OS=Neisseria
meningitidis serogroup C (strain 053442) OX=374833 GN=agrA PE=4 SV=1
MFFDNNYHYNAIPVRLLVNIQDADSDGIQTASENNNGTRMGYNRPMEKNTLSARAPSPW
LPLLLAIAIFMQMLDATILNTALPEIATDLDESPLDMQLAVVAYTLTVALLIPLSGYLADRF
GTKKVFFGSIAVFMGLSALCAASGSLFELTLRVVQGGGSMVPIPRLTILRMYDKSKLL
NAINYAVMPALIGPVLGPLAGGYLVEYASWHWIFLLNLPIGLLGFILGRNIMPDKGNDT
ALDFKGYLTFSAAACLLLLAAESLSHALPPYFALLPLCGLLFARRYFRHMKTTSKPIYSA
DLFLIRTFRLGLAGNLFSLGSIIPFLMPLMFQVAFGFGASLSGWLVAVALSSLLVKPLIA
PLMKRFGYRTVLLWNTKLLAAFIMLLALPDGNSSLWIWIFLSLAIGACNSLQFSAMNTLTL
ADLRPQQTGSGNSLMAVNQQLAISMGIVVGALILKNWTFILPASSGLHSAFRMTLLSIGGI
TLASSLVFNRLHVSDGTNLTRNTPS
>tr|B0SJR0|B0SJR0_LEPBP Glutathione-regulated potassium-efflux system protein KefB putative
membrane protein OS=Leptospira biflexa serovar Patoc (strain Patoc 1 / ATCC 23582 / Paris)
OX=456481 GN=kefB PE=4 SV=1
MKTRSTVFYGFTELLLFGLSGYYLLQAGGVLESTKNLTIAATNGHLDTENFFNRFHHPLALLF
LQIIVVCGSARFVGYLFTRKLLKQPSVMGEIVAGILLGPSLLGYYPETMSFLFPPSSLPTLGT
LSQIGLVLFMFIIGMELDLSVLKNKAHSAMISHASIIFFPFLGMTLAYYYFYTDYAPENVGFLS
FSLFMGIAMSITAFVRLARILQERNLRTPLGAMVLTCAAADDITAWILLAIIVTISKAGNL
NTALFTIGLSFAYILTMIYLVAPFLKRLGSIYISRENLTARTAVAILMILFLSSLTTEVIGIHAL
FGAFLAGVIMPSEGNLKKLIAEKIEDIAVILFLPIFFVITGLRTEVTLLNGSHLWLVFGLVLF
VAVVGKFLGSALAAVSGSNWEDSLSIGALMNTRGLMELVVLNIGYDLGILSPEIFAVFVL
MALVTTLSTGPLLDGIQKFFARTANATYPEPEKPSDSKLRVLVAFQAQKMGKSLVRFAFSL
GNQKKNLELIALHISPNDLSLNEEIRKYRDASFEAIRQTGSSLGIVQTEYRITDNVTYEIVN
FAKIKHTDILLIGAAPLFSRSYTGKIKGILNYCPATVGVLDNGLESIERVAILYKGEKDP
ILGFAQKLTSLKGMKFNKIKVENLIQPETDLNPFPIALSQITGYSLLIDLVNWEELGFEEKMD
LLPTSFLLVRLFTT

>tr|B2FS78|B2FS78_STRMK Putative transmembrane efflux protein OS=Stenotrophomonas maltophilia (strain K279a) OX=522373 GN=Smlt2498 PE=4 SV=1
MSGMTDGGQQLRNAQWGKVSRLFKPAMIISAALTASAETFYRTGAYPRAIFEAGSTDVRT
WLYVALMYLIALPVLFLWMRRLLAGYPMPWNPLKRWLLGAFSLILCSGMIVLPVIVLTV
GGSAAGRKGGLYQLFTGNLFGTFLVGTVLAYGAALGAWLLFIGTPKLLFPKLGSR

>tr|B2V8Y0|B2V8Y0_SULSY Auxin Efflux Carrier OS=Sulfurihydrogenibium sp. (strain YO3AOP1) OX=436114 GN=SYO3AOP1_0770 PE=4 SV=1
MLENLLQIFVFFILGYTAIKLKIIPQEYSKAYIDYIMNFGFPALVVYNIYRLRFSLDVLGIIIL
GWIAIFLTIFVSHLISKSLKLDKKRTVAFIMMSTFSNTGFLGYPFHSLYGEGLRYAVIFDN
LAMFLPIFLLAPFIINYAKEGSTKINIKKLLLFPPFIALVIGVSLKPFDPVEIFLNLLKTLGMTV
IPILFSVGLNLRFSHIGKDLKLLTVNMLVKLFASPLILLILLILKIDLTLPYKVAILQLAMPP
MVLASIYLIDADLEKDFAVSSVAIGIILSFLSVPIWYFLLNSLST

>tr|B4EPG6|B4EPG6_BURCJ Putative auxin efflux carrier family protein OS=Burkholderia cenocepacia (strain ATCC BAA-245 / DSM 16553 / LMG 16656 / NCTC 13227 / J2315 / CF5610) OX=216591 GN=BCAS0049 PE=4 SV=1
MHTELAWVAVAPAFALICIGIAVRRLALVDAAFWPSAEKLTHYVLFPAFLVHSIGLAGPL
DASSKSTIVLLTGLTLAVLAAVVLGCRWCAVPHASFTSIVQGSIRFNSYIFLSVASGLLSRA
DYGIAAVVVAYMVAISNTLVLLSFEHQAGGRGLVRIVGKVAANPLIVASAFGIVLNLTG
WRLPAAVDQTVDLGGAALPLSLICVGAALRLPLPRKEAALVRAGLVTTAIRLVGFPLLA
LTATKAFAVTPLSGNLILLYSVLPCASNSYVLSTQYGGNHRLMAFVVALSTVLSFVPIFLV
ARTM

>tr|B4V7X1|B4V7X1_9ACTN Transmembrane efflux protein OS=Streptomyces sp. Mg1 OX=465541 GN=SSAG_03935 PE=4 SV=1
MMTGARPGGVGRGNCCIMQQDHPSPSSASHPPSPRSPSMLRLASAALAGTAIEFYDFFV
YGTAAALVLGPLFFPSFSPLAGTLAAAFATFGVGFLARPLGSAVFGHIGDRYGRRPVLLGSL
LLTGLATVAVGCVPSYASIGVAAPVLLLLLRFLQGLGLGGEWGGAVLLTAEHAPEGRRL
WSSFPQTGPAVGFLLANGMLGLSATLTDGQFTAWGWRVPFWAAGLLALAGLWLRSSV
EETPQFRALAEETGGRAEAPLTEVVRGHWRLLLLTGGALAVGYAVFYSVTTWSLAYATEH
LRVERTVMLACVMAAVALKALATPMAVLGDRYGRRLPLCLAGCTACALWMFPFVALL
RTTDPLLMTAGCFVALLGMVAMFAVVGAYLPELYAPRIRCTGAAVGYNLGGVLGGALT
PIVATALADGSGPPWGVAVYLTGVALVSLVCFALLPETNPALVRAKEAAGAGTTTGAAE
AAAPA

>tr|B6YZ23|B6YZ23_9RHOB Transmembrane efflux protein, putative OS=Pseudovibrio sp. JE062 OX=439495 GN=PJE062_3819 PE=4 SV=1
MARKHLVLLNMIGALALVMIDQTVLGVLPSLQRTFMFGPVLHLQWSVNAYLIALASMLM
CGGWLGDKFGYFTSLRMGVALFTAASLACAYAPTGEFFITARVFGGAGAALMQPAATAL
VFSAYPADERGKALAHYVGAGLFFLACGPLVGGLLVEFFSWRVVFLNVPIGLAVLIMAF
AIGKSKTNKETGSFDFQGAILFVMALLVFTVAVQLFGDYRLSLGEGVVSAGFVVLACSL
FVRRHRVAHPFIQFSLFENKVYLGCCLLLFCEIPFALLAQVVFVAVFLQNVLSLTPLEAGLS
MLPVVLTIIICAQFGGRLVGNIFRNLAVCGSLAMGIGFATQALVIHFNNLWLLFPGMILM
GAGLGFLISTVSTEALSHVSLARARATALLQTCRQVGGVFGIACVGALINWREKTMISAA
AELMEPNDEDRELLQLLLYKFMGDQPAALLHERWPQSLYILKAISSRALADAYIFSAV
VLFGAAVMSLWAFKGHTPRQRPQGPEGPPPMNSAND

>tr|B8DYY8|B8DYY8_DICTD Auxin Efflux Carrier OS=Dictyoglomus turgidum (strain Z-1310 / DSM 6724) OX=515635 GN=Dtur_0291 PE=4 SV=1
MFLT VFSKFLPVFLLFLLGNLFRIKSYVSENAVSELKKLVVNVFLPSLLFSLFSRTGIEPKHL
IIVVIMFLVCTILLFIGRFFQKLLKVDSKYFYLLFTGFEAGMLGYSLFTVIFYGTENVFKFAI
DLGQVTFVFFVLVGILLSIKEGRRSWNFKSMLYSFLKTPVIIAIFLGIIIFQKTKLIDIFMKNIL
LSSILETIEMLSVMTVPFISLIIGYELKFQKENLSLSFKVVILRNVLIVLGLINIVINKMLG
LDNIFQRALITMFLPPPFIIPLYIRDEDREDKVFISNTLALSTLFTMLIFLLMNILGGVTL

>tr|B9KBM6|B9KBM6_THENN Auxin Efflux Carrier OS=Thermotoga neapolitana (strain ATCC 49049 / DSM 4359 / NS-E) OX=309803 GN=CTN_0246 PE=4 SV=1
MERKAEKGGEKMPYTSFSSIPSFLIILIGYAVGKVFSDEVVGLASKVAIWVMVPTVTFTFI
NKYTPGFSELRDFGLGIIVFLFFLYSSFFKHRRGVVLVTAVTSNAGYLGYPILMSLWGEQ
ALALGVVYALLIVLMTILPAFLGERFNLKNLFLKLPYIYALPAGFITGKLGLHYEDLPSYLL
SAINMLKQAAIPYLLLYVGLSVSRVKMDKRVGTGLGGLIIFNKLFLSPLIALLFVMIYKLDGL
SGKVFILETAMPTAINSVVIVSALGGDSKTVGLGVTLTTFFAIFTLPWAVLLEKIFG
>tr|B9NVI1|B9NVI1_9RHOB Putative transmembrane efflux protein OS=Rhodobacteraceae
bacterium KLH11 OX=467661 GN=RKLH11_3546 PE=4 SV=1
MHHWFIQASMDEPMDRKSIIKVIALMVTGFGIGIDFTGALMLVPAIENSFDTTITSTQWVL
NIYALFFAMTMVAGGRLGDMYGHRKMMIIGLSIFLFASVLCFVSPGLDYLGARALQGIG
AGCVWPCTLAFGATKVSKEEHRALVMGLILAGVTTGNVFGPMISGAVVNLGDWRLFFLA
NVVFSSISMVTALLMERETEHKTGEHIDFAGMGILSFAVLLLLYGLDIGADWGWTSPPLL
LLFFVSAALFFLPKVEKRVREPLLLPQLMQNREFLITLGLNMFNVSAAFVGLLYFPQYMQ
KVLGWSVVFQSALGLAPLTILLAVGSVSGTLYNDFGPKRLLFWGYVCATVGAASIVVMP
AGLGYFQILPGMALIGLGATLTVGPSGTAAVCAVKPERAGLVGGLSFMTHLVYGAIAVA
GATAVMYVTSLSLKTQLAAAGINMPEADQRAINGGTLTTESAKAVLQKLSPGEVEKVK
AAIATAFDSGMNMAFVFATFSVAVGIVLALMLDEKKLHKVEG
>tr|C0EE40|C0EE40_9FIRM Transporter, auxin efflux carrier (AEC) family protein
OS=[Clostridium] methylpentosum DSM 5476 OX=537013 GN=CLOSTMETH_02119 PE=4
SV=1
MQAGLTILNQVFIMFLLILTGYFCHRLGLISARANKQLANLLITIVTAALIIDTYQTDFDPAA
ARNLLISFALSFGILFLGVVVSLLMKRKGSEYSVPTERFGVIYSNSAYMGIPLLLATVGPTG
VFYSSAFMVAFNVMTWAQGATMLTGQRSLRQVLRALVTPVTFSLISLPMFFFRIRLPQPV
GDAIGYLASLLTPLSMLVSGVFIAQTNLVQAFTSLRVYAVSALRLLVIPAITLFALWVLPID
GDLKLTMLILSAAPCATGTMLFASRFGGDVQRASGVFAVSTLLSIVTmplliivaeaiw
>tr|C0K045|C0K045_9BACT Putative efflux outer membrane component OS=uncultured
bacterium 34R1 OX=581113 PE=4 SV=1
MRAGNSVGQFFSLCVLNGKMLSSCAFLHYLCAIINNFMRYGLFIICVALSGVLASAQQ
VLSLDSRSMALRNNKEIKQAQVGEEIAGYQRKQAQAAYLPSVDFQGTYIYNSKKISMVE
KDELLPTKSFNLATGTYYDYNLVINPATGQPLVVDGTPVPSTVALLPKSALTYNHIFVGA
LTITQPIYMGGKIKAMNEITRYAEQLARLTRNRKAEDLIYEVDAAWQVVSRLREKQKLAE
SYVQLVESLDRDVNNMLKEGVATKSTLLSVDVKVNEAHVDLTKVNNGVVLARMLLAQL
CGLPVNEQFVLEDENGNDPDISNLKPARIDMEDVYSRRNDVNSLVLATKIYDEKAKVARA
EMMPTVAAIGAAHTSNPNMYNGFKNRFGFGFSIGAVVKIPLWHWGGLSNKYKEAQAEA
RLKRIELEDAKEKIELQVTQANFRYEEALKTFEATKANLTEANENLRIAQIGFKEGVATAD
DVLAAQTAWLKAHSEEVD AEIDVRMCDVYLAKVLGKMNY
>tr|C0ZNM5|C0ZNM5_RHOE4 Putative drug resistance efflux protein OS=Rhodococcus
erythropolis (strain PR4 / NBRC 100887) OX=234621 GN=RER_05690 PE=4 SV=1
MSSKSSISPCTPTKRCADVTQARLRHPLTTQASPIPTGKELRMSTQPKSTRKWWALALIA
AAQFMVIMDTSIIGVALPQMQLGFSQEGLTWVFNAYVIAFGGLLLLGGRLSDLFGARR
VFSAGWLILLIGSVVAGAAGNVAVELAGRAVQGAGAALIAPSALTLLMMLFGSTQKEMT
KALSIYGAAAPAGGTAGVFLGGVITEYTSWPWVFYLNPIAVIALIATPLLMPNAPARTGSI
DFLGALAVTAGLAVGVFGIVRAPDVGWGSGQTLALAVSAALLGAFVLIQSKRREPLVR
LGIFKAPNLGAANIAQLVLGAAWIPMWFFLNLYLQQVLGYSAFPAGAALLPMTIFVMLG
MVVVAPRAMARFGAKAMIVTGLLVLGIGLGWMSLIRPTGNFWVDVLPASLVAAAGMTL
AFIPSLGTAISAARPEEGGLASGIVNVSQVGSAGVLAVMTAIAAVFGADQLGDLTELNG
FSAVFLGAAAIAVVGAAITAIVMRSTKVDDPRPVQSTVNS
>tr|C5ZWX3|C5ZWX3_9HELI Putative efflux system outer membrane protein OS=Helicobacter
canadensis MIT 98-5491 OX=537970 GN=HCAN_0927 PE=4 SV=1

MSLKTLLFLCILTSTFGYTSLQEAIDLTLKANHAIKEQEFLLEKEAQYNYKTYQSPFYPSINA
 TYSTDRTNKISSQSRKTSIGNIGANIQFNLFNGLSDYYNLASYESLSKAQEHQLQATKEDII
 LLVKTAYIDVLRQKQNVIVAEQSKALLEEQRRRESAEFYKVGLIPKNDLLKVEVELNNSIQA
 LLSAKSNLAYSLKNLERYTRTKINLKDLVELTLHQPTLIESTLKNLMYQKRSELLFLDSVIQ
 SKDYLVKSAKGNFLPNINIIGDYTRYGEDYRLSKRSNTYNDETMITLQINLNLNLFNGFNDKY
 TLESTKVNKLAFESQRITLLEDLDLQLFSALETYNLSLNAYQVALSALTQAEENYRISKNR
 YKERIQSTSDFLDAEYLLTQARTNVVLNRYAILQALAEIERITQTPQVLN
 >tr|C7RFL9|C7RFL9_ANAPD ABC-type Na⁺ efflux pump permease component-like protein
 OS=Anaerococcus prevotii (strain ATCC 9321 / DSM 20548 / JCM 6508 / PC1) OX=525919
 GN=Apre_0228 PE=4 SV=1
 MSRFITVALDSWKKQLKSPAFWL VVFMPHIMMAISGAITYFSADDGIKETYIVA EDEIGAYF
 TENSAYKLNKDEARKAMEDKEIGSFVEIREEDGSLSAKYHTRDLNGQEIAAFNSILREVQ
 NSINIKRAGLGEDKLKILERKPSFKLVEEEGGESFIMYGAYFALVFYMYMMLVMYSNILV
 VEIATEKGSKMIEFIFSSVKAGVYFAGKIFGNFLAVITQTAIYLILALLAYFGAKRYGLFEKF
 NIDLGSLGDLNVLMLVELASLVILSLLIYMLAAMLGSLAKKQEDAGKVGTPILILVIFAFV
 IALSMGKEETLLIKVLSYLPFVSVFFMPMRLIRSSVGLGYGLISILIMLVSIILAYKIASRVY
 KKNILNYSSNSWIKKILRKA
 >tr|C8X5M8|C8X5M8_DESRD Auxin Efflux Carrier OS=Desulfohalobium retbaense (strain
 ATCC 49708 / DSM 5692 / JCM 16813 / HR100) OX=485915 GN=Dret_2443 PE=4 SV=1
 MVTDIVWAVVQIFCVFGLGWLARHLNYLQGM DIGRFSRLAIDFLMPCLVFSATTEHFATE
 RLHELWPLVIAFAIVVFGTCVGAGARLLLKKRTVAQRRTVHHLCAVNNAVFLPVILVEN
 LWGDAAVANLFFSLGAALGLWSIGVVLLGGGSWRDGV RHLLTPTHLALLMALTCLLGG
 ATEAIPITVAQTAFVGSAAIPLVLFLVGASLYPLPDFSPRRLVLLTSCRLIIGIPVLLTLILRQ
 LPIVDDVYNMAVVNAFMPAAAI STILTHRFGGDPQLAASTVVATTLASLITVPLGLSWALI
 >tr|D0SWP0|D0SWP0_ACILW Transporter, auxin efflux carrier (AEC) family protein
 OS=Acinetobacter lwoffii SH145 OX=575588 GN=HMPREF0017_01714 PE=4 SV=1
 MHIILTSFLPLIGLISFGYLLKRRQWLSDDFWRGAEKLNYYALFPVMLFLNLATAKIQMDV
 IQDVVLVVFSSIMAVVSIALYILRHIYQISYARFGVYVQGLLRFNNTYIGLA AVSALFHQQGM
 TIFAVIMVLCIPLVNILSVLAFTRSHDMQLKKIILDL SKNPLILGCIVGGFLNLSGLSLWTGA
 EQFLKQIALCSLPLGLMCMVGAALQFQGFQRDVPLSLITFGRLFGMPLIAFLVCKIFQIDAL
 TTQVLVLFFALPTASASYVLTRVYGGDSELMASISVQTVVAAVSLVLMLSWLI
 >tr|D3CT55|D3CT55_9ACTN ABC-type Na⁺ efflux pump permease component-like protein
 OS=Frankia sp. EUN1f OX=102897 GN=FrEUN1fDRAFT_0722 PE=4 SV=1
 MSTGADGGSDGDTGQLPSFPTQGGRRPDDRGAWVTGPPAAPPAAPASGLASGQASGLAA
 AEAAEPGGFPPLAAWVVVRLVAGRELAILRSLKVFVITTA AFLVLLVGASVVISLLGGHES
 AKSVGFIAAESVLADPLEAVAGGLGVDVATREVPDEATGLREVSDGDLDVLVTAAPSGL
 RVTVKEELSEDLRGVLAVLARQQVLDNEISVLGGDPARVNETVAAAGLDVAELDPVPDD
 QDERLFLGLASAFLIYMGLMLFGPAVSQGVVEEKSSRVVELLSTVRPWTLMAGKVLGIG
 LVALIQMVVIAGGGGLIAALTGALPLPSSEATGTVIWSVAWYVIGFFLYALPFAAVGAMV
 SRQEDLGGISSPIVLALIVPWVVGVSILPGDPDNGLVEILSLVPLFSPLLMPMRIALGVAPL
 WQLVLSVLLALALIGLLIRITGRIYHNAVLRTGARVAFKEAVRRA
 >tr|D4YYV2|D4YYV2_SPHJU RND-family efflux transporter OS=Sphingobium japonicum
 (strain DSM 16413 / CCM 7287 / MTCC 6362 / UT26 / NBRC 101211 / UT26S) OX=452662
 GN=SJA_C1-07000 PE=4 SV=1
 MNKAGYQANLGNMFSRSSGSLNDNMAGPSLYLQQRIWDFGRAKGEIGYARSTEEQRR
 YELESVADQLAEQAALAFQLVKRFELLGREAA RQVEALEHLRELIGLRVDAGISDKSDLM
 LANVRVDSARGDAILAESSLITARAALANLTGAMPTVYQDPNPQITRFGAAEEEPDFASLP
 AIVAADKAEQAAAAARVGQAKAERYPQLGLQLGYTRNNYTYNERNNAFSALVTVTGDLY
 KRGTRYQVRAAEERRAARSARDSVLLDARGRAL TARQEIRGGALRIEAFSHQEKQAEAA

SRIFFEYKLGKRTLTELLNTQLEIYRAASARIVA EYDVLAARIRFENVRGTLRPSLGLPAR
 LTEGEEHGH

>tr|D6KDL8|D6KDL8_9ACTN Transmembrane efflux protein OS=Streptomyces sp. e14
 OX=645465 GN=SSTG_05043 PE=4 SV=1
 MAVLLAANAVAGAGLGAAFAASAAGLAALRDSERAAATTVFGSTVVLALLLAGVPQAD
 HRGGAAAGFAVLAGCCAAAWWLMRYLPDQGRPHPGPHPSAGGQAPPWWFIASVAVLA
 ATDQGAWSYAGVLGERHAGLSAGAVSVILAVAGAAALVGVPVSAAVARRLGRVPTLV
 VIAADAVAKLLAAASGFDPLYAAATVVWQICYLALLAQMLGAVAAVDRSGRWAAAAG
 GALAVGTGLGPAMTGWLLDTAGAPVLGGTLAAVTVVAAPLLRTVRGLALPADSTDA

>tr|D6T174|D6T174_GARVA ABC-type Na⁺ efflux pump, permease component OS=Gardnerella
 vaginalis 5-1 OX=682148 GN=GV51_0406 PE=4 SV=1
 MSGQINQSVSDQATSNSYKTGRSMNAQHRLTFMHSKSEMVKLRGLTSTWWCMALAI
 LPVVFSSIIAIVQKAISKVDFTKQGASASKSSGAVTMGPSDKSSLISSQEGIFNLVISFASISLI
 VIAIFAVLAITAEHSTTSIQASLTSVPRRGMMFTAKFVAIAIYVFVVQLIAMAVSLVAAELAF
 MGENISGLSGSRTWQLPLMLFLGSPVIMVVVAAMAYGFGMICKSTAGGIMCVIGAVMILP
 TVLSIIVISSGFAKWTLVLTQLLPATAVSQFLGDSSSSNGKFASNVNVAFEWWQSGLVVLA
 WAVVMYAIGYVIEKHRDI

>tr|D8F7G2|D8F7G2_9DELTA Putative Potassium efflux system KefA OS=delta proteobacterium
 NaphS2 OX=88274 GN=NPH_3875 PE=4 SV=1
 MFFLLLPACGAVGNAPNSWEALLKHQHRELIETSKSIDQLASKLPHRLSDLQKHLVLLKSR
 FERLMLYFDLKSNDPLVLRDIQGVLDWFSEADRLILPFKQEKASVTRQMENLADLSRKF
 RQEEILIEKAGPQIQAEVTSYKDLADLEARLQPVNKNLAKGIDAAHAFILELEKNRARIEH
 ASSVLKTHLVKRAPVFFSASAWLTGMAALRSWTSRFGLYLLEPIDLRGLGWTMFIKIV
 LFSLLIMGLWVGFKKKIKRYEGLATVRLFPFFLSFSIGIGALLGILSTGLFPSSFFSTLVTVV
 LVYGLLSLSRNLHGVLFDFDQDTRYCRLLPFWGAVSVSGLLVSIHLPEQAFIPVWSIWLLILC
 WYYAGTKVGKEGWETFSRFILIAATPILVLMGMMLFLLFLDIRLAEMLSTALGRMGPDRI
 MTTAPDSSPSKKVRRLLGFPLILLTLLISFAWTFIFVGGGPLFLEVIRYRVGWENFTFSIYRV
 LCIFALLFIIRASIALARSALAKLPDRRRDL DAGSLQTLDTIITYVLWSLFTLGTALFLGLGL
 RNLAVVAGGLSVGLGFLQNIIVNNFLGGLILLFGRSIQPGDLLEIDNIKGHVRKVITIRNTLI
 KAFSGATIFVPNPLLISQKMINWSHSDRRYRQEIKVGVA YGSDVQKVTDLLLEAAKQSPK
 VLD RPPSRVRFLDFGDSTLVFSLRVWIKGWADRYADSEVRYHIDRIFKENGIEISFPQLDLH
 VRS AISPKMEC

>tr|D9XY84|D9XY84_9ACTN Transmembrane efflux protein OS=Streptomyces griseoflavus
 Tu4000 OX=467200 GN=SSRG_05496 PE=4 SV=1
 MNEPPSSSPAVAHRWVSLFAICTAAGMVWLAFGDLSVAIPQIADEFNGNLSSLQWANNAF
 SLVTGALVITAGKFGDLFGRRRMLQVGTVLLAVFSVPAALAPDIGWLVL SRGLMGIGAAL
 ILPASLALIPPEFSGKAETTAFSVWQAVAWGGLSVGPALSGVITDGLGWRWLFWINLPLA
 VITLVVVRVTTPE SRDEKAGHTIDWLGLASIVLAVFALLYALTEGPSQGWGSP LIVALFVA
 TVVLSVWWWFVERHVSQPLVDLKLFIKIRAYNGALANLTMNFTFAGMSFLLVLWLENA
 RGYSAVEAGVLMMLPATVGVFLFIPLGGRLAIRWGGRLPAVVGLVVASAGLTLLGSLGTRS
 STEYLAVALIVIGLGLGLVSTPVANTTVGEVPIDLAGTAAGVFKMSSMLGGALGVAVLTA
 VARELTTRDAASVVEASGLSPADISQFRQALVNSSSFREAIASLPDLGRTVQQA AVSAFSS
 GVADTMAVTAVLTFVGTA AVFFLWPRRRKADATVAGPGPEDRPNP

>tr|E0F2J6|E0F2J6_ACTPL AEC family possible malonate efflux carrier OS=Actinobacillus
 pleuropneumoniae serovar 10 str. D13039 OX=754259 GN=appser10_3610 PE=4 SV=1
 MQAVKFVKNIANLTAYFLLGSRIMFFESLQFSIGVMLPTILLMLLGIFLRRRK FVDDDFCNT
 ASKVMFNFALPTMLFLNVVKSPLDYSKDLNLIFAGLSGTLIYLIAEWWAAKYIRERGYRC
 IFTQGVFRTNAAILGLALTINAYGEAGLATVSIYTASLVILFNVLSVITILNSLSDQKPSAAR
 LAAAVAKNPLIQAIVLGIVVNYLQIRIPKSLMQTAQSLANITLPMALICIGATLDFKALSQF

RQQTAESELTRVVLVYASFSRLILAPLFLFILGKWVFAALNPMQLGILFLTATAPVAAATYAM
 VRAYGGNGKGAANLIGITTIGSIFTASLGLFVLHHLGWI
 >tr|E1SP64|E1SP64_FERBD ABC-type Na⁺ efflux pump, permease component OS=Ferrimonas
 balearica (strain DSM 9799 / CCM 4581 / PAT) OX=550540 GN=Fbal_1485 PE=4 SV=1
 MIALIWLKEMREVLDRDKKTLWVVLFPVLLPALMGGAIVVGASSVKQVYESDLRFQLV
 APEPWGEIAEALTNGERLVWDDQVQVSNREQFDAANEGVLEFVLVVPDDFSATASEVS
 QWQLYYNQADDVGQFDRIHQALQPLFEQWQTEHRNAWNLTESQVQVLKQAVELEQVG
 VADQREFIGEKVGGFLPYALLLLCLMGALLPALDLGAGEKERGTLETLLMAPVSKTTVV
 MAKFMVIAICSLTVALLTMASGVVWSLVLGQVFAIEMLEAISTIGMMDLVLLLLLLPIA
 MFFAALLLAVSFYARTYKEGQNYVAPLNFVAILPAMVALFPGITLTSTLAWIPLVNVTLAS
 KALLKGTFDYWQLMPIMASNTLLAALLLAFCVKWCSREQVLF
 >tr|E2CI87|E2CI87_9RHOB Putative cation efflux system protein OS=Roseibium sp. TrichSKD4
 OX=744980 GN=TRICHSKD4_2787 PE=4 SV=1
 MHSQHQDIGPHARLHGRLFQARPHSPRRFGGGKFTSFWPIYICAGQIPIIAGKGGQALPGE
 AVLSGVIECFMSMSDLV
 >tr|E4LUR2|E4LUR2_9CLOT Transporter, auxin efflux carrier (AEC) family protein
 OS=Clostridium sp. HGF2 OX=908340 GN=HMPREF9406_2375 PE=4 SV=1
 MELSLFMKQLLVMFSLSGIGFLLAKLKLISNEGCKELVNLLLYAVIPLTVLNSFLVEKTPE
 KTQLLLYSLLSLAVFAVSMLLSYIIYGKRKRVENFSAAFSNAFIGIPLVQATVGPHAVFY
 IAGFVAFLNIFQWIYGAYVMGAERRMISFQVIKNAVLLSFITGFTLYLCDLGNILFIKDIA
 NTVAYMNSPLAMIIIGVYMSQISFMRMLQRESSYICSLCRLFVIPLASLGLLAVIPLDCCEV
 KVAICIVLSAPVGANVAMFAQKFHQDYTYAVEIVILSTLMSVVTLPDIVYAAQIVL
 >tr|E6L295|E6L295_9PROT Outer membrane component of efflux system OS=Aerobacter
 butzleri JV22 OX=888827 GN=HMPREF9401_0571 PE=4 SV=1
 MFKNIFIFLISTSLYAIKELLNSVEVTNENYQAQQALQEMSKKQYESATKDNYPFTNLI
 GAYENNSKVLKTEPEDIAYAEKASYTLYDGERIKNNELSKKSLHESQQKTKQYLKQEM
 LEVIKQYFSYQNTKSAIDVINYKINELNGQIKKFEILVKNDLETDKDLQALIASKEALYDI
 ETLKIDLENSILQSLLTGFDILPQDNDKLMEPTYDEKDRFDIEAKRLEAKSVKYTSEGFNY
 LPTISINNSLKKQEYYHYDETYNDKFNNQIMLQINFPIFDGKISKDKKEASQLEALALNKEI
 AYKEKSIQIERKLALKSLESSKVKLDSAISGLEATNTTYEFSKKRFDANLISYTEYLTETK
 KQDANYRVILAKNDIELKKANLAFALGIDLLTLIKE
 >tr|E6XRJ6|E6XRJ6_SHEP2 Catecholate ferric siderophore efflux transporter, permease
 component 1 OS=Shewanella putrefaciens (strain 200) OX=399804 GN=Sput200_3684 PE=4
 SV=1
 MQRLFSPTSTLALALRPAIPALTFGMLLAAGAGVTTLGALWCMIQLIAGHHSLWLAGALI
 FGLVSALLSAGASWVNHNAEAQFSGRLRRDVA AHLVRLPSTLAKYKGEKLRMLVDDI
 ASLHHMIAHLPSELATFIIVPAITIGLLILSAGLVLLALIPGLVAALFYLVVIPRLAAKQGEA
 RFNVMGNITAAVDDYARGAPVFRIYGAQTGAMADYQKATTHFIGDILERVSKVSTSVAV
 ATSLQAVCTFAIVYAIGYEWPEKLAAALFFSLAIVTPALKLGHGLDYLATGRAAAQRLT
 DFLEQSRVPVGNNGNIELNANMQLTTLTNVPSLSTSNQSVPINYQFSSGRVTAVTGISGVGK
 STLLRLLAGMEPLNAGDIRLAGIALKEMDETSINRAIMLLPQGAGLLATSIADNLALTAPY
 ATDDDYLAALHCAQLDNPLNTHASALSGGEIQRVNLRIFLSPARVILLDEPTSALDSETA
 FNVFTVLRHHAKTNHKTIVMVTHTDLTLAELADDKLTCLKHHHREGEGQ
 >tr|F2IEW7|F2IEW7_FLUTR Auxin efflux carrier protein OS=Fluviicola taffensis (strain DSM
 16823 / NCIMB 13979 / RW262) OX=755732 GN=Fluta_0425 PE=4 SV=1
 MEFINILDVDIVESNLTVAVQVNRENHELTSENKMQFLFLIALVCIIIIAYLNLKEK
 >tr|F3ZIL8|F3ZIL8_9ACTN Putative transmembrane efflux protein OS=Streptomyces sp. Tu6071
 OX=355249 GN=STTU_1482 PE=4 SV=1
 MLRPATLIGLAATAGLLLATVYEAPDWTLFVFAAGIGCVPSVSGSMVRSRWAALYRDEPR
 MLHTAYSFESVVDEVCFVLGPIISIGLCTAWFPEAGPLLAGCFLAVGVFWLSGQKATEPAV

HPAGQHERGSAMRSVGLRVLVLTFTVSTGVMFGAIDVVTVAFAEDRGHKAASLVAVY
 ALGSLAGAVFGLFHFTRPPARRWLIGVCLVGVSMIPLQLVGNLPFLAVALFFAGLTIAPT
 MTTTALVEQHVPRAKLTEGMTWVSTGLAVGVALGSSVAGWVIDASGPKAGYAVPGV
 AGAAAVVVAFLGYHRLNRPVPERGGAQDEQRTGSAGGAGAGAGRDTAGGTGAQERAG
 GGAPERDLA
 >tr|F8XUD2|F8XUD2_9PROT Plasma-membrane proton-efflux P-type ATPase, putative
 OS=Acidithiobacillus sp. GGI-221 OX=872330 GN=GGI1_18631 PE=4 SV=1
 MPLFSLGFLFRSFVVTPLLVLFFFANDFVTMSLAEDNVRPSPKPDWRDIHTLVFSSLV
 VAFAWLIYIFAVYGVGRSLGLPLASVQTLDFLGLVFSGLANVFLVRERGHLLWASVPGRFL
 LWASLADILVVGGLAAMGWLMAPLPMPIIVGLLLATMVYTLILDQIKVPLLRRLTSA
 >tr|G2IEB7|G2IEB7_9CLOT ABC-type Na⁺ efflux pump, permease component OS=Candidatus
 Arthromitus sp. SFB-rat-Yit OX=1041504 GN=NaB PE=4 SV=1
 MNKFFIIAAYNFRDIIGRNFFKISTLVISLLIIIVSILPDLIKFNFISKDKSEYLIYISDPKNYIFK
 DDLELNLYIRSIEKSLDNNYYVKLVDKGVKEDELKEKLYNGGIDGYIDVVSKEINIFTKE
 NYPEIKFILDRIYLNQNSDLNISYPNYNVESLSLFKNKVIGIKNYTYPFLLTIFIYIMIFILYGO
 FISMNVNIERTSKIMDIFITKVKFSTIILGKLFGLYLLAALIQLIYFIILFLITGMMSNKYFPLIK
 EIIVFDGLFVLKYISYFVLGFMIYGLLFVFIGSVIDKIEELSLGIPIVFLISIGYFLSMLNLQFP
 NNYFKNILVCIPFFAPFVVITESSFILYKDFASLIMLITIVILIFINISINKQVIKFRGTNLKKNK
 >tr|G2N9R5|G2N9R5_STREK Putative threonine efflux protein OS=Streptomyces sp. (strain
 SirexAA-E / ActE) OX=862751 GN=SACTE_0027 PE=4 SV=1
 MRALNSPLEVGVRALVLLAASFPRPLDLPQLVYLDYAMLHSGEMDGPSPVHPSLPAGPGE
 LAMKRQLEQGLVVLMRAGLADVQADDSGLMYRASEEGPGFLDLLEAPYVGALRERAQ
 WALAFHHRVPADSRAATDDITQRWMGTFFENRLPRQGGDDD
 >tr|G7M0I8|G7M0I8_9CLOT Auxin Efflux Carrier OS=Clostridium sp. DL-VIII OX=641107
 GN=CDLVIII_2401 PE=4 SV=1
 MIISQMLLLFGLMAIGYLAKITKIMDTISDKYFSKFITNIAIPATILSSAIGQNIEDKIGIFKVL
 LVAILVFVVTFFVSIFLVKILKLERTYELMLNYSNLAFMGIPHISSYGYKEYVFYVSIFMMVF
 NISLFSYGVSVLQKENNSGKMQLKSLINPGIISALAALVIFIFEISVPEFITNILKNIGSITPLA
 MIIIGSTLAGVKINSIFTDHKIYIYTILKILVYPLLTWIIHLISLDPVITGITVILCGLPTAGNLS
 MLCADYNSNVELVSKGMFISTICSFITIPLLVIIF
 >tr|G7WEL3|G7WEL3_DESOD Arabinose efflux permease family protein OS=Desulfosporosinus
 orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) OX=768706
 GN=Desor_1241 PE=4 SV=1
 MSGNSKGTCTFFDGHPIGSAHKRFLIIASLAYVFDQMNVINFGFIGPILMKNYGWTMQQFA
 NVNSFNMLGMFIGALFGGWLADKIGRKKGLLTCILIFSLSSLANAAFTNYNIFLIMRTITGF
 GTIGMVTIAMAYISEMMPSESRGKYQALSIAVGVCMPISAILAKVVIPLSYNSWRSVFVL
 GGLGLVITVVGFWLKEPRWLVAKGRLEAAKVLNEIVPDAQLPLNAVELAKSNNSGYI
 ETRVMFSSAYGKRTATLFIVVFGATLGSFYLSNFYPSIHAQMGSQAVVLNLAIYQLFLN
 PVGDYLVSFISDNGGRKTPITVIFSIFGCLFIIQGLCSTVLSISIMLLKGLFVSAAMTITWTY
 LAESYPHTIRTTASGILFGSGRLAASFLLFTVPVYESYGYFGVNLVNGLIYIIPGIVVLFIGD
 STAKVSLEELSPSISMKETS
 >tr|G8R5H8|G8R5H8_OWEHD Putative threonine efflux protein OS=Owenweeksia
 hongkongensis (strain DSM 17368 / CIP 108786 / JCM 12287 / NRRL B-23963 / UST20020801)
 OX=926562 GN=Oweho_2279 PE=4 SV=1
 MLEVILYAVTLGITLSFAAGPVFFVIIETSIISQGKTKALMLDLGAALADVIFILIAFYGSQSLI
 SSLEDNIWVSLIGGLAVIVFGGYIILKSKTPGQFKNRVAVKRKRLFFFKGFLNFLNVGVL
 FYWIATTVAIGSLVHHERSKMIMVYALIMLTLYLTVDMMFKIYFANKFKERFKGRNLQMVE
 KIIGLILLFGVYIVIRAF
 >tr|G8UI28|G8UI28_TANFA Efflux transporter, HAE3 family OS=Tannerella forsythia (strain
 ATCC 43037 / JCM 10827 / FDC 338) OX=203275 GN=BFO_3188 PE=4 SV=1

MNRIAEFIVKKRLAIITAGVAVTLILGYFSTKLTINSNFMSYLPDDDRKVMLFERTDSLYAT
 GNIIVIGMSNTENTIITPEGISVIRQVTDSEIEGVEKVTGLTNVIDIRHRNDGVEIGRLMDE
 EIIPDSLPSLQSYILNKEMYRGRLLSEDGRSTAIIVFVETAADKEKAAREVNDLLDEVRRSH
 PELTVYCDGLPMQQQSLTESTKKDLIRLVPLVCLLIALILASTLHSLRGIFLPLLSVAMGSIW
 SMGAMGLFHVQLSPISGSIPVVLFAVGSAYTIHVLNFFKLENGENHKGIVVRGITIIGVPV
 MLAGLTTIVGFLSFIPGTYSIIRDFGIFMALGTFFCLLSLTFIPAVESYLPPLKHQEKKQKK
 HVLSGVLQWLAGVSIHRNKMVLYCAGGLILLMGAGLFRKLSNIDVLYYFPEKHPLRQSA
 AFLNREFGGTLPVQIKVTADLRSETLAAMQDFEDFLSRLPHVHNPQSVTELIKEMNQAM
 GEGKQIPDTQEKIQNLWFLLEGEPMVEQLCNTDKSEGMIHATMCNAPTGDYHAVSRKIDE
 YAAAHSSGTVQFETTGLPSIYSNFDYNLMQNLFWSLLACILVFICMTFLVKSLKSALVGF
 VPLMSAILFIFGLMGYLGIALNLATVLIAGVAVGIGVDYSIHFISGYRNALVSGKECNEAVI
 QTLQTSKGILFNVTAFAFGFLVLVFADLVPLKEFGLIMFATMFVSGLAATLLPSIILCFHI
 NLNKTQKQ

>tr|H0UME5|H0UME5_9BACT Arabinose efflux permease family protein OS=Jonquetella
 anthropi DSM 22815 OX=885272 GN=JonanDRAFT_0192 PE=4 SV=1

MTPPETEAASSRRLRRSALAFIVLMGVVSMFSDMTHEGGKSILGAYLTLTGASAAAVGFIS
 GFGELAGYSLRYLTGRLADRTKWWTLTILGYAIDLFAVPALALVPENGWLWAAALLIV
 ERGGKALKKKPAKDTLLSFVASQNGVGKSFALQEFLDQLGAFLGPVILFAVMARSSAVSLA
 AYRRCFALLIFPALVTLALLFVARYLFPTPENFEPESSRAENFSRFGWGRRFTLYIAGISLFSL
 GFMDFPLITMHAAKTNLLTPGELPLLYAGAMAVDAFAALFFGWLYDRWDTKALVISTLL
 TAPFGFFVFLAPGQWALWVGASLWGIGMGAQESVLKAAVARLVPKARRSSGYGTFQTAF
 GVCLFLGSWFMGWLYERSLWEMVLSVAAQVLAAILFLLSGRTSTGRLSAEEQ

>tr|H5Y5H2|H5Y5H2_9FIRM Arabinose efflux permease family protein OS=Desulfosporosinus
 youngiae DSM 17734 OX=768710 GN=DesyoDRAFT_3554 PE=4 SV=1

MNWKRTNLVTAIMLVMFLAAVEGTIITMAMPTIAKELQGFELISLVFSVYLLTSAISTPIYG
 KLADLYGRKYVLSISILLFLAGSFLCGLSQSMVMLIAFRAVQGLGAGGIFTVSYTIIGDEFP
 LEERSKIQGGSTVWGVATLVGPFLGGFLIDLSSWHWIFFINIPFGLVAVVLLQORSLQETFE
 KKKQSIDYGGIITLSLAVIALLSIFIFDQNSNSQAYPLFAGTAVTIAILMMLLFYKIEKKAKE
 PILPFGIFTKTSTIVNLLSFLIFAVLMGIDVYIPLYLQNVLGYPRTISGLAMLPMSVSWLIVSII
 LGKLLVKYGGKAVTVTANVVILIGALLTTLGTASPILLVLIYCFVLGIGFGGASTVLTIIIQ
 DSVDYHQRGSAVGANSLLRTLQGQTIGISVFGNIFNSHITGYFINQGIEGVNSSNLYQPSDDL
 ALTSEQISLALNSSMHVLFIAFVIISGLSLILSMAMPGRKEKEANCGINPLQH

>tr|H8XNB6|H8XNB6_FLAIG Probable membrane fusion efflux lipoprotein OS=Flavobacterium
 indicum (strain DSM 17447 / CIP 109464 / GPTSA100-9) OX=1094466 GN=KQS_00090 PE=4
 SV=1

MKNTVLFISTFFLIACSSKEEIHPPKKEIKELVFASGTLEWDNAYNLTAQTDGVLKNVTFD
 VGSTVQINERATIDNPTNENNTESNRKLTSSKENLTAASPALQQLKQNIQFAESKYQQDL
 NQANRYKRLYESQSVAKVEYENMRLAAENSLSQWNALKKQYEQLLQQAQSNINSENQ
 LKNSQVQLSYNQVTVPQTGTVVKKVKDAGDYVKKGEVIAVIADPKKIECVLNVDENSIA
 KVKIGQVVFIQLNTNKQAVFEGEISEILSAYDEQSQSFCICKAIFKKPLPSSLFGTQLEANILIG
 EKKNALLIPRKYLYGNGKVRVKGKEEPVVVKTGIVSTDYVEIVAGLTTEDVVLPIIP

>tr|I1DNN8|I1DNN8_9PROT Putative threonine efflux protein OS=Campylobacter concisus
 UNSWCD OX=929793 GN=UNSWCD_1004 PE=4 SV=1

MNLLFFITLAPISLMPGINMTYAMSIGMSFGYKHSFFVMAGQLLAIAFVSFSCMLGVGAV
 LHHFEYAFKALNIIAGLYMLYLGVMLEFFGKGELSITNVSNLPSKKQMFINGLIVSVSNPKA
 WIFFSALLPTFLDKDDPFSLTRMCVITVTLVFVEFCALNIYALGGAMLKKFLQTHLRLLLEIC
 TAIIVCTIGVLLLFR

>tr|I2IC87|I2IC87_9BURK Arabinose efflux permease family protein OS=Burkholderia sp. Ch1-1
 OX=243261 GN=BCh11DRAFT_03728 PE=4 SV=1

MSEKPATAATNVIEVERVLAETHHPAFQLMLLVLCGLCLVIDGFDAQAMGYVAPSVIGE
WHVSKAALGPVFSASLFGMLLGALGLSVLADRVGRRPVLIGSTFFFALAMLATPFVTTIPA
LIALRFITGLGLGCIMPNAMALVGEFSTPVHRVKRMMLVSCGFTVGAALGGFISAALIPAY
GWRSVFWVGGAAPLLALAMLVVLPESLQFLVLKGHNERALRWLAKFNPMLPIDANTRL
VVREKGNNGGAPVAELFRAGRGPVTLILWAISFMNLIDLYFLSNWLPTVMRDAGYSPSTAV
LVGTVLQTGGVVGTLTLLGWFIERFGFVRVLFVCFAGAALAVGTIGTVAHMLPWLLIVVFA
GGFCVVGQPAVNALAGHFYPTSLRSTGIGWSLGIGRIGSVIGPLIGGQLIALNWSNASLFH
AAAVPVLCSALLVIGLAAATRQRGRPSEPRTA

>tr|I3CIB6|I3CIB6_9GAMM Arabinose efflux permease family protein OS=Beggiatoa alba
B18LD OX=395493 GN=BegalDRAFT_2516 PE=4 SV=1

MQFQNILIIFYITVLSFCALYAPQPLLPLLSQHFQISTDQVSLLISVALIPLGVAPILYGFILS
MAATRLLKITIFLLALGQLPFILIDNFWVLVGFRTEGLLPFAIFTALVTYISTVSTLETIKRN
IALYVAATVLGGFLGRMLSGVMATYFHWTD AFLIIMLGLLGFGLLYRLQSDTRLQLVRP
TWGLLYKALQHPIYNKVYLIIFLVFFCFASVLNPLPFRMTELD SQVSSLRIALTYTG YLVGI
MMALNALRIIRWCSGEMNAILLGLAFYMLSLILLAIPSLIVISLTLFLFCAGMFLMHSVLSG
YLNHLAVENKGIINGLYIASYYAGGSTGSYLPVFIYKNWGWIA YLSCLLGLVFIIMYITLLL
KRVQHNLA

>tr|I3YNM7|I3YNM7_ALIFI Arabinose efflux permease family protein OS=Alistipes finegoldii
(strain DSM 17242 / JCM 16770 / AHN 2437 / CCUG 46020 / CIP 107999) OX=679935
GN=Alfi_2316 PE=4 SV=1

MSANSRKVSPLAWVPTVYFAMGLPFIIVNMVATLMFRGLGIDDARITLWTSILPWSLKP
FWSPLMEMFRTKKFWVATQLVSGGLALVALSLPLPNFFPYAIALMAVVAFSGATHDIA
TDGVYITELSKDLQAKFIGWQGA FYNIAKV FAMGGLVYLAGALKDHVGIVQAWMTVMG
LCGGILFLLGLYHIRMLPSGGAATAHADSF GGAMRETKRIFLEFFKKKYIWIYF AFILFYRF
AEGLVIKIVPLFLNAPLDQQGMGLTEQQIGLYYGTFGVIAFVVG SILGGYFISWLKLRRALF
PLVCIFNVFPVYALLAWFQPSSPVLICAAIVFEYFSYGFGFVGLTLFIMQQVAPGPHQMA
HYAFGSSLANLGVMLPGMISGWLCDSLGGYHYFFMWALLATVPAFLLAARIPFTHPDTEE
VTAEIDKELINE

>tr|I4AES7|I4AES7_DESDJ Arabinose efflux permease family protein OS=Desulfitobacterium
dehalogenans (strain ATCC 51507 / DSM 9161 / JW/IU-DC1) OX=756499 GN=Desde_4201
PE=4 SV=1

MVDNKPMTSTRYMDEATMNKSHYKFLILLAFGYTFEQIDVFSFSFVAPALTKYWGVSME
WIGLVNSCTFVGMLLG CWLGGWFADRIGRRKTFLGSILLFSLCSLVNNGGAPNQEIFLVART
LTGIGMMGMVVVAMVYIAELLPAASRGKWQAIALATALLSIPLIGQLASHIIPNNPEGWR
WILYIGGLGFIVLAFGNWLKESPRWLISKGRFKEAEAVIQFYRPDVKVDLSAEASGKVKE
EKAQETTKTLEVLRLLSKEYRKKTLVLINLVVWNTVGYFMFFAWMPTLLNEYGFSLEDS
LWMVALVSFGSPIGNYLAAFFTDKGGRKVPVIVYGAIIGVLT VIFGTIKAPMLIVGIGFIIRIL
MDGVFVLMWSYLAEAYPTQFRSSGTGIIFSTGRILNVGAMAMVPLIYKQFGYSVLFAIIGA
MYIMIAVVTGIWGERTAGRSLEEIAETDSNKT VSA

>tr|I4CDL2|I4CDL2_DESTA Arabinose efflux permease family protein OS=Desulfomonile tiedjei
(strain ATCC 49306 / DSM 6799 / DCB-1) OX=706587 GN=Desti_5043 PE=4 SV=1

MANLLCNTQFLLIAATNLCLFLVSTWSFLPIVIVELGGNSIDVGLVMGSIGVTSLAALPFI
APLIDSWGRKTFIVGGILVIGLTNALFMLFDSYSPLMIFIRLLQGA AFAACFNGCATAVVDI
VPPDRRAQGIGLFGISGLAVSVGPYLGELFLIHWGRTAYFSLLIAFGLTGFFTALLMRSTE
KRTSQKKIQGFFLTALNDGHIGPMLMAAVFGSGFAAMNTFFPLLAKSLGIQAGLFFV FYGI
SLLSVRIFAGQLVDKVNDRDLILACLVGFGVLLVSTS QLA VRYETILLGSFFGILQGLSYPS
MMARMVD RAGEHNRAVVVSLFTGSFGVGLNVSVLAWGVIADSNGLQFMFLMGGLAVF
AYAFIALCAYMVSPA AESALPERAILETERD

>tr|I4EUA4|I4EUA4_9ACTN Putative Nickel/cobalt efflux system OS=Modestobacter marinus
OX=477641 GN=MODMU_1521 PE=4 SV=1

MTGVGVLA VGLLLCFAGLASIHLAVLASGFALGWLLAESLGGSLGVISIVALCAAVVAW
VLATLVFRAALLVVGGVAGGVIGAKLFGLLLEGDDGNVLLAVLFTLAVAVLAGLAAQHL
HDTALVWICAFGGAGLALSGAARAWPDGLEFLRTPDTTAETVIAAAAWLALGAVGWSV
QRRWASRRDQSRSA

>tr|J0UTS9|J0UTS9_RHIL1 Arabinose efflux permease family protein OS=Rhizobium
leguminosarum bv. viciae (strain WSM1455) OX=755176 GN=Rleg5DRAFT_0772 PE=4 SV=1
MRAIDVSEAI DNNPVGRFQWTVVGLCALLLIVDGYDVFIAGTVLPTLMAEWQLSKPEAG
ALQAWALFGMMFGALIFGPLADKIGRKKGIAISFMLFTIATLSTGFASTPTEFKIFRFIAGLG
CGGLMPNAVALMNEYAPRRLRGTMVALMFSGYSVGGMVAAALGIGLIPHFGWQPMFYI
AAVPLLMLPVILWKLPESLGFLIRQDRQEAKRIYAKIAPSVHLSANDKLTFTETTGAASI
AELFRHQRALRTAMLWVAFFCCLLLVYLLSSWLPKVLQEAGYAERASLLSLFSLNFGGM
AGAIAGGWLGDRFGLPKVVVGFFAAA AVSIALIGFNLPA GMLFMMVFIAGATTIGTQILL
YASVAQLYNLSVRSTGLGWASGVGRIGAIVGPTLGGLLLAKEFPLQQNFLIFAIPAVISAA
AMLVFAVSNARRVSAVSLAAA

>tr|J1I5I4|J1I5I4_9BACT Putative threonine efflux protein OS=Saprospira grandis DSM 2844
OX=694433 GN=SapgrDRAFT_2374 PE=4 SV=1
MLTQAILEGLGLGLLLSIMTGPIFFTILQVSIIEKGSRS GIALVAGQWISDFIYIGISSYLAKFLI
SWTKESELGQDLEFYLSIGGG AFLILLGLLLFSPLPKAKTKEKPLSNKQAGQYFLQGFLIN
SLTPFPLFFWFTSIGTAYSRGYSQTDLVFFGVAIMLMVILTD FLKVFLASRLRQLLNELWLK
RIRWVASFGLIISGLLFWLRLWLWS

>tr|J2HTK7|J2HTK7_9BACL Arabinose efflux permease family protein OS=Brevibacillus sp.
CF112 OX=1144311 GN=PMI08_01031 PE=4 SV=1
MKMRLQPLQALYFTQFLSAFADNMILFVIANLLRENGFSPAMLALVSISFFLPYVFLAPLV
GPFADKHAKSFVLVIGNLIKALGVVLLFVIDHSSILLMLCYFTVGVGAVVYSPAKYGILP
ELTRNEQELFQANARIEAYTIVAILTGIGGGGAIASMTAPLFSSSICLALYLLSLGMTFFIPRI
RGNASIRYGTEARRFFIDFQHLMNRAETS FALIGTGAFWMSSAVLRVAVLAWIPAALGINP
QSFSVSLILATTSIGIIIGAFLAPRLIPLSRFTRSVGYGFGMFLIIVLFPWIHVTVIAICLLLLVG
FMGGVFIIPMNTILQDEGKKMVGSGKTIAIQNFIE NFLMAAGSGIYYLVVFLGASISVAIVA
QGLLLLAFLLYLMKHRSRIAG

>tr|J2TZ31|J2TZ31_9BURK Arabinose efflux permease family protein OS=Polaromonas sp.
CF318 OX=1144318 GN=PMI15_02290 PE=4 SV=1
MNTMPPILYFFALCNLVIGSGAFVLGGILQPMASLGISVAAAGQAMTAYAVATAVLAPL
LIILTARWPRKRAVQLALALFTAGCLVCALAPNPLLLLGRVLMGAGAMFTAAASALAVS
MVVPALRGRALSITFLGMSISYAVGLPIGAWLGFEFGWRVPVWLSAAASGAALAAASWLI
PANMASAGTSFAGFQAAARQGAVLRVWGR TLLYFIAIFSVFAYVGPVLHALNPMNSAQL
SATLAVFGLAGVGGTLMGGWATDRFGALRTMRVQLAVLVAMMCLLPLTRGSVPATMA
VLVLWGIAGFGLMAPQQSRLASLSPAQAPLLLSLNGSMLYVG TALGAVISGALLDHVGFA
QLGWVGVPPFGLLAMLT LVFDRMPARVPASAAA

>tr|J2ZNN3|J2ZNN3_9CAUL Arabinose efflux permease family protein OS=Caulobacter sp.
AP07 OX=1144304 GN=PMI01_05344 PE=4 SV=1
MSSASRLGLFYVVSYLGTGVSLPFIATYFHARGLSGAQIGLILALPMLIRPFTGPALAVWA
DGFALRRTPMAWLALGAGAGYIAMLAPGFSTLLLCWLVGMTCLTTLTPLVDVIALRRS
RIEGFNYGLPRGAGSAAFIVGNLAMGALLTVAAPSIPIWITVAVLGCALIAATVPPDRVH
ETEVA PDKAARWKGLGALLRDRTFLLAVVTVGLIQGTHAFYYGFSTLLWRREGISEPMIG
VLWGVGVAVEVGFMWFAEPWRRKVGPERLLVLGGAAAAIRWTALAFAPPLWLLFPLQA
LHALTFAASFMASLR LIERLAPPQSASAAQAIN SALSAGFMLGVATLASGPLFDAFGVKGY
LVMAAMGGGLGLIGALRLTRLAPRSGFKGQIS

>tr|J3BM71|J3BM71_9RHIZ Arabinose efflux permease family protein OS=Rhizobium sp. CF122
OX=1144312 GN=PMI09_03320 PE=4 SV=1

MTHHRQKFRTLAAEAAMILGGFIFGTSEFAAMGLLPEMAKANGVAIDVAGASVTSYALG
VVFAGPLIAIVSARTPRHLSILLLAIGAVGNILTSLTGNFPMILIVARFVSGPLHGAYFGIAAL
IAAAMAGHGRRAQAVARVMMGLSVANLLGSPIATFIGEGTNWRIPYFLIGAVALVAALG
CHLTVPKMPAAEGSGAAKEMGALARPQVWLTFAGSLGLSGLFAVYTYLVPTLISVTGIG
EQKAPLFLVIIICGMVVGNNFFGGWLADKGVMMRAIGLLLALNVIAFALFLVSVHSAVLIAG
AAFLAGFSALALVAPLQARLMDVAGHAQSLGAMLNGCAINVANAVGASLGGALITTKFG
PASTGVVGVGLGIAALVVFSVSLKIERHHHKRLSLG

>tr|J3EEW6|J3EEW6_9PSED Arabinose efflux permease family protein OS=Pseudomonas sp.
GM21 OX=1144325 GN=PMI22_05569 PE=4 SV=1

MRHSDSRVILNFNYPDDHNMNNQIISPSMDVNLVADTDAGHTAINKKAIAAAVAGNAL
EFYDFVIYAYFAIYIGKAFFPVAGEYGSMAAVATFGVGGFFARPLGGILIGAYADRAGRKP
AMILTVAMITIGTIGLAMTPSYQSIGIAAPIIVVICRLIQGLALGGEVGPATSLLEAAPPHR
GFYSSWQIASQGIAVAVGGVGLGVALSYWLSAEQLETWGWRIFFLSLVLIPIVIYMRRALP
ETHETAQERTSSEIVGVVLRHKKVLLLGILLFASIGVASQIGNYMVSYAVQVLKLSAPVA
QGSVLVGGVLTFAFALIGLLSDRLGRRITNFIPRVILTIAIVPLFMWLVSAPTLTTLFTVNT
VIAALTAMFATAGLVQIPELLPIAVRSTGLSLVYAFGTAIFGGTTQFVVTWLIAVTNSPMAP
AWYLAGVSVVSLAMLFLPESKNVDIRK

>tr|K0EDU3|K0EDU3_ALTMB Putative efflux pump protein OS=Alteromonas macleodii (strain
Balearic Sea AD45) OX=1004787 GN=AMBAS45_05530 PE=4 SV=1

MSQRTPDQEFARYIKLALVAFACFIYFIADIRMPMTPQARVYHQVTQISPQINGPINEVLV
KNNQTVEEGQVLFVIDETPYLIALEKAQIDLANVELENAQIDAKAEAIRAKIEAASAVYDE
RNSEFQRLNSLVQTKAVSQQNVDKAYAQLKSAAEISALEADLNQQVVARGKQGDKNL
KYLEAVNAVKRAELNLAYTKIKAPHDGIMANMQVTQGTAKQSTPLASVVDNTLDVVA
DFREKSLANVKEGIRANVVDALPGKVFEAKVEEFEAGVSDGQLAANGTLASVEKSNRW
VRDAQRRVHIKLEEQEISLSHLTSGARATVQIVPDNPIESVAANIQIHFISSLHFIY

>tr|K6PMY5|K6PMY5_9FIRM Arabinose efflux permease family protein OS=Thermaerobacter
subterraneus DSM 13965 OX=867903 GN=ThesuDRAFT_02000 PE=4 SV=1

MLKGALGYLVLLSLAHLVTDLNQGGMPALLPQVKESYGLTYAQLGVVMLVLNITSSLIQ
PVFGYWSDKRPQGWLVVAGPLLAALGLGLVGYARSYEGVLLAAILCGIGIALFHPEGARA
ARGVSGGQRATAMSIFS VGGNLGFALGPVAAAMVVGLWGPEGLGWLVLPAVVLAAM
VAALPGMKRLEQEAALHEAARRAAAAAGPAGNRHGAPAGDRQGHPPQDGPVAGET
NWLAEALLIGVVGTRSWLQFGVLTLMPLYLEKAGPDGVSTGVLLFVFLVAGAVGTLVG
GPLADRIGTRRVLLGSMVLIPLHWGLVHGPAWATLPLAATGFALVATFSITLVMSQDF
MPRYVAVASGLNTGFSIGLGGIGAAALGALADRWGLETTL SAMVLLPVIGLLLTLVPVP
ERDRRQQLAAGRPRPAET

>tr|K7SFD5|K7SFD5_GLUOY Transmembrane efflux protein OS=Gluconobacter oxydans H24
OX=1224746 GN=B932_0297 PE=4 SV=1

MVGGFSPIDFLFMGFIEPVDVERVRPPHGVPEAMFALMLATFTIGTGEFAMMGLLPEFSH
SLGISISRASSVISAYALGVVVGAPLIAVAGAKLPRRTLLLAMLVLFLVGNIGTILMPNLLDI
EVMRFITGLPHGAFFGVSAALVGASMVERARRGRAVGRVLSGIMFSTVVGSPYSTYAANHL
GWRAAYGAISVLGLLCFLALWYFAPRDKPHPDANALAEAGFKRPQVLLTLLTSAIGFGG
LFEVYTFLTALSDVTHLPDWAVALYQIVWGLGMVAGNSFGGAMADRNINRTILFSLAA
SCVFMLGFWLLPSPIAMLLITFLIPATLIGISPAIQTHLMEVAGDAQTLAASLNNSAFNIAN
AAGTWLGAFLVSSGLGLASIGWGSALLSAGGFLAYLITMAQARLSASR

>tr|K9P6Y1|K9P6Y1_CYAGP Arabinose efflux permease family protein OS=Cyanobium gracile
(strain ATCC 27147 / PCC 6307) OX=292564 GN=Cyagr_2041 PE=4 SV=1

MDQVNAAAQRPGEAPPANPDRWWTLAAVECGNFVYMDGFIIVTLALPAMARQFGVGL
PVLKWWIVAYLLTVTVTLTPAGRLADIWGRRRIVVIGMGVLVVTSLCALAPTVEILIGFR
VLQGVGGGLVLANVMAEITAVFPKQERRKAMAVNASILALAQVTGLVLGGLLIGQFGWR
SLFLVILT VSLAGLILSLWILKARPRSQDRTAMDWTGAVLAVVATSAPFLVIEQLSQDGLN

PASVAILMGGAAALALFVGVEQRLAKPLLTLSLFRSRAFSFGSVAAAFYFVA AVACYFLL
PLYAQLVLGRTPVMSGVLIVPLSLVLTATSLTVSSLGDRVGARTLSTAGMLCVSAGLVGL
SWLGADA AVASIIWPLVLLGMGGGLFHPPNNSATLNTVPAQHLSVANGFLSMARNFGQA
IGTALAASLLAHGLGAAGADATLAGEVGARLGGSQLEAFLGAQQLAFRLAAALGLVGAL
ISVSRGAEAPAAQ

>tr|K9SX29|K9SX29_9SYNE Arabinose efflux permease family protein OS=Synechococcus sp.

PCC 7502 OX=1173263 GN=Syn7502_03334 PE=4 SV=1

MLLLNRYQWTVLFAAWLGGWGFDFDGLLFNYVAPNCVPTLLGLTIGSQPAKTATLFWTGI
LTSVLLVGWAGGGIIFGYIADRIGRSKTLTLLTMVLYALGTACCAFAPNIWILMTCRVIASL
GIGGEWAAGASMVAEVPPEKSRVAAGALLYTSAPAGLLLATFVNYQIAGVILAGSPEISW
RFVFLTGLIPAVIAFVMRLFVKESERWKNTVANTKPPKLVELFNQNLPLTISGFLMAVTA
LLTWWSCNAFIPVVATGLARTA AVDQGLSQTATFALVEHWKVIATNSFNLGGFIGTLLTIP
AAKYLGKRKRMFSTYFILSSAAILMTFGLPLPPEVRLYMYFAIGLTVFGIFGSFTYYLPELFPT
RLRATGSGFCYNTGRLIAAIGPFLVGTIASRGENALSSSLQVLCIGFVPLIGLAFMPWVIET
KDRVLADEFEPIS

>tr|K9UQ14|K9UQ14_CHAP6 Arabinose efflux permease family protein OS=Chamaesiphon

minutus (strain ATCC 27169 / PCC 6605) OX=1173020 GN=Cha6605_6061 PE=4 SV=1

MIKKLSLLLVLCLFVVTIGLGVSLPVLPPFFRHLHSAAVPRETIVHTTFLTSIYAFVQLIASPF
WGQWSDRVGRRPLILLGIAGSAVAQVLFGLASSVAMLYVVRALGGFLSAAMLPAATAY
VADITTD RDRAGMALVGTASSLGAIVGPAFGGLTTREDIHFTLG VVDLKIENYAPPFFLA
AALMFLTLLVAFRWLPESLSSRSTSTVGVGKASRSRSVSERREASRNENRQPPLNWQRLG
KPLLLLLGLTTISQFGLTLFEVVFALQAQDKLGYSPIQTGYVFMMCGGVMTVFQIVAVSFL
TRYVSSIAQVGLGFTLMGSGIFLLLVARSLPIVLGVVAIMAFGMALITPNLIALISKRSSQHT
GTVLGIQNTANSLGQVGGAMLGGLVFAWQFNAPYGFTGVLLVGTGLLLGWRRQKDRQLQR
L

>tr|L0MMP8|L0MMP8_9GAMM Arabinose efflux permease family protein OS=Serratia sp.

FGI94 OX=671990 GN=D781_3868 PE=4 SV=1

MPSRLKISTRLLIVLTGAFLGQFDLFVNVNAAPSVQRSALSDGGLELVVAGYAFMFAA
LLITGGRLGDLYGYQRVYVFGMLGFSLTLLCALSPNGVTLLIARLLQGAAGLMIPQVLA
LLTTVLP AEERTPAMGWYGAATGLGSVLGQFAGGALVSWDFVALGWRWIFLVTVP LGM
VMAGIAWRYLPPCVGSRRRKFDVPGTLGLASAFGLMIGAFLFYGHTRALMAAALLLCAG
MLILVVTLCHEQRLIRQGGDPVVDLRLCRVASLWRGLLAVCLFMLYFSSIFLLTNVLQRG
LMLSPLL AGLVFVPSGLTFISSSLFFRRWAAAHQRLAILTGCGVSAVGLLLAAWGTLFVAA
PVWFLAAAVVITGCGNGLILPVLIGFALRQVPSEQAGMG SALLSSAQQFASALGISAFGTLF
YLLSASQGLVHAMGWCVLIIQLACMALVALITGSGRAAAHHQAA

>tr|L7UBA5|L7UBA5_MYXSD Cation efflux system protein CusC OS=Myxococcus stipitatus

(strain DSM 14675 / JCM 12634 / Mx s8) OX=1278073 GN=MYSTI_04892 PE=4 SV=1

MSPPASRLDAPRSLVVVLALLAPMAALAAQAPLSAPEAQATPVSSLATDETLSKLLTEALEA
RPELRQVEAQEKAAQERVPAQALPDPVLQVGIQNDGFGELMIGEMEGSYFSIMASQALP
FPGKRD LRTQVARLGAKAVSAQVLRARLTIEAELRRAYLDLLMTRERRGLLDRLEAIWK
QSADLARIRYETGDGAQSDLLRAQLELNRIQRVALNAEERTRVQTLNRLSGRPLDEPLP
TTTRVRDLGIPELGEGEAAEKDAMERSPELAEGRANIAQSQQQMALARRERWP DFTVSA
GVMPRG GDFPTMWQANVGVNLPFSGSKQNRAVAESVAMADAATRATETVEQVLRRLRV
RERLTALSALRETATLYRSGLLMQSAATAESTLTQYRVGRASFASVLEANS GIVRDEEDFL
STLVEAQRLAIAQAEVSLEPVAALGGGSAGAGGMPGAGSAPSAPARGAALSGGAAGAAP
SSASSMSGM

>tr|L8MH74|L8MH74_9PSED Auxin Efflux Carrier OS=Pseudomonas furukawaii OX=1149133

GN=ppKF707_1405 PE=4 SV=1

MTNVFFNVILPILIVAAAGAGLKRWRNIPAAPFSQMMLYLLSPALVLD SLLNASLPLEATG
RIVGAILLMSISLVAVSALLSRSLGHNRP MQSGFMLATAFPNAGNMGLPVALLAFGQ EGL

AVAVIIFASQAILGWSLGVFIAARSHNAGLGPLKQTLKLPVVWAIGLAFLLRVTDTTLPLA
 LAQPLEMLGQASIPIMLLILGFQLEKGVALDRGASLLAALGLRLIGSAVLAYLVSELLGLE
 GVAQHTFIVMAAMPTAVFTIILATEFDAEPRFVSSQVIASSLLGFLTTLTVLIMLLQSFGGSI
 >tr|M1MYD9|M1MYD9_9CLOT Putative threonine efflux protein OS=Clostridium
 saccharoperbutylacetonicum N1-4(HMT) OX=931276 GN=Cspa_c58280 PE=4 SV=1
 MISVFSVAQAIAVGFSYGFIAPIGPSGLESVSRISNGFREGFKVSLGAISADIVYIIINLGIF
 TILSKNPKFESLFWIVSGIILVLSNKVSFKRKKTDHNLEKPILKNTYNAFLSGFLITFLNPTTP
 SIWIVSSSTIFTVWRHHGRIFFTLSILSMIIGSISWFCLLNILVSKGVKRFKSNIANHTSKFVN
 YLLFALGIVFIIFGTYKFIF
 >tr|M3CD80|M3CD80_STRMB Arabinose efflux permease family protein OS=Streptomyces
 mobaraensis NBRC 13819 = DSM 40847 OX=1223523 GN=H340_03334 PE=4 SV=1
 MKTAYLHRFVVARTVSMLGDRAAESALPIILLVTDPLVAGLVTASNILPALLFSLPVGH
 LADTRERRGLLITADVWRAVLGLGLALVLLAPEPSVALLVSITFLMGCGDVLFSVASHTY
 LPALVPSTRIMRANTALEAGDAAATLTGPALAGVLVSRFHPVALVNVAGSFVVSALLA
 RLPTARAPHADDHRVSSNCRTARRHGDVLAGFRLLISDPLQRIQLACIYMHLLAAALFVL
 VIVAVSVQTLHIGPFRTGLVLSAAGVGGLIVTLLVTRFVEHLPWGLLLGTALCGLAATFL
 WLAMAQGFVSLFFAALCMDACSAFAFVTAGSVRQVFTPAKALGRLTAAAGLVSAAVRA
 AGVLSSGAVVAWAGGRTAAVVLGVIGLVCAVPLLMARTARRPIAADATPAS
 >tr|M5EHB2|M5EHB2_9RHIZ Amino acid efflux protein OS=Mesorhizobium metallidurans
 STM 2683 OX=1297569 GN=MESS2_1080020 PE=4 SV=1
 MSEVLTIFSILGVFLLGAMSPGPSFVVVSRIAISGERMDGLAAAIGMGIGGLIFASIAVAGLT
 ALLVQVAWLDIGLRIAGGLYLLWIGIRIWRGATEPVEITSDASARPGSFRKALMRALLVQL
 ANPKTAIFYASMFAAMLPASPPLWMLLVLPPLLCNEFVWYAIVAFASFSSSRPRSIYLRAK
 HWIDRAAGAVVGALGVKLVIEGMGAARRAGG
 >tr|M6D6U9|M6D6U9_9LEPT Transporter, auxin efflux carrier domain protein OS=Leptospira sp.
 B5-022 OX=1242992 GN=LEP1GSC192_0879 PE=4 SV=1
 MSNFIVIGLCFLFGILIRSKGKFPSSDHSKVINFSIISVSLPCMEFGPLRHASLDGNFLTFASMP
 WVLFSGFGLFFSLVGKLLHWKESTVVCCLCSAGLGNTSFLGIPLIESYYSKEGLPTVLIIDQ
 LGTFLTALPGTYLGTARHALQSSETKSSIWKTLFTFPFIALLVSLVSRPISVPPELESAIA
 RIGDTLIPLALFSVGFQLPGTIRVNSEEPNAENPKRESDNSFRMRIPLLFGLIFKLIIGPILVWL
 CFGTFFHYSEKNLDSNFLRNFKILIMESAMAPMITGSLLAAEWGLAPRLAVSLVGIGIPLSF
 LTTGLGLYYLLENQAWTGTIFFGQ
 >tr|Q0AAZ7|Q0AAZ7_ALKEH Auxin Efflux Carrier OS=Alkalilimnicola ehrlichii (strain ATCC
 BAA-1101 / DSM 17681 / MLHE-1) OX=187272 GN=Mlg_0636 PE=4 SV=1
 MEVVLAVALPFFALIFTGMAAGRTRLLEGTSTRPLNTFVFYFALPALLLSGTAEMAAADIL
 RPALFLSWLLPALLLFFTTWLGLRWLFGRSAGEGAIQALVATFGNVGFVGLPLVVTAMGT
 HVLPAAMVVIIVDSAIMIAVATAIIEWERDEGSGFRRALRTAGLGVARNPLVIASAVGVTL
 ALLSLSLPAPLLRYLELLGAAAGPTALFALGITLARQPVRSAPEVAILVAAKLLIHAPVV
 WLATWLLGLDGPLQTALVILATLPVAANVHVLAQRYGLYAGPTSTAILISTVLSMVTVSL
 ALSLLL
 >tr|Q0RJR1|Q0RJR1_FRAAA Putative transmembrane efflux protein OS=Frankia alni (strain
 ACN14a) OX=326424 GN=FRAAL3608 PE=4 SV=1
 MLALQGVGAFAARSASRRLTSRLGTRTVVLAGLALAAAGTLPGVTDGPADAVLLAAGL
 LVRGAGIGIVTVLTLAAAYHGLSRHEIGHASGASRILQLGGALGVAGVTTLTAGQLGSPG
 APTHVAFAHFTWLLIASILVGLLPALALPGRAAEDG
 >tr|Q39DB1|Q39DB1_BURL3 AzlC-like efflux pump OS=Burkholderia lata (strain ATCC 17760
 / DSM 23089 / LMG 22485 / NCIMB 9086 / R18194 / 383) OX=482957 GN=Bcep18194_A5961
 PE=4 SV=1
 MLARLSATDRFALIQQGARDYSPTLMAIFSWGLVTGIAMSKSVMTLGQASAMSLLVYAGSS
 QLAVLPLLAALKLPWTILLTAAMVNTRFVIFSAGLAPHFSYLPWRRLAIGYFNGDVIYLLF

QKQGFAYGHVPGKEAYFWGMALASWLSWQVSSLAGILLASFFPASWGLELAGTLALIPIMVSAVANRSTLAAVAVAGVVSLIAFDLPYRLALPLAVLAALAAGCTADFFVERADWRRI
RTETVHEKEIE

>tr|Q83MR3|Q83MR3_TROWT Putative efflux protein OS=Tropheryma whipplei (strain Twist)
OX=203267 GN=TW7_684 PE=4 SV=1

MYHGDVAGYVELFRWKSVTKVVVVQLFARFPIVIFPIALLLFVQKVGHHSIFSAGIVLAVFS
LAQAVFSPVIARFTTIWPHGNVLITCACIFSGIAISVSVLKVPFWLMTIMFALCGVVMPTQ
SIMRTLRYHLVPLRLRSALFSVDTLQELIWWVGPIFVTSVAVSLSPEVSMIFLGVVLLFSSI
WLAFCKEIKNLKIPARNVFGKVLKKPVVSAITVVSILFMGSCATAIELAVVATFRGGEGGH
TSVAHLTGVVIAIWSLGSMLGGLAFGHKPIGRWSIPLRMLPFFVGVVVASLSNNVFWIAIW
LFVCGLGLAPVVSASYSYVASVTNSAESPEAFGWIASGQLLGGSAFSALAGGIIDSNAA
WGFILSGAGAVAAALLAVAVNKLPPALPDRAPTAPIDLIL

>tr|Q8EA69|Q8EA69_SHEON 10 TMS drug/metabolite efflux pump (DME) family
OS=Shewanella oneidensis (strain MR-1) OX=211586 GN=SO_4040 PE=4 SV=2

MNQSHSGPLANNHAQLGLLFISVAVLFWGMLPIALKLSGSFIDPVTLTWFRFLVALIVSILV
QWSAGSLKQFAALDAKVWLRLLAGLFLMLNYVSFVYSLDYLA PGAAQLNFQTSPFFLAF
GGVLFKERLNAIQLSCFASLALGMLMFFHPFLDFSATDNHEIWLGVMIQVFSALSWTTY
ALLQKSLLNRLSPANVLLVIYALGIFAMAPFSDFSQFAQMNSFDWQVALFCAANTLIAYG
CFGQSMKYWPTAQVSAMLALTPVFSFSATALVVSIGWWPEVFRADELDALSFLGIGVIIVS
VMVVQLLPLYRQRRARRLQPI

>tr|R0ELW7|R0ELW7_CAUVI Arabinose efflux permease family protein OS=Caulobacter
vibrioides OR37 OX=1292034 GN=OR37_01103 PE=4 SV=1

MSAEDTQARASRADDGWIGQRPSAARIAAFLAVGSIALIMAGVQPVVLGGLVTAGRLDV
SQLGWSVTIEFLAIGLGVGLADALLPPRRLKLIGLTAALVLAAINFAAFEVSGLGVVTRG
LAGLAEGAIVWLTTLMIVRSPTPGRWSGVFLVSQAVLQVACAAGIPILVSPALGANAGFA
TLGASAALAGIIALVLPDRLAPLAGNRSDEPVLAEPKAAAYVSLAAVFLIFSFFIGFLAYVE
RLAGQAGLTPVQGGLAVALALGASIAGSGLAAVLADKIA YHRALLVCAPIFLAVLVGLW
GLPGSGVFFVLAGLHGLAWGFLQALQAPFVIESDPSRRVLLAPSVQAVGAAAGPMLCSF
FVTVQDARGVLVASGACLALSFLVLAIALWVSRRRRQARSALAVV

>tr|R5DBC8|R5DBC8_9FIRM pH adaptation potassium efflux system protein B 1
sodium/hydrogen antiporter subunit OS=Firmicutes bacterium CAG:83 OX=1262992
GN=BN795_01396 PE=4 SV=1

MSTVFRLLLLAGLLVCAVATALVKKPLRAVIIYMAYSIIIMSVIWILLEAPDLALTEAAVGA
GITGILFFLTLLRIDRIDRDADVEETQGEEEPHEENEATH

>tr|R5HEV3|R5HEV3_9FIRM Macrolide-efflux protein OS=Firmicutes bacterium CAG:114
OX=1263001 GN=BN469_01521 PE=4 SV=1

MGVALLPLVSPIVGYGLITVLSFLVMGVSTLFTVTILAAMQGQTPPDLLGKVMATVLATA
NCAQPLGQAVYGLLFEGLADHAWAVMLGAGLLAACLALRARPVFWALEKETDRSAGD
ATVR

>tr|R5JFN5|R5JFN5_9FIRM ABC-type Na⁺ efflux pump permease component-like protein
OS=Coprococcus sp. CAG:782 OX=1262863 GN=BN781_01587 PE=4 SV=1

MKNKMHGFKTVFFHNLGIHMKS KKYLA VTIILAVFLLAGISIFIMIMSDKNSRKDQYTYNV
DKVYVVDETGLGVPDYSMYGAALGYEDAADTEFVTSDKSPEELVDTDGAQYVVVQKKS
GDSFVLCVIFGNTDNVTDEQVDFNTAAMEEYLVPCFKTHLFQVSGLTGEQIVQVMLPTAI
NVSKIGGESEKQSKHIVAVIMMMAFVMIYFAVLIYGGQICADVPMEKTSKLVEQIMMSV
TPYALVSGKILAMVFASVIQFIIWIGCIVGGVLLGDVLSKTVLGVDTSAVTTALDLLRDWF
DGMGFSGISIVLAVLLFIAGLVFYLMLAGLAGSALARPEDAANVQSIFIPLVA AFMLVLFA
SGLTASGNYNIPLAYNLVPFSAAMTAPASVLIGTLSVPMAIVSLIISVVSGMIILYVAARLY
KGMMFFNGKKAKLKDFISAIKG

>tr|R6GXX2|R6GXX2_9FIRM Auxin Efflux Carrier OS=Oscillibacter sp. CAG:241
OX=1262911 GN=BN557_00130 PE=4 SV=1
MLEILLYAGRAIMPLLLTMALGCWLRRSAHWSDDFYRQLNSFCFHVLLPVQLFLNVYAIE
DLSVLNWRLLGFIIVLCIVGAAGLGVAVAPLFARERAQRVVIAQATFRANQVIMGIPLASA
LGGQDALIFASLVTSCVPVFNMLAVLMLTAYSTDGKSISWREEVRQIFRNPLILGALAGL
VTVLVRQLLPQVDGQPVFSLRSSLSIYKACSDLSKVASPLVLLILGARLRFDVAVQGLWKK
ILAAVSMRLVVVPLIVLTLVLLLREPLGLTTVEMPTVVAIFCSPVAVTSAVMVQEIGGDEQ
LAQQVVAWSSVLSMGTIFCFAAALRAMGVM

>tr|R6PKZ7|R6PKZ7_9FIRM Putative cysteine/O-acetylserine efflux protein OS=Eubacterium sp.
CAG:274 OX=1262888 GN=BN582_00080 PE=4 SV=1
MELSVIGTFLGYVVVSSFTPGPGNLLALNNVTSYGLKKSRNII LGICCGYGIVQFLCTLALY
IVNRHISVLFMLKYIGGAYICFLALHIMLSKKSEDVSVKSPSFKSGCLLQLVNVKIYFYIIT
LITTYFIPNFPTITGLTLAGIGVVAVGCSAII TWALVGVGLKNFFNKYYRIINVVMGVFLLY
CAWDIIRSN

>tr|R6T8R8|R6T8R8_9STAP Cation efflux protein OS=Staphylococcus sp. CAG:324
OX=1262969 GN=BN609_00329 PE=4 SV=1
MSKQNYEFRALIIGVIINLISAIVGFIFFYLTTSMSILLDGLISAILCGSTIVSIFVSNYVNKNDS
KKYPFGRYAIENVFLLFRAIMMLGTIIFTILDGALTILDFINNQTIDNFNASNWQLIVYGLSM
CGLCLLITLVYSILNKKSQVKSEIIRIEIKASLYDGLVTLVAISSLLLFNSIEFLSGIKEIGDSIT
VIILSHIYLYSPLKELIGQIKILIDRRRFVETEKELINNLQHKFLIFKFNDLYFAFSGDHYQIYIS
LYPKQNLKSEEITKKFQDIKNHLLNIYQDSKIYLLLSKEMIHNM

>tr|R7ZLT2|R7ZLT2_9BACT Potassium efflux system KefA protein OS=Lunatimonas lonarensis
OX=1232681 GN=ADIS_4539 PE=4 SV=1
MKSTGLTLLSLCCFLFWSVPAQSQVFDSSVPFVVDSTDFNNLSTPYHTTLTFFYNLQEET
FDPEVSGRALNMSRLTNKDASNLA VKLKQVFDGRGVYVRIGEVPVDANFIDTLRNGQMR
YFFDEQRLPGVFLEKVGQAWLFSSFTVGQIEELHLETYPLGTDRLLNLLPKIGNEVYFGLH
LWQLVGMFLLLLLIFISHQVFTIVVDRGVYYILMKAGYGKMAKKYLLPVARVVSIIYLIVL
LLAVFLRVLQLPILVISWVTVLLNAVKPLLVTIIFYKLVNLLSSYLESMAAKTVSTLDDQLV
PLVRKTLKTFVIVVGTILFDGLQLDIVPFLTGLSIGGLAFALAAQDTIKNFFGSVMIFIDK
PFQVGDWITSGDVGDTVEEVGFRSTRVTRFRNSLVYIPNGKIADATIDNHGLRKYRRFSTH
ITITYDTPPELIEVFVEGLREMVRRHPRHTRKDDFFHIYLNLSAYS LDDIMFYVFFEVPSWGEE
LKAREDMLMATIRLANQLGVRFAFPTQTLHMETFPEKKGLNPTYSDDREAYQKKLAQFIS
KESGTTGRI

>tr|R9GNB9|R9GNB9_9SPHI Potassium efflux system KefA protein OS=Arcticibacter
svalbardensis MN12-7 OX=1150600 GN=ADIARSV_3416 PE=4 SV=1
MLYFKKQFSKYFFLFLCFILTCIASQSNAQGNLLNDTAENVKQEPSWPNDTLGRRTPRGT
VEGFIKAVSQEDYAKAALYLSIDSTLKRKQDRVLQAQGLQQLLDQKGNIFPYSMISDKEE
GQQGDNLGENFDHIGDATVDKDKFEILLENTKGSDGGPIWLFISIQTIRIPLQLDSVSSAPL
LSKLAPKVLEENKWRGVPLAHWMAMLLIIIVAYLLALGITKAAIIVIPLFWHKARIEPVSGI
ITAFALPIRLYLAVWLVFVIGSRQAGIYIIVRQRFSDITVVVLLVAVLLLIWQLVDFVSRYAER
RLARHGNQAGVSAVLFLRRAAKIALVIMCVIMILSTFGFDVTTGLAALGIGGIALALGAQK
TVENFVGSVTLIADQPVRVGDFCKVGDVVGTV EQIGMRSTRIRTLNRTIVTIPNGEFSSNMI
ENYAHRDRFWFHPTFGLRFETTPDQIRYLLVELRSVLYAHPKVDPSPARVRVFEIGSDSLK
LEVFAVYVHAVNFDQFLEIQEDLYLRMMDIITESGTGFAFPSQTLYLAKDHAPSPEKAEIHI
EKVKKWREAGDMPIAFNPDIYDDLKNTIPYPEGSSVYKNDNSFKDEKS

>tr|R9PLK5|R9PLK5_AGAAL Potassium efflux system KefA protein OS=Agarivorans albus
MKT 106 OX=1331007 GN=AALB_2329 PE=4 SV=1
MTLSIFSRGFLVSLFFCLAAQANVGGESHLKGLISSLDTQPSNLNTQQQQLIYEESLALLK
EGNSYREKAKYYRGIINNFSRLRKEQQEQNLNQYQAPVIENLAELNSNQLNEQLTIWQAKL
SNTNSQIDELKQRQYRIDLDVSENHQRSGPLREQLNTVRACLEQLEFGVLNEVEEAERVR

AQVNEASLTAQLAMLELAAQSANHRNELLQLEISLLQRTQLAEKRIVESVKNRLSLEHRA
 EAQRLSDQLAFAPELLNDPIVKNLVEQNQLLQTELSALFEQSEEIADLQEEVNDELEHIKL
 TFANFKEQVSWLKVTRSYGEYLREQISSLPKFKAVAPIEQQIIEVRISKHRHQNLITYTQRNQ
 SQRKAQREFIATLNEEQARIFNKHLKLNQQLSDKYLLELDARLFELARLKLDDYSKLNSQLN
 TINQEANQELFWTADVKAIDLSFFSDIRYSLIWLFSAQQYSQLSDAIAKLSWLWLGWLLLV
 AASVAYIYYLKKHWLKGYLQRIDSKTGNITRDKFSYTLANLLVSAVFATPVALFIGSVGFA
 LMYEWESSFARDLGDALFNVAIVLWLFHLLQQFCQKNGLLNTHFKWPLVNISQAITLIRR
 VVYVSLPLVFILNLCILQTSQPAYSGLARLAFIALLLWVAYGFHSIYRIELPVNYHLDIFKAP
 QLAKKLIWGA AISIPLMAALASAAGFFATAFTVYWQVVSFIIAAVFLG YLLIHRWMLLQ
 RRRIAFDRAKVRRAEMIAQRQSEEDDSSSSNEGVIDSIEEPVIDLDTISAQSLGLLRAALVLS
 LVLVLLLSWSEMTSAFSFLDNITLWESSSSRAGVATVDAITLRSLGSALLVFFFVAVLIRNL
 PGLLELMVLQHLNPGTGFAITTMINYMVILFSIFSGFGLLGIEWSKLQWLVAALT VGLG
 FGLQEIFANFISGLIILFEKPIRIGDVTITRELTGTISNIETRATTIVDWRKEIIVPNKAFITEQF
 INWSLTDPITRVVLMVQVKQGSNDQLVNKLLQEAVDANSLVLANPAPEIYFTEYTNGM
 KFEMRVHVSEMRYRLPMTHELYTLINDKFKANNIEIAYPQLDISLNP

>tr|S0EX62|S0EX62_CHTCT Arabinose efflux permease OS=Chthonomonas calidirosea (strain
 DSM 23976 / ICMP 18418 / T49) OX=1303518 GN=CCALI_00540 PE=4 SV=1
 MRRQSKSGEMRRSPLLILALTLFIDMLGFGILPLIPVYISHYGGGAWVGGMMLGCYSLMQ
 FLTAPIWGRLSDRIGRRPVILIGLCGSAGTFLTFLAPNLLVLFLARVAAGALTSASLPTAQ
 AYIADVTPPEKRASGMAVLGIAFGLGFAFGPVVGGYASRIAIGSLSPIATPALLAFLSFCN
 FLWALAMLPESLSLARREASANATTEKGPLALLRSIAAAFHEPNIRAQLLVFAFVTFATA
 VESSFSWLVLRFHHTLEQTAIRTWQTHHLGQPWASLPDIVRRHQFEKIEAITSRIFLIVGLS
 SLVVQGFIVRGLAHFIGEHYLVRFGAMLMTLTLIGIGLTPSLWGIYLLSICIAIAMGVMTPS
 LNALITHAADPSEIGALSGVQQGLGSLARIAPPINNYLIGLPNATGVPFFCSALLMAVAFL
 SLQLKPMTPSSKRDKEATETTTIEASSIH

>tr|S5R3S5|S5R3S5_9PROT Neutral amino-acid efflux system efflux protein,
 homoserine/homoserine lactone efflux protein OS=Candidatus Profftella armatura OX=669502
 GN=SSDC_00755 PE=4 SV=1
 MIFKTWISFLLFSIITSISPGPGNILTINHALRYGWRKTLSLIIGQEIALVLIILAISEGAELLSS
 SSILIFIKIFGIIWLMYTSFQMWCASINKKDYICETISKKKSFIRGFFTTITNIKAITCLISTLP
 ACLTPIYPIVPQIIIMSLTMTIIDSSVMLLFAITSSYLRFQKSKNIKIQRNISSIFFLFIAISICFL
 >tr|S7XEF2|S7XEF2_9MICO Potassium efflux system KefA protein OS=Leifsonia rubra CMS
 76R OX=1348338 GN=ADILRU_0143 PE=4 SV=1
 MFEWKS WLGLPVAVVIALLA VVIVVGVISLIVRG IARLRPGVYATLAPLRQRLRVLIALLA
 VWVAVAATIPIVEENILNIINYAFRGAVIASGGWLLVAVMNLLFGRAVARYPLDVPDNRV
 ARRVRTQVQVLRRVLTAVIAIVTIGAILMTLPGAQALGASVLASAGLVGVVAGIAAQSAL
 ANVFAGMQLTFSDAIRVDDVVIADGEWGRIEITLTYVVLNIWDQRRLLVLPSTYFTSTPFQ
 NWTRNATELLGVVVFDDLDRVNVNDQMRVQLKKVLAETELWDGRTANVQVVDSTGGFV
 RVRIVASAADSGAQWDLQTHVREEMVSWLQTKNPAALPRTRVLMVENEARSRGKAAAE
 PQDRGLFSGSAEADARRQEFTGAITVQANTPDNTPDNATDNATDNATDNAPEGAADHPP
 KKD

>tr|T0TZF8|T0TZF8_9STRE Potassium efflux system KefA protein/Small-conductance
 mechanosensitive channel OS=Streptococcus sp. HSISM1 OX=1316408 GN=HSISM1_2086
 PE=4 SV=1
 MRVLIDIPLDANTDLDKIYQVIAQVQNQSEQDKHPEVLTGPTILGPQIEKMVVIPSELR
 >tr|U1GP90|U1GP90_9ACTN ABC-type Na⁺ efflux pump permease component-like protein
 OS=Cutibacterium granulosum DSM 20700 OX=1160719 GN=H641_00110 PE=4 SV=1
 MSNNATSSARRDGVGSDGVAGTSSMWWTVARREMSVKIRDRSLLVSLIIVLVIVAVSVG
 VSLITSGTSDDKPTSVAVTDDAGAAIVAQAQKMAQQTGERQILETVRTTSLEQGREVVD
 EKAKLVLHHEDGTWHLESGDEPPSVTSGAGQLIAKAVEARATADLAQKAGVDPQQAVA

DGTVLPGTVDPGQADNWRDTVATFMGVGFAVVYMFTMMFFGNGIAASVVEEKQSRIVEI
LLACIPARQLLAGKIIIGNTILAAGLMLILLVLGCVGVSTPAADLLGTIAAPTAWFVFFIVG
FLSLACLWAAAGALASRTEDLQSTSMPLVMIVMIAVYVFGIQAAQNHGVSASVVPVA
SAIAMPTRVATGGAAWWEVVVSILISVLFSALTIWGGERYRRSVLKTGGKVKLRVAWRS
TDVVA

>tr|U2EMX6|U2EMX6_9PROT Formate efflux transporter OS=Campylobacter concisus ATCC
51562 OX=1242969 GN=ATCC51562_934 PE=4 SV=1

MLNPAETAQAVSSSMHKAHMLPTSIIFLAIMAGAAIAMGDIWAHSTVGMAENQSIGLS
NFIGGITFSCGLMMVVFYGGHLFTSSVLSGVSAYEGKCLKGNTIVYWAIVWIFNFVGGALI
AYMYYYSGLPLKYDGYILQHFVPAAIGKITAPFHELFIKFCNVFVCMISWTATSESNLSG
KFFAIMWMIGAFVACSMHCVANMFIITEAIIKKAHYIAANGGDIAAAAAALGHGITAIEKL
EVLNWNFGNFIGKNLVPVTLGNICGGLFFVGLVGFMANKFDMKKKA

>tr|U2IL81|U2IL81_9BACT Efflux transporter, HAE3 family OS=Prevotella sp. F0091
OX=1227276 GN=HMPREF9148_02286 PE=4 SV=1

MKKLAEFVIRYRWAVIVFFLAALTAFMGFQMKNASFNPDLLTYLPEHLPSRMNQKQIEKMF
GGTDMVMIVVQTDDVVNGKTLKRVEHFSQDMQNIKGIERSVMSVFELKNVRSENDAMTV
DAAVKMIPRTAEDVATIKKELAGNDLVYGSVISKDFTTTAIGLLEPGAKDKDVIDQVEAM
IAKYPGTEKVLLGGSPYMRMQNAGMMQKDMARLIPLGLLLMMVFLFISFRQFRGVWLPI
LIVVMAIFTALGATPLLGWKFAVTTIILVLLIATANSYGIHMFARYQRDNLPGNNTAKE
LSVKMVTSLGAPIHLSGLTTIAGLLCMLGHVLIPGGQMGVLGSIGIGLALIGSLFFIPALSSVL
PKTKPRLRADNNPKSKRGIGLDRLDFIADWVTKKPKTILALFVVISLIGAAGLLRFSINSN
PAELFPDGHPAKESAQIINKELGGFFPLCVVFEGDIKDPALLKKIDDLEKKVREIPEVGTQ
SIAKVTRQISRALYNKGEEGYDKIPDTYDAVSQYFELYLMSGSQKDLEKMFDFNFEEKALL
MIRFKELNTPVLRQCVAQIKEMVKDDPNVKLVGGNADVFTDMDKHVVSGQFLSLLISLV
VVFIIISLGFKSFKAGLLQIVPLMFAMLMFLGMLMGYFGIDLNFMTAFQASILIGVGVDTYIH
VWRYREERRAGYDDKEAVHRLFKATGRGIVFNAIAVIIIGFVLLFSGFLPVRFFGMMM
TIFVCLIAAVLLVPALCMVLKPKFLRQKIHCK

>tr|U2YUG8|U2YUG8_9CAUL Potassium efflux system kefA protein / small-conductance
mechanosensitive channel OS=Brevundimonas abyssalis TAR-001 OX=1391729
GN=MBEBAB_1381 PE=4 SV=1

MAVFARWSRMTSLGSLQALEKIENAPVRLAGTSITAGGLISAAIILTVALVLAWLATRGI
KRLRARSSRSRGALYLLEKLVGYGLIVAGGMLALSATGLNLSSLAVFAGALGIGVGLGLQ
GVVKEFVSGIFLIFDRMVSVDYVEIEGGARGAIMEIGPRATRIRTNINILVPNSQLIEHP
LTNWTLKGDTRRIHIPFSVAYGADRGEVRDVVLAARASPFTSPETDARKCQVWLVNFG
ESGLDFELLVWPTQDAVKRPAAMHAAITWAIAEALEQAGIEIPFPQTDLRIRSLFGREGDE
AMEVMTTGKAPRPKPAARKPKKKATTSSENDAAEDLLLPSAAEAPEPDNS

>tr|W0B7D0|W0B7D0_9GAMM Arabinose efflux permease OS=Legionella oakridgensis ATCC
33761 = DSM 21215 OX=1268635 GN=Loa_00891 PE=4 SV=1

MHQQKSLSSMLSFLVLFIDGMGLGLLPILNTILIDPQAGFLSPNLSMGLRDFLYGLTIGV
FMICWFFGAAILGDLSDSVGRKKSMLICLVGSFLGYFISAIAILTHSFTLLLIGRIIAGFTAGS
QPIAQAAIVDVSSEEQKARNIGLILLSVSLGFVFGPIFGGLSNERLVSWFSFETPMYFAAGL
SLFNAIFLHLTFRETQVKAHDKIQVRWHHAVNIFISAFKQASIKKYSVLLIMIFGWSNYFS
FISLYLLQTYQYSALENSFFLAVMGIGFSIGCGYLVNVCTRHSFSLDGTVISGLLVASLVM
MTLLGKQQWVAWVATLLIGMSLSVAYSVLLTIFSNQVNDDQQGWVMGVTGSIMALCFG
LTSIFTGIIAHVGAVLPMLLAALGLGGSATLLFLFKRGDFQRSRKEMLQP

>tr|W2UC14|W2UC14_9GAMM Threonine efflux protein OS=Gammaproteobacteria bacterium
MOLA455 OX=1411685 GN=rhtC PE=4 SV=1

MDTVFWLSVTMACLLGAMSPGPSLAVIGSLTLNQGRLSGMIGAVAHGLAITAFALLTALG
LVGLVSRYESAFLNLLQLAGCLYLVWMATKLLFAAPNKAPNRAFDQDPGQSADTSNSVVG

PKWAAARDGFLIALINPKIMLFFSALFSQFVSVDSAFWVKLVMAAIAGTVDALWYMLVA
VVISRPGNLLRYQQTG PWLNKLFALLLLFIVAGFFVDLTA
>tr|W4BAJ7|W4BAJ7_9BACL Arabinose efflux permease OS=Paenibacillus sp. FSL R7-269
OX=1226755 GN=C162_27052 PE=4 SV=1
MKAQSGNSASAPRSKRNTVYIMQLVTIFLGFVVFGEISENIKGPAIPRIQLSFNLDEGQLGTL
LSLNALGYLIACSF TAVLVRKWGIKAVTIISFASMVLSGVLIYLSHSYPLFASSYFLMYIGN
GMLEIGLAILGARIFVKNTGMMMNL SHFFYGLSSTVAPLLATGVMSLSVFGHLLDWRGM
YLVMLSCLLPILSALRSTYPGDDL PQEDRTSFR TLTRDPALWMMVMILSFGVVSELAVG
GWL VNFLEKAYAWDTVRASGLLSAFFLVFSLGRLLL GALTD RIGFVLSLIIFSCFSAVCTFA
ALAGGERLAFLFALSGAGIAIHYPTVMAFIARRYPNGSDTAITFVVTLMGLG SVIGNYIIGW
VIEAVKAFYGSTTELGLLRGLQAGYGFGLCAA VCSLSGIVLYVYLKRRRELI
>tr|W7W546|W7W546_9BURK Cation efflux system protein CzcI OS=Methylibium sp. T29
OX=1430884 GN=czcI_1 PE=4 SV=1
MRRWVFAFLLL VVPFQFVWGSAAPYCAHEASVLAKKHFGHHEHKKHQAGGEVTPAADN
QGDAVGAYHADCESCHLGCSAAVQANAPGIHALPQARAPGCREPRYTSYVPSVPQRPDR
VVSAPAARSGSGVVV
>tr|W7ZKE7|W7ZKE7_9BACI Periplasmic component of efflux system OS=Bacillus sp. JCM
19047 OX=1460641 GN=JCM19047_3608 PE=4 SV=1
MKS WKKGIIASLVASVGTFTVYGMTKGKDLAVSSYEETFDLISPMYEDLSTVVMVPGSL
ELVNRQVVQPSTEQGSYQVLVEVGDEVEEGTPILQYSTTEIDFEIQDLELQIEQGQTIRNL
TASEAEITKRKN GPDVKPTYLEDEETGDRTEIEPLVTVAELDAELADQKKAENY AISR
LQNQLETAKKQKGELTLTSTINGRVLSINDQGGNTDDLGNLPLMEIADTTQFTITGNVSE
RQSLDVELGHVASIYSDTIEDGFWSGEVIDVSYPTEGDDWYGDSSGSQYPVTIKITEGETE
NLRPGYQVMAEIVTSEEMGLTLD MELVQYDEVGSFVFVYEDGVAVRREIEIDYANDYSV
KII EGLTEEDLVIADYMQMVTEGMTITVSEFN EEEFYEEGFIEGEFE EGEFE EGEFE EGEFD E
MDQEDETGELEE QEGDDEL
>tr|W8VRK0|W8VRK0_9FLAO Potassium efflux system KefA protein / Small-conductance
mechanosensitive channel OS=Nonlabens marinus S1-08 OX=1454201 GN=NMS_2305 PE=4
SV=1
MQNNTTNKVDFQ NQLTETLSHYEEELIETLPRLGLGLIIILGFLIAGMISRFATRRARARTN
DPLMSRFLGRSIRFLLIVAVIVLGLRVAGFGDISAGIFATAGASAVILGF AFKDIGQNFIAGII
LSFNRPFNVDN TVEIGSNFGKVKSL EFRYTKLKTDFGKD VYIPNSDVITQPVTNYTEDGFF
RWDFLVGLDYEDDINLAKETIMRSINEDPKVVSDEEHSSYVMEDELATSTVNLKVMFWV
DTV DYGRVASETKGRVIGNVKRALMAEGFYLPADIQEIKLYGRETNIPLSLNDLKKSTND
>tr|X4ZQW1|X4ZQW1_9BACL Cysteine and O-acetylserine efflux permease OS=Paenibacillus
sabinae T27 OX=1268072 GN=PSAB_23200 PE=4 SV=1
MTRQKSGVLLLAFLVLVWGINWPLSKIALAYAPLLFSGIRT VIGGVLLILIALPKARLLRF
KTLWPVYLG SALLSIALY YGVQTIGLQYVPAGL FSAIVFLQP VLLGIFSWLWLGEEMHGQ
KIGGLVLGFLGVACLSAGGLTGSISLLGILLALATALC WALGTVYMKRNAVRVDMLWMT
AMQITLGG LILLVAGSAAEPWKAIRWSTDFVAVTLFISIFVIALGWL VYFKLIHEGEAGKV
ASYTFLVPLV SIGSSVLFLNEKITINLVIGLILVVISIILVNVRFR RSPASAVAEIRALEEGDYD
F
>tr|X5MF18|X5MF18_9RHIZ pH adaptation potassium efflux system protein D 3 OS=Candidatus
Phaeomarinobacter ectocarpi OX=1458461 GN=BN1012_Phect3075 PE=4 SV=1
MMEFIMYHLPALQVVVPMLAAPICLLMMRGS LAGLVALVTGVLCFVMSLLLLQQVIVSG
PISYQLGGWAPPFGIEYRVDAMNAFVLVIVAATSALVLPFARRSIRAEIEPSKQALFYTVFT
LCLTGLLGVTITGDAFN VFV FLEISSLSTYVLVAMGARRDRRALTAGYTYLVMGTIGATF
YVIGLGLLYQATGTLN MEDLAVRLQPLGDLTSVRAGFAFIMVGLALKLAMFPIHAWLPN
AYTYAPS VVSIFLAATSTKVAVYVLLRFMFTVFGYDFPVVELSLSTVFLPLAVIAMFVASA
VAVFQTDFKRLLAYSSVAQIGYMV LGFSMASVTGLTATMVH LFNHAAMKGV MFMVAG

AVVYRVGSTAVTSFAGLGRQMPWTMAAMVVGGLSLIGVPLTVGFISKWYLILGALETGD
WIIAFMIVASSLIAVIYVWRMVEMAYLTPAPEGSKPVREAPLSMLLPMWTLALVCLYFGI
NAELTASIGQAVAETLLNGGVDAASVIPMDEVVEGVAP

3. Non-efflux antibiotic resistance (non-EAR): 189 protein sequences

>sp|P62593|BLAT_ECOLX Beta-lactamase TEM OS=Escherichia coli OX=562 GN=bla PE=1 SV=1

MSIQHFRVALIPFFAAFCPLPVFAHPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEE
RFPMMSTFKVLLCGAVLSRVDAGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELC
SAAITMSDNTAANLLLTIGGPKELTAFLHNMGDHVTSLDRWEPELNEAIPNDERDITMP
AAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPLLSALPAGWFIADKSGAGERGS
RGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIAEIGASLIKH

>sp|P0A0B2|MECR_STAEP Methicillin resistance mecR1 protein OS=Staphylococcus epidermidis OX=1282 GN=mecR1 PE=3 SV=1

MLSSFLMLSIISSLLTICVIFLVRMLYIKYTQNIMSHKIWLLVLVSTLIPLIPFYKISNFTFSKD
MMNRNVSDTTSSVSHMLDGGQSSVTKDLAINVNQFETSNITYMILLIWVFGSLLCLFYMI
KAFRQIDVIKSSSLESSYLNERLKVCQSKMQFYKKHITISYSSNIDNPMVFGLVKSQIVLPT
VVVETMNDKEIEYIILHELSHVKSHDLIFNQLYVVFKMIFWNPALYISKTMMDNDCEKV
CDRNVLKILNRHEHIRYGESILKCSILKSQHINNVAQAQYLLGFNSNIKERVKYIALYDSMPK
PNRNKRIVAYIVCSISLLIQAPLLSAHVQQDKYETNVSYKKLNQLAPYFKGFDGSFVLYNE
REQAYSINPEPEKQRYSPNSTYKIYLALMAFDQNLNHNTEQQWDKHQYPFKEWNQD
QNLNSSMKYSVNWYYENLNKHLRQDEVKSYLDLIEYGNEEISGNENYWNESLKSIAIEQ
VNLLKNMKQHNMFHDNKAIEKVENSMTLKQKDTYKYVGKTGTGIVNHKEANGWFVGY
VETKDNTYYFATHLKGEDNANGEKAQQISERILKEMELI

>sp|A4W6F7|RSMA_ENT38 Ribosomal RNA small subunit methyltransferase A OS=Enterobacter sp. (strain 638) OX=399742 GN=rsmA PE=3 SV=1

MNTRVHQHGLARKRFGQNFLNDQFVIESIVSAINPQKGQAMVEIGPGLAALTEPVGERLD
EMTVIELDRDLAARLKTHPFLGPKLTIIYQQDAMTMNFAELSEKLGQPLRVFGNLPYNISTP
LMFHLFSYTDADMFHMLQKEVVNRLVAGPNSKAYGRLSVMAQYYCQIIPVLEVPPTAF
TPAPKVESAVVRLVPHAVMPHPVKELRVLSRITTEAFNQRRKTIRNSLGNTFTVDVLTELG
IDPAMRAENISVEQYCKLANYSISDNAPPKES

>sp|P25910|BLAB_BACFG Metallo-beta-lactamase type 2 OS=Bacteroides fragilis OX=817 GN=ccrA PE=1 SV=1

MKTVFILISMLFPVAVMAQKSVKISDDISITQLSDKVYTYVSLAEIEGWGMVPSNGMIVIN
NHQAALLDTPINDAQTEMLVNWVTDSLHAKVTTFIPNHWGDCIGGLGYLQRKGVQSY
ANQMTIDLAKEKGLPVPEHGFTDSLTVSLDGMPLQCYLGGGHATDNIVVWLPTENILFG
GCMLKDNQATSIGNISDADVTAWPKTLDKVKAKFPSARYVVPVGHGDYGGTELIEHTKQI
VNQYIESTSKP

>sp|P06107|LINA_STAHA Lincosamide resistance protein OS=Staphylococcus haemolyticus OX=1283 GN=linA PE=1 SV=1

MKNNNVTEKELFYILDLEFHEMKVTYWLDGGWGVVDVLTGKQQREHRDIDIDFDAQHTQK
VIQKLEDIGYKIEVHWMPSRMELKHEEYGYLDIHPINLNDGSGITQANPEGGNYVFQNDW
FSETNYKDRKIPCSKEAQLLFHSGYDLTETDHFIDIKNLKSIT

>sp|P0AE05|AADB1_KLEPN 2"-aminoglycoside nucleotidyltransferase OS=Klebsiella pneumoniae OX=573 GN=aadB PE=1 SV=1

MDTTQVTLIHKILAAADERNLPLWIGGGWAIDARLGRVTRKHDDIDLTFFPGERRGELEAIV
EMLGGRVMEELDYGFLAEIGDELDDCEPAWDAEAYEIAEAPQGSCEAAEGVIAGRPV
RCNSWEAIIWDYFYADEVPPVDWPTKHIESYRLACTSLGAEKVEVLRAAFRSRYAA

>sp|A4WEI9|UPPP_ENT38 Undecaprenyl-diphosphatase OS=Enterobacter sp. (strain 638)
OX=399742 GN=uppP PE=3 SV=1
MSDMHSLLVAAILGVVEGLTEFLPVSSSTGHMIIVGHLLGFEGETAKTFEVVIQLGSILAVV
VMFWRRFLGLIGIHFGRPPQHEGEGKGRLTLIHILLGMVPAVVLGLIFHDAIKSLFNPINVM
YALVVGGVLLIAAELLKPKEPKAPGLDDMTYRQAFMIGCFQCLALWPGFSRSGATISGGM
LMGVSRYAASEFSFLLAVPMMMGAALDLYKSYHFLTAADFPMFAVGFTAFVLVALVAI
KTFLQLIKRISFIPFAIYRFIVAAAVYVVF

>sp|Q87K03|QNR_VIBPA Pentapeptide repeat protein VPA0095 OS=Vibrio parahaemolyticus
serotype O3:K6 (strain RIMD 2210633) OX=223926 GN=VPA0095 PE=1 SV=1
MLKTDLIFERENFSHHDFQNATFKNCHFYMCSFDHADLRDAKFIDCRFIESKALEGCSFRF
ANLKDASFTNCMLAMSLFNGANCMGLELRKCDLKGANFQGANFANRVSNMTMFFCSAFIT
GCNLTYCNFERVLLEKCDLFENRWNGANLAGATLKGSDLSRCEFSPEQWGTFNVEQCDL
THVELDGLDIRRVSLFGVKICDWQQEQQLLAPFGLIIL

>sp|Q7DJ53|BLE_STAAU Bleomycin resistance protein OS=Staphylococcus aureus OX=1280
GN=ble PE=1 SV=1
MLQSIPALPVGDIKKSIGFYCDKLGFTLVHHEDGFAVLMCNEVRIHLWEASDEGWRSRSN
DSPVCTGAESFIAGTASCRIEVEGIDELYQHILPLGILHPNTSLKDQWWDERDFAVIDPDNN
LISFFQQIKS

>sp|P31776|PBPA_HAEIN Penicillin-binding protein 1A OS=Haemophilus influenzae (strain
ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=mrcA PE=1 SV=2
MRIAKLILNTLLTLCILGLVAGGMLYFHLKSELQQPMQIYTADGKLIGEVGEQRRIPVKLA
DVPQRLIDAFLATEDSRFYDHHGLDPIGIARALFVAVSNGGASQGASTITQQLARNFFLTSE
KTIIRKAREAVLAVEIENTLNKQEILELYLNKIFLGYRSYGVA AAAAQTYFGKSLNELTLSE
MAIIAGLPKAPSTMNPLYSLKRSEERNVLSRMLDEKYISKEEYDAALKEPIVASYHGAK
FEFRADYVTEMVVRQEMVRRFGEENAYTSGYKVFTTVLSKDQAEAQA VRNNLIDYDMR
HGYRGGAPLWQKNEAAWDNDRIVGFLRKLDPSEPFIPAAVIGIVKGGADILLASGEKMTL
STNAMRWTGRSNPVKVGEQIWIHQ RANGEWQLGQIPAANSALVSLNSDNGAIEAVVGGF
SYEQSKFN RATQSLVQVGSSIKPFIYAAALEKGLTLSSVLQDSPISIQKPGQKMWQPKNSPD
RYDGPMRLRVGLGQSKNIIAIRAIQTAGIDFTA EFLQRFQKRDQYFASEALALGAASFTPL
EMARAYAVFDNGGFLIEPYII EKIQDNTGKDLFIANPKIACIECNDIPVIYGETKDKINGFAN
IPLGENALKPTDDSTNGEELDQQPETVPELPELQSNMTALKEDAIDLMAAAKNASSKIEYA
PRVISGEL AFLIRSALNTAIYGEQGLDWKGT SWRIAQSIRSDIGGKTGTTNSSKVAWYAG
FGANLVTTT TYVGFDDNKRVLGRGEAGAKTAMP AWITYMKTALSDKPERKLSLPPKIVEK
NIDTLTGLLSPNGGRKEYFIAGTEPTRTYLSEMQERGYVPT ELQQRLNNEGNTPATQPQE
LF

>sp|P52700|BLA1_STEMA Metallo-beta-lactamase L1 type 3 OS=Stenotrophomonas maltophilia
OX=40324 PE=1 SV=1
MRSTLLAFALAV ALPAAHTSAAEVPLPQLRAYTV DASWLQPMAPLQIADHTWQIGTEDL
TALLVQTPDGAVLLDGGMPQMASHLLDNMKARGVTPRDLRLILLSHAHADHAGPVAEL
KRRTGAKVAANAESAVLLARGGSDDLHFGDGITYPPANADRIVMDGEVITVGGIVFTAHF
MAGHTPGSTAWTWT DTRNGKPVRIAYADSLSAPGYQLQGNPRYPH LIEDYRRSFATVRA
LPCDVLLTPHPGASNWDYAAGARAGAKALTCKAYADAAEQKFDGQLAKETAGAR

>sp|Q06239|VANR_ENTFC Regulatory protein VanR OS=Enterococcus faecium OX=1352
GN=vanR PE=3 SV=1
MSDKILIVDDEHEIADLVELYLNENYTVFKYYTAKEALECIDKSEIDLAILDIMLPGTSGL
TICQKIRDKHTYPIIMLTGKDTEVDKITGLTIGADDYITKPF RPLELIARVKAQLRRYKKFSG
VKEQNENVIVHSGLVINVNTH ECYLNEKQLSLTPTEFSILRILCENKGNVVSSELLFHEIWG
DEYFSKSNNTITVHIRHLREKMNDTIDNPKYIKTVWGVGYKIEK

>sp|I6YBX3|MFPA_MYCTU Pentapeptide repeat protein MfpA OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) OX=83332 GN=mfpA PE=1 SV=1

MQQWVDCEFTGRDFRDEDLSRLHTERAMFSECDGSGVNLAESQHRGSAFRNCTFERTTL
 WHSTFAQCSMLGSVVFACRLRPLTLDDVDFTLAVLGGNDLRGLNLTGCRLRETSLVDTD
 LRKCVLRGADLSGARTTGARLDDADLRGATVDPVLWRTASLVGARVDVDQAVAFAAA
 HGLCLAGG
 >sp|P25051|VANA_ENTFC Vancomycin/teicoplanin A-type resistance protein VanA
 OS=Enterococcus faecium OX=1352 GN=vanA PE=1 SV=1
 MNRIKVAILFGGCSEEHDSVSKSAIEIAANINKEKEYEPLYIGITKSGVWKMCEKPCAEWEN
 DNCYSAVLSPDKKMHGLLVKKNHEYEINHVDVAFSALHGKSGEDGSIQGLFELSGIPFVG
 CDIQSSAICMDKSLTYIVAKNAGIATPAFWVINKDDRPAATFTYPVFVKPARSGSSFGVK
 KVNSADELDYAIESARQYDSKILIEQAVSGCEVGC AVLGN SAALVVGEVDQIRLQYGIFRI
 HQEVEPEKGSENA VITVPADLSAEERGRIQETAKKIYKALGCRGLARVDMFLQDNGRIVL
 NEVNTLPGFTSYSRYPRMMAAAGIALPELIDRLIVLALKG
 >sp|P67919|BLA1_MANHA Beta-lactamase ROB-1 OS=Mannheimia haemolytica OX=75985
 GN=rob1 PE=3 SV=1
 MLNKLKIGTLLLLTLTACSPNSVHSVTSNPQPASAPVQQSATQATFQQTLANLEQQYQARI
 GVVVWDTETGHSLSYRADERFAYASTFKALLAGAVLQSLPEKDLNRTISYSQKDLVSYS
 ETQKYVGKGMTIAQLCEAAVRFSDNSATNLLKELGGVEQYQRILRQLGDNVTHTNRLE
 PDLNQAKPNDIRDTSTPKQMAMNLNAYLLGNTLTESQKTILWNWLDNNATGNPLIRAAT
 PTSWKVYDKSGAGKYGVRNDIAVVRIPNRKPIVMAIMSTQFTEEAKFNNKLVEDAAKQV
 FHTLQLN
 >sp|Q05709|VANH_ENTFC D-specific alpha-keto acid dehydrogenase OS=Enterococcus faecium
 OX=1352 GN=vanH PE=1 SV=1
 MNNIGITVYGCEQDEADAFHALSPRFGVMATIINANVSESNAKSAPFNQCISVGHKSEISAS
 ILLALKRAGVKYISTRSIGCNHIDTTAAKRMGITVDNVAYSPDSVADYTMMLILMAVRNV
 KSIVRSVEKHDFRLDSDRGKVLSDMTVG VVG TGQIGKAVIERLRGFGCKVLAYSRSRSIEV
 NYVPFDELLQNSDIVTLHVPLNTDTHYIISHEQIQRMKQGAFLINTGRGPLVDTYELVKAL
 ENGKLGAALDVLEGEFFYS DCTQKPIDNQFLLKLQRM PNVIITPHTAYYTEQALRDTV
 EKTIKNCLDFERRQEHE
 >sp|Q06241|VANX_ENTFC D-alanyl-D-alanine dipeptidase OS=Enterococcus faecium OX=1352
 GN=vanX PE=1 SV=1
 MEIGFTFLDEIVHGVRWDAKYATWDNFTGKPVDGYEVNRIVGTYELAESLLKAKELAAT
 QGYGLLLWDGYRPKRAVNCFMQWAAQPENNLTKESYYPNIDRTEMISKGYVASKSSHRSR
 GSAIDLTLYRLDTGELVPMGSRFDFMDERSHHAANGISCNEAQNRRRLRSIMENSGFEAY
 SLEWWHYVLRDEPYPN SYFDFPVK
 >sp|P00382|DYR1_ECOLX Dihydrofolate reductase type 1 OS=Escherichia coli OX=562
 GN=dhfrI PE=1 SV=1
 MKLSLMVAISKNGVIGNGPDIPWSAKGEQLLFKAITYNQWLLVGRKTFESMGALPNRKY
 AVVTRSSFTSDNENVLIFPSIKDALTNLKKITDHVIVSGGGEIYKSLIDQVDTLHISTIDIEPE
 GDVYFPEIPSNFRPVFTQDFASNINYSYQIWQKG
 >sp|P52699|BLAB_SERMA Metallo-beta-lactamase type 2 OS=Serratia marcescens OX=615
 PE=1 SV=1
 MSKLSVFFIFLFCSIATAAESLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVLVNAE
 AYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFS DSTGGIEWLNSRSIPTYASELTNELL
 KKD GKVQATNSFSGVNYWL VKNKIEVFYPGPGHTPDNVVWVLP ERKILFGGCFIKPYGL
 GNLGDANIEAWPKSAKLLKSKY GKAKLVVPSHSEVG DASLLKLTLEQAVKGLNESKKPS
 KPSN
 >sp|P30897|BLAC_PROMI Beta-lactamase OS=Proteus mirabilis OX=584 GN=blaP PE=1 SV=1
 MNVRQHKASFFSVVITFLCLTSLNANATDSVLEAVTNAETELGARIGLAHDLTGKRW
 EHKSNERFPLSSTFKTLACANVLQRVDL GKERIDRVVRFSES NLVTYSPVTEKHVGKKGM
 SLAELCQATLSTSDNSAANFILQAIGGPKALTKFLRSIGDDTTRLDRWEPELNEAVPGDKR

DTTTPIAMVTTLEKLLIDETLSIKSRQQLESWLKGNEVGDALFRKGVPSPDWIVADRTGAG
 GYGSRITAVMWPPNRKPIVAALYITETDASFEERNAVIAKIGEQUIAKTVLMENSRN
 >sp|P85302|AMPC_PSEFL Beta-lactamase OS=Pseudomonas fluorescens OX=294 GN=ampC
 PE=1 SV=1
 ATDIRQVVDSTVEPLMQQQDIAGLSVAVIQNGKAQYFNYGVANKDSKQPITENTLFEIGS
 VSKTFTATLAGYALANGKLLSDPASQYLPALRGDKFDHISLLNLGTYTAGGLPLQFPES
 DNTGKMISYYQHWKPAFAPGTQRLYSNPSIGLFGHLAAQSLGQPFKLEQTVLPKLGLK
 HTFISVPETQMSLYAQGYDKAGKPVRVSPGALDAEAYGIKTSTSDLIHYVEVNMHPAKLE
 KPLQQAIAATHTGYYTVDGMTQGLGWEMYPYPIKVDALVEGNSTQMAMEPHKVNWLT
 PPQAAPLDTLVNKTGSTGGFGAYVAYVPSKGLGVVILANKNYPNAERVKAAHAILSAMD
 Q
 >sp|P13082|STR_KLEPN Streptomycin 3"-kinase OS=Klebsiella pneumoniae OX=573 GN=str
 PE=3 SV=1
 MERWLLRDGELLTTHSSWILPVRQGDMPAMLKVARIPDEEAGYRLLTWWDGQGAARV
 FASAAGALLMERASGAGDLAQIAWSGQDDEACRILCDTAARLHAPRSGPPDLHPLQEW
 FQPLFRLAAEHAALAPAASVARQLLAAPREVCPLHGDLHHENVLDFGDRGWLAIDPHGL
 LGERTFDYANIFTNPDLSDPGRPLAILPGRLEARLSIVVATTGFEPERLLRWIIAWTGLSAA
 WFIGDGDGEGEGAIDLAVNAMARRLLD
 >sp|P0C003|DHP1_PSEAI Dihydropteroate synthase type-1 OS=Pseudomonas aeruginosa
 OX=287 GN=sulI PE=3 SV=1
 MVTVFGLNLTEDSFFDESRRDPAGAVTAAIEMLRVGSVDVDVGPAASHPDARPVSPAD
 EIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLNDIQGFDPALYPDIAEADCRL
 VVMHSAQRDGIATRTGHLRPEDALDEIVRFFEARVSALRRSGVAADRLILDPGMGFFLSPA
 PETSLHVLNLQKLKSALGLPLLVSVSRSFLGATVGLPVKDLGPASLAAELHAIGNGADY
 VRTHAPGDLRSAITFSETLAKFRSRDARDRGLDHA
 >sp|P18150|APHE_STRGR Streptomycin 3"-kinase OS=Streptomyces griseus OX=1911
 GN=aphE PE=3 SV=1
 MSDHPGPGAVTPELFGVGGDWLAVTAGESGASVFRAADATRYAKCVPAADAAGLEAER
 DRIAWLSGQGVPGPRVLDWYAGDAGACLVTRAVPGVPADRVGADDLRTAWGAVADAV
 RRLHEVPVASC PFRRGLDSVVDAARDVVARGAVHPEFLPVEQRLVPPAELLARLTGELAR
 RRDQEAADTVVCHGDLCLPNIVLHPETLEVSGFIDLGR LGAADRHADLALLANARETW
 VDEERARFADAFAERYGIAPDPERLRFYLHLDPLTWG
 >sp|Q47747|VANW_ENTFA Vancomycin B-type resistance protein VanW OS=Enterococcus
 faecalis (strain ATCC 700802 / V583) OX=226185 GN=vanW PE=2 SV=1
 MNRKRLTQRFPLLPMRQAQRKICFYAGMRFDGCCYAQTIGEKTLPYLLFETDCALYNHN
 TGFDMIYQENKVFNKLAAKTLNGLLIKPGETFSFWRLVRHADKDTKYDGLTVANGKL
 TTMSGGGMCMQSNLLFWVFLHTPLTIIQRSGHVVKFPEPNSDEIKGV DATISEGWIDLV
 RNDTDCTYQIWVTLDDDEKIIQGVFADKQPQALYKIANGSIQYVRESGGIYEYAKVERMQV
 ALGTGEIIDCKLLYTNKCKICYPLPESVDIQEANQ
 >sp|P26839|VATA_STAAU Virginiamycin A acetyltransferase OS=Staphylococcus aureus
 OX=1280 GN=vat PE=1 SV=2
 MNLNNDHGPDPENILPIKGNRNLQFIKPTITNENILVGEYSYD SKRGESFEDQVLYHYEVI
 GDKLIIGRFCSIGPGTTFIMNGANHRMDGSTYPFHLFRMGWEKYMP SLKDLPLKGDIEIGN
 DVWIGRDVTIMPGVKIGDGAIIAAEAVVTKNVAPYSIVGGNPLKFIRKRFSDGVIEEWLAL
 QWWNLDMKIINENLPFIINGDIEMLRKRKLLDDT
 >sp|E1ANH6|BLC97_ECOLX Beta-lactamase CTX-M-97 OS=Escherichia coli OX=562 GN=bla
 PE=1 SV=1
 MMTQSIGRSMMLTVMATLPLLFSSATLHAQANSVQQQLEALEKSSGGRLGVALINTADNSQ
 ILYRADERFAMCSTSKVMAAAAVLKQSESDKHLLNQRVEIKKSDLVNYNPIAEKHVNGT
 MTLAELGAAALQYSDNTAMNKLIAHLGGPDKVTAFARSLGDETFR LDRTEPTLNTAIPGD

PRDTTTPPLAMAQTLKNLTLGKALAETQRAQLVTWLKGNTTGSASIRAGLPKSWVVGDKT
 GSGDYGTTNDIAVIWPENHAPLVLVITYFTQPEQKAESRRDILAAAAKIVTHGF
 >sp|P26841|CAT4_PSEAE Chloramphenicol acetyltransferase OS=Pseudomonas aeruginosa
 (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 /
 PAO1) OX=208964 GN=cat PE=1 SV=3
 MGNYFESPFRGKLLSEQVSNPNIRVGRYSYYSYGYHGHHSFDDCARYLMPDRDDVDKLV
 GSFCSIGSGAAFIMAGNQGHRAEWASTFPFHFHMEEPVFAGAVNGYQPAGDTLIGHDVWI
 GTEAMFMPGVRVGHGAIIGSRALVTGDVEPYAIVGGNPARTIRKRFSDGDIQNLLEMAW
 WDWPLADIEAAMPLCTGDIPALYRHWKQRQATA
 >sp|Q06242|VANZ_ENTFC Protein VanZ OS=Enterococcus faecium OX=1352 GN=vanZ PE=4
 SV=2
 MGKILSRGLLALYLVTLIWLVLFLKLQYNILSVFNYHQRSNLTPFTATGNFREMIDNVIIFIP
 FGLLLNVNFKEIGFLPKFAFVLVLSLTFEIIQFIFAIGATDITDVITNTVGGFLGLKLYGLSNK
 HMNQKKLDRVIIFVGILLVLLLVRTHLRINYV
 >sp|P13018|STA_ECOLX Streptothricin acetyltransferase OS=Escherichia coli OX=562 GN=sat-
 1 PE=3 SV=1
 MKISVIPEQVAETLDAENHFIVREVFDVHLSAQGFELSTRSVSPYRKDYISDDSDSDSAC
 YGAFIDQELVGKIELNSTWNDLASIEHIVVSHTHRGKGVASHLIEFAKKWALSRLGIRL
 ETQTNNVPACNLYAKCGFTLGGIDLFTYKTRPQVSNETAMYWYWFSGAQDDA
 >sp|P17585|AADK_BACSU Aminoglycoside 6-adenylyltransferase OS=Bacillus subtilis (strain
 168) OX=224308 GN=aadK PE=1 SV=1
 MRSEQEMMDIFLDFALNDERIRLVTLEGSRTNRNIPPDNFQDYDISYFVTDVESFKENDQW
 LEIFGKRIMMQKPEDMELFPPELGNWFSYIILFEDGNKLDLTLPIREAEDYFANNDGLVKV
 LLDKDSFINYKVTNPDRQYWIKRPTAREFDCCNEFWMVSTYVVKGLARNEILFAIDHLN
 EIVRPNLLRMMAWHIASQKGYFSMGKNYKFMKRYLSNKEWEELMSTYSVNGYQEMW
 KSLFTCYALFRKYSKAVSEGLAYKYPDYDEGITKYTEGIYCSVK
 >sp|P50858|AAC6_KLEAE Aminoglycoside N(6')-acetyltransferase type 1 OS=Klebsiella
 aerogenes OX=548 GN=aacA7 PE=3 SV=1
 MDSSPLVRPVETTDASWLSMRCELWPDGTCQEHQSEIAEFLSGKVARPAAVLIAVAPDG
 EALGFAELSIRPYAEECYSGNVAFLEGWYVVPARRQGVGVVALVKAAEHWARGRGCTEF
 ASDTQLTNSASTSAHLAAGFTEVAQVRCFRKPL
 >sp|Q2PT27|QNRB4_ECOLX Pentapeptide repeat protein QnrB4 OS=Escherichia coli OX=562
 GN=qnrB4 PE=3 SV=2
 MMTLALVGEKIDNRNFTGEKVENSTFFNCDFSGADLSGTEFIGCQFYDRESQKGCNFSRA
 NLKDAIFKSCDLSMADFRNINALGIEIRHCRAQGSDFRGASFMNMITTRTWFC SAYITNTN
 LSYANFSKVLEKCELWENRWMGTQVLGATFSGSDLGGEFSSFDWRAANVTHCDLTNS
 ELGDLDIRGVLDLQGVKLDSYQASLLLERLGIAVMG
 >sp|A8A2C2|ARNA_ECOHS Bifunctional polymyxin resistance protein ArnA OS=Escherichia
 coli O9:H4 (strain HS) OX=331112 GN=arnA PE=3 SV=1
 MKTVVFAYHDMGCLGIEALLAAGYEISAIFTHTDNPGEKAFYGSVAHLAAERGIPVYAPD
 NVNHPLWVERIAQLSPEVIFSFYRHLICDEILQLAPAGAFNLHGSLLPKYRGRAPLNWVL
 VNGETETGVTLHRMVKRADAGAIVAQLRVAIAPDDIAITLHHKLCHAARQLLEQTLPAIK
 HGNILEIAQRENEATCFGRRTPDSSFLEWHKPASVLHNMVRAVADPWPGAFSYVGNQKF
 TVWSSRVPHASKAQPGSVISIAPLLIACGDGALEIVTGQAGDGITMQGSQLAQTLGLVQG
 SRLNSQPACTARRRTRVLILGVNGFIGNHLTERLLREDHYEVYGLDIGSDAISRFLNHPHFH
 FVEGDISIHSEWIEYHVKKCDVVLPLVAIATPIEYTRNPLRVFELDFEENLRIIRYCVKYRKR
 IIFPSTSEVYGMCSKDYFDEHNSNLIVGPVNKPRWIYSVSKQLLDRVIWAYGEKEGLQFTL
 FRPFNWMPRLDNLNAARIGSSRAITQLILNLVEGSPIKLIDGGKQKRCFTDIRDGIEALYRI
 IENAGNRCDGEIINIGNPENEAIEELGEMLLASFEKHPLRHHFPFAGFRVVESSSYGKG
 YQDVEHRKPSIRNAHRCLDWEPKIDMQETIDETLDFFLRTVDLTDKPS

>sp|P59676|PBPX_STRR6 Penicillin-binding protein 2X OS=Streptococcus pneumoniae (strain ATCC BAA-255 / R6) OX=171101 GN=pbpX PE=1 SV=1
 MKWTKRVIRYATKNRKSPAENRRRVGKSLSLLSVVFVFAIFLVNFAVIIGTGTRFGTDLAKE
 AKKVHQTTTRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNK
 VAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDF
 TTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLG
 NIVPGTEQVSQRTMDGKDVTYTTISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEIL
 ATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAIDNNTFPGGGEVFNSS
 ELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFK
 FGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISA
 IYDPNDQTARKSQKEIVGNPVSKDAASLTRTNMVLVGTDVPVYGTMYNHSTGKPTVTVPG
 QNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGE
 FANPILERASAMKDSLNLQTTAKALEQVSQQSPYPMPSVKDISPGDLAEELRRNLVQPIVV
 GTGTKIKNSSAEEGKNLAPNQVLILSDKAEEVPDMYGWTKETATLAKWLNIELEFQGS
 GSTVQKQDVRANTAIKDIKKITLTLGD

>sp|C7C422|BLAN1_KLEPN Metallo-beta-lactamase type 2 OS=Klebsiella pneumoniae OX=573
 GN=blaNDM-1 PE=1 SV=1

MELPNIMHPVAKLSTALAAALMLSGCMPGEIRPTIGQQMETGDQRFGDLVFRQLAPNVW
 QHTSYLDMPGFGAVASNGLIVRDGGRVLVVDTAWTDDQTAQILNWIKQEINLPVALAVV
 THAHQDKMGGMDALHAAGIATYANALSNQLAPQEGMVAAQHSLTFAANGWVEPATAP
 NFGPLKVFYPPGHTSDNITVGIDGTDIAFGGCLIKDSKAKSLGNLGDADTEHYAASARAF
 GAAPKASMIVMSHSAPDSRAAITHTARMADKLR

>sp|Q06893|VANB_ENTFA Vancomycin B-type resistance protein VanB OS=Enterococcus faecalis (strain ATCC 700802 / V583) OX=226185 GN=vanB PE=1 SV=2

MNKIKVAIIFGGCSEHDVSVKSAIEIAANINTEKFDPHYIGITKNGVWKLCKKPCTEWEA
 DSLPAIFSPDRKTHGLLVMKEREYETRRIDVAFVVLHGKCGEDGAIQGLFELSGIPYVGCDI
 QSSAACMDKSLAYILTKNAGIAVPEFQMIKGDKPEARLTLYPVFVKPARSGSSFGVTKV
 NSTEELNAAIEAAGQYDGKILIEQAISGCEVGCVMGNEDDLIVGEVDQIRLSHGIFRIHQE
 NEPEKGSENAMIIVPADIPVEERNRVQETAKKVYRVLGCRLARVDLFLQEDGGIVLNEV
 NTLPGFTSYSRYPRMAAAAGITLPALIDSLITLAIER

>sp|P00555|KKA5_STRFR Aminoglycoside 3'-phosphotransferase OS=Streptomyces fradiae
 OX=1906 GN=aph PE=3 SV=1

MDDSTLRRKYPHHEWHAVNEGDSGAFVYQLTGGPEPQPELYAKIAPRAPENSADFSLGE
 ADRLEWLHRHGIPVPRVVERGADDTAAWLVTAVPGVAAAEEWPEHQRFVVEAMAEL
 ARALHELPVEDCPSDRRLDAVAEARRNVAEGLVDLDDLQEERAGWTGDQLLAELDRT
 RPEKEDLVVCHGDLCPNNVLLDPGTCRVTGVIDVGRLGVADRHADIALAARELEIDEDPW
 FGPAYAERFLERYGAHRVDKEKLAFYQLLDEFF

>sp|P09885|KKA6_ACIBA Aminoglycoside 3'-phosphotransferase OS=Acinetobacter baumannii
 OX=470 GN=aphA-6 PE=3 SV=1

MELPNIIQQFIGNSVLEPNKIGQSPSDVYSFNRNNETFFLKRSSTLYTETTYSVSREAKMLS
 WLSEKLKVPPELIMTFQDEQFEFMITKAINAKPISALFLTDQELLAIYKEALNLLNSIAIIDCPF
 ISNIDHRLKESKFFIDNQLDDIDQDDFDTELWGDHKTYLSLWNETTETRVEERLVFSGHD
 ITDSNIFIDKFNEIYFLDLGRAGLADEFVDISFVERCLREDASEETAKIFLKHLLKNDRPDKRN
 YFLKLDELN

>sp|P0A2Q8|MERR_SALTI Mercuric resistance operon regulatory protein OS=Salmonella typhi
 OX=90370 GN=merR PE=3 SV=1

MENNLENLTIGVFAKAAGVNVETIRFYQRKGLLREPDKPYGSIRRYGEADVVRVKFVKSA
 QRLGFSLEIAELLRLDDGTHCEEASSLAEHKLKDVREKMADLARMETVLSSELVCACHA
 RKGNVSCPLIASLQGEAGLARSAMP

>sp|P06689|MERD_PSEAI HTH-type transcriptional regulator MerD OS=Pseudomonas aeruginosa OX=287 GN=merD PE=4 SV=1
 MNAYPVSRALDAGVSVHIVRDYLLRGLLRPVACTPGGYGLFDDAALQRLCFVRAAFEAGIGLDALARLCRALDAADGDEAAQALALLRQFVERRREALADLEVQLATLPTEPAQHAE SLP

>sp|O84955|BLO20_PSEAI Beta-lactamase OXA-20 OS=Pseudomonas aeruginosa OX=287 GN=bla PE=3 SV=1
 MIIRFLALLFSAVVLVSLGHAQEKTHESSNWGKYFSDFNAKGTIVVVDERTNGNSTSVYN ESRAQQRYSPASTFKIPHTLFALDAGAVRDEFHVFRWDGAKRSFAGHNQDQNLRSAMRN STVWVYQLFAKEIGENKARSYLEKLNIGNADPSTKSGDYWIDGNLAISANEQISILKKLY RNELPFRVEHQRLVKDLMIVEAKRDWILRAKTGWGQMGWVVGWVWPTGPVFFALN IDTPNRMEDLHKREAIARAILQSVNALPPN

>sp|P12921|TMRB_BACSU Tunicamycin resistance protein OS=Bacillus subtilis (strain 168) OX=224308 GN=tmrB PE=1 SV=4
 MIIWINGAFGSGKTQTAFELHRRLLNPSYVYDPEKMGFALRSMVPQEIAKDDFQSYPLWRA FNYSLLASLTDITYRGILIVPMTIVHPEYFNEIIGRLRQEGRIVHHFTLMASKETLLKRLRTRA EGKNSWAAKQIDRCVEGLSSPIFEDHIQTDNLSIQDVAENIAARAELPLDPDTRGSLRRFAD RLMVKLNHIRIK

>sp|Q45726|BLAC_BACTU Beta-lactamase OS=Bacillus thuringiensis OX=1428 GN=bla PE=3 SV=1
 MMILKNKRMLKIGICVGILGLSITSLEAFTGGALQVEAKQKTGQVKHKNQATHKEFSQLE KKFDARVGVYAIDTGTNQTISYRSNERFAFASTYKALAAGVLLQQNSIDTLNEVITFTKED LVDYSPVTEKHVDTGMLKGEIAEA AVRSSDNTAGNILFNKIGGPKGYEKALRKMGRVT MSDRFETELNEAIPGDIRDTSTAKRIATNLKAFTVGNALPAEKRKILTEWMKGNATGDKLI RAGVPTDWVVGDKSGAGSYGTRNDIAIVWPPNRAPIIIAILSSKDEKEASYDNQLIAEATE VIVKALK

>sp|P12055|STR_STAAU Streptomycin resistance protein OS=Staphylococcus aureus OX=1280 GN=str PE=4 SV=1
 MRTEKEILNLVSEFAYQRSNVKIIALEGSRTNENIKKDKFQDYDFAFFVSDIEYFTHEESWL SLFGELLFIQKPEDMELFPPDLDYGYSYIMYFKDGIKMDITLINLKDLNRYFSDSDGLVKIL VDKDNLVTQEIVPDDSNYWLKKPTEREFYDCCNEFWSVSTYVAKGVFRREILFALDHFN ILRPELLRMISWYIGFNRGFD FSLGKNYKFINKYLT DKEFNMLLATFEMNGYRKTYQSFKL CCELFKYYSNKVSCLGNYNYPNYEKNIENFIRNNYEN

>sp|P05193|AMPC_CITFR Beta-lactamase OS=Citrobacter freundii OX=546 GN=ampC PE=1 SV=1
 MMKKSICCALLLTASFSTFAAAKTEQQIADIVNRTITPLMQEQAIIPGMAVAIIYEGKPYFYFT WGKADIANNHPVTQQTLELGSVSKTFNGVLGGDRIARGEIKLSDPVTKYWPELTGKQW RGISLLHLATYTAGGLPLQIPGDVTDKAELLRFYQNWQPQWTPGAKRLYANSSIGLFGAL AVKSSGMSYEEAMTRRVLQPLKLAHTWITVPQSEQKNYAWGYLEGKPVHVSPGQLDAE AYGVKSSVIDMARWVQANMDASHVQEKTLQQGIELAQSRYWRIGDMYQGLGWEMLN WPLKADSINGSKVALAALPAVEVNPPAPAVKASWVHKTGSTGGFGSYVAFVPEKNL GIVMLANKSYPNPARVEAAWRILEKLQ

>sp|Q9X3P3|VANT_ENTGA Serine/alanine racemase OS=Enterococcus gallinarum OX=1353 GN=vanT PE=1 SV=1
 MKNKGIDQFRVIAAMMVVAIHCLPLHYLWPEGDILITLTIFRVAVPFFFFMISGYVFAELA VANSYPSRQRVFNFIKKQLKVYLLATLMFLPLALYSQTIGFDLPVGTLVQVLLVNGILYHL WYFPALITGSLLLTSLLIHV SFKKVFWLAAGLYLIGLGGDSWFGLIQQTPIEPFYTAVFHLL DGTRNGIFFTPLFLCLGVLVRKQSEKRSLSKTALFFLISLIGLLIESAYLHGFSIPKHDSMYLF LPVVLFFLPLILRWHPHRTWKHPGQLSLWLYLLHPYTIAGTHFLSQKISILQNNLINYL VV LILTIGFICLFLRQKHSWFRHKQTTPVKRAVKEFSKTALLHNLQEIQRIISPKTKVMAVKA

DAYGCGAKEVAPVLEQAGIDFFAVATIDEGIRLRKNAVKSPILVLGYTSPKRIKELRRYSLT
QSIISEGHAVALSQRKVAIDCHLAIDTGMHRLGVPTIDSILSIFDLPLTISGVYSHLGSADR
LNPDSMIRTQKQIACFDQILLELDQRQISYGITHLQSSYGILNYPDLNYDYVRPGILLTGSL
DTNEPTKQRVSLQPILTLKAQLITKRVAKGGEAIGYGQTAVANQETTVGVVSGYCDGLP
RSLSNQEFCLSYRGQSLPQIGLICMDMLLIDLHCPTIPIESEIEILTDWSDTAEQVQTITNELI
CRIGPRVSARIK

>sp|P45439|ERMS_STRFR rRNA adenine N-6-methyltransferase OS=Streptomyces fradiae
OX=1906 GN=ermSF PE=3 SV=1

MARAPRSPHPARSRETSRAHPPYGTRADRAPGRGRDRDRSPDSPGNTSSRDGGRSPDRAR
RELSQNFLARRAVAERVARLVRPAPGGLLLEVAGARGVLTEALAPYCGRLVAHEIDPRLL
PALRDRFGGPHHAHVRISSGGDFLAAPVPREPFALAGNIPYSRTAGIVDWALRARTLTSATF
VTQLEYARKRTGDYGRWSLLTVRTWPRHEWRLGRVSRREFRPVPRVDSGILRIERRERP
LLPSAALGDYHRMVELGFSGVGGSYASLRRRAHRAGPLDAAFRAARLDRSVVAVYTPE
QWLTVFRTLRPVRSRPAGR

>sp|P07944|PBP_STAAU Beta-lactam-inducible penicillin-binding protein OS=Staphylococcus
aureus OX=1280 GN=pbp PE=2 SV=1

MKKIKIVPLILIVVVVGFGIYFYASKDKEINNTIDAIEDKNFKQVYKDSSYISKSDNGEVEM
TERPIKIYNLSGVKDINIQRKIKKVSNNKRVDAQYKIKTNYGNIDRNVQNFVKEDGM
WKLDWDHVSIIIPGMQKDQSIHIENLKSERGKILDRNNVELANTGTHMRLGIVPKNVSKKD
YKAIKELSESIEDYINNKKWIKIGYKMIPSFHFKTVKKMDEYLSDFAKKFHLTTNETESRNY
PLGKATSHLLGYVGPINSEELKQKEYKGYKDDAVIGKKGLEKLYDKKLQHEDGYRVTIV
RVDDNSNTIAHTLIEKKKKDGKDIQLTIDAKVQKSIYNNMKNDYSGGTAIHPQTGELLAL
VSTPSYDVYPFMYGMSNEEYNKLTEDKKEPLLNFQITTSPGSTQKILTAMIGLNNKTLDD
KTSYKIDGKGWQKDKSWGGYNVTRYEVVNGNIDLKQAISSDNIFFARVALELGSKKFE
KGMKKLGVGEDIPSDYPFYNAQISNNKLDNEILLADSGYGQGEILINPVQILSIYSALENNG
NINAPHLLKDTKNKVWKKNIISKENINLLNDGMQQVVKTHKEDIYRSYANLIGKSGTAE
LKMKQGETGRQIGWFISYDKDNPNMMMAINVKDVQDKGMASYNKISGKVYDELYEN
GNKKYDIDE

>sp|P07287|ERME_SACEN rRNA adenine N-6-methyltransferase OS=Saccharopolyspora
erythraea (strain ATCC 11635 / DSM 40517 / JCM 4748 / NBRC 13426 / NCIMB 8594 / NRRL
2338) OX=405948 GN=ermE PE=3 SV=2

MSSSDEQPRPRRRNQDRQHPNQNRPVLGRTDRNRNRQFGQNFLRDRKTIARIAETAELR
PDLPVLEAGPGEGLLTRELADRARQVTSYEIDPRLAKSLREKLSGHPNIEVVNADFLTAEP
PPEPFAFVGAIPYGITSIVDWCLEAPTITATMTVQLEFARKRTGDYGRWSRLTVMTWPL
FEWEFVEKVDRLFKPVPKVDASIMRLRRRAEPLLEGAALERYESMVELCFTGVGGNIQA
SLLRKYPRRRVEAALDHAGVGGGAVVAVYVRPEQWLRLFERLDQKNEPRGGQPQRGRRT
GGRDHGDRRTGGQDRGDRRTGGRDHRDRQASGHGDRRSSGRNRDDGRTGEREQGDQG
GRRGPSGGGRTGGRPGRRGPGQR

>sp|Q9KJA7|BLAB8_ELIME Metallo-beta-lactamase type 2 OS=Elizabethkingia meningoseptica
OX=238 GN=blaB8 PE=3 SV=1

MKGLKGLLVLAGFTGLQVFGQQNPDIKIEKLKDNLYVYTTYNTFKGTKYAANAVYMV
TDKGVVVIDSPWGEDKFKSFTDEIYKKHGGKVMINIATHSHDDRAGGLEIFGKLGAKTY
STKMTDSILAKENKPRAKYTFDNNKSFKVGKTEFQVYYPGKGHTADNVVWVFPKDKVL
VGGCIVKSGDSKDLGFIGEAYVNDWTQSIHNIQQKFPDVQYVVAGHDDWKDQTSIQHTL
DLISEYQQKQKASN

>sp|P58777|CAT_KLESP Chloramphenicol acetyltransferase OS=Klebsiella sp. OX=576 GN=cat
PE=1 SV=1

MEKKITGYTTVDISQWHRKEHFQAFQSVACQCTYNQTVQLDITAFKTVKKNKHKFYPAFI
HILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSSLWSEYHDDFRQFLHIY

SQDVACYGENLAYFPKGFIEENMFFVSANPWVSFTSFDLNVAAMDNFFAPVFTMGKYYTQ
GDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGGA
>sp|O69773|AMPC_PROST Beta-lactamase OS=Providencia stuartii OX=588 GN=ampC PE=3
SV=1
MDNSMKNIFRQGRFLIALSLAMTSISAFALTQQEVDDIHKPLMKQEQIPGMSVAISVNGKQ
AIYHYGVQSKQTQIPVSDRTLYEIGSLSKTFTATLATYAQIQGKLDFSQSVSHYLPKLSA
FDNVSVMLNATHTSGLSLFVPSDIKTNDQLMAYYQKWLPDNEVGQYRSYSNLGVLLGI
VTAKQLNMPFSQAMEKLMPLSLGLKHTYIHVPKSQEKYYAQGYNKQNQPVRNLNLEILGP
EAYGLKSNADLIRYLEINMQSIKVAKTWQEAIENTHTGVYLTDSFVQDMMWESYPWPV
SLSQLLQGNRDDMALPKPKVELIKPAMAPEVRAYYNKTGSSNGFATYAIFIPEEKIAIVML
SNKWIPQIRITATYQLLEKIER
>sp|P14559|BLAC_STRAL Beta-lactamase OS=Streptomyces albus G OX=1962 PE=1 SV=1
MHPSTSRPSRRTLLTATAGAALAAATLVPGTAHASSGGRGHGSGSVSDAERRLAGLERAS
GARLGVYAYDTGSGRTVAYRADELFP MCSVFKTLSSAAVLRDLDRNGEFLSRILYTQDD
VEQADGAGPETGKPQNLANAQLTVEELCEVSITASDNCAANLMLRELGGPAAVTRFVRS
LGDRVTRLDRWEPELNSAEPGRVTDTTSPRAITRTYGRVLVGDALNPRDRRLTSWLLAN
TTSGDRFRAGLPDDWTLGDKTGAGRYGTNNDAGVTWPPGRAPIVLTVLAKTEQDAAR
DDGLVADAARVLAETLG
>sp|Q44056|BLA1_AERHY Beta-lactamase AER-1 OS=Aeromonas hydrophila OX=644
GN=aer1 PE=3 SV=2
MYVLSVEKPTLRNKFAAGIGVVLVCVVASFIPTPVFALDTTKLIQAVQSEESALHARVGM
TVFDSNTGTTWNYRGDERFPLNSTHKTFS CAALLAKVDGKSLSLGQSVSISKEMLVTYSPI
TEKSLSPETVTFGKICQAAVSYSNTAANVVFDAIGGATGFNAYMRSIGDEETQLDRKEPE
LNEGTPGDVRDTTTTPNAMVNSLRKILLGDALSASSRSQLTQWMLDDQVAGALLRASLPS
DWKIADKTGAGGYGSR SIVAVIWPPSKQPLVVGIIYTQTKASMQASNQAIARIGVVLKDT
VAP
>sp|P26840|MATA_LYSSH Probable macrolide acetyltransferase (Fragment) OS=Lysinibacillus
sphaericus OX=1421 PE=3 SV=1
DHKNSPEKFYDNIEHHYEFIGDKLIIGKFCIAAEGVKFIMNGANHRMDGITTYPFNIFGCG
WEKVTPTIEQLPFGKDTVIGNDVWIGQNVTIMPGVIIGDGAIIAANSTVVKSVPEYSISGN
PAKFIKKRFSDEKIEFLKLEWWNWSGEEIFDNLEILTSEAGLEELMNKYSKRDAIN
>sp|P23364|CAT4_AGRFC Chloramphenicol acetyltransferase OS=Agrobacterium fabrum (strain
C58 / ATCC 33970) OX=176299 GN=cat PE=3 SV=1
MENYFESPFRGITLDKQVKSPNLVVGKYSYYSGYHGHSGFEDCARYLLPDEGADRLVIGS
FCSIGSGAAFI MAGNQGHRNEWISTFPFFFMPEVPEFENAANGYLPAGDTVIGNDVWIGSE
AIIMPGITVGDGAVIGTRALVTKDVEPYAIVGGNPAKTIRKRFDDDSIALLEMKWWGWP
AERLKAAMPLMTSGNVAALYRFWRSDSL
>sp|Q52424|AAC2_PROST Aminoglycoside 2'-N-acetyltransferase OS=Providencia stuartii
OX=588 GN=aac PE=1 SV=1
MGIEYRSLHTSQLTLSEKEALYDLLIEGFEGDFSHDDFAHTLGGMHVMAFDQQKLVGHV
AIIQRHMA LDNTPISVGYVEAMVVEQSYRRQGIGRQLMLQTNKIIASCYQLGLLSASDDG
QKLYHSVGWQIWKGKLFELKQGSYIRSIEEEGGVMGWKADGEVDFTASLYCDFRGGDQ
W
>sp|Q55002|OTRA_STRRM Oxytetracycline resistance protein OS=Streptomyces rimosus
OX=1927 GN=otrA PE=3 SV=1
MNKLNGLILAHVDAGKTS LTERLLHRTGVIDEVGSVDAGTTTTDSMELERQRGITIRSAV
ATFVLDDLVNLDTPGHSDFI SEVERALGVLDGAVLVVSAVEGVQPQTRILMRTLRLGI
PTLVFVNKIDRGGARPDGVLREIRDRLTPAAVALSAVADAGTPRARAIALGPDTPDFAV
RVGELLADHDDAFLTAYLDEEHVLT EKEYAEELAAQTARGLVHPVYFGSALTGEGLDHL
VHGIRELLPSVHASQDAPLRATVFKVDRGARGEAVAYLRLVSGTLGTRDSVTLHRVDHT

GRVTEHAGRITALRVFEHGSATSETRATAGDIAQAWGLKDVRVGDRAHLDGPPPRNFF
APPSLETVIRPERPEEAGRLHAALRMLDEQDPSIDLRQDEENAAGAVVRLYGEVQKEILGS
TLAESFGVRVRFDPTRTVICIEKPVGTGEALIELDTRTHNYFWGAPWVCASDRPSPARAITF
RLAVELGSLPLAFHKAIEETVHTTLRHGLYGWQVTDCAVTLTRTGVRSPVSAADDFRKA
NARLVLM DALGRAGTEVHEPVSSFELEVPAARLSPVLAKLAELGATPGVPTAEGDVFRLE
GTMPTSLVHDFNQVRPGLTQGEGVFLAEHRGYRPAVGQPPVRPRPEGNPLNRDEYILHV
LKR

>sp|P00552|KKA2_KLEPN Aminoglycoside 3'-phosphotransferase OS=Klebsiella pneumoniae
OX=573 GN=neo PE=1 SV=1

MIEQDGLHAGSPAAWVERLFGYDWAQQTIGCSDAAVFRLSAQGRPVLVFKTDLSGALNE
LQDEAARLSWLATTGVPCAAVLDDVTEAGRDWLLGEVPGQDLLSSHLAPAELKVSIMAD
AMRRLHTLDPATCPFDHQA KHRIERARTRMEAGLVDQDDLDEEHQGLAPAELFARLKAR
MPDGEDLVVTHGDACLPNIMVENGRFSGFIDCGRLGVADRYQDIALATRDIAEELGGEW
ADRFLVLYGIAAPDSQRIAFYRLLEFF

>sp|P22782|CAT_CAMCO Chloramphenicol acetyltransferase OS=Campylobacter coli OX=195
PE=3 SV=1

MQFTKIDINNWTRKEYFDHYFGNTPCTYSMTVKLDISKLLKKGKLYPTLLYGVTTIINR
HEEFRTALDENGQVGVFSEMLPCYTVFHKETETFSIWTETADYTEFLQNYQKIDIDAFGE
RMGMSAKPNPPENTFPVSMIPWTSFEGFNLNLKKG YDYLLPIFTFGKYEEGGKYYIPLSI
QVHHAVCDGFHVCRFLDELQDLLNK

>sp|Q56415|FOSA_SERMA Glutathione transferase FosA OS=Serratia marcescens OX=615
GN=fosA PE=1 SV=1

MLQSLNHLTLAVSDLQKSVTFWHELLGLTLHARWNTGAYLTCGDLWVCLSYDEARQYV
PPQESDYTHYAFTVAEEDFEPLSQRLAQAGVTIWKQNKSEGFYFLDPDGHKLELHVGS
LAARLAACREKPYAGMVFTSDEA

>sp|P26918|BLAB_AERHY Metallo-beta-lactamase type 2 OS=Aeromonas hydrophila OX=644
GN=cphA PE=1 SV=1

MMKGWMKCGLAGAVVLMASFWGGSVRAAGMSLTQVSGPVYVVEDNYYVQENSMVY
FGAKGVTVVGATWTPDTARELHKLIKRVSRKPVLEVINTNYHTDRAGGNAYWKSIGAKV
VSTRQTRDLMKSDWAEIVAFTRKGLPEYPDLPLVLPNVHDGDFTLQEGKVRAFYAGPA
HTPDGIFVYFPDEQVLYGNCILKEKLG NLSFADV KAYPQTLERL KAMKLPIKT VIGGHDSPL
HGP ELIDHYEALIKAAPQS

>sp|P94958|AMPC_MORMO Beta-lactamase OS=Morganella morganii OX=582 GN=ampC
PE=3 SV=1

MKKSLSATLISALLAFSAPGFSAADNVA AVVDSTIKPLMAQQDIPGMAVAVSVKGKPYF
NYGFADVQAKQPVTENTL FELGSVSKTFTGVLGAVSVAKKEMTLNDPAEKYQPELALPQ
WKGITLLDLATYTAGGLPLQVPDAVKSRADLLHFYQQWQPSRKPGDMRLYANSSIGLFG
ALTANAAGMPYEQLLTARILAPLGLSHTFITVPESAQSQYAYGYKNKKPV RVSPGQLDAE
SYGVKSASKDMLRWAEMNMEPSRAGNADLEMAMYLAQTRYKTAAINQGLGWEMYD
WPQQKDMIINGVTNEVALQPHPVTDNQVQPYNRASWVHKTGATTGFGAYVAFIPEKQV
AIVILANKNYPNTERVKAAQAILSALE

>sp|Q93A44|VANTE_ENTFL Amino-acid racemase OS=Enterococcus faecalis OX=1351
GN=vanTE PE=3 SV=1

MKHRANGIDLFRIFAATMVVAIHTFPFQSIAPFLDEVITLTVFRVAVPFFFMITGYFLLGRLS
LNFSYNNNRVKKYLYKIGMIYLYSILLYFPLSLLNGTISLKMNILLKLVFIFDGTIFYHLW
YFPASIIGTILVTLLRSIGFKLTVA FSTCLYL VGLGGDSWYGITNQVPLL NKLYTFIFSWSD
YTRSGVFFTPVFLCLGIFAYRVSKKL TASKILNLLFYVFIIGMTFESIFLHRFTNVKHDSMYL
LLPSCALILFLMLLNWQPKLKVKESADLTLLVYILHPLVIVIVHSISKYIPILKNSLLNLLV
VVC SFILAQLLLNLKRKL RVSKQKIPFERASKEISASAIHNNINEIRKIIPKNTNIMGVVKAN
AYGCGMVEVAYELEKIGISFFCVATIEEAIALRKSGNQGDILILGYTHPNRINDIKKYNLIQS

IVSEEHGKVLNLKKIPIRCHLQVDTGMHRLGVTPNVTHIQQMYLFSNLKIEGIYSHLGSSDS
LEQESIARTNTQIFLNNILSDLEQMGISYGYTHIQSSYGILNYPELSFDFVRIGILCYGFLSD
YNSPTKIPIDLQPIVKVKASLITERIVEAGEYVGYGLGAKVEKRTRIGVVSIGYADGIPRALS
NAKLTLEFKGQSIKQIGNICMDMMLVLDSEVEDISLNDELIVLPNISKIADDEEQTITNELLSR
LGSRLGTELN

>sp|P45460|AMPC_YEREN Beta-lactamase OS=Yersinia enterocolitica OX=630 GN=ampC
PE=3 SV=1

MMKKSIIINTLIFTSIATFPLYTLAQTCLTELQVATIVNNTLTPLLEKQGIPGMAVAVFYDGK
PQFFNYGMADIKAGRPVTENTL FELGSVSKTFTGVAGEYAMQTGIMNLNDPVTEYAPELT
GSQWKDVKMLHLATYTAGGLPLQLPDSVTDQKSLWQYYQQWQPQWAPGVMRNYSNA
SIGLFGALAVKRSQ LTFENYMKYVFQPLKLDHTFITIPESMQSNYAWGYKDGQPVRVTL
GMLGEEAYGVKSTSQDMVRFMQANMDPESLPAGNDKLKEAIIASQSR YFQAGDMFQGL
GWEMYSWPINPQGV IADSGNDIALKPRKVEALVPAQPAVRASWVHKTGATNGFGAYIVF
IPEEKVGIVMLANKNYPNPVRVQAAYDILQALR

>sp|P16898|ERMA_CORDP rRNA adenine N-6-methyltransferase OS=Corynebacterium
diphtheriae OX=1717 GN=ermA PE=3 SV=1

MSAYGHRHEHGQNFLT NHKIINSIIDLVKQTSGPIIEIGPGSGAL THPMAHLGRAITAVEV
DAKLA AKITQETSSAAVEVVHDDFLNFRLPATPCVIVGNIPFHLTTAILRKLLHAPAWTDA
VLLMQWEVARRRAGVGASTMMTAQWSPWFTFHLGSRVPRSAFRPQPNVDGGILVIRRV
GDPKPIEQRKAFQAMVHTVFTARGRGIGEILRRQGCFFHVQKHNHGCAREESTPRPYLPD
CTPTTGSISSR

>sp|Q03680|BLA1_STRCI Beta-lactamase 1 OS=Streptomyces cacaoi OX=1898 GN=blaL PE=1
SV=1

MRIRPTRRLLLGAVAPLALVPLVACGQASGSESGQQPGLGGCGTSAHGSADAHEKEFRAL
EKKFDAHPGVY AIDTRDGQEITHRADERFAYGSTFKALQAGAILAQVLRDGREVRRGAEA
DGMDKV VHYGQDAILPNSPVTEKHVADGMSLRELCDAVVAYS DNTAANLLFDQLGGRR
GSTRVLKQLGDHTTSM DRYEQELGSAVPGDPRDTSTPRAFAEDLRAFAVEDGEKAALAP
NDREQ LNDWMSG SRTGDALIRAGVPKDWKVEDKSGQVKYGTRNDIAVVRPPGRAPIVVS
VMSHGDTQDAEPHDELVAEAGLVVADGLK

>sp|Q59514|BLA1_MORCA Beta-lactamase BRO-1 OS=Moraxella catarrhalis OX=480 GN=bla
PE=3 SV=1

MQRRHFLQKTLLALPIIFSGNLLTGCKTNLSDDYLPDDKITNNPNLLQNKLKEILPIWENKF
NAKIGMTIADNGELSSH RGNEYFPVNSTIKAFIASHILLVDKEKLDLNEKIIKESDLIEYS
PVCKKYFDENKPISISELCEATITLSDNGSANILLDKIGGLTAFNQFLKEIGADMVLANNP
LLNRSHYGETSDTAKPIPYTKSLKALIVGNILSNQSKEQLITWLINDKVADNLLRKLYLPKN
WRIGDKTGTGSESKNIIA VIWNENNKP YFISLFITQPHDGKSLDFKNQKDEIMAQIGKEIYPF
L

>sp|P13079|CARB_STRTH rRNA methyltransferase OS=Streptomyces thermotolerans
OX=80858 GN=carB PE=2 SV=1

MAALLKRILRRRMAEKRSRGRMAAARTTGAQSRKTAQRSGRSEADRRRRVHGQNFLV
DRETVQRFVRFADPD PGEVVLEV GAGNGAITRELARLCRRVVAYEIDRHFADRLREATAE
DPRIEVVAGDFL KTSQPKVPFSVVG NIPFGNTADIVDWCLNARRLR TTTTLVTQLEYARKRT
GGYRRWSRLTVATWPEVEWRMGERISR RWF RPVPAVDSAVLRLERRPVPLIPPGLMHDF
RDLVETGFTGKGGS LDASLRRRFPARRVAAGFRRARLEQGVV VAYVTPGQWITLFEELH
GR

>sp|P52676|NMCR_ENTCL Carbapenem-hydrolyzing beta-lactamase transcriptional activator
OS=Enterobacter cloacae OX=550 GN=nmcR PE=3 SV=1

MRARLPLNALRAFEASARYLNFTKAGLELHVSQA AVSQQVVRTLEQMLGVALFTRVPRGL
QLTDEGMHLLPSITEALQMMSSAMDKFHEGKIKEVLTIAVVGTF AIGWLLPRITAF LNENP
WIDIRILTHNNVVNLAAEGIDASIRFGTGGWINTENILLFQAPHTVLCSPETSKKLYIPSDLK

KVCLLSYRKEEWNWFKAAAGIDPWTITGPIFDSTRLMIDAVKLGDYAALVPYHMFQKE
 LNERSVAKPFEIYATLGGYWLTLQKSRVNHNSEALNVFKEWIEHSREFVLKS
 >sp|P14509|KKA8_ECOLX Aminoglycoside 3'-phosphotransferase OS=Escherichia coli OX=562
 GN=aphA PE=3 SV=1
 MNDIDREEPCAAAAVPESMAAHVMGYKWARDKVGQSGCAVYRLHSGSGSDLFLKHG
 KDAFADDVTDEMVRRLRWLAGHISVPSVVSFVRTPNQAWLLTTAIHGKTAYQVLKSDFGA
 RLVVVDALAAFMRRLLHAIPVSECSVQQWTTAGLPERGSIEAGVVDVDDFDKEREKGT
 EQVWEAMHRLPLAPDPVVTHGDFSLDNLIVEGKVVGVCIDVGRAGIADRYQDLAVLWN
 CLEEFESLQERLVAQYGIADPDRRLQFHLLDELF
 >sp|Q07448|S3AD_ENTFL Streptomycin 3"-adenylyltransferase OS=Enterococcus faecalis
 OX=1351 GN=spc PE=4 SV=1
 MRRIYLNTEYEQINKVKKILRKHLKNNLIGTYMFGSGVESGLKPNSDLDFLVVSEPLTDQS
 KEILIQKIRPISKKIGDKSNLRYIELTIIQQEMVPWNHPPKQEFYGEWLQELYEQGYIPQKE
 LNSDLTIMLYQAKRKNKRIYGNYDLELLPDIPFSDVRRAIMDSSEELIDNYQDDETNSILT
 LCRMILTMDTGKIIPKDIAGNAVAESSPLEHRERILLAVRSYLGENIEWTNENVNLTYNLN
 NRLKKL
 >sp|P50868|CAT4_KLEAE Chloramphenicol acetyltransferase OS=Klebsiella aerogenes OX=548
 GN=catB4 PE=3 SV=1
 MTNYFDSFPKGLLSEQVKNPNIKVGRYSYYSYSGYYHGHSFDDCARYLFPDRDDVDKLIIG
 SFCSIGSGASFIMAGNQGHRYDWASSFPFFYMQEPAFSSALDAFQKAGNTVIGNDVWIGS
 EAMVMPGIKIGHGAVIGSRSLVTKDVEPYAIVGGNPAKKIKKRFTDEEISLLEMEWWNW
 SLEKIKAAAMPMLCSSNIVGLHKYWLEFAV
 >sp|P50870|VATD_ENTFC Streptogramin A acetyltransferase OS=Enterococcus faecium
 OX=1352 GN=vatD PE=1 SV=1
 MGNPNMKMYPIEGNKSQFIKPILEKLENVEVGEYSYYDSKNGETFDKQILYHYPILNDKL
 KIGKFCSIGPGVTIIMNGANHRMDGSTYPFNLFGNGWEKHMPKLDQLPIKGDTHIGNDVWI
 GKDVVIMPGVKIGDGAIVAANSVVVKDIAPYMLAGGNPANEIKQRFDQDTINQLLDIKW
 WNWPIDIINENIDKILDNSIIREVIWKK
 >sp|Q49157|AAC2_MYCFO Aminoglycoside 2'-N-acetyltransferase OS=Mycobacterium
 fortuitum OX=1766 GN=aac PE=3 SV=1
 MPFQDVSAPVRGGILHTARLVHTSDLDQETREGARRMVIEAFEGDFSDADWEHALGGMH
 AFICHHGALIAHAAVVQRRLLYRDTALRCGYVEAVAVREDWRGQGLATAVMDAVEQVL
 RGAYQLGALSASDTARGMYLSRGWLPWQGPTSVLQPAGVTRTPEDDEGLFVLPVGLPAG
 MELDTTAEITCDWRDGDVW
 >sp|P05789|EREB_ECOLX Erythromycin esterase type II OS=Escherichia coli OX=562
 GN=ereB PE=4 SV=1
 MRFEWVKDKHIPFKLNHPDDNYDDFKPLRKIIGDTRVVALGENSHFIKEFFLLRHTLLRF
 FIEDLGFTTFAFEFGFAEGQIINNWIHGQGTDDDEIGRFLKHFYYPEELKTTFLWLREYNKAA
 KEKITFLGIDIPRNGGSYLPNMEIVHDFRTADKEALHIIDDAFNIAKKIDYFSTSQAALNLH
 ELTDSEKCRLTSQLARVKVRLEAMAPIHIEKYGIDKYETILHYANGMIYLDYNIQAMSGFI
 SGGGMQGDMDGAKDKYMADSVLWHLKNPQSEQKVIVVAHNAHIQKTPILYDGFSLCLPM
 GQRLKNAIGDDYMSLGITSYSGHTAALYPEVDTKYGFRVDNFQLQEPNEGSVEKAISGCG
 VTNSFVFFRNIPEDLQSIPNMIRFDSIYMKAELEKAFDGFQIEKSSVSEVVYE
 >sp|P10051|AAC6_CITKO Aminoglycoside N(6')-acetyltransferase type 1 OS=Citrobacter koseri
 OX=545 GN=aacA1 PE=3 SV=1
 MNYQIVNIAECSNYQLEAANILTEAFNDLGNNSWPDMTSATKEVKECIESPNLCFGLLINN
 SLVGWIGLRPMYKETWELHPLVVRPDYQNKIGIGKILLKELENRAREQGIIGIALGTDDEYY
 RTSLSLITITEDNIFDSIKNIKNINKHPYEFYQKNGYYIVGIIPNANGKNKPDIMWWSLIKE
 >sp|P23181|AACC1_PSEAI Gentamicin 3-N-acetyltransferase OS=Pseudomonas aeruginosa
 OX=287 GN=aacC1 PE=1 SV=1

MLRSSNDVTQQGSRPKTKLGGSSMGIIRTCRLGPDQVKSMAALDLFGREFGDVATYSQH
 QPDSYLGNLLRSKTFIALAAFDQEAUVGALAAAYVLPREFEQRSEIYIYDLAVSGEHRREQ
 IATALINLLKHEANALGAYVIYVQADYGDDPAVALYTKLGIREEVMHFDIDPSTAT
 >sp|Q54441|AAC6C_SERMA Aminoglycoside N(6')-acetyltransferase type 1 OS=Serratia
 marcescens OX=615 PE=1 SV=1
 MIVICDHDNLDLAWLALRTALWPSGSPEDHRAEMREILASPHHTAFMARGLDGAFVAFAE
 VALRYDYVNGCESSPVAFLEGIYTAERARRQGWAAARLIAQVQEWAKQQGCSELASDTDI
 ANLDSQRLHAALGFAETERVVFYRKTG
 >sp|Q44057|AAC6_ACIHA Aminoglycoside N(6')-acetyltransferase type 1 OS=Acinetobacter
 haemolyticus OX=29430 PE=1 SV=1
 MNIKPASEASLKDWLELRNKLWSDSEASHLQEMHQLLAEKYALQLLAYSDHQAIAMLEA
 SIRFEYVNGTETSPVGFLEGIYVLPARRSGVATMLIRQAQVWAKQFSCTEFASDAALDNV
 ISHAMHRSGLGFQETEKVVYFSKKID
 >sp|Q9R381|AAC6_SALEN Aminoglycoside N(6')-acetyltransferase type 1 OS=Salmonella
 enteritidis OX=149539 PE=1 SV=1
 MDIRQMKNKTHLEHWRGLRKQLWPGHPDDAHLADGEEILQADHLASFIAMADGVAIGFA
 DASIRHDYVNGCDSSPVVFLGIFVLPSPFRQGVAKQLIAAVQRWGTNKGCREMASDTSP
 ENTISQKVHQUALGFEETERVIFYRKR
 >sp|P18622|STRA_STRGA Streptomycin 6-kinase OS=Streptomyces glaucescens OX=1907
 GN=sph PE=3 SV=1
 MSTSKLVEIPEPLAASYARAFGEEGQAWIAALPALVEELDRWELTADGASASGEASLVL
 PVLRTDGTRAVLKLQLPREETSAAITGLRTWNGHGVVRLLDHDPSSMTLLERLDASRTL
 ASVEDDDAAMGVLAGLLARLVSVAPRGLRGLGDIAGAMLEEVPRAVAALADPADRRL
 LNDWASAVAELVGEPGDRMLHWDLHYGNVLAAREPWLAIDPEPLAGDPGFDLWPALD
 SRWDDIVAQRDVVRVRRRFDLLTEVLGLDRARAAGWTYGRLLQNALWDIEDGSAALD
 PAAVTLAQALRGH
 >sp|P13081|BLE_KLEPN Bleomycin resistance protein OS=Klebsiella pneumoniae OX=573
 GN=ble PE=1 SV=1
 MTDQATPNLPSRDFDSTAIFYERLGFVFRDAGWMILQRGDLMEFFAHPGLDPLASWF
 SCCLRLDDLAIFYRQCKSVGIQETSSGYPRIHAPELQEWGGTMAALVDPDGTLLRLIQNEL
 LAGIS
 >sp|P30899|BLAC_BACVU Beta-lactamase OS=Bacteroides vulgatus OX=821 GN=cfxA PE=3
 SV=1
 MEKNRKKQIVVLSIALVCIFILVFSLFHKSATKDSANPPLTNVLTDSISQIVSACPGEIGVAVI
 VNNRDTVKNVNNKSVYPMMSVFKVHQALALCNDFDNKGISLDTLVNINRDKLDPKTSWSP
 MLKDYSGPVISLTVRDLLRYTLTQSDNNASNLMMFKDMVNVAQTDSTFIATLIPRSSFQIAYT
 EEEMSADHNKAYSNYTSPLGAAMLMNRLFTEGLIDDEKQSFINKTLKECKTGVDRIAAPL
 LDKEGVVIAHKTGSGYVNENGVLAAHNDVAYICLPNNISYTLAVFVKDFKGNKSQASQY
 VAHISAVVYSLLMQTSVKS
 >sp|P96465|BLA2_STEMA Beta-lactamase L2 OS=Stenotrophomonas maltophilia OX=40324
 PE=3 SV=1
 MLARRRFLQFSGAAVASSLALPLLARAAGKTAASAPTDAAALTAATDFAALEKAVRGRFG
 VTLLDTASGRRIGHRQDERFPMCSTFKSVLAATVLSQAERQPALLDTRVPVRDADLLSHA
 PVTRRHAGKDMTVRDLCRATIITSDNTAANLLFGVVGGPPAVTAFLRSIGDAVSRTDRLEP
 ELNSFAKGDPRDTTTPAAMAATLQRVVLGEVLQLASRQQADWLIDNETGDACLRAGLG
 KLWRVRDKTGSNGEDARNDIAVLWPVAGGAPWVLTAYLQAGAISYEQRATVLAQVGRI
 ADRLIG
 >sp|P0A9Z9|BLA2_KLEPO Beta-lactamase SHV-2 OS=Klebsiella pneumoniae subsp. ozaenae
 OX=574 GN=bla PE=3 SV=1

MRYIRLCIISLLATLPLAVHASQPQLEQIKLSESQLSGRVGMIEMDLASGRTLTAWRADERF
PMMSTFKVVLGAVLARVDAGDEQLERKIHQRQDLVDYSPVSEKHLADGMTVGELCA
AAITMSDNSAANLLLATVGGPAGLTAFLRQIGDNVTRLDRWETELNEALPGDARDTTTPA
SMAATLRKLLTSQRLSARSQRQLLQWMVDDR VAGPLIRSVLPAGWFIADKTGASERGAR
GIVALLGPNKKAERIVVIYLRDTPASMAERNQQIAGIGAALIEHWQR

>sp|P28585|BLC1_ECOLX Beta-lactamase CTX-M-1 OS=Escherichia coli OX=562 GN=bla
PE=1 SV=2

MVKKSLRQFTLMATATVTLLLGSVPLYAQTADVQQKLAELERQSGGRLGVALINTADNS
QILYRADERFAMCSTSKVMAVA AVLKKSESEPNLLNQRVEIKKSDLVNYNPIAEKHVDGT
MSLAELSAAALQYSDNVAMNKLISHVGGPASVTAFARQLGDETFRLDRTEPTLNTAIPGD
PRDTTSPRAMAQTLRNLTGKALGDSQRAQLVTWMKGNTTGAASIQA GLPASWVVGDK
TGSGDYGTNDIAVIWPKDRAPLILVTYFTQPQPKAESRRDVLASAAKIVTNGL

>sp|Q47746|VANY_ENTFA D-alanyl-D-alanine carboxypeptidase OS=Enterococcus faecalis
(strain ATCC 700802 / V583) OX=226185 GN=vanYB PE=1 SV=1

MEKSNYHSNVNHHKRHMKQSGEKRAFLWAFIISFTVCTLFLGWRLVSVLEATQLPPIPAT
HTGSGTGVAENPEENTLATAKEQGDEQEWSLILVNRQNPIPAQYDVELEQLSNGERIDIRIS
PYLQDLFDAARADGVYPIVASGYRTTEKQQEIMDEKVAEYKAKGYTSAQAKAEAETWV
AVPGTSEHQLGLAVDINADGIHSTGNEVYRWLDENSYRFGFIRRYPPDKTEITGVSNEPWH
YRYVGIEAATKIYHQGLCLEEYLNTEK

>sp|P0AG05|S3AD_ECOLX Streptomycin 3"-adenylyltransferase OS=Escherichia coli OX=562
GN=aadA PE=4 SV=1

MREAVIAEVSTQLSEVVGVIERHLEPTLLAVHLYGSAVDGGLKPHSDIDLLVTVTVRLDET
TRRALINDLLETSPGGESEILRAVEVTIVVHDDIIPWRYPAKRELQFGEWQRNDILAGIFEP
ATIDIDLAILLTKAREHSVALVGPAAEELFDPVPEQDLFEALNETLTLWNSPPDWAGDERN
VVLTLRSRIWYSAVTGKIAPKDVAADWAMERLPAQYQPVILEARQAYLGQEEDRLASRAD
QLEEFVHYVKGEITKVVGK

>sp|Q7N8V7|RSMA_PHOLL Ribosomal RNA small subunit methyltransferase A
OS=Photobacterium luminescens subsp. laumondii (strain DSM 15139 / CIP 105565 / TT01)
OX=243265 GN=rsmA PE=3 SV=1

MNNRVHQGHFARKRFGQNFLTQDFVIDSIAAANPQPGQAVLEIGPGLGALTEPVGERMD
KMTVVELDRDLAARLQVHPQLKDKLTIIQQDAMTVNFGELSQQRGKPLRVFGNLPYNIST
PLMFHLFSYTDIAIDMHFMLQKEVVNRLVAGPGSKTFGRLSVMAQYYCQVIPVLEVPPT
AFTPAPKVDSAVVRLVPHKSIHPVKNIRMLSRIITQAFNQRRKTIRNSLGDLFTVEQLTEL
GIDPSTRAENISVEQYCKMANWLSEQPEMQS

>sp|Q7N0B9|UPPP_PHOLL Undecaprenyl-diphosphatase OS=Photobacterium luminescens subsp.
laumondii (strain DSM 15139 / CIP 105565 / TT01) OX=243265 GN=uppP PE=3 SV=1

MTDLSTLFHAAILGVVEGLTEFLPVSSSTGHMIIIVGHMLGFTGDKAETFEVIIQLGSILAVVV
VFWRRLFGLIGIHFGEVPHEGKTNGKLKLSHILAMLPAVTLGLMFHDVIKSLFNPQSVMY
ALVIGGVLLITAEILKPKTPKAEGLDITRYQAFMIGCFQCLALWPGFSRSGATISGGMLM
GVNRYTASEFSFILAVPMMMGASGLDLYKSLHFLSASDIPMFAVGFTAFVVALVAIKTF
LALIKRISFIPFAIRFIVAAAVYWVFM

>sp|Q00982|BLO5_PSEAI Beta-lactamase OXA-5 OS=Pseudomonas aeruginosa OX=287
GN=bla PE=3 SV=1

MKTIAAYLVLVFYASTALSESISENLAWNKEFSSES VHGVFVLCKSSSNSCTTNNAARAST
AYIPASTFKIPNALIGLETGAIKDERQVFKWDGKPRAMKQWEKDLKLRGAIQVSAVPVFQ
QIAREVGEIRMQKYLNLFSYGNANIGGGIDKFWLEGQLRISAFNQVKFLESYLYLNNLPASK
ANQLIVKEAIVTEATPEYIVHSKTGYSVGVTESSPGVAWWVGWVEKGTEVYFFAFNMID
DNESKLPSRKSISTKIMASEGIIIGG

>sp|Q51574|BLO15_PSEAI Beta-lactamase OXA-15 OS=Pseudomonas aeruginosa OX=287
GN=bla PE=1 SV=1

MAIRIFAILFSIFSLATFAHAQEGTLERSDWRKFFSEFQAKGTIVVADERQADRAMLVFDPV
RSKKRYSPASTFKIPHTLFDALDAGAVRDEFQIFRWGDNRGFAGHNQDQDLRSAMRNST
VWVYELFAKEIGDDKARRYLLKKIDYGNAGPSTSNNGDYWIEGSLAISAQEQIAFLRKLYRN
ELPFRVEHQRLVKDLMIVEAGRNWILRAKTGWEGRMGWVVGWVEWPTGVSFFALNIDT
PNRMDDLKREAIVRILRSIEALPPNPAVNSDAAR
>sp|P10738|ERMB_ECOLX rRNA adenine N-6-methyltransferase OS=Escherichia coli OX=562
GN=ermBC PE=3 SV=1
MNKNIKYSQNFLTSEKVLNQIIKQLNLKETDVTVEIGTGKGHLTTKLAKISKQVTSIELDSH
LFNLSSEKLKSNTRVTLIHQDILQFQFPNKQRYKIVGNIPYHLSTQIIKKVVFESHASDIYLIV
EEGFYKRTLDIHRTLGLLLHTQVSIQQLKLPAECFHPKPRVNSVLIKLTRHTTDVPDKYW
KLYTYFVSKWVNREYRQLFTKNQFHQAMKHAKVNNLSTVTYEQVLSIFNSYLLFNGRK
>sp|Q00014|ERMG_LACRE rRNA adenine N-6-methyltransferase OS=Lactobacillus reuteri
OX=1598 GN=ermGT PE=3 SV=1
MNKKNIKDSQNFITSKHHINEILRNVLNLTNDNIIIGSGKGHFSFELAKRCNYVTAIEIDPK
LCRITKNKLIYEYENFQVINKDILQFKFPKNKSYKIFGNIPYNISTDIIRKIVFESTATESYLIVE
YGFARLLNTNRSLALFLMTEVDISILSKIPREYFHPKPRVNSSLIVLKRHPSKISLKDRKQY
ENFVMKWVNKEYIKLFSKNQFYQALKYARIDDLNNISFEQFLSLFNSYKLFNR
>sp|P29806|AADB2_KLEPN 2"-aminoglycoside nucleotidyltransferase OS=Klebsiella
pneumoniae OX=573 GN=aadB PE=4 SV=1
MDTTQVTLIHQILAAADERNLPLWIGGGWAIDARLGRVTRKHDDIDLTTFPGERRGELEAM
VEMLGGRVTEELDYGFLAEIGDELDDCEPAWWADEAYEIAEAPQGSCEAAEGVIAGRPV
RCNSWEAIIWDYFYADEVPVDPWPTKHIESYRLACTSLGAEKVEVLRAAFRSRYAA
>sp|P19650|AAC6_KLEPN Aminoglycoside N(6')-acetyltransferase type 1 OS=Klebsiella
pneumoniae OX=573 GN=aacA4 PE=3 SV=1
MSIQHFQTKLGITKYSIVTNSNDSVTLRLMTEHDLAMLYEWNLRSHIVEWWGGEEARPTL
ADVQEQLPSVLAQESVTPYIAMLNGEPIGYAQSYVALGSGDGWWEETDPGVRGIDQL
LANASQLGKGLGTLKLVRLVELLFNDPEVTKIQTDPSPSNLRAIRCYEKAGFERQGTVTTP
DGPAVYVMVQTRQAFERTRVA
>sp|P37711|VANY_ENTFC D-alanyl-D-alanine carboxypeptidase OS=Enterococcus faecium
OX=1352 GN=vanY PE=2 SV=1
MKKLFFLLLLLLFLIYLGYYDYVNEALFSQEKVEFQNYDQNPKEHLENSGTSSENTQEKTITEE
QVYQGNLLINSKYPPVRQESVKSIVNLSKHDELINGYGLLDSNIYMSKEIAQKFSEMVND
AVKGGVSHFIINSGYRDFDEQSVLYQEMGAEYALPAGYSEHNSGLSLDVGSSSLTKMERAP
EGKWIEENAWKYGFILRYPEDKTELGTIYQYEPWHIRYVGLPHSAIMKEKNFVLEEYMDYL
KEEKTISVSVNGEKYEIFYYPVTKNNTTIHVPTNLRYEISGNNIDGVIVTVFPGSTHTNSRR
>sp|P69413|MERR_PESP Mercuric resistance operon regulatory protein OS=Pseudomonas sp.
OX=306 GN=merR PE=3 SV=1
MENNLENLTIGVFKAAGVNVETIRFYQRKGLLLEPDKPYGSIRRYGEADVTRVRVFKSA
QRLGFSLEIAELLRLLEDGTHCEEASSLAEHKLKDVREKMA DLARMEAVLSELVCACHA
RRGNVSCPLIASLQGGASLAGSAMP
>sp|P00808|BLAC_BACLI Beta-lactamase OS=Bacillus licheniformis OX=1402 GN=penP PE=1
SV=1
MKLWFSTLKLKKA AAVLLFSCVALAGCANNQTNASQPAEKNEKTEMKDDFAKLEEQFD
AKLGIFALDTGTNRTVAYRPDERFAFASTIKALTVGVLLQKQSIEDLNQRITYTRDDL VNY
NPITEKHVD TGMTLKE LADASLRYS DNAAQNLILKQIGGPESLKKELRKIGDEV TNPERFE
PELNEVN PGETQDTSTARALVTSLRAFALEDKLPSEKRELLIDWMKRNTTG DALIRAGVP
DGWEVADKTGAASYGTRNDIAIHWPPKGDPVVLAVLSSRDKKDAKYDDKLIAEATKVVM
KALNMNGK
>sp|P30180|AACC7_STRRY Aminoglycoside N(3)-acetyltransferase VII OS=Streptomyces
rimosus subsp. paromomycinus OX=92743 GN=aacC7 PE=3 SV=1

MDELALLKRS DGPVTRTRLARDLTALGLGDGDTVMFHTRMSAVGYVAGGPETVIGALR
DVVGERGTLMTVCWNDAPPYDFTDWPQTWQDARRAEHPAYDPVLSEADHNNGR LPE
ALRRRPGAVRSRHPDASFAALGAAATALTADHPWDDPHGPDSP LARLVAMGGRVLLLG
APLEALTLLHHAELADAPGKRFVDYEQPILVDGERVWRRFHDIDSEDGAFDYSALVPEG
TEAFEIIGRDMRAAGIGRRGTVGAADSHLFEARDVVDFGVAWMEEKLGRERGGPGG
>sp|Q02652|TETM_STRLI Tetracycline resistance protein TetM OS=Streptomyces lividans
OX=1916 GN=tetM PE=3 SV=1
MRTLNI GILAHVDAGKTS LTERLLFDHGAVDRLGSDAGDTRTV DGGIERRRGITIRSAVA
AFTVGDTRVNLIDTPGHSDFVAEVERALEVLDGAVLLLSAVEGVQARTRVLMRALRRRLR
LPTIVFVNKIDRAGARTDGLLG DVRRLLTPHVAPL TEVADAGTPRARVTRRPPDGRTAEA
LAEVDTEVLAALVDGPEPTGEDVARALAARTADGSFHP LYHGSALGGQGVAELVEGLLG
LIPAAATPGTSGGTSGGTEPRGTVF AVRPGPAGERTAYLR LYGGEVHPRRRLTFLRRES DGR
TTEVSGRVTRLDVVGGDATLTAGNIAALTVP GGLRVGDRLGGPTDRAPQFAPPTLQTLVR
ARHPEQAAPLRSALLALADQDPLLHARPAASGATALL YGEVQMEVLAATLAEDFGIEAE
FTPGRVRFLERPAGTDEAAEEMPWLDRTYFATIGLR VEPGPRGSGGAFGYETELGALPR
AFHQAVEETVHDTLRTGLTGAAVTDYRVTLIRSGFSSPLSTAADFRGLTPLVLRRALARA
GTVLHEPYQAFEA EVPADTLAAVTALLASLGADFTGTTGGDPAWIVTGELPARRVREAEL
RLPGLTHGEAVWSSRPCEDRPLKAGNSGPGTGVGGHSGE
>sp|B3U538|BL133_ACIRA Beta-lactamase OXA-133 OS=Acinetobacter radioresistens
OX=40216 GN=blaOXA-133 PE=2 SV=1
MNKYFTCYVVASLFFSGCTVQHNLINETQSQIVQGHNQVIHQYFDEKNTSGVLVIQTDKKI
NLYGNALSRANTEYVPASTFKMLNALIGLENQKTDINEIFKWKGEKRSFTTWEKDMTLGE
AMKLSAVPVYQELARRIGLDLMQKEVERIDFGNAEIGQQVDNFWLIGPLKVTPIQEVEFVS
QLAHTQLPFSEKVQANVKNMLLLEENNGYKIFGKTGWAMDIKPQVGWLTGWVEQPDGK
IVAFALNMEMRSEMPASIRNELLMKSLKQLNII
>sp|P24735|AMPC_PSEAE Beta-lactamase OS=Pseudomonas aeruginosa (strain ATCC 15692 /
DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964
GN=ampC PE=1 SV=2
MRDTRFPCLCGIAASTLLFATTPA IAGEAPADRLKALVDAAVQPV MKANDIPGLAVAISLK
GEPHYFSYGLASKEDGRRVTPETLFEIGSVSKTFTATLAGYALTQDKMRLDDRASQHWPA
LQGSRFDGISLLDLATYTAGGLPLQFPDSVQKDQAQIRDYYRQWQPTYAPGSQR LYSNPSI
GLFGYLAARSLGQPFERLMEQQVFPALGLEQTHLDVPEAALAQYAQGYGKDDRPLRVGP
GPLDAEGYG VKTSAADLLRFVDANLHPERLDRPWAQALDATHRGYYKVGDMTQGLGW
EAYDWPISL KRLQAGNSTPMALQPHRIARLPAPQALEGQRLLNKTGSTNGFGAYVAFVPG
RDLGLVILANRNYPNAERVKIA YAILSGLEQQGKVPLKR
>sp|P05364|AMPC_ENTCL Beta-lactamase OS=Enterobacter cloacae OX=550 GN=ampC PE=1
SV=1
MMRKS LCCALLLGISCSALATPVSEKQLAEVVANTITPLMKAQSVPGMAVAVIYQGKPH
YYTFGKADIAANKPVTPQTLFELGSISK TFTGVLGGDAIARGEISLDDAVTRYWPQLTGKQ
WQGIRMLDLATYTAGGLPLQVPDEVT DNASLLRFYQNWQPQWKPGTTRLYANASIGLFG
ALAVKPSGMPYEQAMTTRVLKPLKLDHTWINVPKAE EAHYAWGYRDGKAVRVSPGML
DAQAYGVKTNVQDMANWVMANMAPENVADASLKQ GIALAQSR YWRIGSMYQGLGWE
MLNWPVEANTVVEGSDSKVALAPLVAE VNPPAPPVKASWVHKTGSTGGFGSYVAFIPE
KQIGIVMLANTSYPNPARVEAAYHILEALQ
>sp|Q03170|BLP1_PSEAI Beta-lactamase PSE-1 OS=Pseudomonas aeruginosa OX=287
GN=psel PE=1 SV=1
MKFLLAFSLLIPSVVFASSSKFQQVEQDVKAIEVSLSARIGVSVLDTQNGEYWDYNGNQRF
PLTSTFKTIACAKLLYDAEQGKVNP NSTVEIKKADLV TYSPVIEKQVGQAITLDDACFATM
TTSDNTAANIILSAVGGPKGVTD FLRQIGDKETRLDRIE PDLNEGKLGDLRDTTTPKAIAS T

LNKFLFGSALSEMNOQKKLESWMVNNQVTGNLLRSVLPAGWNIADRSGAGGFGARSITAV
VWSEHQAPIIVSIYLAQTQASMAERNDIVKIGHSFVDVYTSQSR

>sp|P06548|BLA3_BACCE Beta-lactamase 3 OS=Bacillus cereus OX=1396 GN=blaZ PE=1
SV=1

MFVLNKFFTNSHYKKIVPVVLLSCATLIGCSNSNTQSES NKQTNQTNQVKQENKRNHAF
KLEKEYNAKLGIYALDTSTNQTVAYHADDRFAFASTSKSLAVGALLRQNSIEALDERITYT
RKDLSNYPITEKHVDTGMTLKLADASVRYSDSTAHNLILKKLGGPSAFEKILREMGDT
VTNSERFEPNEVNPGETHDTSTPKAIAKTLQSFTLGTVPSEKRELLVDWMKRNTTGD
KLIRAGVPKGWEVADKTGAGSYGTRNDIAIWPNNKKPIVLSILSNHDKEDAEYDDTLIAD
ATKIVLETLKVTNK

>sp|P80545|BLAC_SERFO Beta-lactamase OS=Serratia fonticola OX=47917 PE=1 SV=1

QPANAKANIQQQLSELEKNSGGRLGVALIDTADNSQILYRGDERFPMCSTSKVMAVSALL
KQSETDKNLLAKRMEIKQSDLVNYPNIAEKHLDTGMTLAEFSAATIQYSDNTAMNKILEH
LGGPAKVTEFARTIGDKTFRLDRTEPTLNTAIPGDKRDTTSPQAMASLQNLTLGKALAE
PQRAQLVEWMKGNTTGGASIRAGLPTTWVVGDKTGSGDYGTTNDIAVIWPANHAPLVLV
TYFTQPQQNAEARKDVLAAA AKIVTAGL

>sp|P22390|BLAC_CITKO Beta-lactamase OS=Citrobacter koseri OX=545 PE=1 SV=2

MFKKRGRQTVLIAAVLAFFTASSPLLARTQGEPTQVQQKLA ALEKQSGGRLGVALINTAD
RSQILYRGDERFAMCSTSKTMVAAAVLKQSETQHDILQQKMVIKKADLTNWNVPTEKYV
DKEMTLAELSAATLQYSDNTAMNKLEHLGGTSNVTAFARSIGDTTFRLLDRKEPELNTAI
PGDERDTTCPLAMAKSLHKLTLGDALAGA QRAQLVEWLKGNTTGGQSIRAGLPEGWV
GDKTGAGDYGTTNDIAVIWPEDRAPLILV TYFTQPQQDAKGRKDILAAA AKIVTEGL

>sp|P18623|VPH_STRVI Viomycin phosphotransferase OS=Streptomyces vinaceus OX=1960
GN=vph PE=3 SV=1

MRIIETHRDLLSRLLPGDTVGG LAVHEGQFHV VIGSHRVVCFARTRAAADRLPGRADV
RALAGIDLGFRTQPPLSEGAQGTDEPPYL VLSRIPGAPLEDDVLTSPEVAEAVARQYATL
LSGLAAAGDEEKVRAALPEAPANEWQEFATGVRT ELPMSDGGRERAERELAALDALP
HLTSAVVHGD LGGENVLWETVDGVPRMSGVVDWDEVGIGDPAEDLAAIGASYGEELG
RVLALGGWADNGTAERISAIRGTFALQQALYAQRDGDEEELADGLSGYR

>sp|Q0K7S4|UPPP_CUPNH Undecaprenyl-diphosphatase OS=Cupriavidus necator (strain ATCC
17699 / H16 / DSM 428 / Stanier 337) OX=381666 GN=uppP PE=3 SV=2

MEIALALKAVILGIVEGLTEFLPISSTGHLILAGQLLDFNDEKKGKIFEIVIQFGAILAVCWEFR
ARIGNVVRGLRAEPLAQRFAANVVIASVPAIVLAFIFGKWIKAHLFNPISVALAFIVGGVVI
LLAEWRDARRGT VSH PQGNALLEAAKAGAPRIESVDDL NWRDALKVGLAQCFALVPGTS
RSGATIIGGMLFGLSRQVATEFSFFLAIPVIFGATVYELYKARALLNGDDL GIFA VGFVFAF
LSAFLCVRWLLRFVATHDFKPF AWYRIAFGIVVLLTAYSGLVSWHA

>sp|P13661|BLO1_ECOLX Beta-lactamase OXA-1 OS=Escherichia coli OX=562 GN=bla PE=1
SV=2

MKNTIHINFAIFLIANIYSSASASTDISTVASPLFEGTEGCFLLYDASTNAEIAQFNKAKCA
TQMAPDSTFKIALSLMAFDAEIIDQKTIFKWDKTPKGMEIWNSNHTPKTWMQFSVVWVS
QEITQKIGLNKIKNYLKDFDYGNQDFSGDKERNNGLTEAWLESSLKISPEEQIQFLRKIINH
NLPVKNSAIENTIENMYLQDLDNSTKLYGKTGAGFTANRTLQNGWFEGFIISKSGHKYVF
VSALTGNLGSNLTSSIKAKKNAITILNTLNL

>sp|Q8CTJ6|UPPP_STAES Undecaprenyl-diphosphatase OS=Staphylococcus epidermidis (strain
ATCC 12228) OX=176280 GN=uppP PE=3 SV=1

MFLLELIKGIILGIVEGLTEFAPVSSTGHMILVDDMWL KSTNFLGSQSAFTFKVVIQLGVSF
AAAWVFRERFLEILHIGQHKPEPSTSGDRRSKPRRLNLHV LVGMVPAGILGFLFDDLIEKY
LFSVPTVLIGLFIGAIYMIADKYSKTVQHPQTVDQINYFQAFVIGISQAIAMWPGFSRSGSTI
STGVLMKLNHKAASDFTFIMSVPIMLAASGLSLLKH YEYIHLAHIPFYILGFLAAFIVGLIAI
KTFLLHLINKVKLVPF AIYRIVLVIFIAILYFGFGIGKGI

>sp|Q51355|BLC4_PSEAI Beta-lactamase CARB-4 OS=Pseudomonas aeruginosa OX=287
GN=carB4 PE=3 SV=1
MKLLLVSLLIPSMVFNSSKFQQVEQDAKVIEASLSAHIGISVLDTQTGEYWDYNGNQRF
PLTSTFKTIACAKLLYDAEQGEINPKSTIEIKKADLVITYSPVIEKQVGQAITLDDACFATMT
TSDNAAANIILNALGGPESVTDFLRQIGDKETRLDRIEPELNEGKLGDLRDTTPNAIVNTL
NELLFGSTLSQDGQKKLEYWMVNNQVTGNLLRSVLPEGWNIADRSGAGGFGARSITAVV
WSEAQSPIIVSIYLAQTEASIADRNDIVKIGRSIFEVYSSQSR

>sp|Q831R1|UPPP1_ENTFA Undecaprenyl-diphosphatase OS=Enterococcus faecalis (strain
ATCC 700802 / V583) OX=226185 GN=uppP PE=3 SV=1
MLFANLWKAILGIIIEGITEWLPISSTGHLILVDEFIKLDLSKDFMEMFNVVVIQLGAIMAVVI
LYFHKLNPFPKKNKEEKKDTWILWSKVLVACLPAAVIGLKFDDYLDHFYNFLTYSIML
IVYGIAFIIEKRKNVAPKCTNLKDFTYKAALIVGAFQVLALIPGTSRSGATILGAILIGASR
FVATEFSFFLGIPVMFGASFLKIFKFLAKGNTFGSEIIILITGSIVAFVVSIIAIKFLNLNLYLKK
DFTVFGWYRVILGAILIGYWLFS

>sp|P58740|UPPP1_AGRFC Undecaprenyl-diphosphatase 1 OS=Agrobacterium fabrum (strain
C58 / ATCC 33970) OX=176299 GN=uppP1 PE=3 SV=1
MGDQSIISALLGIIIEGLTEFIPVSSTAHLVLLAGHFLGFKSPGNTFAVLIQLGAILAILLVYFQ
KLVSIAVAMPTSARARRFVLAVLVAFLPAAVIGALAHDFIKTVLFETPMLICVVLIIGGFILL
AVDRMPLPKPYTDIMDYPPSLAFKIGLFQCLAMIPGTSRSGATIVGALLMGTDKRSAAEFS
FFLAMPTMLGAFVLDLYKNRDALSFDSDALIAVGFAAFVSGLFVVRSLDFVSRRGFAP
FAWWRIVIGALGLVALLVIG

>sp|A5W499|UPPP_PSEP1 Undecaprenyl-diphosphatase OS=Pseudomonas putida (strain ATCC
700007 / DSM 6899 / BCRC 17059 / F1) OX=351746 GN=uppP PE=3 SV=1
MDFWTAFAQAILGVVEGLTEFLPISSTGHQIIVADLIGFGERAMAFNIIQLAAILAVVWEF
RSKIFEVVFGLTHQPKARRFTGNLLLAFMPAVVLGVLFADLIHEYLFNPVTVAAALVVG
VIMLWAERRKHRVEVDHVDDMRWSHALKIGFIQCLAMIPGTSRSGSTIIGGLLFGLSRKA
ATEFSFFLAMPTMVGAAVYSGYKYRDLFQPGDLPVFALGFVTSFIFAMIAVRALLKFIANH
SYAAFAWYRIVFGLFILATWQFGWVDWSTAHG

>sp|P08988|AACC4_SALSP Aminoglycoside N(3)-acetyltransferase IV OS=Salmonella sp.
OX=599 GN=aacC4 PE=3 SV=2
MQYEWKRAELIGQLNLGVTPGGVLLVHSSFRSVRPLEDGPLGLIEALRAALGPGGTLVM
PSWSGLDDEPFDPATSPVTPDLGVVSDTFWRLPNVKRSAHPFAFAAAGPQAEQIISDPLPLP
PHSPASPVARVHELDGQVLLLGVGHDAANTTLHLAELMAKVYPYGVPRHCTILQDGKLVRV
DYLENDHCCERFALADRWLKEKSLQKEGPVGHAFARLIRSRDIVATALGQLGRDPLIFLH
PPEGGMRRMRCSRSPVDWLSS

>sp|P62594|BLAT_SALTI Beta-lactamase TEM OS=Salmonella typhi OX=90370 GN=bla PE=3
SV=1
MSIQHFRVALIPFFAAFCPLPVFAHPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEE
RFPMMSTFKVLLCGAVLSRVDAGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELC
SAAITMSDNTAANLLLTIGGPKELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDITMP
AAMATTLRKLTLGELLTLASRQQLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERGS
RGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIAEIGASLIKH

>sp|P9WQG9|AAC2_MYCTU Aminoglycoside 2'-N-acetyltransferase OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=aac PE=1 SV=1
MHTQVHTARLVHTADLDSETRQDIRQMTGAFAGDFTETDWEHTLGGMHALIWHHGAII
AHAAVIQRRLIYRGNALRCGYVEGVAVRADWRGQRLVSALLDAVEQVMRGAYQLGALS
SSARARRLYASRGWLPWHGPTSVLAPTGPVTRTPDDDGTVFVLPIDISLDTSAELMCDWRA
GDVW

>sp|A9VRT9|FOSB_BACWK Metallothiol transferase FosB OS=Bacillus weihenstephanensis
(strain KBAB4) OX=315730 GN=fosB PE=3 SV=1

MLKGINHLCFSVSNLENSITFYEKVLEGELLVKGRKLAYFNICGVWIALNEETHIPRKEIHQ
SYTHLAFSVEQKDFERLLHRLEENNVHILQGRERDVRDCESIYFVDPDGHKFEFHSGTLQD
RLNYYRDEKPHMTFY

>sp|B9IY29|FOSB_BACCQ Metallothiol transferase FosB OS=Bacillus cereus (strain Q1)
OX=361100 GN=fosB PE=3 SV=1

MLKGINHLCFSVSNLEDSITFYEKVLEGELLVRGRKLAYFNICGVWIALNEEIHIPRNEIHQ
SYTHIAFSVEQKDFERLLQRLEENDVHILQGRERDVRDCESIYFVDPDGHKFEFHSGTLQD
RLNYYREGKPHMTFY

>sp|P04190|BLA2_BACCE Metallo-beta-lactamase type 2 OS=Bacillus cereus OX=1396
GN=blm PE=1 SV=1

MKKNLTLLKVGLCVLLGTIQFVSTISSVQASQKVEKTVIKNETGTISISQLNKNVWVHTEL
GSFNGEAVPSNGLVLNTSKGLVLVDSSWDDKLTKELIEMVEKKFQKRVTDVIIITHAHADR
IGGIKTLKERGIKAHSTALTAELAKKNGYEEPLGDLQTVTNLKFGNMKVETFYPGKGHTE
DNIVVWLPQYNILVGGCLVKSTSADKLGNAVADAYVNEWSTSIENVLKRYRNINAVVPGH
GEVGDKGLLLHTLDLLK

>sp|Q02736|CAT_CLOBU Chloramphenicol acetyltransferase OS=Clostridium butyricum
OX=1492 GN=catB PE=3 SV=2

MNFNLDINHWSRKPYFEHYLNNVKCTYSMTANIEITDLLYEIKLKNIKFYPTLIYMIATVV
NNHKEFRICFDHKGSLGYWDSMNPSYTFHKENETFSIWTENKSFRLFYSYDYLDDIKNY
GNIMKFTPKSNEPDNTFSVSSIPWVSFTGFNLNVYNEGTYLIIFTAGKYFKQENKIFIPISIQ
VHHAICDGYHASRFINEMQELAFSFEWLENK

>sp|P07641|CAT_PROMI Chloramphenicol acetyltransferase OS=Proteus mirabilis OX=584
GN=cat PE=3 SV=1

MDTKRVGILVVDLSQWGRKEHFQAFQSAQCTFSQTVQLDITSLLKTVKQNGYKFYPTFI
YIISLLVNKHAEFRMAMKDGELVIWDSVNPNGYNIFHEQTETFSLSWSYHKDINRFLKTYS
EDIAQYGDDLAYFPKEFIENMFFVSANPWVSFTSFNLNMANINNFAPVFTIGKYTQGDK
VLMPLAIQVHHA VCDGFHVGRLLNEIQYCYDEGCK

>sp|P57296|PBPB_BUCAI Penicillin-binding protein 1B OS=Buchnera aphidicola subsp.
Acyrtosiphon pisum (strain APS) OX=107806 GN=mrcB PE=3 SV=1

MFFNFKKYFLIKVFFFLVLTLCYGLYLYVKINRFINGKVWNFPTSIYGRIVNLEPGNSYSQ
KEVLHLLKSTMYRKVDLVMLPGEYSIKNNTIEFIRRAFDPDFDIREDEFHARLYFNKDTLVKI
KNIDNNHDFSFRLEPKLIAMLSPEAKKRMFIPRNQYPEMLVKTLAIEDKYFYEHDGIH
LSSIGRAFLVNL MAGRTIQGGSTLTQQLIKNLFLTNTSRILRKINEIYMALILDRFYTKDRIL
ELYLNEVYLGQDGEQIRGFPLASIYYFGRPINELNEQYALLVGMVKGASLYSPWTNPN
LALKRRNLVFLLYKQKYITRKIYKDLCKRSLNVQPKGNISSHPSFIQLVCEEFHKKIYNPI
KNFPGTKIFTTLDYTSQNAVEQAVKIEIPILKRKKRLKDLEVAMIVIDRFTGEVQALIGSSKP
EFNGYNRALKTRRSIGSLSKPITYLTALSQPEKYHLNTWISNYPLSIKLDGQYWTPKNNN
FSFSKKVLLLDALHSINIPTVNLSINIGLKKLVDSWLLLGISKKYITPLPSISLGAINLTPFEIA
QVFQIIGSGGYKSSLSSVRSIISDDGKVLVYQNL PQSIHIESSEASYLTLYGMQQVVKSGTAK
SLGTIFKEFSLAGKTGTTNNLVDNWFVVGIDGKQIVITWIGRDNNHTTRYSSSGAMQIYKR
YLQYQRPVPLVLKAPNNINMFYINNLGELFCKKNNQHNRMLPIWSIKNKKICNDKLSERFS
IKKKKNFLFWLKNLF

>sp|P18539|AMPC_SERMA Beta-lactamase OS=Serratia marcescens OX=615 GN=ampC PE=3
SV=1

MTKMNRCAALIAALILPTAHAAQQQDIDAVIQPLMKKYGVPGMAIAVSVDGKQQIYPYG
VASKQTGKPITEQTLFEVGSLSKTFATLAVYAQQQSKLSFKDPASHYLPDVRGSAFDGVS
LLNLATHTSGLPLFVPDDVTNNAQLMAYYRAWQPKHPAGSYRVYSNLGIGMLGMIAAKS
LDQPFIQAMEQGMLPALGMSHTYVQVPAAQMANYAQGYSKDDKPVRVNPGLDAESYG
IKSNARDLIRYLDANLQQVKVASVARRWPRRTSVITSAGAFTQDLMWENYPYPVKLSRLI

EGNNAGMIMNGTPATAITPPQPELRAGWYNKTGSTGGFSTYAVFIPAKNIAVEMLANKW
 FPNDDRVEAAYHIIQALEKR
 >sp|Q06240|VANS_ENTFC Sensor protein VanS OS=Enterococcus faecium OX=1352 GN=vanS
 PE=3 SV=1
 MVIKLNKKNNDYSKLERKLYMYIVAIVVVAIVFVLYIRSMIRGKLGDWILSILENKYDLNH
 LDAMKLYQYSIRNNIDIFIYVAIVISILILCRVMLSFKAFKYFDEINTGIDVLIQNEDKQIELSA
 EMDVMEQKLNTLKRTEKREQDAKLAEQRKNDVVMYLAHDIKTPLTSIIIGYLSLLDEAPD
 MPVDQKAKYVHITLDKAYRLEQLIDEFFEITRYNLQTITLTKTHIDLYYMLVQMTDEFYPQ
 LSAHGKQAVIHAPEDLTVSGDPDKLARVFNNILKNAAAYSEDNSIIDITAGLSGDVVSIEFK
 NTGSIPKDKLAAIFEKIFYRLDNARSSDTGGAGLGLAIAKEIIVQHGGQIYAESNDNYTTFRV
 ELPAMPDLVDKRRS
 >sp|P29753|VANC_ENTGA Vancomycin C-type resistance protein VanC OS=Enterococcus
 gallinarum OX=1353 GN=vanC PE=2 SV=1
 MKKIAVLFGGNSPEYSVSLTSAASVIQAIDPLKYEVMTIGIAPTMDWYWYQGNLANVRN
 DTWLEDHKNCHQLTFSSQGFILGEKRIVPDVLFVPLHGKYGEDGCIQGLLELMNLPYVGC
 HVAASALCMNKWLLHQLADTMGIASAPTLILLSRYENDPATIDRFIQDHGFPIFIKPNEAGS
 SKGITKVTDKTALQSALTAFAYGSTVLIQKAIAGIEIGCGILGNEQLTIGACDAISLVDGFF
 DFEKYQLISATITVPAPLPLALESQIKEQAQLLYRNLGLTGLARIDFFVTNQGAIYLNEINT
 MPGFTGHSRYPAMMAEVGLSYEILVEQLIALAEEDKR
 >sp|P37321|BLE1_PSEAI Extended-spectrum beta-lactamase PER-1 OS=Pseudomonas
 aeruginosa OX=287 GN=per1 PE=1 SV=1
 MNVIKAVVTASTLLMVSFSSFETSQAQSPLLKEQIESIVIGKKATVGVAVWGPDDLEPLLIN
 PFEKFPMQSVFKLHLAMLVLHQVDQGKLDLNQTVIVNRAKVLQNTWAPIMKAYQGDEF
 SVPVQQLQYSVSHSDNVACDLLFELVGGPAALHDYIQSMGIKETAVVANEAMHADDQ
 VQYQNWTSMKGAAEILKKFEQKTQLSETSQLLWKWMVETTTGPERLKGLLPAGTVVA
 HKTGTSGIKAGKTAATNDLGIILLPDGRPLLVAVFVKDSAESSRTNEAIIAQVAQTAYQFEL
 KKLSALSPN
 >sp|P14171|BLAC_RHOCA Beta-lactamase OS=Rhodobacter capsulatus OX=1061 PE=3 SV=1
 MRFTATVLSRVATGLALGLSMATASLAETPVEALSETVARIEEQLGARVGLSLMETGTGW
 SWSHREDELFLMNSTVKVPVCGAILARWDAGRLSLSDALPVRKADLVPIYAPVTETRVGG
 NMTLDELCLAAIDMSDNVAANILIGHLGPEAVTQFFRSVGDPTSRLDRIEPLNDFASGD
 ERDTTSPAAMSETLRALLLGDVLSPEARGLAEWMRHGGVTGALLRAEAEDAWLILDKS
 GSGSHTRNLVAVIQPEGGAPWIATMFISDTDAEFEVRNEALKDLGRAVVAVVRE
 >sp|P29809|AACC8_STRFR Aminoglycoside N(3)-acetyltransferase VIII OS=Streptomyces
 fradiae OX=1906 GN=aacC8 PE=3 SV=1
 MDEKELIERAGGPVTRGRLVRDLEALGVGAGDTVMVHTRMSAIGYVVGPPQTVIDAVR
 DAVGADGTL MAYCGWNDAPPYDLAEWPPAWREAARAEPAYDPLLSEADRGNGRVPE
 ALRHQPGAVRSRHPDASFVAVGPAAHPLMDDHPWDDPHGPDSPARLAGAGGRVLLLG
 APLDTLTLHHAEARAEAPGKRFAVEQPVTVGGRRVWRRFRDVTSRGVVPYGRVPEG
 VVPFTVIAQDMLAAGIGRTGRVAAAPVHLFEAADVVRFVGVWIESRMGGAAGGA
 >sp|P16897|BLP4_PSEAI Beta-lactamase PSE-4 OS=Pseudomonas aeruginosa OX=287 GN=pse4
 PE=1 SV=1
 MKFLLAFSLLIPSVVFASSSKFQQVEQDVKAIEVSLSARIGVSVLDTQNGEYWDYNGNQRF
 PLTSTFKTIACAKLLYDAEQGKVNPNSTVEIKKADLVITYSPVIEKQVGQAITLDDACFATM
 TTSNTAANIILSAVGGPKGVTDFLRQIGDKETRLDRIEPLDNEGKLGDLRDTTTPKAIAS
 LNKFLFGSALSEMNOQKLESWMVNNQVTGNLLRSVLPAGWNIADRSGAGGFGARSITAV
 VWSEHQAPIIVSIYLAQTQASMEERNDAIVKIGHSIFDVYTSQSR
 >sp|P29810|AACC9_MICCH Aminoglycoside N(3)-acetyltransferase IX OS=Micromonospora
 chalybeata OX=1874 GN=aacC9 PE=3 SV=1

MEEMSLLNHSGGPVTRSRIKHDLDLGLKGDVVIFHTRMSAIGYVAGGTQTIIGALLDV
VGARGTLMVPCGWNNAPPYDFLDWPRDWQDALRAEHPAYDPDLSEADYNNGRLLPEALP
RWPGAIRSRHPDASFAALGPAAELMAEHPWDHPHGPDTPLARLIAHSGRVLLLGAPLDT
MTLLHHAELADVRSKRFTYEQPILVNGQRVWRQFRDIDSEEGAFDYSTVRRGVEPFEA
IARDMLSAGIGRQGRVGAADSYLFDAGPVFNFAINWIEAKLKR

>sp|Q00983|BLL1_PSEAI Beta-lactamase LCR-1 OS=Pseudomonas aeruginosa OX=287

GN=lcr1 PE=3 SV=1

MLKSTLLAFGLFIALSARAENQAIKFLFRAGVDGTIVIESLTTGQRLVHNDPRAQQRYPA
ASTFKVLNTLIALEEGAISGENQIFHWNGTQYSIANWNQDQTLDSAFKVCVWCYQQIAL
RVGALKYPAYIQQTNYGHLLEPFNGTEFWLDGSLTISAEQVAFLRQVVERKLPPKASSY
DSLKKVMFADENAQYRLYAKTGWATRMTPSVGWYVGYVEAKDDVWLFALNLATRDA
NDLPLRTQIAKDALKAIKAFPTK

>sp|P0A3M2|BLA5_PSEAI Beta-lactamase SHV-5 OS=Pseudomonas aeruginosa OX=287

GN=bla PE=3 SV=1

MRYIRLCIISLLATLPLAVHASPQPLEQIKLSSESQSLSGRVGMIEMDLASGRTLTAWRADERF
PMMSTFKVVLGAVLARVDAGDEQLERKIHQRQDLVDYSPVSEKHLADGMTVGECA
AAITMSDNSAANLLLATVGGPAGLTAFLRQIGDNVTRLDRWETELNEALPGDARDTTTPA
SMAATLRKLLTSQRLSARSQRQLQWMVDDR VAGPLIRSVLPAGWFIADKTGASKRGAR
GIVALLGPNKAERIVVIYLRDTPASMAERNQQIAGIGAALIEHWQR

>sp|P00485|CAT1_STAAU Chloramphenicol acetyltransferase OS=Staphylococcus aureus

OX=1280 GN=cat PE=2 SV=1

MNFNKIDLDNWKKEIFNHYLNQQTTF SITTEIDISVLRYNIKQEGYKFYPAFIFLVTRVINS
NTAFRTGYNSDGELGYWDKLEPLYTIFDGVSKTFSGIWTPVKNDKFEDYDLYLSDVEKYN
GSGKLFPKTPIPENAFSLSIIPWTSFTGFNLNINNSNYLLPIITAGKFINKGNSIYLPLSLQVH
HSVCDGYHAGLFMNSIQELSDRPNDWLL

>sp|P05051|AMPR_ENTCL HTH-type transcriptional activator AmpR OS=Enterobacter cloacae

OX=550 GN=ampR PE=3 SV=3

MTRSYLPLNSLRAFEAAARHLSFTHAAIELNVTHSAISQHVKTLEQHLNCQLFVRVSRGL
MLTTEGENLLPVLNDSFDRIAGMLDRFANHRAQEKLKIGVVGTFATGVLFSQLDFRRGY
PHIDLQLSTHNNRVDPAAEGLDYTIRYGGGAWHGTEAEFLCHAPLAPLCTPDIAASLHSPA
DILRFTLLRSYRRDEWTAWMQAAGEHPPSPTHRVMVFDSSVTMLEAAQAGVGIAIAPVD
MFTHLLASERIVQPFATQIELGSYWLTRLQSRAETPAMREFSRWLVEKMKK

>sp|Q04515|DYR10_ECOLX Dihydrofolate reductase type A10 OS=Escherichia coli OX=562

GN=dfrA10 PE=3 SV=1

MNISLIFANELITRAFGNQGKLPWQFIKEDMQFFQKTTENSVVVMGLNTWRSLPKMKKLG
RDFIVISSTITEHEVLNNNIQIFKSFESFLEAFRDTTKPINVIGGVGLLSEAIEHASTVYMSSIH
MVKPVHADVYVPVELMNKLYSDFKYPENILWVGDPIDSVYSLSIDKFVRPASLVGVPNDI
NT

>sp|P0A0U9|PBP2_NEIMB Probable peptidoglycan D,D-transpeptidase PenA OS=Neisseria

meningitidis serogroup B (strain MC58) OX=122586 GN=penA PE=3 SV=1

MLIKSEYKPRMLPKEEQVKKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ
GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSSAAQLERLSELVDV
PVDVLRNKLEQKGKSFIIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG
FTDIDGKGQEGLESLHGEDGAEVVLRDRQGNIVDSLDSRPNKAPKNGKDIILSLDQ
RIQTLAYEELNKAVEYHQAAGTVVVLDARTGEILALANTPAYDPNRPGRADSEQRRNR
AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQK
SSNVGTSKLSARFGAEEMYDFYHELIGVVRMHSGFPGETAGLLRNWRRWRPIEQATMSF
GYGLQLSLLQLARAYTALTHDGVLLPVSFQKQAVAPQGKRIFKESTAREVRNLMVSVTEP
GGTGTAGAVDGFVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA
HGYGYYGGVVAGPPFKKIMGGSLNILGISPTKPLTAAAVKTPS

>sp|P38422|DACF_BACSU D-alanyl-D-alanine carboxypeptidase DacF OS=Bacillus subtilis (strain 168) OX=224308 GN=dacF PE=2 SV=2
MKRLLSTLLIGIMLLTFAPSAFAKQDGKRTSELAHEAKSAVLIERTDTGKVLYNKNSNERLA
PASMTKIMTMLLIMEALDKGKIKMSDKVRTSEHAASMGGSQIFLEPGEEMTVKEMLKZIA
IASGNDASVAMAEFISGSEEEFVKKMNKKAKELGLKNTSFKNPTGLTEEGHYSSAYDMAI
MAKELLKYESITKFTGTIEDYLRENTDKKFWLVNTNRLIKFYPGVDGVKTGYTGAEAKYC
LTASAKKGNMRAIAVVFGASTPKERNAQVTKMLDFAFSQYETHPLYKRNQTVAKVKVK
KGKQKFIELTTSEPISILTKKGEDMNDVKKEIKMKDNISAPIQKGQELGTLVLKKDGEVLA
ESPVAAKEDMKKAGFITFLKRTMGDWTKFK

>sp|A2AXI2|CFR_STAWA Ribosomal RNA large subunit methyltransferase Cfr
OS=Staphylococcus warneri OX=1292 GN=cfr PE=3 SV=1
MNFNNTKTKYGKIQEFLRSNNPDYRIKQITNAIFKQIRSFEDMKVLPKLLREDLINNFGET
VLNIKLLAEQNSEQVTKVLFEVSKNERVETVNMKYKAGWESFCISSQCGCNFGCKFCATG
DIGLKKNLTVDEITDQVLYFHLLGHQIDSISFMGMGEALANRQVFDALDSFTDPNLFALSP
RRLSISTIGIIPSIKKITQEYPQVNLTFSLHSPYSEERSKLMPINDRYPIDVMNILDEHIRLTS
RKVYIAYIMLPGVNDSLEHANEVVSLLKSRYSKGLYHVNLRYNPTISAPEMYGEANEG
QVEAFYKVLKSAGIHVTIRSQFGIDIDAACGQLYGNYSQ

>sp|P40883|PCHR_PSEAE Regulatory protein PchR OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)
OX=208964 GN=pchR PE=2 SV=1
MTITIIAPPQADAAAPAPGNRPGVAHIDPNMKLVGTGFCASSEDWFEEPLERGLRLILVQSG
QLRCRIPGQPEHLIEGPSLCTIANDGDFTSAQIYGTDKPLRYTIVQLGVEALDSRLGWLPEQ
LIRRPGGDPRIMSCAPRAMQALASQIATCQMLGPTRDLYLGKALELAALSAQFLSGEG
RPVEEPRITCSEVERIHAARDLLVGALQEPPSLDTLASRVGMNPRKLTAGFRKVFVGASVFG
YLQEYRLREAHRLCDEEANVSTVAYRVGYSPAHSIAFRKRYGISPSEIR

>sp|Q06650|BLAC_STRCE Beta-lactamase OS=Streptomyces cellulosa OX=1968 GN=bla PE=3 SV=1
MRKPTSSLTRRSVLGAGLGLGGALALGSTTASAASAGTTPSENPAAVRRLRALEREHQAR
IGVFALNLATGASLLHRAHELFPMSVFKTLAAAVALRDLHDGSQLARVIRYTEADVTK
SGHAPVTKDHIDTGMTIRDLCDATIRYSDNCAANLLLRELGGPTAVTRFCRSLGDPVTRLD
RWEPELNSGEPDRRTDTTSPYAIARTYQRLVLGNALNRPDRALLTDWLLRNTTTLTTFRT
GLPKGWTVADKSGGGDTYGRNEAAIAWTPDGAPVLLTALTHKPSLPTAPGDTPLIILKLA
TVLSEAVAPA

>sp|Q59517|BLAF_MYCFO Beta-lactamase OS=Mycobacterium fortuitum OX=1766 GN=blaF PE=1 SV=1
MTGLSRRNVLIGSLVAAAAGVAGVGGAAPAFAPIDDLAELERRDNVLIGLYAANLQS
GRRITHRLDEMFMFCSTFKGYAAARVLQMAEHGEISLDNRVFDADALVPNSPVTEARA
GAEMTLAELCQAALQRSNTAANLLLKTIGGPAAVTAFAFSVGDERTRLDRWEVELNSA
IPGDPRTDTSTAAALAVGYRAILAGDALSPQGRLLLEDWMRANQTSSMRAGLPEGWTTAD
KTGSGDYGSTNDAGIAFGPDGQRLLLVMMTRSQAHDPAENLRPLIGELTALVLPSSL

>sp|A9HXK3|UPPP_BORPD Undecaprenyl-diphosphatase OS=Bordetella petrii (strain ATCC BAA-461 / DSM 12804 / CCUG 43448) OX=340100 GN=uppP PE=3 SV=1
MTDSTLYLIKAFFLGIIIEGLTEFIPVSSTGHLILIGDWINFTSSSGKVFEVVIQFGSILAVMWIF
RARLWQLIRGTLTGVPETAFTRNLLAFLPAAVVGAIKTIKQVFYHPGVVAVTLVLGG
LIMLWVERKTHHTPGDAPGAADDITASDERASAHTLEQISWKQALGVGVAQCLAMVPGT
SRSGATIIGGMIAGIQRKTATEFSFFLAMPTMLGAATYDLYRNIDLLSQHDLIAVGVFAA
AFISALVVVRAVLRVFNHTYRGFAWYRIALGIVVAAWLMTK

>sp|Q184H7|UPPP2_PEPD6 Undecaprenyl-diphosphatase 2 OS=Peptoclostridium difficile (strain 630) OX=272563 GN=uppP2 PE=3 SV=1

MMSLDVIFILKSVIIAIVEGLTEFIPVSSTGHMILVGNLIDFKGQFAEMFEVVIQLGAILAVV
VLYWKKIKDSVIEFFKFIFTGGKEGKIGFRFGMNVIIGCIPFAIIGVLFYDNIKSLFNLQSVIIG
FIVGGILLLVVETLFRKKNHSTDNIDKITPIQALKVGTQLQVLSAWPGMSRSASTIMGGWIA
GLNSPTAAEFSFFLAVPAMVASSGKDLFEFDYSIMTPTLWIALVVGFIIVAFIVSIIVMEKFV
NFLKKKPMRVFAVYRIIMGVVLAFLAFTNIISV

>sp|Q13V13|UPPP1_PARXL Undecaprenyl-diphosphatase 1 OS=Paraburkholderia xenovorans
(strain LB400) OX=266265 GN=uppP1 PE=3 SV=1

MDWLLACKALILGVVEGLTEFLPVSSTGHLIVAGSLLNFTDEHAKTFDVIQLGAILAVC
WEYRRRIGSVVSGLPSRPDARRFTLNVIIATIPAIVLGLLFEKTIKAALFSPVPVAFALVAGG
VVILWAESRQRTRGETVARVQNVDDLALDALKVGLAQCFALIPGMSRSGSTIIGGMLFG
LDRRVATEFSFFLAIPFIIFGATAYELHKDWHLLSVDALGTALGFVAAFVSAFACVRWLLR
YIAAHDTAFAWYRIGFGLLILLVGYSGALNWE

>sp|P43433|MYRB_MICGR Mycinamicin-resistance protein MyrB OS=Micromonospora
griseorubida OX=28040 GN=myrB PE=3 SV=1

MSSIRRRHAAASLDTPAVGGRHELGNFLVDRGVCTRIAEVVSSTTAHPVLELGAGDGAI
TRALVAANLPVTALELDPRRVRRLQRTFADGVTVVHGDMLRYDFGPYPHHVVSTVPFSIT
TPLRLRLIGQRFWHTAVLLVQWEVARKRAGVGGTMTLTAASWPWYEFTLVERVPKTSFD
PVPSVDGGILVIERRSAPLLDDRCVGDYQNLVREVYTGPRGLAAILRTRLPGREVDWL
RRERVDPAALPRDLKAGHWASLYRLYREVGTTPAPAGRSVRARPGSVGPDRSLPPRGLRS
GPPRRRRRGGA

>sp|A4VLM0|UPPP1_PSEU5 Undecaprenyl-diphosphatase 1 OS=Pseudomonas stutzeri (strain
A1501) OX=379731 GN=uppP1 PE=3 SV=1

MDLWVAIQALILGVVEGITEFLPVSSTGHQIIVADLIGFGERALAFNIIIQLGAILAVIWEY
RRKIIDVVVGLPEERQAQKFTVNLLIAFMPAVVLGVAFADLIHEYLFNPITVAAALVIGGIV
MLWAERRDHAIARAETVDDMTWTLALKVGFAQCLALVPGTSRSGSTIIGLLFGLSRKAAT
EFSFFLAMPTMVGAADVSGYKYRDLFQPGDFAVFAIGFVTSFIFAMLA VRALLKFIGNHSY
AAFAWYRIGFGLLILATWQLGMIDWSTAIG

>sp|Q4KC13|UPPP_PSEF5 Undecaprenyl-diphosphatase OS=Pseudomonas fluorescens (strain
ATCC BAA-477 / NRRL B-23932 / Pf-5) OX=220664 GN=uppP PE=3 SV=1

MDLWTAQAALILGIVEGLTEFLPISSTGHQIIVADLLDFGGERAMAFNIIIQLGAILAVVWE
FRRKILDVVIGLPTQPKAQRFTINLLIAFLPAVVLGVIFADLIHAYLFNPITVATALVVGGLI
MLWAERRQHQAETVDDITWKDALKVGCAQCLAMIPGTSRSGSTIIGLLFGLSRKTAT
EFSFFLAMPTMVGAADVSGYKYRHLFQPDFFPVFAIGFVTAFFVAMIAVKGLLKFIASHSY
AAFAWYRIAFGLLILATWQFGWVDWTAACP

>sp|O07293|BLO18_PSEAI Beta-lactamase OXA-18 OS=Pseudomonas aeruginosa OX=287
GN=bla PE=1 SV=1

MQRSLMSGKRHFIFAVSFVISTVCLTFSPANAAQKLSCTLVIDEASGDLLHREGSCDKAF
APMSTFKLPLAIMGYDADILLDATTPRWYKPEFNNGYKSQQKPTDPTIWLKDSIVWYSQE
LTRLRGESRFSYVQRFDYGNKDVSGDPGKHNLTHAWLASSLKISPEEQVRFLRRFLRG
ELPVSEDALEMTKAVVPHFEAGDWDVQGKTGTGSLSDAKGGKAPIGWFIGWATRDDR
VVFARLTVGARKGEQPAGPAARDEFLNTPALSENF

>sp|Q5WCX5|UPPP2_BACSK Undecaprenyl-diphosphatase 2 OS=Bacillus clausii (strain KSM-
K16) OX=66692 GN=uppP2 PE=3 SV=1

MDVWEWVVAAILGLVEGLTEYAPVSSTGHMIIVDDLWLKSELVGSQNAYVFKIVIQLGS
ILAVALLFKDRLLQLAGFKKQAATQSEGRGLTLGKVAVGLLPAAVLGLLFEDKMESIFHV
RTVAFALIAGAFLMIAADFINKRNNKKKQVDDISYKQALAIGLFQCLALWPGFSRSGSTI
SGGVMLGLTHRAAANFTFIMAIPIMVGASALSLIKNWDALDISLLPFYATGFISAFVLVSLVV
VRFFLKLINKIKLVFPALYRIALGLLLLFLFS

>sp|P14489|BLO10_PSEAI Beta-lactamase OXA-10 OS=Pseudomonas aeruginosa OX=287
GN=bla PE=1 SV=1

MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNGVFLCKSSSKSCATNDLARASK
EYLPASTFKIPNAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQ
QIAREVGEVRMQKYLKKFSYGNQNISSGIDKFWLEGQLRISAVNQVEFLESYLNKLSAS
KENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEKETEVYFFAFNM
DIDNESKLPLRKSIPTKIMESEGIIG

>sp|P29808|AACCC3_PSEAI Aminoglycoside N(3)-acetyltransferase III OS=Pseudomonas
aeruginosa OX=287 GN=aacC3 PE=3 SV=1

MTDLNIPHTHAHLVDAFQALGIRAGQALMLHASVKAVGAVMGGPNVILQALMDALTPD
GTLMMYAGWQDIPDFIDSLPDALKAVYLEQHPPFDPATARAVRENSVLAEFLRTWPCVH
RSANPEASMVAVGRQAALLTANHALDYGYGVESPLAKLVAIEGYVLMGLAPLDTITLLH
HAEYLAKMRHKNVVRYPILRDGRKVWVTVEDYDTGDPHDDYSFEQIARDYVAQGGG
TRGKVGADADAYLFAAQDLTRFAVQWLESRFGDSASYG

>sp|A0KQI1|UPPP_AERHH Undecaprenyl-diphosphatase OS=Aeromonas hydrophila subsp.
hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240)

OX=380703 GN=uppP PE=3 SV=1

MTESYALFVAFVLGIVEGLTEFLPVSSTGHMIIVGHLLGFDGPKAATFEVVIQMGSLAVV
AVFWRRLFGLIGHFGQKPAQGHATLSLVHIILGMLPAVIIGLAIHSWIKAHFLFGPQTVMYA
LVAGGILLIIAEKFRPAVRSETLDDISYKQALGIGLFQCLALWPGFSRSGATISGGMLMGIS
RQAAAEFSFILAVPMMVAASGLDLYKSRDLLSMADFPMFVAVGFITAFVAMIAIKTFLALI
RRLDFIPFAIYRFVVAFAVYLVFVA

>sp|Q01515|AAC3_SERMA Aminoglycoside N(3)-acetyltransferase III OS=Serratia marcescens
OX=615 GN=aac3-Vb PE=3 SV=1

MNTIESITADLHGLGVRPGDLIMVHASLKAVGPVEGGAASVVSALRAAVGSAGTLMGYA
SWDRSPYEETLNGARMDEELRRRWPPFDLATSGTYPGFLLNRFLLEAPDARRSAHPDAS
MVAVGPLAATLTEPHRLGQALGEGSPLEFVGHGGKVLLLGAPLDSVTVLHYAEIAPI
NKRRVTYEMPMLGPDGRVRWELAEDFDSNGILDCFAVDGKPDVETIAKAYVELGRHRE
GIVGRAPSYLFEAQDIVSFGVTYLEQHFGAP

>sp|A0R8Y3|UPPP1_BACAH Undecaprenyl-diphosphatase 1 OS=Bacillus thuringiensis (strain
Al Hakam) OX=412694 GN=uppP1 PE=3 SV=1

MSDIIAFILGIVEGLAEFLPISSTGHLILVGHLLGFEGERAKTFEIVIQLGAILAIAILYHKRLV
SLCNIKPLLKKEKFNFAHFVFLGVFPAVVAGLLLDHVIKTYLFQPYTVVIGLVAGAILMIF
AEVKKQEATSYSLDDLTyrQALTIGLFQCLAVYPGFSRAGSTISGLLAKVNYKTASEFSF
LIALPVMVGATGLDLLKSWTYLSVDDIPMFVAVGFITSFIVAMLAVVTFLLKLEKIGLKPF
YYRILLAILFTVFL

>sp|P14508|KKA7_CAMJU Aminoglycoside 3'-phosphotransferase OS=Campylobacter jejuni
OX=197 GN=aphA-7 PE=3 SV=1

MKYIDEIQILGKCSEGMSPAENVYKCKQLKNTVCYLKKIDDIFSKTTYSVKREAEMMMWLSD
KLKVPDVIEYGVREHSEYLIMSELRGKHIDCFIDHPIKYIECLVNALHQLQAIDIRNCPFSSK
IDVRLKELKYLLDNRIADIDVSNWEDTTEFDDPMTLYQWLCENQPQEELCLSHGDMSANF
FVSHDGIYFYDLARCGVADKWLDIAFCVREIREYYPDSYEFKFFNMLGLEPDYKKINYYI
LLEDMF

>sp|P37414|YTL1_SALTY Uncharacterized protein pSLT049 OS=Salmonella typhimurium
(strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=PSLT049 PE=4 SV=1

MKPAPGAEPVRMYKSPYGGKYGVWRLADCVPMRAKRPQTEKQRLASTRLGLQARMKS
ERGRFAMLAHTWLALGPVFLDTETTGLDAGAQALEIGLVNARGERIFETRLKPTVGIDPA
AAAVQIVTEPYRFPVLSVRLA

>sp|P00487|CAT_BACPU Chloramphenicol acetyltransferase OS=Bacillus pumilus OX=1408
GN=cat86 PE=2 SV=1

MFKQIDENYLKKEHFHHYMTLTRCSYSLVINLDITKLHAILKEKKLVYPVQIYLLARAVQ
KIPEFRMDQVNDDELGYWEILHPSYITLNKETKTFSSIWTPFDENFAQFYKSCVADIETFSKS

SNLFPPKPHMPENMFNISSLPWIDFTSFNLSNVSTDEAYLLPIFTIGKFKVEEGKIILPVAIQVH
HAVCDGYHAGQYVEYLRWLIEHCDEWLNDLSLHIT
>sp|Q47744|VANR_ENTFA Regulatory protein VanRB OS=Enterococcus faecalis (strain ATCC
700802 / V583) OX=226185 GN=vanRB PE=3 SV=1
MSIRILLVEDDDHICNTVRAFLAEARYEVDACDGTGNEAHTKIFYENTYQLVILDIMLPGMN
GHELLREFRAQNDDTPILMMTALSDDENQIRAFDAEADDYVTKPFKMRILLKRVEALLRRS
GALAKEFRVGRILTLLPEDFRVLCDDGTTELPLTRKEFEILLVQNKGRTLTHEIILSRIWGYD
FDGDGSTVHTHIKNLRAKLPENIKTIRGVGYRLEESL
>sp|A7Z3A4|FOSB_BACVZ Metallothiol transferase FosB OS=Bacillus velezensis (strain DSM
23117 / BGSC 10A6 / FZB42) OX=326423 GN=fosB PE=3 SV=1
MLNEVGKINIKGINHLLFSVSNLEKSIEFYEKVFHAQLLVKGQKTAYFDLNGWLALNLE
ADIPRNEIHKSYTHMAFTIDPKDFDAIHHRLKNLNVNINLNGRPRDKQDQKSIYFTDPDGHK
FEFHTGTQLQDRLSYYKKDKPHMKFYI
>sp|Q9KBZ6|FOSB_BACHD Metallothiol transferase FosB OS=Bacillus halodurans (strain
ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) OX=272558 GN=fosB PE=3
SV=1
MRIQGINHLLFSVKCLERSIEFYKKALGAKLLVKGRTTAYFDLQGIWLALNEEPDIPRNEIH
QSYTHIAFTVGEEEMEEAYERLAGLVNILKGRPRDPRDRQSIYFTDPDGHKFEFHCCTLN
DRLDYYREAKPHMTFFDD
>sp|A4IS40|FOSB_GEOTN Metallothiol transferase FosB OS=Geobacillus thermodenitrificans
(strain NG80-2) OX=420246 GN=fosB PE=3 SV=1
MRIGGINHLTFSVSDLEKSIHFYQNVFGAKLLVKGRNLAYFDLNGIWLALNVQQDIPRNDI
QHSYTHIAFSVKEEDFDHVVEKLKELGVNILPGRERDERDKRSVYFTDPDGHKFEFHTGT
NDRLSYYKSEMHHMQFFD
>sp|P72533|TETO_STREE Tetracycline resistance protein TetO OS=Streptococcus pneumoniae
OX=1313 GN=tetO PE=3 SV=1
MKIINLGILAHVDAGKTTLTESLLYTSGAIAEPGSVDKGTTRTDTMNLERQRGITIQTAVTS
FQWEDVKVNIIDTPGHMDFLAEVYRSLSVLDGAVLLVSAKDGIQAQTRILFHALQTMKIP
TIFFINKIDQEGIDLPMVYQEMKAKLSSEIIVKQKVGQHPHINVTNDNDMEQWDAVIMGN
DELLEKYMSGKPFKMSELEQEENRRFQNGTLFPVYHGS AKNNLGIRQLIEVIASKFYSSTP
EGQSELGQVFKIEYSEKRRRFVYVRIYSGTLHLRDVIKISEKEKIKITEMCVPTNGELYSS
DTACSGDIVILPNDVLQLNSILGNEMLLPQRKFIENPLPMLQTTIAVKKSEQREILLGALTEI
SDGDPLLKYYVDTTTHEIILSFLGNVQMEVICAILEEKYHVEAEIKEPTVIYMERPLRKA
EYTIHIEVPPNPFWASVGLSIEPLIGSGVQYESRVSLGYLNQSFQNAVMEGVLYGCEQGLYG
WKVTDCKICFEYGLYSPVSTPADFRLLSPIVLEQALKKAGTELLEPYLHFEIYAPQEYLSR
AYHDAPRYCADIVSTQVKNDEVILKGEIPARCIQEYRNDLTFTNGQGVCLTELKGYQPAI
GKFICQPRRPNSRIDKVRHMFHKL
>tr|D2JGC2|D2JGC2_STAAU Lincosamide nucleotidyltransferase OS=Staphylococcus aureus
OX=1280 GN=lnu(A) PE=4 SV=1
MKNNNVTEKDLFYILDLFEHMKVITYWLDGGWGVLDVLTGKQQREHRDIDIDFDAQHTQK
VIQKLEDIGYKIEVDWMPARMELKHEEYGYLDIHPINLNDGSGITQANPEGGNYVFQNDW
FSETNYKGRKIPCISKEAQLLFHSGYDLTEKDHFDIKNLKSIT
>sp|A0A0D2YG02|FUB7_FUSO4 Sulfhydrylase FUB7 OS=Fusarium oxysporum f. sp.
lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) OX=426428 GN=FUB7
PE=1 SV=1
MAEQVFQNFETLQLHAGYTPDPHTRSTAVPIYATSSYTFNDSAHGARLFGKELGNIYSRL
MNPTVDVFEEKRIAALLEGIAAAATSSGQAAQFLTIATLAKAGDNIVASSHLYGGTYNQLN
VLLPRFGIKTKFVRSGLLEDYAAAIDDQTRAIYVESMSNPDYVVPDFEGIAKIAHEHGIPLV
VDNTLGAGGYYIRPIEHGADIVVHSATKWIGGHGTTIGGVIVDSGRFNWNKHSERFPEMV
EPSPSYHGLKYWEAFGPATFITRIRVEMLRDIGACLSFSAQQLLGIETLGLRAERHAQNT

EKLAKYFESSPNVSWVLWPGSESHPTYAQAKKYLTRGFGAMLSIGVKGDASAGSKVVDG
LKLVSNLANVGDAKSLAIHPWSTTHEQLSEDERLASGVTEDMIRISVGIEHVDDIADFEQS
FQKAYGS

>sp|A0R066|ILVE_MYCS2 Branched-chain-amino-acid aminotransferase OS=Mycobacterium
smegmatis (strain ATCC 700084 / mc(2)155) OX=246196 GN=ilvE PE=1 SV=1
MNSGPLEFTVSANTNPATDAVRESILANPGFGKYTDHMSIDYTVDEGWHNAQVIPYGP
IQLDPSAIVLHYGQEIFEGLKAYRWADGSIVSFRPEANAARLQSSARRLAIPELPEEVFIESL
RQLIAVDEKWVPPAGGEESLYLRPFVIATEPGLGVRPSNEYRYLLIASPAGAYFKGGIKPVS
VWLSHEYVRASPGGTGAAKFGGNYAASLLAQAQAEMGCDQVWLDIERRYVEEMG
GMNLFFVFGSGGSARLVTPELSGSLLPGITRDSLLQLATDAGFAVEERKIDVDEWQKKAG
AGEITEVFACGTAAVITPVSHVKHHDGEFTIADGQPGEITMALRDTLTGIQRGTFADTHGW
MARLN

>sp|A0AI83|CODY_LISW6 GTP-sensing transcriptional pleiotropic repressor CodY OS=Listeria
welshimeri serovar 6b (strain ATCC 35897 / DSM 20650 / SLCC5334) OX=386043 GN=codY
PE=3 SV=1

MTLLEKTRKINAMLQNAAGKTVNFKEMADTLTDVIEANTYIVSRKGKLLGYSESLPIEND
RMKQMLTERQFPPEYTQSLFNVGETSSNLEVSSQYTAFFIENSDFTKGLTTIVPIVGGGER
LGTLLSRLESNFTDDDLLAEYGGTVVGMEILHEKAEEIEEARSRAVVQMAISSLSYSEL
EAIEHIFDELNGKEGLLVASKIADRVGITRSVIVNALRKLESAGVIDSRSLGMKGTFFIRVLN
DKFLVELEKLN

>sp|A0AJY3|MNTR_LISW6 HTH-type transcriptional regulator MntR OS=Listeria welshimeri
serovar 6b (strain ATCC 35897 / DSM 20650 / SLCC5334) OX=386043 GN=mntR PE=3 SV=1
MPTPSMEDYIEKIYSLIETKGYARVSDIADLDFVHPSSVTKMVQKLDKDEYLIYEKYRGLIL
TPKGTQMGRLLERHALLESFLSIIGVDSSHIYHDVEGIEHHLSWNSIDRIGNVVQFFENHP
DALEALKAMETTKPETNE

>sp|A0LLH2|YIDD_SYNFM Putative membrane protein insertion efficiency factor
OS=Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB) OX=335543 GN=Sfum_2596
PE=3 SV=1
MIRSIFLGLIRFYQIVLSPLKGPRCRFLPTCSQYAYEAIERYGIWRGLFLGGKRLLRCHPFHA
GGYDPVPRPSANNHPSR

>sp|O06474|YFMP_BACSU HTH-type transcriptional regulator YfmP OS=Bacillus subtilis
(strain 168) OX=224308 GN=yfmP PE=2 SV=1
MEWMKIDQVAKRSGLTAKRTIRFYEEIGLIPAPKRTDGGVRLYSEDDMEELEKVVISTKEVLG
FSLQELQHFMTSRQLELNKEGYLLSLDPKERKEKLEEIQETLNHQLDLIDEKIRTFQSFKE
RLQGMKGKAERAIQSIE

>sp|B1Q2A8|NPHR_RHOSO Transcriptional activator NphR OS=Rhodococcus sp. OX=1831
GN=nphR PE=1 SV=1
MAEREQSNDARTDVPAIVSLRTRELDTGEGRMQWASTLERLYCETDVAWPEPRRHFDA
EWGGRPFGLHVSTIRADAHTVVRSPAMIQSDSGEGLVCLVTDGVSVEVRQSGRATVVEP
GSFALLDCAAPFVFHSPAPFRQVVVRSPREVLTSRLPGRIVEHGTARSIHGDTGAGGLVGR
LFVDIADMDAPMSQGAAVSFASSAVDMLATALTEGLLATSAADLHRTEDLTRVQRVIEQ
NLHDADITLSDIAAAAGMSLRTVHKLFNAEGTTTRAWLYQARLEAARRYLLTTDLSVAD
VSECAGFRDVSHFSRLFRSTFGSSPGLYRKEHARIGS

>sp|P0A3M3|BLO9_KLEPN Beta-lactamase OXA-9 OS=Klebsiella pneumoniae OX=573
GN=bla PE=3 SV=2
MKKILLHMLVFVSATLPISSVASDEVETLKCTIADAITGNTLYETGECARRVSPCSSFKLP
LAIMGFDGILQSPKSPTWELKPEYNPSPRDRTYKQVYPALWQSDSVVWFSQQLTSLRGV
DRFTEYVKKFEYGNQDVSGDSGKHNGLTQSWLMSSLTISPKEQIQFLLRFVAHKLPVSEA
AYDMAYATIPQYQAAEGWAVHGKSGSGWLRDNNGKINESRPQGWFVGWAEKNGRQVV
FARLEIGKEKSDIPGGSKAREDLVELPVLGMNK

>sp|A0A0H3MDW1|CHXR_CHLT2 Atypical response regulator protein ChxR OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) OX=471472 GN=chxR PE=1 SV=1
MAGPKHVLLVSEHWDLFFQTKELLNPEEYRCTIGQQYKQELSADLVVCEYSLLPREIRSPK
SLEGSFVLVLLDFFDEETSVDLLDRGFWYLIRPITPRILKSAISLFLSQHSLHSVPESIRFGPN
VFYVLKLTVETPEGSVHLTPSESGILKRLLINKGQLCLRKHLLLEEIKNHAKAIVARNVDVHI
ASLRKKLGAYGSRIVTLRGVGYLFSDDGDKKFSQQDTKLS

>sp|A0PWB3|MPRB_MYCUA Signal transduction histidine-protein kinase/phosphatase MprB
OS=Mycobacterium ulcerans (strain Agy99) OX=362242 GN=mprB PE=3 SV=1
MVGFRRGPRAPLRATSSLSLRWRVMLLAMSMVAMVVVLMMSFAVYAVISAALYSDIDNQ
LQSRQLLIASGSLAADPGKAIEGTAYSDVNAMLVNPGRSIYTANQPGQTLPGGAPEKAVI
HGDFLSRRTVSDQRVLAIHLPNGSSLLISKSLKPTEAVMTKLRAVLLIVGGVGVAVAAV
AGGMVTRAGLRPVGRLTEAAERVARTDDLPIPVFGSDELARLTEAFNLMLRALAESRER
QARLVSDAGHELRTPLTSLRTNVLLMASMEPGAPRLPEQEMVGLREDVVAQIEELSTLV
GDLVDLTRGDAGVVVHEPVDMAEVVDRSLERVRRRRNDIHFDVDVVGWQVYGDAAGL
SRAALNLMDNAAKWSPPGGRVGIRLRQLDPSHAELVSDNGPGISPQERRLVFERFYRST
SARAMPGSGLGLAIVKQVVLNHGGSRLIEDTVPGGQPPGTAICMLLPGRPMPDSAYPAAP
DDKKTEPVDTRGANGANSRGSANVISVDSQSARAR

>sp|A0A067XMV2|PTAH_PESFW Methyltransferase ptaH OS=Pestalotiopsis fici (strain W106-1 / CGMCC3.15140) OX=1229662 GN=ptaH PE=2 SV=1
MSTNDEVFAKDNEFWKTYLRGRAQPPESSFERIFRYHEDHGGHFGTVHDCGAGNGPYSQ
KLRSRFKHVIVSDVAPGNVELAKERLGNDGFSFRVARVEDFDDIPTGSVDLVFATNVMH
WVEPSRGAKAIVSQLKSGGTFFAAGFGPARFEDQKVQDIWTRISQSGGRRLLMKADDPTKI
LKVAVRSSRYVDVAPTDTSLFVPGTQRIHLNMNNGGLTDIVYPEDYVAAAEPSTYGPQDD
EIFESEDGWSFETDLEGVKDHFATFPFSKEDPEVFAELWAELEKYVADGRPIRGCPAKII
LATRV

>sp|O66565|Y178_AQUAE Universal stress protein Aq_178 OS=Aquifex aeolicus (strain VF5)
OX=224324 GN=aq_178 PE=1 SV=1
MKVLLVLTDAYSDEKAITYAVNFSEKLGAELDILAVLEDVYNLERANVTFGLPFPPEIKE
ESKKRIERRLREVWEKLTGSTIEPGVEYRIGPLSEEVKKFVEGKGYELVWWACYPSAYLCK
VIDGLNLASLIVK

>sp|A0JZC7|TYSY_ARTS2 Thymidylate synthase OS=Arthrobacter sp. (strain FB24)
OX=290399 GN=thyA PE=3 SV=1
MSIPTPYEDLLRDVLANGTHKSDRTGTGTLSVFGRQMRFDLSQSFPLITTKRVHFKSVAVE
LLWFLRGETNVKWMQDQGVTIWNEWADADGELGPVYGVQWRSWPTPDGGHIDQIAEL
VENLKSNPDSRRHIVSAWNVAELQDMALPPCHAFFQFYVADGKLSCQLYQRSADTFLGV
PFNIASYALLTCMLAQVVGLEPGFVWTGGDVHIYDNHMDQVLKQLKREPYEYPQLKIL
RKPDSIFDYTLDDFEVVGYYHHPTIKAPIAV

>sp|A0AJY0|TYSY_LISW6 Thymidylate synthase OS=Listeria welshimeri serovar 6b (strain ATCC 35897 / DSM 20650 / SLCC5334) OX=386043 GN=thyA PE=3 SV=1
MKQYLDLEKYVLENGTQKGDRTGTGTISTFGYQMRFDLQEGFPIMTTKRVPFKLVVSELL
WFLHGD TNIRYLLQHNNNIWNEWAFERFVKSADYKGEDMTDFGLRAERDPAFKEVYQA
EMEQFKTRILEDEGFANKYGELGNIYGKQWREWKTSQGETIDQLADVIEMIKTNPNSRRLI
VSAWNPEDIPNMALPPCHSLFQFYVADGKLSCQLYQRSADIFLGVPFNIASYALLTHLIAR
EVGLDVGEFIHTMGDAHLYNNHIEQVKEQLSRTPHALPKLVLSDKPTTIFDFDVADISLDG
YHPDPAIKAPISV

>sp|A0AHA7|RF3_LISW6 Peptide chain release factor 3 OS=Listeria welshimeri serovar 6b (strain ATCC 35897 / DSM 20650 / SLCC5334) OX=386043 GN=prfC PE=3 SV=1
MSQDLQKEVASRKTFAIISHPDAGKTTITEQLLLFGGVIRSAGTVKGKKSGKFATSDWMEI
EKQRGISVTSSVMQFDYNGSRINILDTPGHSDFSEDTYRTLMAVDSAVMVIDAAKGIEAQT
LKLFKVCRMRIPIFTFINKMDRQGGKMPLELLAELEEVLIESYPMNWPIMGMGKELAGLYD

RYHRVIEQYRSEEDERFLPLGEDGDLKEAHEIQKSLYYDQALEEIMLLDEAGNDFSRRERIL
AGEQTPVFFGSALTNFGVETFLRTFVDFAPAPSSSHESNEGIIHADNPKFSGFIFKIQANMNPA
HRDRIAFIRICSGEFERGMNVTLTRTGKSIKLANSTQFMADDRETVNRAVAGDIIGLYDTG
NYQIGDTITNGSKKLEFEKLPQFTPELFMRVYAKNVMKQKHFFHKGVEQLVQEGAIQLFKT
WRTEEYIIGAVGQLQFEVFEHRMRGEYNSEIRMEPIGKKIARWVKEEDADEKLSTARSML
VKDRFDQPLFLFENEFAINWFNDKNPDIELTSSL

>sp|A0ALY8|EFTU_LISW6 Elongation factor Tu OS=*Listeria welshimeri* serovar 6b (strain ATCC 35897 / DSM 20650 / SLCC5334) OX=386043 GN=tuf PE=3 SV=1

MAKEKFDRSKPHVNIGTIGHVDHGGKTTLTAAITTVLAKKGYADAQAYDQIDGAPEERER
GITISTAHVEYQTD SRHYAHVDCPGHADYVKNMITGAAQMDGAILVVSAAADGMPMQTRE
HILLSRQVGVPYIVVFMNKCDDMVDEELLELVEMEIRDLLTEYEFPGDDIPVIKGSALKAL
QGEADWEAKIDELMEAVDSYIPTPERDTDKPFMMPVEDVFSITGRGT VATGRVERGQVK
VGDEVEVIGIEEESKKVVVTGVEMFRKLLDYAEAGDNIGALLRGVAREDIQRGQVLAKPG
SITPHTNFKAETYVLTKEEGGRHTPPFNRYRPQFYFRITDVTGIVTLPEGTEMVMPGDNIE
LAVELIPIAIEDGTFKSIREGGRTVGAGVVSNIK

>sp|A4JGI0|RLMH_BURVG Ribosomal RNA large subunit methyltransferase H

OS=*Burkholderia vietnamiensis* (strain G4 / LMG 22486) OX=269482 GN=rlmH PE=3 SV=1

MKLYILAVGHKMPGWIASGFDEYTKRMPPELRIELREIKPELRSGGRSAESVMAAERQKIE
AALPKGARIVALDERGRDWTMQLAQALPGWQQDGRDVA FVIGGADGLDPEL KARADL
LLRISSMTLPHGMVRVLLAEQLYRAWSITQNHYPYHRA

>sp|B2IHG2|KHSE_BEII9 Homoserine kinase OS=*Beijerinckia indica* subsp. *indica* (strain ATCC 9039 / DSM 1715 / NCIB 8712) OX=395963 GN=thrB PE=3 SV=1

MAVYTHISETDLKTFLASYDIGNALVLKGIAEGVENSNNFFLQTERGFFILTLYEKRVEEKDL
PFFLGLMEHLSRRGLNCPQPVHNRSGLALGRLAGRPVIVTFLEGVGADVADARRCAAV
GEALARLHQAGADFAGKRTNALGLAAWRPLFETVRDRADTVAPALAAATIAEELDFLEAH
WPRALPQGVIIHADLFPDNLVFRGETLSGLIDFYFACVDAYAYDIAICLNAWCFEPDLTFNI
GKGLAFFTGYEHVRKLTAEAAAALPVLARGGALRFALTRLVDWLNVPKGAMVNP KDPL
EYMGKLAHFHQTVGT VRELGLLR

>sp|P0A5I5|KGUA_MYCBO Guanylate kinase OS=*Mycobacterium bovis* (strain ATCC BAA-935 / AF2122/97) OX=233413 GN=gmk PE=3 SV=1

MSVGEGPDTPKPTARGQPAAVGRVVVLSGPSAVGKSTVVRCLRERIPNLHFSVSATTRAPR
PGEVDGVDYHFIDPTRFQQQLIDQGELLEWAEIHGGLHRSGLTAQPVRAAAATGVPVLIEV
DLAGARAIKKTMPEAVTVFLAPPSWQDLQARLIGRGTTETADVIRRLDTARIELAAQGDF
DKVVVNRRLESACAELVSLVGTAPGSP

>sp|A1E9Q2|RR12_SORBI 30S ribosomal protein S12, chloroplastic OS=*Sorghum bicolor*
OX=4558 GN=rps12-A PE=3 SV=1

MPTVKQLIRNARQPIRNARKSAALKGCPQRRGTCARVYTINPKKPNSALRKVARVRLTSG
FEITAYIPGIGHNLQEHSVVLVRGGRVKDLPVRYRIIRGTLDAAVAVKNRQQGRSKYGAK
KPKK

>sp|B3DMA2|ACD11_RAT Acyl-CoA dehydrogenase family member 11 OS=*Rattus norvegicus*
OX=10116 GN=Acad11 PE=1 SV=1

MEMDVTRDTVEVLPQHKFDIRSLEAYLNQHLPFGSDHRAVLTVTQYRSGQSNPTFFLQK
GSQAYVLRKKPPGSLPKAHKIDREFKVQKALFSVGFPVPKPLLYCSNASIIIGTEFYVMEH
VQGRIFRDFSIPGVSPAERAAIYVSLVETLAWLHSLDIHSLGLDRYGTGVGYCKRQVSTWT
KQYQASAHQSIPAMDQLSTWLMRNLPDSNNEELVHGDFKLDNIVFHPKECRVIAVLDW
ELSTFGHPLS DLAHLSLFYFWPRTLPMINRGSHIQENTGIPLMEELISIIYCRRRGIDPNLPNW
NFFMALSFFKLAGIAQGVYSRYLMGNNSSDSFLTANTVQPLAETGLQLSRRTLSTVPPQA
DAKSRLFAQSRRGQEVLTRVKQFMKQHVFPAEKEVAEYQAQNGNSAEKWEHPLVIEKLG
EMAKAEGLWNFLPAVSGLSQVDYALIAEETGKCFAPDVFNCQAPDTGNMEVLHLYGS
EQQKQQWLEPLLRGDITSVFCMTEPNVSSSDATNMECSIQRDGGSYIVHGKKWWSSGAG

NPKCKIAVVLGRTESPSVSRHKVHSMILVPM DTPGV ELIRPLSVFGYMDNVHGGHWEVHF
 NHVRVPASNILGEGRGFEISQGR LGPGR IHHCMRSVGLAERILQIMCDRAVQREAFGKKL
 YEHEVVAHWIAKSRIAIEEIRLLTLKAAHSIDTLGSAAARKEIAMIKVAAPKAVCKIADRAI
 QVHGGAGVSQDYPLANMYAIIRTLRLADGPDEVHLSAIAKMELQDQARQLKARM

4. Non-efflux prokaryotic proteins (Non-efflux): 554 Protein Sequences

>sp|P0C0R7|RLME_ECOLI Ribosomal RNA large subunit methyltransferase E OS=Escherichia coli (strain K12) OX=83333 GN=rlmE PE=1 SV=1
 MTGKKRSASSSRWLQEHFSDKYVQQAQKKGLRSRAWFKLDEIQQSDKLFKPGMTVVDL
 GAAPGGWSQYVVTQIGGKGRIIACDLLPMDPIVGVDLQGD FRDEL VMKALLERVGDSK
 VQVMSDMAPNMSGTPAVDIPRAMYLV ELALEMCRDVLAPGGSFVVKVFQGE GFDEYL
 REIRSLFTKVKVRKPDSSRARSREVYIVATGRKP

>sp|P61068|RL4_RHOPA 50S ribosomal protein L4 OS=Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009) OX=258594 GN=rpL4 PE=1 SV=1
 MELKVTTLLEGKEAGSVQLSDEIFGLEPRSDI IQRCVIWQLAKRQAGTHKAKGRAEVWRTG
 KKMYKQKGTGGARHGSQRVPQFRGGGRAFGPVVRSHAIDL PKKVRVLALRH ALSAKAK
 GGGLIVLDKAELEAAKTKTLVGHFSGLGLESALIIDGAEVNNGFAAAARNIPNIDVLPVQG
 INVYDILRRKKLVLTAAVDALEARFK

>sp|B0B7N2|RL7_CHLT2 50S ribosomal protein L7/L12 OS=Chlamydia trachomatis serovar L2 (strain 434/Bu / ATCC VR-902B) OX=471472 GN=rpL7 PE=1 SV=1
 MTTESLETLVEQLSGLTVLELSQLKKLLEEKWDVTAAAPVVAVAGAAAAGDAPASAEPT
 EFAVILEDVPSDKKIGVLKVVREVTGLALKEAKEMTEGLPKTVKEKTSKSDAEDTVKKLQ
 EAGAKAVAKGL

>sp|P60456|RL3_RHOPA 50S ribosomal protein L3 OS=Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009) OX=258594 GN=rpL3 PE=1 SV=1
 MRSGVIAQKVG MTRVFTEAGEHIPVTVLKLGNCQVLGHRTKEKNGYVALQVGS GSRKTV
 YMPKAERGQFAAAKVEPKRKVEEFRVSEDALLPVGA EIQADHFVVGQFVDVTGTSTGKG
 FAGGMKRWNFGGLRATHGVS VSHRSIGSTGGRQDPGKTFKNKKMPGHMGVDRVTTLNL
 RVVQTDVERGLILVEGAVPGTKGGWIRVRDAVKKALPADAPKPGKFR LANGDAAAEAP
 AAQEAGA

>sp|P9WN65|RMLB_MYCTU dTDP-glucose 4,6-dehydratase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=rmlB PE=1 SV=1
 MRLLVTTGGAGFIGTNFVHSAVREHPDDAVTVLDALTYAGRRESLADVEDAIRLVQGDITD
 AELVSQLVAESDAVVHFAAESHVDNALDNPEPFLHTNVIGTFTILEAVRRHGVRLHHISTD
 EVYGDLELDDRARFTSTPYNPSPYSATKAGADMLVRAWVRSYGV RATISNCSNNYGP
 YQHVEKFIPRQITNVLTGRRPKLYGAGANVRDWIHVDDHNSAVRRILDRGRIGRTY LISSE
 GERDNLTVLRTLRLMDRDPDDFDHVTDRVGHDLRYAIDPSTLYDEL CWAPKHTDFEEG
 LRTTIDWYRDNESWWRPLKDATEARYQERGQ

>sp|Q07465|RNI_AERHY Ribonuclease OS=Aeromonas hydrophila OX=644 PE=1 SV=1
 MKKIVVLLGMLLAPWFSSAVQAKGEAGEFDYYAMALSW SPEHCAIKPADRDQCSRQLGF
 VLHGLWPQYQRGYPSSCTRERLDPAMEQE FAGLYPSRFLYRHEWEKHGTC SGLSQHDFH
 QLASDLRQKREDPGRLSVSCRAAAQKPLPAQGGSGQCQRLAGPGQH HGGLRRRWRFLRE
 VYICLNKEGTDAVTCSDQMREL PSCGQPDFLLRTVR

>sp|P32684|RLUF_ECOLI 23S rRNA pseudouridine(2604) synthase OS=Escherichia coli (strain K12) OX=83333 GN=rluF PE=1 SV=1
 MLPDSSVRLNKYISESGICSRREADRYIEQGNVFLNGKRATIGDQVKPGDVVKVNGQLIEP
 REAEDLVLI ALNKPVGIVSTTEDGERDNIVDFVN HSKRVFPIGR LDKDSQGLIFLTNHGDLV
 NKILRAGNDHEKEYLVTVDKPITEEFIRGMSAGVPILGTVTKKCKVKKEAPFVFRITLVQG

LNRQIRRMCEHFGYEVKKLERTRIMNVSLSGIPLGEWRDLTDDELIDLFKLIENSSSEVKPK
 AKAKPKTAGIKRPVVKMEKTAEEKGGRPASNGKRFTSPGRKKKGR
 >sp|A0R1W8|RNPH_MYCS2 Ribonuclease PH OS=Mycobacterium smegmatis (strain ATCC
 700084 / mc(2)155) OX=246196 GN=rph PE=1 SV=1
 MSRREDGRLLDELRPVVITRGFTSHPAGSVLVEFGQTRVMCTASVTEGVPRWRKGGSGQG
 WLTAEYAMLPAATHDRSDRESVKGRIGGRTQEISRLIGRSLRACIDLAALGENTIAIDCDV
 LQADGGTRTAAITGAYVALSDAVTWLAAAGRLSDPRPLSCAIAAVSVGVVDGRVRVDLP
 YSEDSRAEVDMMNVVATDTGTLVEIQGTGEGATFPRSTLDKMLDAALGATEQLFVLQREA
 LDAPYPGVLPEGPAPKKAFGS
 >sp|P17622|RIBT_BACSU Protein RibT OS=Bacillus subtilis (strain 168) OX=224308 GN=ribT
 PE=1 SV=1
 MLIRYKKSFEKIAMGLLSFMPNEKDLKQLQQTIKDYETDTRQLFLWKEDEDIVGAIGVE
 KKDSEVEIRHISVNPISHRHQIGIGKQMMMDALKHLFKTQVLVPNELTQSFFERCQGGQQDQDI
 SYNN
 >sp|P9WH95|RL332_MYCTU 50S ribosomal protein L33 2 OS=Mycobacterium tuberculosis
 (strain ATCC 25618 / H37Rv) OX=83332 GN=rpmG2 PE=1 SV=1
 MASSTDVRPKITLACEVCKHRNYITKKNRRNDPDRLELKKFCPNCGKHQAHRER
 >sp|P03051|ROP_ECOLX Regulatory protein rop OS=Escherichia coli OX=562 GN=rop PE=1
 SV=1
 MTKQEK TALNMARFIRSQTLTLLEKLNELDADEQADICESLHDHADELYRSCLARFGDDG
 ENL
 >sp|Q6G3V6|RPIA_BARHE Ribose-5-phosphate isomerase A OS=Bartonella henselae (strain
 ATCC 49882 / DSM 28221 / Houston 1) OX=283166 GN=rpiA PE=1 SV=1
 MNVQQLKKMAALKALEFVEDDMRLGIGSGSTVNEFIPLGERVANGLRVTCVATSQYSE
 QLCHKFGVPITLEKIPELDLDIDGADEIGPEMTLIKGGGALLHEKIVASASRAMFVIAD
 TKMVKTLGAFALPIEVNPFGIHATRIAIEKAADNLGLSGEITLRMNGDDPFKTDGGHFIFDA
 FWGRILQPKLLSEALLAIPGVVEHGLFLGLASRAIVAMADSQIKVLEPFDF
 >sp|Q5SII2|RSMF_THET8 Ribosomal RNA small subunit methyltransferase F OS=Thermus
 thermophilus (strain HB8 / ATCC 27634 / DSM 579) OX=300852 GN=rsmF PE=1 SV=1
 MLPKAFLSRMAELLGEEFPAFLKALTEGKRTYGLRVNTLKLPPFAFQRISPWPLRPIPWCQ
 EGFYYPEEARPGHPFFYAGLYYIQEPSAQAVGVLLDPKPGERVLDLAAAPGGKTTHLAA
 RMGGKGLLLANEVDGKRVRGLENVERWGAPLAVTQAPRALAEAFGTFFHRVLLDAP
 CSGEGMFRKDREAARHWGPSAPKRMAEVQKALLAQASRLGPGGVLVYSTCTFAPEENE
 GVVAHFLKAHPEFRLEDARLHPLFAPGVPEWGEGNPELLKTARLWPHRLEGEHFLARFR
 KEGGAWSTPRLERPSPLSQEALRAFRGFLEEAGLTLEGPVLDRAHLYLLPEGLPTLLGLK
 APAPGLYLKGVQKGRFLPARALALAFGATLPWPEGLPRLALTPEDPRALAFATGEGVAW
 EGEDHPLALVVLKTAAGEFPLDFGKAKRGVLRPVGVGL
 >sp|Q8ZKB0|RSGA_SALTY Small ribosomal subunit biogenesis GTPase RsgA OS=Salmonella
 typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=rsgA PE=1 SV=2
 MSKNKLSKGQQRRVNANHQRRLKTSAEKADYDDNLFGEPAEGIVISRFGMHADVESADG
 EVHRCNIRRTIRSLVTGDRVVWRPGKAAEGVNVKGIVEAVHERTSVLTRPDFYDGVKPI
 AANIDQIVIVSAILPELSLNIIDRYLVGCETLQVEPLIVLNKIDLLDDEGMDFVNEQMDIYRN
 IGYRVL MVSSHTQDGLKPLEEALTGRISIFAGQSGVGKSSLLNALLGLQNEILTNDVSNVS
 GLGQHTTTAARLYHFPHGDDVIDSPGVREFGLWHLEPEQITQGFVEFHLYLGHCKYRDCK
 HDADPGCAIREAVENGAI AETRFENYHRILESMAQVKTRKNFSDTDD
 >sp|P26420|SCRK_KLEPN Fructokinase OS=Klebsiella pneumoniae OX=573 GN=scrK PE=1
 SV=1
 MNGKIWVLGDAVVDLLPDGEGRLLQCPGGAPANVAVGVARLGGDSGFIGRVGDDPFGR
 FMRHTLAQEQVDVNYMRLDAAQRTSTVVVDLDSHGERTFTFMVRPSADLFLQPEDLPF
 AAGQWLHVCSIALSAEPSRSTTFAALEAIKRAGGYVSFDPNIRSDLWQDPQDLRDCLDRA

LALADAIKLSEEELAFISGSDDIVSGIARLNARFQPTLLLVTQGKAGVQAALRGQVSHFPA
RPVVAVDTTGAGDAFVAGLLAGLAAHGIPDNLAALAPDLALAQTGALATTAKGAMTA
LPYKDDLQRS

>sp|A5W4E3|TODS_PSEP1 Sensor histidine kinase TodS OS=Pseudomonas putida (strain ATCC 700007 / DSM 6899 / BCRC 17059 / F1) OX=351746 GN=todS PE=1 SV=1

MSSLD RKKPQNRSKNYYNICLKEKGSEELTCEEHARIIFDGLYEFVGLLDAHGNVLEVN
QVALEGGGITLEEIRGKPFWKARWWQISKKTEATQKRLVETASSGEFVRCDVEILGKSGG
REVIAVDFSLLPICNEEGSIVYLLAEGRNITDKKKAEMALALKNQELEQSVECIKLDNAK
SDFFAKVSHELRTPLSLILGPLEAVMAAEAGRESPYWKQFEVIQRNAMTLLKQVNTLLDL
AKMDARQMGLSYRRANLSQLTRTISSNFEGIAQQKSITFDTKLPVQMVAEVDCEKYERIIL
NLLSNAFKFTPDPGGLIRCCLSLRPNYALVTVSDSGPGIPPALRKEIFERFHQLSQEGQQAT
RGTGLGLSIVKEFVELHRGTISVSDAPGGGALFQVKLPLNAPEGAYVASNTAPRRDNPQV
VDTDEYLLLAPNAENAEVLPFQSDQPRVLIVEDNPDMRGFIKDCSSDYQVYVAPDGAK
ALELMSNMPPDLLITDLIMPVMSGDMLVHQVRKKNELSHIPIMVLSAKSDAELRVKLLSE
SVQDFLLKPFSAHELRARVSNLVSMKVAGDALRKELSDQGDDIAILTHRLIKSRHRLQQSN
IALSASEARWKAVYENSAAGIVLTDPENRILNANPAFQRITGYGEKDLEGLSMEQLTPSDE
SPQIKQRLANLLQGGGAEYSVERSYLCKNGSTIWANASVSLMPQRVGESPVILQIIDDITEK
KQAQENLNQLQQQLVYVSRSATMGEFAAYIAHEINQPLSAIMTNANAGTRWLGNEPSNIP
EAKEALARIRDSDRAAEIIRMVRSFLKRQETVLKPIDLKALVTDTSILKAPSQNNSVNLD
VVADDELPEIWGDGVQIQQLINLAMNAIEAISQADCETRQLTSLFSGNDTGDALVISVKD
TGPGISERQMAQLFNAFYTTKKEGLGMGLAICLTITEVHNGKIWVECPPAGGACFLVSIPA
RQSGT

>sp|P9WFY9|TRMB_MYCTU tRNA (guanine-N(7)-)-methyltransferase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=trmB PE=1 SV=1

MVHHGQMHAQPGVGLRPDTPVASGQLPSTSIRSRSGISKAQRETWERLWPELGLLALPQ
SPRGTPVDTRAWFGRDAPVVLEIGSGSGTSTLAMAKAEPHVDVIAVDVYRRGLAQLLCAI
DKVGS DGINIRLILGNAVDVLQHLIAPDSL CGVRVFFPDPPWPKARHHKRLLQPATMALIA
DRLVPSGVLHAATDHPGYAEHIAAAGDAEPRLVRVDPDTELLPISVVRPATKYERKAQLG
GGAVIELLWKKHGCSERDLKIR

>sp|P05845|TNSE_ECOLX Transposon Tn7 transposition protein TnsE OS=Escherichia coli OX=562 GN=tnsE PE=1 SV=1

MVRLATFNDNVQVVHIGHLFRNSGHKEWRIFVWFNPMQERKWTRFTHLPLLSRAKVVNS
TTKQINKADRVIEFEASDLQRAKIIDFPNLSSFASVRNKDGAQSSFIYEAEPTYSKTRYHIPQ
LELARSLFLINSYFCRSCLSSTALQQEFDVQYEVERDHLEIRILPSSSFPGGALEQSAVVQLL
VWLFSDQDVMDSYESIFRHYQQNREIKNGVESWCFSFDPPPMQGWKLHVKGRRSSNEDKD
YLVEEIVGLEINAMLPSTTAISHASFQEKEAGDGSTQHIAVSTESVVDDEHLQLDDEETANI
DTDTRVIEAEPTWISFSRPSRIEKSRRARKSSQTILEKEEATTSENSNLVSTDEPHLGGVLAA
ADVGGKQDATNYNSIFANRFAAFDELLSILKTKFACRVLFEETLVLPKVGRSRLHLCKDGS
PRVIKAVGVQRNGSEFVLLEVDASDGVKMLSTKVLSGVDSETWRNDFEKIRRGVVKSSL
NWPNSLFDQLYGQDGHGRGVNHPKGLGELQVSREDMEGWAERVVREQFTH

>sp|Q813X6|TOX1_BACCR Ribonuclease BC_0920 OS=Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711) OX=226900 GN=BC_0920 PE=1 SV=1

MSLNMYLGEVQGQTQSMNAV CNATIQGMEQVIQSIDAF AIDTVLQGQTYSSAKSFFVQTF
RPLAQGGIYLCEELIRQNDAFPSQFQSQVASTDVIEQEILEQIREIDRMKASMEAISQAMPI
GMDAMANLFTVMRKKLQEKLDHLYQFNQTSSNNYSTALQLAASIAAGLAEVQSGKGFSP
ASGTFSTQGLNMEWTTSIQAITEERARQAANSIEEGEMCGKLPEKSTGEKIWDGIVEGTGQ
AVSDTIDGIKALGDWETWENMGNAALHPIDTLSTMYNTLSDSFINDVINGDAESRAKWGS
YALTQVGLGLIGDKGLSKASKLGQAGKVTKLAKNKIPQAVSHITSNLQMGRFAFAGGN
SLRFRFDTPDFKKAEKLSYQFARGESNYGGSNFVNENHRSSLSNREIISNLQHTEKFRPN

TLKHILEGEINWRGDAMGYHTEVLENTPGKIISGTEEILNDQGIYKARVEVNGTPKTGNRG
FSTFFPKDWSPQKIVDNINEAYNNRTYEFNGTYSIGSEGIRISMYIDGNGKIISAFPAE
>sp|P9WGV5|TAER_MYCTU Trans-acting enoyl reductase OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) OX=83332 GN=Rv2953 PE=1 SV=1
MSPAEREFDIVLYGATGFSGKLTAEHLAHSNSTARIALAGRSSERLRGVRMMLGPNAAD
WPLILADASQPLTLEAMAARAQVVLTTVGPYTRYGLPLVAACAKAGTDYADLTGELMFC
RNSIDLYHKQAADTGARIILACGFDSIPSDLVYQLYRRSVEDGTGELCDTDLVLRFSQR
WVSGGSVATYSEAMRTASSDPEARRLVTDPTYTLTTDRGAEPGLGAQPDFLRRPGRDLAPE
LAGFWTGGFVQAPFNTRIVRRSNALQEWAYGRRFRYSETMSLGKSMAAPILAAAVTGTV
AGTIGLGNKYFDRLPRRLVERVTPKPGTGPSRKTQERGHYTFETYTTTTTGARYRATFAH
NVDAYKSTAVLLAQSGLALALDRDLAELRGVLTAAAMGDALLARLPAGGVVMGTTR
LS
>sp|Q03304|TMOF_PSEME Toluene-4-monooxygenase system, ferredoxin--NAD(+) reductase
component OS=Pseudomonas mendocina OX=300 GN=tmoF PE=1 SV=1
MFNIQSDDLHHEADSNDTLLSAAALRAELVFPYECNSGGCGACKIELLEGEVSNLWPD
PGLAARELRKNRFLACQCKPLSDLKIKVINRAEGRASHPPKRFSTRVSKRFLSDEMFLR
LEAEQKVVFSPGQYFMVDVPELGTRAYSANPVDGNTLTIVKAVPNGKVSCALANETIE
TLQLDGPYGLSVLKTADETQSVFIAGGSGIAPMVSMVNTLIAQGYEKPITVFYGSRLAE
EAAETLFGWKENLKLINVSSSVVGNSEKKYPTGYVHEIPEYMEGLLGAEFYLCGPPQMIN
SVQKLLMIENKVPFEAIHFDRFF
>sp|P24546|T2A1_ACICA Type-2 restriction enzyme AccI OS=Acinetobacter calcoaceticus
OX=471 GN=accIR PE=1 SV=1
MDYYDRIRELTKNVPVELVDFEQPRDLARTPTQASSNFITNKEQGDWAEDLVTRAINENS
KNFVAVKYGKSDNLVAGENGFDTFYQDFQTELDITIGKRPDLLIFKKTDFTTLGFDVSQIP
HHQITDYVKKAIAGIEVRSSAFLIDKYEEAMQVVRTQRFTEIAFQTRDKILAEFLDVLHPSR
SKYITLLNTLTLETISIFDFKVPGWRSNERLIEVNNLFKRLKVAIKEIQKRDYLSITPKVEDIK
VYKWIETFNVPHFYFQVFFDKVYGISFEQILTIISNSDNDGVIFSVEKDVQNQNKTITIKINS
KTGYPIASKVDEPTHEIRKEMDRGRLLFYVTFKGGTAYLDLDNLRTILGIEEAEF
>sp|P83615|TPAP_STRMB Prolyl tri/tetrapeptidyl aminopeptidase OS=Streptomyces mobaraensis
OX=35621 GN=ptp PE=1 SV=2
MRKALRSLAASMLIGAIGAGSATAEAASITAPQADIKDRILKIPGMKFVEEKPYQGYRYL
VMTYRQPVDRNPGKGTFEQRFLLHKDTRPTVFFTSNGYNVSTNPSRSEPTRIVDGNQV
SMEYRFFTPSRPQPADWSKLDIWQAASDQHRLYQALKPVYGKNWLATGGSKGGMTATY
FRRFYPNDMNGTVAYVAPNDVNDKEDSAYDKFFQNVGDKACRTQLNSVQREALVRRDE
IVARYEKWAKENGKTFKVVGSAKAYENVVLDLVWSFWQYHLQSDCASVPATKASTDE
LYKFIDDISGFDGYTDQGLERFTPYYYQAGTQLGAPTIVKNPHLKGVLRYPGINQPRSYVPR
DIPMTFRPGAMADVDRWVREDSRNMLFVYQGNDPWSGEPFRLGKGAAARHDYRFYAPG
GNHGSNIAQLVADERAKATAEVLKWAGVAPQAVQKDEKAAKPLAPFDAKLDRVKNDK
QSALRP
>sp|E0U4V7|TARQ_BACPZ Poly(ribitol-phosphate) beta-glucosyltransferase OS=Bacillus
subtilis subsp. spizizenii (strain ATCC 23059 / NRRL B-14472 / W23) OX=655816 GN=tarQ
PE=1 SV=1
MKISIVIPVYNSEDLISECLDSLVNQTMPKEDYEIICVDDKSTDSSLDILNQYKKKYENVVV
IERTVNSSGGPGAPRNDAIKIAKGEYILFVDSDDYIGSEALLRWYNFSKENQSDITLGKLKGI
NGRGVPSKSMFKETNPVDVLDVSKIVFTLGPQKLKFKASLLKENKITFPTHIKAAEDQVFTMN
AYLKAKKISVSADYDYYYLVKRDGEHMSVAYVPPENFYGAMEDIIISAIKASDLEEARKIK
LMAVFLNRHFDIFSRTKNVTIKMKTDEERAWEFRYLSSFIHAVPEEADQFVLPHIKLRLLFI
RNNDLRGLTQYEREEQDIKKFCTVNNGELIARYPSLERYSSIEELLKVNYKNKLEHYLQNI
EFSHSLSIQGTITHKLLDDETNNKQSLTGVFVHRDTKAEKYIAPASYDNSTFTFECKFDEL
ASAEEDLGVWDFFISSIDGYKLRARIGNKRAAYKYSTKTMYLGHNALFVYSARPYFTMN

YDNLSDIDIKKHAYTEAELSYETESKDLSFIFKDKQIYLPNHSKIIVNTGQSEISLPVKRIDLEP
NCTKLTNVNQSLLEQLAHVKKERLIEFAINTSQNKISAKVDNQAIILDTKSVERKSMLFFN
KMVEVQYKLLTSKSKFYFYQY
>sp|P0AEV1|RSSB_ECOLI Regulator of RpoS OS=Escherichia coli (strain K12) OX=83333
GN=rssB PE=1 SV=1
MTQPLVGKQILIVEDEQVFRSLDSWFSSLGATTVLAADGVDALELLGGFTPDLMICDIAM
PRMNGLKLLHIRNRGDQTPVLVISATENMADIAKALRLGVEDVLLKPVKDLNRLREMFV
ACLYPSMFNSRVEEEERLFRDWDAMVDNPAAAALLQELQPPVQQVISHCRVNYRQLVA
ADKPGVLVDIAALSENDLAFYCLDVTRAGHNGVLAALLLRALFNGLLQEQLAHQNRQLP
ELGALLKQVNHLLRQANLPGQFPLLVGYYHRELKNLILVSAGLNATLNTGEHQVQISNGV
PLGTLGNAYLNQLSQRCDAWQCQIWGTGGRLRLMLSAE
>sp|P46850|RTCB_ECOLI RNA-splicing ligase RtcB OS=Escherichia coli (strain K12)
OX=83333 GN=rtcB PE=1 SV=3
MNYELLTTENAPVKMWTGKVPVEADARQQLINTAKMPFIFKHIAVMPDVHLGKGSTIGS
VIPTKGAIIPAAVGVDIGCGMNALRTALTAEDLPENLAELRQAIETAVPHGRTTGRCKRDK
GAWENPPVNVDAKWAELEAGYQWLTQKYPRFLNTNNYKHLGTLGTGNHFIEICLDESQ
VWIMLHSGSRGIGNAIGTYFIDLAQKEMQETLETLP SRDLAYFMEGTEYFDDYLKAVAW
AQLFASLNRDAMMENVVTALQSITQKTVRQPQTLAMEEINCHHNYVQKEQHFGEEIYVT
RKGAVSARAGQYGIIPGSMGAKSFIVRGLGNEESFCSCSHGAGRVMSTRKAKKLFSVEDQ
IRATAHVECRKDAEVIDEIPMAYKDIDAVMAAQSDLVEVIYTLRQVVCVKG
>sp|P46228|RS1_SYNP6 30S ribosomal protein S1 OS=Synechococcus sp. (strain ATCC 27144 /
PCC 6301 / SAUG 1402/1) OX=269084 GN=rpsA PE=1 SV=4
MVTQDIPAVDIGFTHEDEFAALLDQYDYHFNP GDTVVGTVFNLEPRGALIDIGAKTAAFLP
VQEMSINRVESPEEVLQPSEMREFFILSDENEDGQLTSLIRRIEYMRATERVRQLQTEDAT
VRSEVFATNRGGALVRIEGLRGFIPGSHISTRKAKEDLVGEELPLKFLEVDEDNRNLVLSH
RRALVERKMNRLLEVGEVVVGAVRGIKPYGAFIDIGGVSGLLHISEISHDHIETPHSVFNVN
DEVKVMIIDLDAERGRISLSTKQLEPEPGDMVRNPEVVYEKAEEMAAQYREKLKQQAEG
LVVTE
>sp|B0FYK7|RPPA_STRC0 1,3,6,8-tetrahydroxynaphthalene synthase OS=Streptomyces
peucetius subsp. caesius OX=55158 GN=rppA PE=1 SV=1
MRVPVAVDDL VAPSTMGERHTVIDRGTSVAAVHTALPPHRYAQSDLTELIADLCLEPGAD
RALLRRLHTSAGVRTRHLALPIEQYAGLGDFGQANAAWLTVGLALAEALSGALDAAGL
TAADIDLLVCTSITGVAAPSLDARLAVRMGMRADVKRVPVFGLGCVGGAAGLGR LHDYL
LGHPDDTAVLLSVELCSLT LQRDGLANLVAGALFGDGAAAVVARGGDAGR RGAGWPM
VAATRGLYPDTEHLLGWRIGASGRVVDAGIPDVVRTHLGGDLRNFLATHGLVPDDI
GTWICHPPGGPKVLA AVGDALELPD GALDSSWRSLAGVGNLSSASVLRVLEDVATRCRPD
PGTWGVLLAMGPGFCAEFVLLRW
>sp|O25503|SPEE_HELPY Polyamine aminopropyltransferase OS=Helicobacter pylori (strain
ATCC 700392 / 26695) OX=85962 GN=speE PE=1 SV=1
MWITQEITPYLRKEYTIEAKLLDVRSEHNILEIFKSKDFGEIAMLNRQLLFKNFLHIESELLA
HMGGCTKKELKEVLIVDGFDELAHQLFKYDTHIDFVQADEKILDSFISFFPHFHEVKNNK
NFTHAKQLLDLDIKKYDLIFCLQEPDIHRIDGLKRLMKEDGVFISVAKHPLLEHVSMQNAL
KNMGGVFSVAMPFVAPLRILSNKGYIYASFKTHPLKDLMTPKIEALTSVRYYNEDIHRAAF
ALPKNLQEVFKDNIKS
>sp|P37506|STA_BACSU Streptothricin acetyltransferase A OS=Bacillus subtilis (strain 168)
OX=224308 GN=satA PE=1 SV=1
MIMKMTHLNMKDFNKPNEPFVVFGRMIPAFENGWWTYTEERFSKPYFKQYEDDDMDVS
YVEEEGKAAFLYYLENNCIGRIKIRSNWNGYALIEDIAVAKDYRKKGVGTALLHKAIEWA
KENHFCGLMLETQDINISACHFYAKHHFIIGAVDTMLYSNFPTANEIAIFWYYKF

>sp|P25052|TENA_BACSU Aminopyrimidine aminohydrolase OS=Bacillus subtilis (strain 168)
OX=224308 GN=tenA PE=1 SV=1
MKFSEECRSAAAEWWEGSFVHPFVQGIGDGTLPIDRFKYYVLQDSYYLTHFAKVQSFGA
AYAKDLYTTGRMASHAQGTYEAEMLHREFAEELLEISEEERKAFKPSPTAYSYTSHMYRS
VLSGNFAEILAALLPCYWLYYEVGEKLLHCDPGHPIYQKWIGTYGGDWFRQQVEEQINRF
DELAENSTEEVRAKMKENFVISSYYEYQFWGMAYRKEGWSDSAIKEVEECGASRHNG

>sp|P32143|SQUV_ECOLI Sulfofructose kinase OS=Escherichia coli (strain K12) OX=83333
GN=yihV PE=1 SV=2
MIRVACVGITVMDRIYYVEGLPTESGKYVARNYTEVGGGPAATAAVAAARLGAQVDFIG
RVGDDDTGNSLLAELESWGVNTRYTKRYNQAKSSQSAIMVDTKGERIIINYPSPDLLPDAE
WLEEIDFSQWDVVLADVRWHDGAKKAFTLARQAGVMTVLDGDITPDISELVALSDHA
AFSEPLARLTGVKEMASALKQAQTLTNHGVYVTQGSAGCDWLENGGRQHQPFAFKVDV
VDTTGAGDVFHGAVALATSGDLAESVRFASGVAALKCTRPGGRAGIPDCDQTRSFLSL
FV

>sp|Q7WY75|SSPK_BACSU Small, acid-soluble spore protein K OS=Bacillus subtilis (strain 168)
OX=224308 GN=sspK PE=1 SV=3
MVRNKEKGFPYENENKFQGEPRAKDDYASKRADGSINQHPQERMTRASGKR

>sp|O70023|TYLN_STRFR O-mycaminosyltransferase
OS=Streptomyces fradiae OX=1906 GN=tylN PE=1 SV=2
MRIALLTMGSRGDVQPFVALGTGLRARGHEVVLGAPEALRPLVEQAGLEYRATPGDPDG
FFTMEVVETLRRGPAMRDLMKALPPAPEEYDQEVLDRIERAGEGVDLVVHAPLTVTTAL
GEPSTPWLSVNWPNSTSTWTFPAVESGQRRMGPLTPLYNRLTHWRAEREDWGWRRRAEV
NEFRGRRGLPPFGKSSPLRRLGHRPHLYPFSPSVLPKPRDWPGQCHVTGYWFDWQPGW
RPSPELEDFLADGEPPVLLTLGSTWPVHRQEEMVEYAVAAARGARRRLLLVGGPEGALPG
DALRVPSADYSWLMPTAAVHHGGFGTTADAVRAGVPQVLVPVFADHPFWAARLRR
MGTAARPVPLARMNREALAASVRTAVTDPAMAVRARRLGEAVAAERGVENACVLIIEEW
AETRTTAHTPG

>sp|Q46871|YQJH_ECOLI NADPH-dependent ferric-chelate reductase OS=Escherichia coli
(strain K12) OX=83333 GN=yqjH PE=1 SV=1
MNNTPRYPQVRNDRFRELTVLRVERISAGFQRIVLGGEALDGFSTRGFDDHSLFFPQP
DAHFVPPTVTEEGIVWPEGPRPPSRDYTPLYDELRLHELAIIDFFIHDGGVASGWAMQAQPG
DKLTVAGPRGSLVVPEDYAYQLYVCDESGMPALRRRLETLSKLAVKPQVSALVSVRDNA
CQDYLAHLDFNIEWLAHDEQAVDARLAQMQUIPADDFIWIWITGEGKVVKNLSSRRFEAEQ
YDPQVRVAAAYWHAK

>sp|P9WMC7|Y2912_MYCTU Uncharacterized HTH-type transcriptional regulator Rv2912c
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv2912c PE=1
SV=1
MARTQQQRREETVARLLQASIDTIEVGYARASAAVITKRAGVSVGALFRHFETMGDFMA
ATAYEVLRRQLETFTKQVAEIPADRPALPAALTILRDITAGSTNAVLYELMVAARTDEKLL
ETLQNVLGQYSAKIHDAARALPGAESFPEETFPVIVALMTNVFDGAAIVRGVLPQPELEEQ
RIPMLTALLTAGL

>sp|P9WPI9|Y2232_MYCTU Uncharacterized protein Rv2232 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) OX=83332 GN=Rv2232 PE=1 SV=1
MSSPRERRPASQAPRLSRRPPAHQTSRSSPDTTAPTGSGLSNRFVNDNGIVTDTTASGTNCP
PPPRAAARRASSPGESPQLVIFDLDTLDSARGIVSSFRHALNHIGAPVPEGDLATHIVGPP
MHETLRAMGLGESAEIAIVAYRADYSARGWAMNSLFDGIGPLADLRTAGVRLAVATSK
AEPTARRILRHFGIEQHFEVIAGASTDGSRGSKVDVLAHALAQLRPLPERLVMVGDRSHD
VDGAAAHGIDTVVVGWGYGRADFIDKTSTTVVTHAATIDELREALGV

>sp|P9WL51|Y2645_MYCTU Uncharacterized protein Rv2645 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) OX=83332 GN=Rv2645 PE=1 SV=1

MTTTPRQPLFCAHADTNGDPGRACGQQLADVGPATPPPPWCEPGTEPIWEQLTERYGG
 VTICQWTRYFPAGDPVAADVWIAADDRVVDGRVLRTPAIHYTEPPVLGIGPAAARRLA
 AELLNAADTLDDGRRQLDDLGEHRR
 >sp|Q7VKS7|Y1794_HAEDU UPF0301 protein HD_1794 OS=Haemophilus ducreyi (strain
 35000HP / ATCC 700724) OX=233412 GN=HD_1794 PE=1 SV=1
 MFGNLQGKFIIATPEMDDEYFDRTVIYICEHNDNGTIGVIINTPTDLSVLELLTRMDFQMAK
 PRIYTQDQMVLNGGPVNQDRGFIVHSKTDHEFTHSYKVTDDITLTTSGDVLDSTFGTQTAP
 KFIVCLGCSTWKPHQLEQEIAQNYWLLSEANNQTLFETSYLDRWVEANEMLGISGILAPA
 GRA
 >sp|P9WGA5|Y2603_MYCTU Probable transcriptional regulatory protein Rv2603c
 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv2603c PE=1
 SV=1
 MSGHSKWATTKHKKAVVDARRGKMFARLIKNIIEVAARVGGGDPAGNPTLYDAIQKAKK
 SSVPNENIERARKRGAGEEAGGADWQTIMYEGYAPNGVAVLIECLTDNRNRAASEVRVA
 MTRNGGTMAADPGSVSYLFSRKGVTLEKNGLTEDDVLAADVLEAGAEDVNDLGDSFEVIS
 EPAELVAVRSALQDAGIDYESAEASFQPSVSPVDLDGARKVFKLVDALEDSDDVQNVW
 TNVDVSDEVLAALDDE
 >sp|A5A614|YCIIZ_ECOLI UPF0509 protein YciZ OS=Escherichia coli (strain K12) OX=83333
 GN=yCiZ PE=1 SV=1
 MSEFDAQRVAERIDIVLDILVAGDYHSAIHNLKLEILKAELLRQVAESTPDIPKAPWEI
 >sp|P9WL31|Y2895_MYCTU Uncharacterized protein Rv2895c OS=Mycobacterium tuberculosis
 (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv2895c PE=1 SV=1
 MAGRPLHAFEVVATRHLAPHMVRVVLGGSGFDTFVPSDFTDSYIKLVFVDDDDVDVGRLP
 RPLTLDSEADLPTAKRPPVRTMTVRHVDAAAREIAVDIVLHGEHGVAGPWAAGAQRGQP
 IYLMGPGGAYAPDPAADWHLLAGDESAIPAIAAALEALPPDAIGRAFIEVAGPDDEIGLTA
 PDAVEVNWVYRGGADLVPEADGRAGDHAPLIEAVTTTAWLPQGVHVFHGEAQAVMHNL
 RPYVRNERGVDAKWASSISGYWRRGRTEEMFRKWKKELEAEAEAGTH
 >sp|P9WQ89|Y2231_MYCTU Uncharacterized aminotransferase Rv2231c OS=Mycobacterium
 tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv2231c PE=1 SV=1
 MLWILGPHTGPLLFDASLDTSPLAAARYHGDQDVAPGVLDFAVNVRHDRPPEWLVRQ
 LAALLPELARYPSTDDVHRAQDAVAERHGRTRDEVLPVGAAGFALLHNLSVRAAIV
 VPAFTEPAIALSAAGITAHVVLKPPFVLDTAHVPDDADLVVVGNPTNPTSVLHLREQLLE
 LRRPGRILVVDEAFADWVPGEPQSLADDSLPDVLVLRSLTKTWSLAGLRVGYALGSPDVL
 ARLTVQRAHWPLGLTLQTAIAACCAPRAVAAAAADAVRLTALRAEMVAGLRSVGAEEV
 DGAAPFVLFNIADADGLRNYLQSKGIAVRRGDTFVGLDARYLRAAVRPEWPVLVAAIAE
 WAKRGGR
 >sp|P44886|Y827_HAEIN Uncharacterized acyl-CoA thioester hydrolase HI_0827
 OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421
 GN=HI_0827 PE=1 SV=1
 MSANFTDKNGRQSKGVLLRLTLAMPSTDNANGDIFGGWIMSQMDMGAILAKEIAHGR
 VVTVAVESMNFIPISVGDVVCCYQGCLKVGRSSIKIKVEVWVKKVASEPIGERYCVTDA
 VFTFVAVDNNGRSRTIPRENNQELEKALALISEQPL
 >sp|P9WJ01|Y480_MYCTU Hydrolase Rv0480c OS=Mycobacterium tuberculosis (strain ATCC
 25618 / H37Rv) OX=83332 GN=Rv0480c PE=1 SV=1
 MRLALAQIRSGTDPAAANLQLVGKYAGEAATAGACL VVFPEATMCRLGVPLRQVAEPVDG
 PWANGVRRATEAGITVIAGMFTPTGDGRVTNTLIAAGPGTPNQPDAAHYHKIHLDAFGF
 TESRTVAPGREPVVVVVDGVRVGLTVCYDIRFPALYTELARRGAQLIACASWGS GPGL
 EQWTLLARARALDSMSYVAAAGQADPGDARTGVGASSAAPTGVGGS LVASPLGEVVVS
 AGTQPQLLVADIDVDNVAAARDRIA VLRNQTD FVQIDKAQSRG

>sp|Q9HYR3|Y3332_PSEAE Uncharacterized PhzA/B-like protein PA3332 OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=PA3332 PE=1 SV=1
MNAKEILVHSLRLLENGDARGWCDLFHPEGVLEFPYAPPGWKTRFEGRETIWAHMRLFP
EHLTVRFTDVQFYETADPDLAIGEFHGDGVATVSGGKLAQDYISVLRTDQGILLRYRDFW
NPLRHLEALGGVEAAAKIVQGA

>sp|Q9RRH3|RQKA_DEIRA DNA damage-responsive serine/threonine-protein kinase RqkA OS=Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422) OX=243230 GN=rqkA PE=1 SV=1
MPLTPGTLLAGRYELLALLGEGGSAQVYRAQDGLLGREVALKVMHDYLPESDRSRFLRE
VRTLARLTHPGVVPVLDLGQEPEAGRPFPTMPLLTGGPITRLGPLDAPGPLARFLTAAAF
ASRALHHVHSHGIVHRDLTPGNVLLDDTGLPRIMDFGLVALSEQTRHLTRSGVTLGTPAY
MAPEQAKGGGVGDARSPLYALGAVLYRVACGSPPFVGSDSDQSVLYQHVEPVPDPRDLN
PAVPDAVARVLLWLLAKRADRRPQSGAALAHLLWALARRDLWTTHARGQYRGGRARTG
EHPDGPARGVSDMQELWSVALPGEVTWPAAVVGEGLDVAVGTRGGQLVLTHTSGRPFAT
YAARDEVTA PATLIGGHVLYGAWDGTLLRRVELQSGSEVWRHQARA EFTGAPT VWGGRL
LAPSRDGHLLHALSLRTGELAWAYRAGGSLAASPLVWAGAALQCDETGWLHALDARSGT
PLWKVEVGTVHATPALLPGPPGTATLVIATWEGEVHAIGLEVQNGRAALAGEDAIRWTY
DVEDEVWASPALTALDLPDPSGAAPDASAAPGGVVVVAGWGGKVRGLRLADGEDLWE
RTLDGRVTASPVISAGLVFLATEGGELLALDVRNGEVRWTCRERSGVQATPLAASGTLYV
AFMDGTLLRAYRNAHPEWRSEQEG

>sp|Q9KI19|RPOS_COXBU RNA polymerase sigma factor RpoS OS=Coxiella burnetii (strain RSA 493 / Nine Mile phase I) OX=227377 GN=rpoS PE=1 SV=1
MKTKTTKKTIKKA AKKIKKPSKRKIKKTAKKSRPKKPIKASDHGLIFAKTKKETTEKEDAE
LANAKAKTKKRRETRSSDPTQIYLRELGFQPLLNAKEELKIARRVHKGDPKARKQMIEAN
LRLVVKIARHYVNRGLPFLDLIEEGLNGLLTAVEKFDPERGFRFSTYATWWIRQTIERAIM
NQSRTVRLPIHVIKELNVYLRTAKKLTQEV DHEATPEDVAHLIDKPVQEIR RIMDLAPSAT
SIDVPISEDGQKSLVDLTLADDNNIDPARLIQNVDLQDHIERWLAQLDERHREVVILRFGLH
ENEKGTLEAVGKAVGLTRERVRQIQIDALQQLRHILEMEGVTGEEVED

>sp|P66715|RPOE_STAAN Probable DNA-directed RNA polymerase subunit delta OS=Staphylococcus aureus (strain N315) OX=158879 GN=rpoE PE=1 SV=1
MKIQDYTKQMVDEKSFIDMAYTLLNDKGETMNL YDIIDEFRALGDYEEYEEIENRVVQFYT
DLNTDGRFLNVGENLWGLRDWYSVDDIEEKIAPTIQKFDILDADDEEDQNLKLLGEDEMD
DDDDIPAQTDDQEELNDPEDEQVEEEINHSDIVIEEDEDEDEDEEVEFEDEEDFND

>sp|P68817|RECU_STAAN Holliday junction resolvase RecU OS=Staphylococcus aureus (strain N315) OX=158879 GN=recU PE=1 SV=1
MNYPNGKPYRKNSAIDGGKKTA AFSNIEYGGRGMSLEKDIEHSNTFYLKSDIAVIHKKPTP
VQIVNVNYPKRSKAVINEAYFRTPSTTDYNGVYQGYIDFEAKETKNKTSFPLNNIHDHQ
VEHMKNA YQQKGIVFLMIRFKTLDEVYLLPYSKFEVFWKRYKDN IKKSITVDEIRKNGYH
IPYQYQPRLDYLKAVDKLILDESEDRV

>sp|Q9HXQ0|RIMM_PSEAE Ribosome maturation factor RimM OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=rmmM PE=1 SV=1
MPTPADDLVVIGKIVSVYGIRGEVKVYSFTDPLDNL LDYRRWTLRRDGEIRQAELVRGRL
HGKVLAAKLKGLDDREEARTFTGYEICIPRSELP SLEEGEYYWHQLEGLKVIDQGRQLLG
VIDHLL ETGANDVMVVKPCAGSLDDRERLLPYTGQCVLSIDL AAGEMRVDWDADF

>sp|Q51559|RHIA_PSEAE 3-(3-hydroxydecanoyloxy)decanoate synthase OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=rhlA PE=1 SV=2

MRRESLLVSVCKGLRVHVERVVGQDPGRSTVMLVNGAMATTASFARTCKCLAEHFNVL
FDLPFAGQSRQHNPQRGLITKDDEVEILLALIERFEVNLVLSASWGGISTLLALSRNPRGIR
SSVVMFAFAPGLNQAMLDYVVGRAQALIELDDKSAIGHLLNETVGKYL PQRLKASNHQHM
ASLATGEYEQARFHIDQVLALNDRGYLACLERIQSHVHFINGSWDEYTTAEDARQFRDYL
PHCSFSRVEGTGHFLDLESKLA AAVRVH RALLEHLLKQPEPQRAERAAGFHEMAIGYA
>sp|A5U2B7|RIBBA_MYCTA Riboflavin biosynthesis protein RibBA OS=Mycobacterium
tuberculosis (strain ATCC 25177 / H37Ra) OX=419947 GN=ribBA PE=1 SV=1
MTRLDSVERAVADIAAGKAVIVIDDEDRENEGDLIFAAEKATPEMVAFMVRYTSGYLCVP
LDGAICDRLGLLPMYAVNQDKHGTAYTVTVDARNIGITGISASDRATTMRLLADPTSA
DDFTRPGHV VPLRAKDGGVLRPGHTEAAVDLARMAGLQPAGAICEIVSQKDEGSMAHT
DELRVFADEHGLALITIADLIEWRRKHEKHIERVAEARIPTRHGEFRAIGYTSIYEDVEHVA
LVRGEIAGPNADGDDVLVRVHSECLTGDVFGSRRCDGCPQLDAALAMVAREGRGVVLY
MRGHEGRGIGLMHKLQAYQLQDAGADTV DANLKLGLPADARDY GIGAQILVDLGVRS
M RLLTNNPAKRVGLDGYGLHIIERVPLPVRANAENIRYLMTKRDKLGHDLA GLDDFHE
SVH LPGEFGGAL
>sp|P9WHL9|PURK_MYCTU N5-carboxyaminoimidazole ribonucleotide synthase
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=purK PE=1
SV=1
MMAVASSRTPAVTSFIAPLVAMVGGGQLARMTHQAAIALGQNLRLVLTSAADDPAAQVTP
NVVIGSHTDLAALRRVAAGADVLTFDHEHVPNELLEKL VADGVNVAPSPQALVHAQDKL
VMRQRLAAAGVAVPRYAGIKDPDEIDVFAARVDAPIVVKAVRGGYDGRGVRMARDVAD
ARDFARECLADGVAVLVEERVDLRRELSALVARSPFGQGAAWPVVQTVQRDGTCLVIA
PAPALPDDLATAAQRLALQLADELG VVGVLAVELFETTDGALLVNELAMRPHNSGHWI
DGARTSQFEQHLRAVL DYPLGSDAVVPVTVMANVLGAAQPPAMSVDERLHHLFARM
P DARVHLYGKAERPGRKVGHINFLGSDVAQLCERAELAAHWSHGRWTDGWDPHRASD
DAVGVPACGGRSDEEERRL
>sp|P37940|ODBA_BACSU 2-oxoisovalerate dehydrogenase subunit alpha OS=Bacillus subtilis
(strain 168) OX=224308 GN=bfmBAA PE=1 SV=1
MSTNRHQALGLTDQEAVDMYRTMLLARKIDERMWLLNRSGKIPFVISCQGQEEAAQVGA
AFALDREMDYVLPYYRDMGVVLAFGMTAKDLMMSGFAKAADPNSGGRQMPGHFGQK
KNRIVTGSSPVTQVPHAVGIALAGRMEKKDIAAFVTFGEGSSNQGDFHEGANFAAVHKL
PVIFMCENNKY AISVPYDKQVACENISDRAIGYGM PGVTVNGNDPLEVYQAVKEARERA
RRGEGPTLIETISYRLTPHSSDDDDSSYRGREEVEEAKKSDPLLT YQAYLKETGLLSDEIEQ
TMLDEIMAI VNEATDEAENAPYAAPESALDYVYAK
>sp|Q9LCQ7|OPH_PESP Oxidized polyvinyl alcohol hydrolase OS=Pseudomonas sp. OX=306
GN=pvaB PE=1 SV=1
MNQSLGVLRLTRGVIALALASVASGCSSTGADR TAATPAAANPAATEPVKWECPAGYEV
KEGLNVDFPHKGMKRAFIVYPAKNVSGPAPVWVPMTGSVESTNDNLTVARSGANSILAD
HGYTVIAPVRACANQDPNIRGERCNGPGSNGWNWNPWFEGRAADPSGEHWKNDEGPDS
SFFVAMVQCVGTKYKLDARRLF LGGISSGGTMTNRALLFRSNFWAGGLPISGEWYVTSD
DGTPLSFDDARA AAVAAAPT KIHQGRVGPYPLPAKVGPLIVMTVWGGEKDLWNCTRPDGS
RFLCADYRPSTQAGSNFFSAQPDVVHVACSS THGHMWPQLNTQEFNRWALDTLASHPKG
SDPRSFKLTQPPEGYTCHVGPFTGLY
>sp|Q04681|PMFA_PROMH Major fimbrial subunit OS=Proteus mirabilis (strain HI4320)
OX=529507 GN=pmfA PE=1 SV=1
MKLSKIALAAALVFGINSVATAENETPAPKVSSTKGEIQLKGEIVNSACGLAASSSPVIVDF
SEIPTSALANLQKAGNIKKDIELQDCDTTVAKTATVSYTPSVVNAVNKDLASFVSGNASG
AGIGLMDAGSKAVKWNTATTPVQLINGVSKIPFVAYVQAESADAKVTPGEFQAVINFQV
DYQ

>sp|P0A7X6|RIMM_ECOLI Ribosome maturation factor RimM OS=Escherichia coli (strain K12)
OX=83333 GN=rimM PE=1 SV=1
MSKQLTAQAPVDPIVLGKMGSSYGIRGWLRVFSSTEDAESIFDYQPWFIQKAGQWQQVQ
LESWKHHNQDMIKLKGVDDRDAAANLLTNCEIVVDSSQLPQLEEGDYWKDLMGCQVV
TTEGYDLGKVVDMMETGSNDVLVIKANLKDAFGIKERLVPFLDGQVIKKVDLTTRSIEVD
WDPGF

>sp|O31677|QUEE_BACSU 7-carboxy-7-deazaguanine synthase OS=Bacillus subtilis (strain 168)
OX=224308 GN=queE PE=1 SV=1
MAKGIPVLEIFGPTIQGEGMVIGQKTMFVRTAGCDYSCSWCDSAFTWDGSAKKDIRWMT
AEEFAELKDIGGDAFSHVTISGGNPALLKQLDAFIELLKENNIRAALETQGTVYQDWFTLI
DDLTISPKPPSSKMVTNFQKLDHILTSLQENDRQHAVSLKVVFNDLEDLEFAKTVHKRYPG
IPFYLQVGNDDVHTTDDQSLIAHLLGKYEALVDKVAVD AELNLVRVLPQLHTLLWGNKR
GV

>sp|P22635|PCYA_SPHSK Protocatechuate 4,5-dioxygenase alpha chain OS=Sphingobium sp.
(strain NBRC 103272 / SYK-6) OX=627192 GN=ligA PE=1 SV=1
MTEKKERIDVHAYLAEFDDIPGTRVFTAQRARKGYNLNQFAMSLMKAENRERFKADESA
YLDEWNLTPAAKAAVLARDYNAMIDEGGNVYFLSKLFSTDGKSFQFAAGSMTGMTQEE
YAQMMIDGGRSPAGVRSIKGGY

>sp|Q9JMQ2|PPAX_BACSU Pyrophosphatase PpaX OS=Bacillus subtilis (strain 168)
OX=224308 GN=ppaX PE=1 SV=1
MSDKQVTTILFDLDGTLINTNELIIASFLHTLEHYYP SKYKREDVLAFIGPSLFDTFSSMDPD
KCEDMIAMYRAYNHDMHDSLVTEYETVYETLDALKKAGFTLGIVTTKLRDVTNMGLKL
TGIGEFFETVVTLD DVTNAKPDPEPVLLALKQLGSEPAEAIMVGDNYHDVLAGKNAGTKT
AGVAWTIKGPEMLAKHEPDMLEKMSDLLQIVGVK

>sp|Q79FE1|PPE41_MYCTU PPE family protein PPE41 OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) OX=83332 GN=PPE41 PE=1 SV=1
MHFEAYPPEVNSANIYAGPGPDSMLAAARAWRSLDVEMTAVQRSFNRTLLSLMDAWAG
PVVMQLMEAAKPFVRWLTDL CVQLSEVERQIHEIVRAYEWAHHD MVPLAQIYNNRAER
QILIDNNALGQFTAQIADLDQEYDDFWDEDEGEVMRDYRLRVSDALSKLTPWKAPPPIAHS
TVLVAPVSPSTASSRTDT

>sp|Q7BSH1|RHAM_RHILT L-rhamnose mutarotase OS=Rhizobium leguminosarum bv. trifolii
OX=386 GN=rhaM PE=1 SV=1
MTLEKHAFKMQLNPGMEAEYRKRHDEIWPELVDLLHQSGASDYSIHLDRETNTLFGVLT
RPKDHTMASLPDHPVMKKWWAHMADIMATNPDNSPVQSDLVTLFHMP

>sp|P41409|RIHA_ECOLI Pyrimidine-specific ribonucleoside hydrolase RihA OS=Escherichia
coli (strain K12) OX=83333 GN=rihA PE=1 SV=2
MALPILLDCDPGHDDAIAIVLALASPELDVKAITSSAGNQTP EKTLRNVLRMLTLLNRTDIP
VAGGAVKPLMRELIIADNVHGESGLDGPALPEPTFAPQNCTAVELMAKTLRESAEPVTIVS
TGPQTNVALLLN SHPELHSKIARIVIMGGAMGLGNWTPAAEFNIYVDPEAAEIVFQSGIPV
VMAGLDVTHKAQIHVEDTERFRAIGNPVSTIVAELL DFFLEYHKDEKWGFV GAPLHDPCT
IAWLLKPELFTSVERWVG VETQGKYTQGMTVVDY YYYLTGNKPNATVMVDVDRQGFVD
LLADRLKFYA

>sp|P75589|RBFA_MYCPN Ribosome-binding factor A OS=Mycoplasma pneumoniae (strain
ATCC 29342 / M129) OX=272634 GN=rbfA PE=1 SV=1
MASYKKERLENDIIRLINRTVIHEIYNETVKTGHVTHVKLSDDLHVTYVYLD CYNREQIDR
VVGAFNQAKGVFSRVL AHNLYLAKAVQIH FVKDAIDNAMRIESIINSLKKS KPN

>sp|Q8KZ94|REBMT_NOCAE Demethylrebeccamycin-D-glucose O-methyltransferase
OS=Lechevalieria aerocolonigenes OX=68170 GN=rebM PE=1 SV=1
MTESKSEGTAVAAPTPEEVRQMYDDFTDPFARIWGENLHFGY WEDAGADVSVD DATDR
LTDEMIALLDVRS GDRVLDVGC GIGKPAVRLATARDVRVTGISISRPQVNQANARATAAG

LANRVTF SYADAMDLPFEDASFDVWALESLHHMPDRGRALREMARVLRPGGTVAIADF
VLLAPVEGAKKEAVDAFRAGGGVLSLGGIDEYESDVRQAELVVTSTVDISAQARPSLVKT
AEAFENARSQVEPFMGAEGLDRMIATFRGLAEVPEAGYVLIGARKP
>sp|Q8ZKW0|RBSD_SALTY D-ribose pyranase OS=Salmonella typhimurium (strain LT2 /
SGSC1412 / ATCC 700720) OX=99287 GN=rbsD PE=1 SV=1
MKKGTVLNSEISSVISRLGHTDTLVVCDAGLPIPNSTARIDMALTQGVPSFMQVVDVVTRE
MQVEAAILATEIKQQNPQLHETLLTHLEQLQQHQGNTIKISYTTHEQFKKLTADSQAVIRS
GECSPYANVILCAGVTF
>sp|P75691|YAHK_ECOLI Aldehyde reductase YahK OS=Escherichia coli (strain K12)
OX=83333 GN=yahK PE=1 SV=1
MKIKAVGAYS AKQPLEPMDITRREPGPNVDKIEIAYCGVCHSDLHQVRSEWAGTVYPCVP
GHEIVGRVVAVG DQVEKYAPGDLVGVGCIVDSCKHCEECDGLENYCDHMTGTYNSTPT
DEPGHTLGGYSQQIVVHERYVLRIRHPQEQLAAVAPLLCAGITTYSPLRHWQAGPGKKVG
VVGIGGLGHMGIKLAHAMGAHVVAFTTSEAKREAAKALGADEVVNSRNADEMAAHLKS
FDFILNTVAAPHNLDDFTLLKRDGTM TLVGAPATPHKSPEVFNLMKRRAIAGSMIGGIP
ETQEMLDFCAEHGIVADIEMIRADQINEAYERMLRGDVKYRFVIDNRTLTD
>sp|P9WNG1|Y892_MYCTU Uncharacterized monooxygenase Rv0892 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv0892 PE=1 SV=1
MTGRCPTVAVVGAGMSGMCVAITLLSAGITDVCIEKADDVGGTWRDNTYPGLTCDVPS
RLYQYSFAKNPNWTQMFSRGGEIQDYLRGIAERYGLRHRIRFGATVVSARFDDGRWVLR
TDSGTESTVDFLISATGVLHHPRIPPIAGLDDFRGTVFHSARWDHTVPLLGRRIAVIGTGST
GVQLVCGLAGVAGKVTMFQRTAQWVLPWPNP RYSKLARVFHRAFPCLGSLAYKAYSLS
FETFAVALSNPGLHRKLVGAVCRASLRVRDPRLRRALTPDYEPMCKRLVMSGGFYRAIQ
RDDVELVTAGIDHVEHRGIVTDDGVLHEVDVIVLATGFDSHAFFRPMQLTGRDGIRIDDV
WQDGPAAHQTV AIPGFPNFFMMLGPHSPVGNFPLTAVAESQAEHIVQWIKRWRHGEFDT
MEPKSAATEAYNTV LRAAMPNTVWTTGCDSWYLNKDG IPEVWPFAPAKHRAMLANLHP
EEYDLRRYA AAVRATSRPQSA
>sp|O31521|URHG1_BACSU Unsaturated rhamnogalacturonyl hydrolase YesR OS=Bacillus
subtilis (strain 168) OX=224308 GN=yesR PE=1 SV=1
MAQLIFDEEKVTSVIDRIVKRTFQMDFAWDWPGGVAFYGVAEAYEATENEEYINLLK TW
VDEQLEDGLPPLSINGVSIGHTLLFLHKVTGDDVYLETAAEMA EYVLHKAPRFGE GILQHT
VNAAEYVFPEQAWADTLMMAGLFMLRIGRVMEREDYFEDGLRQFHGHEDVLQDPVTNL
YYHAWDNKAQNHLSGIYWGRANGWAALTMAKALPLIEVTHPSFMIIDGSLRDQLSALVR
LQDESGLWHTILDDPDSYLEVSASAGIASALMSSGKLYTKYVQKSLAAILDAVEEDGRVS
RVSAGTAVMKN AEGYKQVPYKRIQG WGQGLALTFLADVLKTKKRLYQ
>sp|P44882|Y817_HAEIN UPF0149 protein HI_0817 OS=Haemophilus influenzae (strain ATCC
51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=HI_0817 PE=1 SV=1
MLISHSDLNQQ LKSAGIGFNATELHGFLSGLLCGGLKDQSWLPLLYQFSNDNHAYPTGLV
QPVTLEYEQISQTLSDVEGFTFELGLTEDENVFTQADSLSDWANQFLLGIGLAQPELAKEK
GEIGEAVDDLQD ICQLGYDEDDNEEELAEALEEII EYVRTIAMLFYSHFNEGEIESKPV LH
>sp|O07779|VPB27_MYCTU Antitoxin VapB27 OS=Mycobacterium tuberculosis (strain ATCC
25618 / H37Rv) OX=83332 GN=vapB27 PE=1 SV=3
MKAVVDAAGRIVVPKPLREALGLQPGSTVEISRYGAGLHLIPTGRTARLEEENGVLVATG
ETTIDDEVVFGLIDSGRK
>sp|P9WF97|VPC15_MYCTU Ribonuclease VapC15 OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) OX=83332 GN=vapC15 PE=1 SV=1
MIVDTSVWIA YLSTSESLASRWLADRIAADSTVIVPEVVM MELLIGKTDEDTAALRRRL LQ
RFAIEPLAPVRDAEDAAAIHRRRCRRGGDTVRSLIDCQVAAMALRIGVAVAHDRDRDYEAIR
THCGLRTEPLF

>sp|C0H3X4|YEZG_BACSU Probable antitoxin YezG OS=Bacillus subtilis (strain 168)
OX=224308 GN=yezG PE=1 SV=1
MQDLYQLIGEKLNDIIPGEWTKIYLYAEVLDDSTMVLFHFRTPENNQIIYSQDIPSHYNVSK
DIFKTLLRELRELFEELRTEHRNNDDVWTNLTLTLDRSGEFQLDYNDDILASELDGYER
IAIWEYKNLGLPEDEDDKEFVISYLGL

>sp|P64594|YHAV_ECOLI Ribonuclease toxin YhaV OS=Escherichia coli (strain K12)
OX=83333 GN=yhaV PE=1 SV=1
MDFPQRVNGWALYAHPCFQETYDALVAEVETLKGKDPENYQRKAATKLLAVVHKVIEE
HITVNPSSPAFRHGKSLGSGKNKDWSRVKFGAGRYRLFFRYSEKEKVIILGWMNDENTLR
TYGKKTDAYTVFSKMLKRGHPPADWETLTRETEETH

>sp|P40943|XYN1_GEOSE Endo-1,4-beta-xylanase OS=Geobacillus stearothermophilus
OX=1422 PE=1 SV=1
MRNVVRKPLTIGLALTLLLPMGMTATSAKNADSYAKKPHISALNAPQLDQRYKNEFTIGA
AVEPYQLQNEKDVQMLKRHFNSIVAENVMKPISIQPEEGKFNFQADRIVKFAKANGMDI
RFHTLVWHSQVPQWFFLDKEGKPMVNETDPVKREQNKQLLLKRLETHIKTIVERYKDDIK
YWDVVNEVVGDDGKLNRNSPWYQIAGIDYIKVAFQAARKYGGDNIKLYMNDYNTEVEPK
RTALYNLVKQLKEEGVPIDGIGHQSHIQIGWPSEAEIEKTINMFAALGLDNQITELDVSMY
GWPPRAYPTYDAIPKQKFLDQAARYDRLFKLYEKLSDKISNVTFWGIADNHTWLDSRAD
VYYDANGNVVDPNAPYAKVEKGKGDAPFVFGPDYKVKPAYWAIIDHK

>sp|Q97QT7|Y1112_STRPN DegV domain-containing protein SP_1112 OS=Streptococcus
pneumoniae serotype 4 (strain ATCC BAA-334 / TIGR4) OX=170187 GN=SP_1112 PE=1 SV=1
MTKIKIVTDSSVTIEPELVKQLDITIVPLSVMIDNVVYSADLKEEGKFLQLMQESKNLPKT
SQPPVGVFAEIFEDLCKDGGQILAIHMSHALSGTVEAARQGASLSTADVTVVDSSFTDQAL
KFQVVEAAKLAQEGKDMEMAILSHVEEVKNHTELYIGVSTLENLVKGGGRISRVTGLLSSLL
NIRAVMQMKDHELQPMVKGRGTKTFKKWLDELITSLSERAVAEIGISYSGSDDWAKEMK
ESLQAYVEKPISVLETGSIQTHTGENAWAILIRYHS

>sp|Q3MUH7|XG74_PAESP Xyloglucanase OS=Paenibacillus sp. OX=58172 GN=xeg74 PE=1
SV=1
MKTFLGKKLWMASLAVALAAGSFAALPEMTSAAPSEPYTWKNVVTGAGGGGFVPGIIFNE
SEKDLIYARTDIGGAYRWNPANESWIPLTDFVGWDDWNKNGVDALATDPVDPDRVYLA
VGTYTNSWDKNNGAILRSTDRGDTWQTTLPFKVGGNMPGRSMGERLVVDPNDNRILYF
GARSNGNLWRSSDYGATWSKVTSFPNPGTYVQDPANEYGSDIVGLAWITFDKSSGQVGG
ATQTIYVGVADTAQSIYRSTDGGATWTA VPGQPTGYLPHHGVLADAGSLYITYSNGVGP
YDGTKGDVWKLNTSTGAWTNISIPSSSADNYFGYGGLAVDAQEPGTLMVATLNSWWP
DAILFRSKDGGTTWTRIWEFDGYPNRKFRYTQNISAAPWLTFGTTPAPPEVSPKLGWMIG
DLEIDPFDSDRMMYGTGATIYGTNNLTNWDNNEKIDISVMAKGVEEMAVLDLVSPPSGA
HLVSGLGDVNGFRHDDLQPPAKMFSSPNYASTESLDFAE LNPSTMVRVGKADYAADPN
AKSIGLSSDGGTNWYKANAEPAGTAGGGTVAISSDGSKLVWSTSDKG VHYSSSTGGNSWT
ASTGIPAQAKVISDRVNPKNFYGFAAGKIYVSVNGGVSFQSQTAAAGLPVDGNADLDAVPG
VEGELWFAGGNEDGGPYGLWHSTDSGASFALSNVEEADSIGFGKAAPGRNSAALYAVA
QIDGTRGFFRSDDGGASWVRINDDAHQYARVTTITGDPRIYGRVYLG TNGRGILYADPVG
GNNGGETPPVSHSGISPQSTEFDLNADRQADIPVALTLNGNTLASIRNGNHVLVQGS DYT
MSGSQVFLSKTYLATLSKGVQSLVFRFSAGNDATLSITVKDTTQVPLPEGSIRIEMYNGTTS
ATANSINPKFKLTNTGTAPLQLADVNI RYYYTIDGEKPLNFFCDWATAGSANVTGTFSALP
AAVNGADHVLEIGFTASAGTLAAGQSTEVQVRFSKTDWTNFTQTDDYSFAASSTAYENW
SKVTGYVSGTLQWGIEP

>sp|P76584|YPHB_ECOLI Uncharacterized protein YphB OS=Escherichia coli (strain K12)
OX=83333 GN=yphB PE=1 SV=1
MTIYTLSHGSLKLDVSDQGGVIEGFWRDTPLLRPGKKSGVATDASCFPLVPFANRVSGN
RFVWQGREYQLQPNVEWDAHYLHGDGWLGEWQCVSHSDDSLCLVYEHRSGVYHYRVS

QAFHLTADTLTVTLSTVNQGAETLPFGTGWHPYFPLSPQTRIQAQASGYWLEREQWLAGE
FCEQLPQELDFNQAPLPRQWVNNGFAGWNGQARIEQPQEGYAIIMETTPPAPCYFIFVSD
PAFDKGYAFDFFCLEPMSHAPDDHHRPEGGDLIALAPGESTTSEMSLRVEWL

>sp|P45931|YQBO_BACSU Uncharacterized protein YqbO OS=Bacillus subtilis (strain 168)

OX=224308 GN=yqbO PE=1 SV=2

MAKLTATFELHDKISRKLRLMIQGNAERLKRANGPLIFEADRTERVMRQIDRSANRLTA
RARLLEMGLDDRVSNGLHSIRQQAEDLTEGSHEVTVSVDQATPRFRLIRGGLTDLNSSH
AEPTVSVRDHASNQLDEIRRHVTDVDSEHAETVSIKDRASAALDAIEAKIDSLKGATITLA
VAGGFSAGSIMGSGKSTMSQDAYVSATSNVNKKDVAKMTDQIYFNNKAGSSREEVSLSL
RNLSQQTGASKKALAELETSSSKIAQLMNADQAEVDRAFSSMYNNLKLKSGKQSGDLIAY
VYRNAGDQADDLLDTMNEYSSTFKDLKLTGGQIANAMIKGTKGGARNFDNLADSMREF
NIRRTMSDSQVDAFKTLFGAKETKKMFKGFKDGSISGEESLFRVAKALSKVKDKTKRAA
IATELIGTQYEDLKQPILDMAEGIGTSAKTSGELERSFTKLDRDNNPMTVPNDAMRDFESISK
DMGTSLLTGLGPAFDKISSFINSKEGQEKLEIKKDIADLGEEIGDKLNVAIEWSVNHWDD
LKTAIKVVIPSLIGLIGYLKILRPLLKGIGTVGSDAAGVIRKLIPKRTPKAGTNTQSERNRN
SNRNASTRGRESKTATGPTSLPRSGSLTYCCCSDDGGKNDRIRRRRGKRVLGRRGNPNRMN
PSDSSIAVSSERLERRRSGRTVGTNPTRDSRSAITTRSELYSAGRAAGGTSKFGKVLSPKLS
VGKFAKGVPLLGTALAATDLIGMNKDNVGEKIGSAGGGLAGAATGAAIGSVIPGVGTAG
GLVGGIAGTMGGSSLGKAFDGSEVKKKLNSTLFDQKWWSEKWSGIKSNKTSINGLSDT
WSNVKEKVKSTLFNSEWWSEKWSGVKSWAQNKWNSASSVWESVKGKIKSTLFSEKWW
SGKWEKVKSWAQSKWDSASSVWQSVKGKLGKSTLFSEKWWSGKWESVKSWSKNKWDN
AKSIWKS VKSSISETLFSKKWWSEKWSVKELGSSILGGVKEVGGKVASSAKKTAGKAW
GYVKSGVNYLFGSGKEKPKKHATGGYITKPTISWIGEAGKEFVIPVENNKGRGKMLLSQA
ASKLGMSVDDIASASSAGGEPATSPLVRSAAVTASVSPIIDTSSLDEQATSFGQQFTKSFD
QGIRDNVVSMEAWKQKNVGQPMNNLISYSPNYGKQVVNGYAKGQNSTSTGTDGFLQTK
VKMPFQNTV NKSSSWGSGTIKGFASGQNSSQTGTDQYVSTHINKPFIRSKESSNGWGS
GMIGNFVSGMTSKASEVNEAAKELAKKVEKAFREELDIHSPSRVMMSLGRFASIGIVKGLDSV
DVKKFAEKQAGSLAAAYSGMGAVSGNVKQWLMAAIMATKTPMSWLPGLMTIAQHESG
GNPKAINLWDSNAKAGHPSQGLMQTIPSTFNAHKLPGMNNILNPIHNAAAAIGYIKSRYGS
INNVPGIRSMRHGGPYVGYANGGLITKEQIARVGEKNKREWIPEERGIRGRYLLAQA
AKALGMEVTDPSKQTELSGQVTAATTGRNQTTFKAAAGGKEVIIQFNGDQHFHNDQDMNS
LVAKIKQALVDELEQDINIGTKGVVAFD

>sp|P9WLF7|Y2271_MYCTU Uncharacterized protein Rv2271 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv2271 PE=1 SV=1

MTTPPDKARRRFLRDAYKNAERVARTALLTIDQDQLEQLLDYVDERLGEQPCDHTARHA
QRWAQSHRIEWETLAEGLQEFGGYCDCEIVMNVEPEAIFG

>sp|P07773|CATA_ACIAD Catechol 1,2-dioxygenase OS=Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) OX=62977 GN=catA PE=1 SV=1

MEVKIFNTQDVQDFLRVASGLEQEGGNPRVKQIIHRVLSPLYKAIEDLNITSDEYWAGVA
YLNQLGANQEAGLLSPGLGFDHYLDMRMDAEDAALGIENATPRTIEGPLYVAGAPESVG
YARMDDGSDPNGHTLILHGTIFDADGKPLPNAKVEIWHANTKGFYSHFDPTGEQQAFNM
RRSIITDENGQYRVRTILPAGYGCPPEGPTQQLLNQLGRHGNRPAHIIHYFVSADGHRKLTT
QINVAGDPYTYDDFAYATREGLVVDAVEHTDPEAIKANDVEGPFAEMVFDLKLTRLVDG
VDNQVVDRPRLAV

>sp|Q5SHW0|CBL_THET8 Cystathionine beta-lyase OS=Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579) OX=300852 GN=TTHA1620 PE=1 SV=1

MDLPPRTGSLKWGTYPEDVLPLWVADMDFPFAEAIQQALAERARGFLGYPPREGDREL
ELILEALGLEAELAFMPGVVVGLYAAVA AFTAPGQGVLTQVPIYPPFLAAIRDQRRTVLA
NPLRETPEGYRLDLAGLERLAFATRLLLFCHPHNPTGRVFGEEELAALAQAIRRHDLIVS
DELHAPLTYEKPHVPLARFLPERTLTLVGPGKTYNLAGLPIGAVLGPKPLVEAVKRHLPHV

FPNVLAMAAWKAALKEGGPWLKATLEQLRANRDRVAAWAKARGLGHHHPPEGTYLAWI
 QTPFPKAAAYFLERARVALNPGESFGRGYDTYVRLNFATYPEVLEEALRRLDGALK
 >sp|Q81UB2|AZOR1_BACAN FMN-dependent NADH-azoreductase 1 OS=Bacillus anthracis
 OX=1392 GN=azoR1 PE=1 SV=1
 MNKTLIINAHPKVDDTSSVSIKVFKEHFLSYKELISNNETIEQINLYDDVVPIDKTVLSAW
 EKQNGNGQELTREEQKVTERMSEILQQFKSANTYVIVLPLHNFNIPSKLKDYMNDNIMIARET
 FKYTETGSGVLLKDGRMLVIQASGGIYTNDWYTDVEYSHKYLKAMFNFLGIEDYQIV
 RAQGTAVLDPTEVLQNAAYKEVEEAASRLANKYIFSLEE
 >sp|P76364|CBEA_ECOLI Cytoskeleton bundling-enhancing antitoxin CbeA OS=Escherichia coli
 (strain K12) OX=83333 GN=cbeA PE=1 SV=1
 MSDTLPGTTLPDDNHDRPWGLPCTVTPCFGARLVQEGNRLHYLADRAGIRGLFSDADA
 YHLDQAFPLLMKQLELMLTSGELNPRHQHTVTLYAKGLTCKADTLSSCDYVYLA VYPTP
 EMKN
 >sp|Q936X2|ATZF_PSED Allophanate hydrolase OS=Pseudomonas sp. (strain ADP) OX=47660
 GN=atzF PE=1 SV=1
 MNDRAPHPERSGRVTPDHLTDLASQAAAYAGTDAADVISDLYARIKEDGENPIWISLLP
 LESALAMLADAQQRKDKGEALPLFGIPFGVKDNIDVAGLPTTAGCTGFARTPRQHAFVVQ
 RLVDAGAIPIGKTNLQDQFATGLNGTRTPFGIPRCVFNENYVSGGSSSGSAVAVANGTVPFS
 LGTDTAGSGRIPAAFNVLVGLKPTKGLFSGSLVPAARSLDCISVLAHTVDDALAVARVA
 AGYDADDAFSRKAGAAALTEKSWPRRFNFGVPAAEHRQFFGDAEAEALFNKAVRKLEE
 MGGTCISFDYTPFRQAAELLYAGPWVAERLAAIESLADEHPEVLHPVVRDIILSAKRMSAV
 DTFNGIYRLADLVRAAESTWEKIDVMLLPTAPTIYTVEDMLADPVRLNSNLGFYTNFVNL
 MDLSAIAVPAGFRTNGLPFGVTFIGRAFEDGAIASLGKAFVEHDLAKGNAATAAPPKDTV
 AIAVVG AHLSDQPLNHQLTESGGKLRATTRTAPGYALYALRDATPAKPGMLRDQNAVGS
 IEVEIWDLPVAGFGAFVSEIPAPLGIGTITLEDGSHVKGFLCEPHAIETALDITHYGGWRAY
 LAAQ
 >sp|Q83AJ3|AROK_COXBU Shikimate kinase OS=Coxiella burnetii (strain RSA 493 / Nine Mile
 phase I) OX=227377 GN=aroK PE=1 SV=1
 MKKNLTNIYLIGLMGAGKTSVGSQAKLTKRILYDSKDKEIEKRTGADIAWIFEMEGEAGF
 RRREREMIEALCKLDNIILATGGGVVLDEKNRQQISETGVVIYLTASIDTQLKRIGQKQKGM
 RRPLFIKNSKEKLQQLNEIRKPLYQAMADLVYPTDDLNRQLATQILVDIKQTYSDL
 >sp|O87692|CBIC_BACME Cobalt-precorrin-8 methylmutase OS=Bacillus megaterium OX=1404
 GN=cbiC PE=1 SV=1
 MDRTEFKPLTVQPQQIEGKSFEMITEELGHPFTDEQYPIVQRVIHRSADFELGRSMLFHP
 DAIQAGIKAIRSGKQVADVQMVQVGTNKQRIEKHGGEIKVYISDSVMEEAKRLNTTRA
 IISMRAIKEADGGIFAIGNAPTALLELIRLIKEGEAKPGLVIGLPVGFVSAAESKEELAKLY
 VPFITNIGRKGGSTVTVAALNAISILADSGVTYEGSAKRT
 >sp|I6X7F9|CDDTR_MYCTU Transcriptional regulator Rv3488 OS=Mycobacterium tuberculosis
 (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv3488 PE=1 SV=1
 MREFQRAAVRLHILHHAADNEVHGAWLTQELSRHGYRVSPGTLYPTLHRLEADGLLVSE
 QRVVDGRARRVYRATPAGRAALTEDRRALEELAREVLGGQSHTAGNGT
 >sp|Q84CG1|CAMYS_STRVI Capreomycin synthase OS=Streptomyces vinaceus OX=1960
 GN=vioD PE=1 SV=1
 MTGPLGAGPQALPAAPLEDWLRERYFQAKTDISSSGVHNYTFGELRALDPALLGTRELDQ
 LMFRDGPLGDERLRAAVAARVRPGPGHVMTTHGSSEALYLAFALVRPGDEVVVATP
 AYHSLSGLATAAGASLRPWPLRPENGFAFDLDDLRVLSRTRLVVVNFHPNPSGACVDP
 RGRTELLDLVANSQAVLLWDGAFTDLVHDHPPLAEPQDLDRVLSFGTSLKAYGLPGLR
 VGWCVVPPQDLVSELVRIRDYLTLSLSPVERVA AVAVEHADALITPRLTEARHNRRRVLE
 WAAASEGAIDCPVPRGGVTAFFRFTAHTDVTDL CERLLARHGVLVVPGRVFGQADRMRI
 GFSCPRPELERGLAAISEELGTHARGRRRG TG

>sp|P63264|CBPM_ECOLI Chaperone modulatory protein CbpM OS=Escherichia coli (strain K12) OX=83333 GN=cbpM PE=1 SV=1
MANVTVTFTITEFCLHTGISEEELNEIVGLGVVEPREIQETTWFDDHAAIVVQRAVRLRH
ELALDWPGIAVALTLMDDIAHLKQENRLLRQRLSRFVAHP

>sp|A0A0H5BN57|CLDD_STRCP (12E)-labda-8(17),12,14-triene synthase OS=Streptomyces
cyslabdanicus OX=1470456 GN=cldD PE=1 SV=1
MTRTGDAVTILQPDFTATFPGPFPPTSPHGERTERQLLGWLEEYPLLPSARARSVLVNITSH
GVSRTLPTADADDLVLFAELLWLTAFFDDMHGESNAARDLVALVDRTAELTLVLAGGSP
PPLTNPFPAALYDLLARFRARTGPAAYLRLAASLRDTIMALVWEAHHVAEPERVALETYL
EMRPHTVFVRTIFAAAEIVLDYELTDAQRALAPVRHLETAVANLAGWINDLASYEREAAR
GPAQPLSLPTLLRARHGGSLLEEAFARAGGMCENEAAVARQGITSLAGDPPSALTAHARAL
EDIARSFVWHTSHARYQGPKRGAAPTSR

>sp|P75919|CLSC_ECOLI Cardiolipin synthase C OS=Escherichia coli (strain K12) OX=83333
GN=clsC PE=1 SV=2
MPRLASAVLPLCSQHPPGQCGLFPLEKSLDAFAARYRLAEMAETLDVQYYIWQDDMSGR
LLFSALLAAAKRGVRVRLLLDDNNTPLGDDILRLLDLSDHPRIEVRVLFNPFSFRLLRPLGYITD
FSRLNRRMHNKSFTVDGVVTLVGGRNIGDAYFGAGEEPLFSDLDVMAIGPVVEDVADDF
ARYWYCKSVSPLQQVLDVPEGEMADRIELPASWHNDAMTHRYLRKMESSPFINHLVDGT
LPLIWAKTRLLSDDPAKGEKAKRHSLLPQRLFDIMGSPSERIDISSYFVPTRAGVAQLLR
MVRKGVKIAILTNSLAANDVAVVHAGYARWRKLLRYGVELYELKPTREQSSTLHDRGI
TGNSGASLHAKTFSIDGKTVFIGSFNFDPRSTLLNTEMGFVIESETLAQLIDKRFIQSQYDAA
WQLRLDRWGRINWVDRHAKKEIILKKEPATSFWKRVMLASILPVEWLL

>sp|Q38M35|CNBH_COMTE 2-amino-5-chloromuconic acid deaminase OS=Comamonas
testosteroni OX=285 GN=cnbH PE=1 SV=2
MNAAHLSLAEHAARLRRRELTAVALIDTCAQHHEARMEPRLNAYKTWDGARARSAAA
DTLLDQGQDLGPLMGLPVSVKDLYGVPGLPVFAGSDEALPEAWQAAGPLVARLQRQLGI
VVGKTHTVEFAFGGLGVNAHWGTPRNPWSPHEHRVPGGSSAGAGVSLVQGSALLALGT
DTAGSVRVPASMTGQVGLKTTVGRWPVEGIVPLSSSLDTAGVLTRTVEDLAYAFAALDT
ESQGLPAPAPVRVQGLRVGVPTNHFWDIDPSIAAAVEAAVQRLAQAGAQQVRFPLPHC
EEAFDIFRRGGLAASELAAYLDQHFPKHVERLDPVVRDRVRWAEQVSSVEYLRRKAVLQ
RCGAGAAARLFDDVDVLLTPTVPASPPRLADIGTVETYAPANMKAMRNTAISNLFGWCAL
TMPVGLDANRMPVGLQLMGPPRAEARLIGIALGIEALIGQGHALLGAPDLP

>sp|P37975|CNRR_CUPMC Nickel and cobalt resistance protein CnrR OS=Cupriavidus
metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) OX=266264 GN=cnrR
PE=1 SV=2
MMKSRTRRSLSTLFGALLGVSVAAAWLYYSHRNEAGHGDLHEILHEAVPLDANEREILE
LKEDAFARRRREIETRLRAANGKLADAIKNPASPEVEAATQEVERAAGDLQRATLVH
VFEMRAGLKPEHRPAYDRVLIDALRRGSQ

>sp|P9WPQ3|BCCA_MYCTU Acetyl-/propionyl-coenzyme A carboxylase alpha chain
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=accA1 PE=1
SV=1
MFDTVLVANRGEIAVRVIRTLRRLGIRSVAVYSDPDVDARHVLEADAAVRLGPAPARESY
LDIGKVLDAARTGAQAIHPGYGFLAENADFAAACERARVVFLGPPARAIEVMGDKIAA
KNAVAAFDVPVPGVARAGLTDDALVTAAAEVGYPVLIKPSAGGGGKGMRLVQDPARL
PEALVSARREAMSSFGDDTLFLERFVLRPRHIEVQVLADAHGNVVHLGERECSLQRRHQK
VIEEAPSPLLDPQTRERIGVAACNTARCVDYVGAGTVEFIVSAQRPDEFFFMEMNTRLQVE
HPVTEAITGLDLVEWQLRVGAGEKLGFAQNDIELRGHAIEARVYAEDPAREFLPTGGRVL
AVFEPAGPGVRVDSSLLGGTVVGSDDYDPLLTKVIAHGADREEALDRLDQALARTAVLGV
QTNVEFLRLLADERVRVGDLDTAVLDERSDFTARPAPDDVLAAGGLYRQWALARRA
QGDLWAAPSGWRGGGHMAPVRTAMRTPLRSETVSVWGPPESAQVQVGDGEIDCASVQV

TREQMSVTISGLRRDYRWAEADRHLWIADERGTWHLREAEEHKKIHRAVGARPAEVSMP
PGSVIAVQVESGSQISAGDVVVVVEAMKMEHSLEAPVSGRVQVLVSVGDQVKVEQVLAR
IKD

>sp|P22805|BIOA_LYSSH Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
OS=Lysinibacillus sphaericus OX=1421 GN=bioA PE=1 SV=1

MKQVLTELQEKDLQHVWHPCSQMKDYEAFPPIVIKKGEGVWLYDEQNQRYLDAVSSW
WVNLFGHANPRISQALSEQAFTLEHTIFANFSHEPAIKLAQKLVALTPQSLQKVFFADNGS
SAIEVALKMSFQYHMQTGKTQKKRFLALTDAYHGETLGALS VGGVDLYNEVYQPLLLDT
VRAQGPDCFRCPFKHHPDSCHAQCISFVEDQLRMHHKEITAVIIEPLIQAAAGMKMYPAY
LRLRELCTQYDVHLIADEIAVGFGRTGTLFACEQANISPDFMCLSKGLTGGYLPLSVMT
TNDVYQAFYDDYATMKAFLHSHSYTGNTLACRVALEVLAIIEEEQYIDVVQDKGERMRK
LALFAFDLPFVGEYRQVGFGAIELVANRDTKEPLSEERIGYQIYKRALAKGLLIRPLGN
VLYFMPPIIITDDEMQMFIQTTKDTIVQFFEEREG

>sp|Q7A3F4|CLPL_STAAN ATP-dependent Clp protease ATP-binding subunit ClpL
OS=Staphylococcus aureus (strain N315) OX=158879 GN=clpL PE=1 SV=1

MNNGFFNSDFDSIFRRMMQDMQGSNQVGNKKYYINGKEVSPEELAQLTQQGSNQSAEQS
AQAFQQAQRQQGQGGNGNYLEQIGRNLTQEARDGLDPVIGRDKEIQETAEVLSRRT
KNNPILVGEAGVGKTAIVEGLAQAVEGNVPAAIKDKEIISVDISSLEAGTQYRGAFEEINQ
KLIEGVKSSQNAVLFFDEIHQIIGSGATGSDSGSKGLSDILKPALSARGEISIIGATTQDEYRNN
ILKDAALTRRFNEVLVNEPSAKDTVEILKGIREKFEEHHQVKLPDDVLKACVDLSIQYIPQR
LLPDKAIDVLDITAAHLSAQSPA VDKVETEKRISELENDKRKAVSAEEYKKADDIQNEIKS
LQDKLENSNGEHTAVATVHDISDTIQRLTGIPVSQMDDNDIERLKNISNRLRSKIIGQDQAV
EMVSRAIRNRAGFDDGNRPIGSFLFVGPTGVGKTELAKQLAIDLFGNKDALIRLDMSEYS
DTTAVSKMIGTTAGYVGYDDNSNTLTEKVRNPNYSVILFDEIEKANPQILTLLQVMDDG
NLTDGQGNVINFKNTIIICTSNAGFGNGNDAEEKDIMHEMKKFFRPEFLNRFNGIVEFLHL
DKDALQDIVNLLLDDVQVTLDDKKGITMDVSDAKDWLIEEGYDEELGARPLRRIVEQQV
RDKITDYLDHTDVKHVDIDVEDNELVVKGK

>sp|Q9ZN78|AFRP_STRGR A-factor receptor protein OS=Streptomyces griseus OX=1911
GN=arpA PE=1 SV=1

MAKQARAVQTWRSIVDAAASVFDDYGYERA AISEILRRAKVTKGALYFHFASKEAIAQAI
MDEQTSTVEFEQEGSPLQSLVDGGQQFAFALRHNSMARAGTRLSIEGVFLGGPHPWGDWI
DATARMLELGQERGEVFPQIDPMVSAKIIVASFTGIQLVSEADSGRADLRGQVAEMWRHI
LPSIAHPGVIAHIKPEGRVDLAAQAREKAEREEQEARIAAEAKGAGSDAATDSGSRSGGSG
LRGGGSGRGP RAGGAGDEGEDEEPAGAGVAAGGVVA

>sp|P14941|ADH_THEBR NADP-dependent isopropanol dehydrogenase
OS=Thermoanaerobacter brockii OX=29323 GN=adh PE=1 SV=1

MKGFAMLSIGKVGWIEKEKPAPGPFDAIVRPLAVAPCTSDIHTVFEGAIGERHNMILGHEA
VGEVVEVGSEVKDFKPGDRVVVPAITPDWRTSEVQRGYHQHSGGMLAGWKFSNVKDG
FGEFFHVNDADMNLAHLPKEIPLEAAVMIPDMMTTGFHGAELADIELGATVAVLGIGPVG
LMAVAGAKLRGAGRII AVGSRPVCVDAAKYYGATDIVNYKDGPIESQIMNLTEGKGVDA
AIIAGGNADIMATAVKIVKPGGTIANVN YFGEGEVLPVPRLEWGCGMAHKTIKGGLCPGG
RLRMERLIDL VFYKRVDPSKLVTHVFRGFDNIEKAFMLMKDKPKDLIKPVVILA

>sp|Q0KDL6|ADH_CUPNH Alcohol dehydrogenase OS=Cupriavidus necator (strain ATCC
17699 / H16 / DSM 428 / Stanier 337) OX=381666 GN=adh PE=1 SV=1

MTAMMKAAVFVEPGRIELADKPIPDIGPNDALVRITTTTICGTDVHILKGEYPVAKGLTVG
HEPVGIIKLGSAVTGYREGQRVIAGAICPNFNSYAAQDGVASQDGSYLMASGQCCHGY
KATAGWRFGNMIDGTQAEYVLV PDAQANLTPIDGLTDEQVLMCPDIMSTGFKGAENAN
IRIGDTVAVFAQGPIGLCATAGARLCGATTIIAIDGNDHRLEIARKMGADVVLNFRNCDVV
DEVMKLTGGRGVDASIEALGTQATFEQSLRVLPKGGTSSLGVYSSDLTIPLSAFAAGLGD

HKINTALCPGGKERMRLINVIESGRVDLGALVTHQYRLDDIVAAYDLFANQRDGVLKIA
IKPH

>sp|Q8NQ97|ACNR_CORGL HTH-type transcriptional repressor AcnR OS=Corynebacterium
glutamicum (strain ATCC 13032 / DSM 20300 / JCM 1318 / LMG 3730 / NCIMB 10025)
OX=196627 GN=acnR PE=1 SV=1
MSVAAGDKPTNSRQEILEGARRCFAEHGYEGATVRRLEEATGKSRGAIFHHFGDKENLFL
ALAREDAARMAEVVSENGLVEVMRGMLEDPERYDWMSVRLEISKQLRTDPVFRAKWID
HQSVLDEAVRVRLSRNVDKGQMRTDVPIEVLHTFLETVLDGFISRLATGASTEGLSEVLDL
VEGTVRKRD

>sp|P9WNE5|BFRB_MYCTU Ferritin BfrB OS=Mycobacterium tuberculosis (strain ATCC
25618 / H37Rv) OX=83332 GN=bfrB PE=1 SV=1
MTEYEGPKTKFHALMQEQIHNEFTAAQQYVAIAVYFDSLEDLPQLAKHFYSQAVEERNHA
MMLVQHLLDRDLRVEIPGVDTVRNQFDRPREALALALDQERTVTDQVGRLTAVARDEG
DFLGEQFMQWFLQEIEEVALMATLVRVADRAGANLFELENFVAREVDVAPAASGAPHA
AGGRL

>sp|O33731|CYC3_SHEFN Tetraheme cytochrome c-type OS=Shewanella frigidimarina (strain
NCIMB 400) OX=318167 GN=cctA PE=1 SV=1
MSNKLLSALFAAGFAVMMMSSASFAAETLAEFHVEMGGCENCHADGEPKDGAYEFE
QCQSCHGSLAEMDDNHKPHDGLLMCADCHAPHEAKVGEKPTCDTCHDDGRTAK

>sp|Q8DGH2|CHLN_THEEB Light-independent protochlorophyllide reductase subunit N
OS=Thermosynechococcus elongatus (strain BP-1) OX=197221 GN=chlN PE=1 SV=1
MTVTAPNALNFECETGNYHTFCPISCVAWLYQKIEDSFVLVIGTKTCGYFLQNAMGVMIF
AEPYAMAELEEGDISAQLNDYEELKRLCLEIKRDRNPSVIVWIGTCTTEIHKMDLEGLAPK
LEAEIGIPIVVARANGLDYAFTQGEDTVLAAMAARCPTSTAISDPEERNPIQRLLNFGKKKE
EVQAQSSQYHPHPLVLFGLPDPVVTQLTLELKKQGIKVSGLWPAKRYTELPVIDEGYY
VAGVNPFLSRTATTLIRRRKCQLITAPFPIGPDGTRTWIEQICATFGIQPQGLAEREAEWQ
KLSDYLELVRGKSVFFMGDNLLEISLARFLIRCGMRVLEIGIPYMDKRYQAAELALLSQT
AEMGHPLPTIVEKPDNYNQLQRIKALQPDLVITGMAHANPLEARGISTKWSVEFTFAQIHG
FGNARDILELVTRPLRRNQALAGLGWQKLVAH

>sp|P33665|CHIS_STRSN Chitosanase OS=Streptomyces sp. (strain N174) OX=69019 GN=csn
PE=1 SV=1
MHSQHRTARIALAVVLTAPASLATAGVGYASTQASTAVKAGAGLDDPHKKEIAMELVSS
AENSSLDWKAQYKYIEDIGDGRGYTGGIIGFCSGTGDMLELVQHYTDLEPGNILAKYLP
LKKVNGSASHSGLGTPFTKDWATAAKDTVFQQAQNDERDRVYFDPAVSQAKADGLRAL
GQFAYYDAIVMHGPGNDPTSFGGIRKTAMKKARTPAQGGDETTYLNAFLDARKAAMLT
EAAHDDTSRVDTEQRFVLKAGNLDLNPPLKWKTYGDPYVINS

>sp|P86319|CYC2_RHOBL Cytochrome c2 OS=Rhodobacter blasticus OX=1075 PE=1 SV=1
QDAPTGDAAAGAKVFNKCQTCHMVVAPDGTVLGKAGKTGNPLYGLDGRAPASYPDF
AYGDGIKELGAAGEVWNEADFLQYVADPTKFLKTKTGDTKAKGKMTFKLPNEKEAHDV
WAFLNSLAPAPAAAEAAAPAADAAAPAAADAAAPAEPAEAAEGAAT

>sp|P00097|CYC2_RUBGE Cytochrome c2 OS=Rubrivivax gelatinosus OX=28068 PE=1 SV=1
ATPAELATKAGCAVCHQPTAKGLGPSYQEIAKKYKGQAGAPALMAERVRKGSVGIFGKL
PMTPTPPARISDADLKLVIDWILKTP

>sp|D5MP61|3XYN1_VIBSX Beta-1,3-xylanase XYL4 OS=Vibrio sp. OX=678 GN=xyl4 PE=1
SV=1
MKRTYLSLIAAGVMSLSVSAWSLDGVLVPESGILVSVGQDVDSVNDYASALGTIPAGVTN
YVGIVNLDGLNSDADAGAGRNNIAELANAYPTSALVVGVSMMNGEVDASGRYNANID
TLLNTLAGYDRPVYLRWAYEVDGPWNGHSPSGIVTSFQYVHDRIIALGHQAKISLVWQV
ASYCPTPGGQLDQWWPGSEYVDWVGLSYFAPQDCNWDVRVNEAAQFARSKGKPLFLNES
TPQRYQVADLTYSADPAKGTRNRQSKTSQQLWDEWFAPYFQFMSDNSDIVKGFTYINADW

DSQWRWAAPYNEGYWGDSRVQANALIKSNWQQEIAKGQYINHSETLFTLGYGSTGGG
DNGGGDNGGTNPPEPCNEEFGRYVSDSTIEVFHKNNGWSAEWNYVCLNGLCLQGEIKN
GEYVKQFDAQLGSTYGIEFKVADGESQFITDKSVTFENKQCGSTGTPGGGDNGSGGDNGG
DNGSGGDNGSGGGTDPSCSADFGYNYRSDTEIEVFHKDLGWSASWNYICLDDYCVPGD
KSGDSYNRSFNATLGSDYKITFKVEDSASQFITEKNITFVNTSCAQ

>sp|Q04416|4HBT_ARTSP 4-hydroxybenzoyl-CoA thioesterase OS=Arthrobacter sp. OX=1667
GN=fcbC PE=1 SV=1

MHRTSNGSHATGGNLPDVASHYPVAYEQTLDTGTVGFVIDEMTPERATASVEVTDTLRQR
WGLVHGGAYCALAEMLATEATVAVVHEKGMMAVGQSNHTSFFRPVKEGHVRAEAVRI
HAGSTTWFWVDVSLRDDAGRLCAVSSMSIAVRPRRD

>sp|P9WQD3|ACPS_MYCTU Holo-[acyl-carrier-protein] synthase OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=acpS PE=1 SV=1

MGIVGVGIDLVSIPTFAEQVDQPGTVFAETFTPGERRDASDKSSSAARHLAARWAAKEAV
IKAWSGSRFAQRPVLPEDIHRDIEVVTDMWGRPRVRLTGAIAYELADVTIHVSLTHEGDT
AAAVAILEAP

>sp|Q9WYN9|CHEB_THEMA Protein-glutamate methylesterase/protein-glutamine glutaminase
OS=Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) OX=243274
GN=cheB PE=1 SV=1

MTDRVIRVLVVDSDAFMRMVLKDIIDSQPDMMKVVGFAKDGLAVEKAIELKPDVITMDIE
MPNLNGIEALKLIMKKAPTRVIMVSSLTEEGAATIEALRNGAVDFITKPHGSISLTFRQVA
PELLEKIRQAMNVDPRITLLFKPKVSRLTITKPAVSGKIVVIGSSTGGPRSLDMIIPNLPKNFP
APIVVVQHMPPGFTKSLAMRLDSTSELTVKEAEDGEEVKPGFVYIAPGDFHLGLKAQNGK
VFFFLDKSDKINNVRPAVDFTLDKAAEYKSKTIAVILTGMGKDGTKGAFKVKFYGGTVIA
EDKETCVVFGMPKSVIEEGYADYVLPAYKIPEKLIELV

>sp|P17998|CEAD_ECOLX Colicin-D OS=Escherichia coli OX=562 GN=cda PE=1 SV=1

MSDYEGSGPTEGIDYGHSMVWPSTGLISGGDVKPGGSSGIAPSMPPGWDYSPQGIALV
QSVLFPGIIRRIILDKELEEGDWSGWSVSVHSPWGNEKVSAAARTVLENGLRGGLPEPSRPA
AVSFARLEPASGNEQKIIRLMVTQQLEQVTDIPASQLPAAGNNVPVKYRLMDLMQNGTQ
YMAIIGGIPMTVPVVDAPVPDRSRPGTNIKDVYSAPVSPNLPDLVLSVGQMNTPVLSNPE
IQEEGVIAETGNYVEAGYTMSSNNHDVIVRFPEGSDVSPLYISTVEILDSNGLSQRQEAENK
AKDDFRVKKEEAVARAEAEKAKAELEFSKAGVNQPPVYTQEMMERANSVMNEQGALVL
NNTASSVQLAMTGTGVWTAAGDIAGNISKFFSNALEKVTIPEVSPLLMRISLGALWFHSEE
AGAGSDIVPGRNLEAMFSLSAQMLAGQGVVIEPGATSVNLPVRGQLINSNGQLALDLLKT
GNESIPAAVPVLNAVVRDTATGLDKITLPAVVGAPSRITLVNVPVQPSVPTDTGNHQPVPVT
PVHTGTEVKSVEMPVTTITPVSDVGGRLDFIYWRPDAAGTGVEAVYVMLNDPLDSGRFSR
KQLDKKYKHAGDFGISDTKKNRETLTKFRDAIEEHLSDKDTVEKGTYRREKGSKVYFNP
TMNVVVIKSNGEFLSGWKINPDADNGRIYLETGEL

>sp|P9WP95|COBQ_MYCTU Cobyric acid synthase OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) OX=83332 GN=cobQ PE=1 SV=1

MSGLLVAGTTSDAGKSAVTAGLCRALARRGVRVAPFKAQNMSNNSMVCGRPDGTGVEI
GRAQWVQALAAARTTPEAAMNPVLLKPASDHRSHVVLGMKPWGEVASSSWCAGRRA
EAACRAFDALAARYDVVVAEGAGSPAELNLRAGDYVNMGLARHAGLPTIVVGDIDRGGV
FAAFLGTVALLAEDQALVAGFVVNKFGRDSDLLAPGLRDLERVTGRRVYGTLPWHPDL
WLDSEDALDLQGRRAAGTGARRVAVVRLPRISNFTDVALGLEPDLVVFASDPRALDD
ADLIVLPGRATIALDLAWLRARDLDRALLVHVAAGKPLLIGCGGFQMLGRVIRDPYGIEG
PGGQVTEVEGLGLLDVETAFSPHKVLRPRGEGLGVPASGYEIIHGRITRGDTAEFFLGGA
RDGPVFGTMWHGSLEGDALREAFRLRETLGLAPSGSCFLAARERRLDLLGDLVERHLDVD
ALLNLARHGCPTLPFLAPGAP

>sp|P0A9H7|CFA_ECOLI Cyclopropane-fatty-acyl-phospholipid synthase OS=Escherichia coli
(strain K12) OX=83333 GN=cfa PE=1 SV=2

MSSSCIEEVSV PDDN WYRIANELL SRAGIANGSAPADIRVKNP DFFKRV LQEGSLGLGESY
MDGWWECDRLDMFFSKVLRAGLENQLPHHFKDTLRIAGARLFNLQSKKRAWIVGKEHY
DLGNDLFSRMLDPFMQYSCAYWKDADNLESAQQAKLKMICEKLQLKPGMRVLDIGCGW
GGLAHYMASNYDVS VVGVTISAEQQKMAQERCEGLDVTILLQDYRDLNDQFDRIVSVG
MFEHVGPKNYDTYFAVVDRLNKPEGIFLLHTIGSKKTDLNVDPWINKYIFPNGCLPSVRQI
AQSSPHFVMEDWHNFGADYDTTLMAWYERFLAAWPEIADNYSERFKRMFTYYLNACA
GAFRARDIQLWQVVF SRGVENGLRVAR

>sp|P21161|DCMA_METED Dichloromethane dehalogenase OS=Methylobacterium extorquens
(strain DSM 6343 / CIP 106787 / DM4) OX=661410 GN=dcmA PE=1 SV=1

MSPNPTNIHTGKTLRLLYHPASQPCRSAHQFMYEIDVPFEEEVVDISTDITERQEFRDKYNP
TGQVPILVDGEFTVWESVAIARYVNEKFDGAGNWFGRGTQERAQINQFLQWYAYTLRLG
GGAFHWNIFGCLYGEKPYSKFTAEQNKGRITLLYEAMGTLENYWLRDREYVCGDEVSY
ADLAAFHEFVSHEAGKIIPDRVWQGFPIAAWFKKLSERPHAKTVSEWQYTNVGIIRGE
LTASMFKRKTAVLKGTEVFSGHNHGIPYLNKAEDYFKRVEKEGAAVA

>sp|P64141|DHPS_STAAM Dihydropteroate synthase OS=Staphylococcus aureus (strain Mu50 /
ATCC 700699) OX=158878 GN=folP PE=1 SV=1

MTKTKIMGILNVTPDSFSDGGKFNNVETAINRVKAMIDEGADIIDVGGVSTRPGHEMVTL
EEELNRVLPVVEAIVGFDVKISVDTFRSEVAEACLKLGVDMINDQWAGLYDHRMFQIVA
KYDAEILMHNGNGNRDEPVVEMLTSLLAQAHAQAKIAGIPSNKIWLDPGIGFAKTRNEEA
EVMARLDELVATEYPVLLATSRKRFTKEMMGYDTPVERDEVTAATTAYGIMKGVRAV
RVHNVELNAKLAKGIDFLKENENARHNLS

>sp|P42305|DBPA_BACSU ATP-dependent RNA helicase DbpA OS=Bacillus subtilis (strain 168)
OX=224308 GN=dbpA PE=1 SV=2

MSHFKNYQISHDILRALEGLGYTEPTKVQQSVIPAALERKDLVVKSQTGSGKTASFGIPLC
ELANWDENKPPQALILTPRELAVQVKEDITNIGRFKRIKATAVFGKSSFDKQKAELKQKSH
IVVGTPGRVLDHIEKGTLPDLRLSYLVIDEADMLNMGFIEQVEAIKHLPTERTTMLFSAT
LPQDIEKLSRQYMQNPEHIEVKAAGLTTRNIEHAVIQVREENKFSLLKDVLMTENPDSCIIF
CRTKEHVNQLTDELDDLGYPCDKIHGGMIQEDRFDVMNEFKRGEYRYLVATDVAARGID
IENISLVINYDLPLEKESYVHRTGRTGRAGNKGKSAISFVTAFEKRFLADIEEYIGFEIQKIEAP
SQEEVARKKPEFLAKLNDRPESKKDKSEELNKDIMKLYFNNGGKKKKIRAVDFVGTIAKID
GVSADDIGIITIMDNASYVEILNGKGPHVLKVMKNNTTVKGKQLKVNKANK

>sp|P71889|DDAH_MYCTU N(G),N(G)-dimethylarginine dimethylaminohydrolase
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv2323c PE=1
SV=1

MENTQRPSFDCEIRAKYRWFMTDSYVAAARLGSPARRTPRTRRYAMTPPAFFAVAYAINP
WMDVTAPVDVQVAQAQWEHLHQTYLRLGHSDVLEIPISGLPDMVYTANGGFIAHDIAVV
ARFRFPERAGESRAYASWMSSVGYRPVTTRHVNEGQGDLLMVGERVLAGYGFRTDQRA
HAEIAAVLGLPVVSLELVDPRFYHLDALAVLDDHTIAYYPPAFSTAAQEQLSALFPDAIV
VGSADAFVFGFLNAVSDGLNVVLPVAAMGFAAQLRAAGFEPVGVLDSELLKGGGSVKCC
TLEIHP

>sp|E2JA29|DDAD_ENTAG Dapdiamide synthesis protein DdaD OS=Enterobacter agglomerans
OX=549 GN=ddaD PE=1 SV=1

MHSVETFNLPALNSLLETTARRFGNRLAVQDDNGSLTFADFVEKVGILSAKLRLVIKRG
HVAVQLPRGINYIVAAYAIWEAGGVYLPDLNQWPSSRIEGLHRSHVRVLIHTSQADQGLE
LTELPAETRAESPVAGTPAYIIHTSGTTGEPKGVVVSHESLIHLVESHQRDIYQAYDVTEGP
VAINASFCFDSALERMALVALGYSLHVSDQVRKSPYELVKYLRDINSIVNVLDLVP SHLKV
LLSAGLNEKCDALRLVIVGGEAIDAELWREIVQNQAIYINVYGP TENTINTSFCEIRGETPHI
GRPFGKNTCLLLNENGERCAAGEEGELLVAGRHLAQGYYNAPDLTDRV FVHIDGIRYYR
TGDRVRQNEQGNLLYLGRIDDQVKINGFRIELADVQHNLTLQLPGVKYAAVTPIKLPTGQG
LLASIVWNSDAPEQTFSNLEALLGEKLPSYMPTRWQKLDALPLTDNLKLDHKSLLSHW

KNSQEQIGEKFAAESISATEHQIKNLWQKILRQPSLSPDAHFFASGGDSMAAMTLLVELKK
VTPQDVS LGDIFKYPTIRKMAAWLDASSVQAES

>sp|P14295|DHL2_WEICO L-2-hydroxyisocaproate dehydrogenase OS=Weissella confusa
OX=1583 PE=1 SV=3

MARKIGIIGLGNVGA AVAHGLIAQGVADDYVFIDANEAKVKADQIDFQDAMANLEAHGN
IVINDWAALADADVISTLGNIKLQQDNPTGDRFAELKFTSSMVQSVGTNLKESGFHGV
LVVISNPVDVITALFQHVTGFPAHKVIGTGTLTDTARMQRAVGEAFDLDPRSVSGYNLGEH
GNSQFVAWSTVRVMGQPIVTLADAGDIDLAAIEEEARKGGFTVLNGKGYTSYGVATSAIR
IAKAVMADAHAE LVVSNRRDDMGMYLSYPAIIGRDGVLAETTLDTTDEQEKLQSRDYI
QQRFDEIVDTL

>sp|P0C0X1|DHPS1_MYCLE Dihydropteroate synthase OS=Mycobacterium leprae (strain TN)
OX=272631 GN=folP1 PE=1 SV=1

MSLAPVQVIGVLNVT DNSFS DGGRYLDPDDAVQHGLAMVAEGAAIVDVGGESTRPGAIR
TDPRVELSRIVPVKELAAQGITVSIDTTRADVAAALQSGARIVNDVSGGRADPAMAPL
VAEAGVAWVLMHWRLMSAERPYEAPNYRDVVAEVRADLLAGVDQAVAAGVDPGSLVI
DPGLGFAKTGQHNWALLNALPELVATGVPILLGASRKRLGRLLAGADGAVRPPDGRET
ATAVISALAALHGAWGVRVHDVRASVDALKVVGAWLHAGPQIEKVRCDG

>sp|P12293|DHM1_PARDE Methanol dehydrogenase [cytochrome c] subunit 1 OS=Paracoccus
denitrificans OX=266 GN=moxF PE=1 SV=1

MNRNTPKARGASSLAMAVAMGLAVLTAPATANDQLVELAKDPANWVMTGRDYNAQ
NYSEMTDINKENVKQLRPAWSFSTGVLHGHEGTPLVVGDRMFIHTPPNTTFALDLNEPG
KILWQNKPKQNPTARTVACCDVVRGLAYWPGDDQVKPLIFRTQLDGHIVAMDAETGET
RWIMENS DIKVGSTLT IAPYVIKDLVLVGSSGAELGVRGYVTAYDVKSGEMRWRAFATG
PDEELLLAEDFNAPNPHYGQKNLGLETWEGDAWKIGGGTNWGWYAYDPEVDLFYYGSG
NPAPWNETMRPGDNKWTMAIWGREATTGEAKFAYQKTPHDEWDYAGVNVMMMLSEQE
DKQGQMRKLLTHPDRNGIVYTLDRTNGLISADKMDDTVNWWKEVQLDTGLPVRDPEF
GTRMDHKARDICPSAMGYHNQGHDSYDPERKVFMLGINHICMDWEPFMLPYRAGQFFV
GATLTMYPGPKATAERAGAGQIKAYDAISGEMKWEKMERFSVWGGTMATAGGLTFYVT
LDGFIKARDSDTGDLLWKFKLPSGVIGHPMTYKHDGRQYVAIMYGVGGWPGVGLVFDL
ADPTAGLGSVGAFAKRLQEFTQMGGGVMVFSLDGESPYSDPNVGEYAPGEPT

>sp|P32436|DEGV_BACSU Protein DegV OS=Bacillus subtilis (strain 168) OX=224308
GN=degV PE=1 SV=2

MNIAVVT DSTAYIPKEMREQHQIHMIPLQVVFREETYREEIELDWKSFYEEVKKHNELPTT
SQPPIGELVALYEELGKSYDAVISIHLSSGISGTFSSAAAADSMVDNIDVYPFDSEISCLAQG
FYALKAAELIKNGASSPEDIKELEEMKKT VRAYFMVDDLHLQRGGRLSSAQAFIGSLLK
VKPILHFDNKVIVPF EKIRTRKKAISRIYELLDEDASKGLPMRAAVIHANREEEA AKIIEELS
AKYPHVEFYNSYFGAVIGTHLGEALGICWCFK

>sp|P22441|DHMA_FLAS1 N-acylmannosamine 1-dehydrogenase OS=Flavobacterium sp. (strain
141-8) OX=240 PE=1 SV=3

MTTAGVSRRPGRLAGKAAIVTGAAGGIGRATVEAYLREGASVVAMD LAPRLAATRYEEP
GAIPACDLADRAAIDAAMADAVARLGGLDILVAGGALKGGTGNFLDLSADWDRYVD
VNMTGTFLT CRAGARAMVAAGAGKDGRSARIITIGSVNSFMAEPEAAAYVAAKGGVAM
LTRAMAVDLARHGILVNMIAPGPVDVTGNNTGYSEPRLAEQVLDEVALGRPGLPEEVAT
AAVFLAEDGSSFITGSTITIDGGLSAMIFGGMREGRR

>sp|P45523|FKBA_ECOLI FKBP-type peptidyl-prolyl cis-trans isomerase FkpA OS=Escherichia
coli (strain K12) OX=83333 GN=fkpA PE=1 SV=1

MKSLFKVTLLATTMAVALHAPITFAAEAAKPATAADSKAAFKNDDQKSAYALGASLGRY
MENS LKEQEKLGIKLDKDQLIAGVQDAFADKSKLS DQEIEQTLQAFEARVKSSAQAKMEK
DAADNEAKGKEYREKFAKEKG VKTSSTGLVYQVVEAGKGEAPKDSDTVVVNYKGTLD

GKEFDNSYTRGEPLSFRLDGVIPGWTEGLKNIKKGGKIKLVIPPELAYGKAGVPGIPPNSTL
VFDVELLDVKPAPKADAKPEADAKAADSACK

>sp|P9WQ85|BIOF2_MYCTU Putative 8-amino-7-oxononanoate synthase 2 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=bioF2 PE=1 SV=1

MPTGLGYDFLRPVEDSGINDLKHYFYMADLADGQPLGRANLYSVCFDLATTDRKLTPAW
RTTIKRWFPGFMTFRFLECGLLTMVSNPLALRSDTDLERVLPVLAGQMDQLAHDDGSDFL
MIRDVDPEHYQRYLDILRPLGFRPALGFSRVDTTISWSSVEEALGCLSHKRRLPLKTSLEFR
ERFGIEVEELDEYAEHAPVLARLWRNVKTEAKDYQREDLNPEFFAACSRHLHGRSRLWLF
RYQGTPIAFFLNVWGADENYILLEWGIDRDFEHYRKANLYRAALMLSLKDAISRDKRRM
EMGITNYFTKLRIPGARVIPTIYFLRHSTDPVHTATLARMMMHNIQRPTLPDDMSEEFRCRW
EERIRLDQDGLPEHDIFRKIDRQHKYTGLKLGGVYGFYPRFTGPQRSTVKAELGEIVLLG
TNSYLGLATHPEVVEASAEATRRYGTGCSGSPLLNGTLDLHVSLEQELACFLGKPAAVLC
STGYQSNLAAISALCESGDMIIQDALNHRSLFDAARLSGADFTLYRHNDMDHLARVLRRT
EGRRIIVVDAVFSMEGTVADLATIAELADRHGCRVYVDESALGVLGPDGRGASAAALG
VLARMDVVMGTFSKSFASVGGFIAGDRPVVDYIRHNGSGHVFASLPPAAAAATHAALR
VSRREPDRRARVLAAAEYMATGLARQGYQAEYHGTAIVPVILGNPTVAHAGYLRLMRSG
VYVNPVAPPVPEERSGFRTSYLADHRQSDLDLALHVFAGLAEDLTPQGAAL

>sp|Q84HH6|BOXC_AZOEV Benzoyl-CoA-dihydrodiol lyase OS=Azoarcus evansii OX=59406
GN=boxC PE=1 SV=1

MQAVANKPVAELVDYRTEPSKYRHWSLATDGEIATLTNLNIDEDGGIRPGYKLKLNSYDLG
VDIELHDALQVRFEHPEVRTVVVTSGKPKIFCSGANIYMLGLSTHAWKVNFCFTNETR
NGIEDSSQYSGLKFLAACNGTTAGGGYELALACDEIVLVDDRNSVSLPEVPLLGVLPGTG
GLTRVTDKRRVRRDHADIFCTISEGVRGQRAKDWRLVDDVVKQQQFAEHIQARAKALAQ
TSDRPAGAKGVKLTTLERTVDEKGYHYEFVDAIDADGRTVTLTVRAPAAVTAKTAAEIE
AQGIKWVPLQMARELDDAILNLRTNHLDVGLWQLRTEGDAQVVLIDATIDANRDNWF
VRETIGMLRRTLARIDVSSRSLYALIEPGSCFAGTLLEIALAADRSYMLDAAEAKNVVGLS
AMNFGTFPMVNGLSRIDARFYQEEAPVAAVKAKQGSLLSPAEAMELGLVTAIPDDLDDWA
EEVRIAIEERAALSPDALTGLEANLRFGPVETMNTTRIFGRLSAWQNWIFNRPNAVGENGAL
KLFSGSKKAQFDWNRV

>sp|Q8RJB2|BZRD_BACCE Benzil reductase ((S)-benzoin forming) OS=Bacillus cereus
OX=1396 GN=yueD PE=1 SV=1

MRYVIITGTSQGLGEAIATQLLEESTTVISISRRENKELTKLAEQYNSNCIFHSLDLQDVHNL
ETNFKEIISIKEDNVSSIHLINNAGTVAPMKPIEKAESEQFITNVHINLLAPMILTSTFMKHT
KEWKVDKRVINISSGAGKNPYFGWGAYCTTKAGVNMFTQCVATEEEVEKEYPVKIVAFAP
GVVDTNMQAQIRETAKEDFTNLDRFIALKEEGKLLSPEYVAKAIRNLLETEEFPPQGEVIRID
E

>sp|Q72C18|ARGB_DESVH Acetylglutamate kinase OS=Desulfovibrio vulgaris (strain
Hildenborough / ATCC 29579 / DSM 644 / NCIMB 8303) OX=882 GN=argB PE=1 SV=1
MDCVENARLQSKVLIESLPYLRQFHGETVVIKYGGHAMKDEALKKAFALNVALLKLVGI
NPVIVHGGGPQIGKMLEQLNIQSHFREGLRVTDATMDVVEMVLVGKVNKEIVNQMNLA
GAKAVGLSGKDGMILIRARKMEMVISKEAQAPEIIDLGKVGEVMGVNTTLRLSLERDGFV
PVIAPVGVDDNGETYNNINADAVAGAVAAALKAKRLLLLTDVAGILDHDKKLIRSVNMRE
AVNLFSDGTLTGGMIPKVKCCLEALEEGVEKAMIIDGRTENCILLELLTDKGVGTEIVSDR
AAQAACNCVLR

>sp|O66440|AROD_AQUAE 3-dehydroquininate dehydratase OS=Aquifex aeolicus (strain VF5)
OX=224324 GN=aroD PE=1 SV=1

MLIAVPLDDTNFSENKKAKEKGADIVELRVDQFSDSLNYVKEKLEEVHSQGLKTILTIR
SPEEGGREVKNREELFEELSPLSDYTDIELSSRGLLVKLYNITKEAGKKLIISYHNFEITPPN
WIIREVLREGYRYGGIPKIAVKANSYEDVARLLCISRQVEGEKILISMGDYGKISRLAGYVF
GSVITYCSLEKAFAPGQIPLEEMVELRKKFYRL

>sp|P9WPY1|AROC_MYCTU Chorismate synthase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=aroC PE=1 SV=1
MLRWITAGESHGRALVAVVEGMVAGVHVTSADIADQLARRRLGYGRGARMTFERDAVT
VLSGIRHGSTLGGPIAIEIGNTEWPKWETVMAADPVDPAELADVARNAPLTRPRPGHADY
AGMLKYGFDDARPVLERASARETAARVAAGTVARAFLRQALGVEVLSHVISIGASAPYE
GPPRAEDLPAIDASPVRAYDKAAEADMIAQIEAAKKDGDRTLGGVVEAVALGLPVGLGSF
TSGDHRLDSQLAAAVMGIQAIKGVEIGDGFQTARRRGSRAHDEMYPGPDGVVRSTNRAG
GLEGGMTNGQPLRVRAAMKPISTVPRALATVDLATGDEAVAIHQRSVDCAVPAAGVVVE
TMVALVLARAALAEKFGGDSLAEQTQRNIAAYQRSVADREAPAARVSG

>sp|P31552|CAIC_ECOLI Crotonobetaine/carnitine--CoA ligase OS=Escherichia coli (strain K12) OX=83333 GN=caiC PE=1 SV=2
MDIIGGQHLRQMWDDLADVYGHKTALICESSGGVVNRYSYLELNQEINRTANLFYTLGIR
KGDKVALHLDNCPEFIFCWFLAKIGAIMVPINARLLCEESAWILQNSQACLLVTSAQFYF
MYQQIQQEDATQLRHICLTDVALPADDGVSSFTQLKNQQPATLCYAPPLSTDDTAELFTS
GTTSRPGKVVITHYNLRFAGYYSAWQCALRDDDVLTVMPAFHIDCQCTAAMAAFSAG
ATFVLVEKYSARAFWGQVQKYRATVTECIPMMIRTLMVQPPSANDQQHRLREVMFYLN
SEQEKDAFCERFGVRLTSYGMTETIVGIIGDRPGDKRRWPSIGRVGFCYEAIEIRDDHNR
LPAGEIGEICKIPGKTIFKEYFLNPQATAKVLEADGWLHTGDTGYRDEEDFFYFVDRRC
NMIKRGGENVSCVELENIAAHPKIQDIVVVGKDSIRDEAIKAFVVLNEGETLSEEEFFRFC
EQNMAKFKVPSYLEIRKDLPRNCSGKIIRKNLK

>sp|P9WPK3|CARB_MYCTU Carbamoyl-phosphate synthase large chain OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=carB PE=1 SV=1
MPRRDTHLHVLVIGSGPIVIGQACEFDYSGTQACRVLRAEGLQVSLVNSNPATIMTDPEFA
DHTYVEPITPAFVERVIAQQAERGNKIDALLATLGGQTALNTAVALYESGVLEKYGVLEIG
ADFDAIQRGEDRQRFKDIVAKAGGESARSVCFTMAEVRETVAELGLPVVVRPSFTMGGL
GSGIAYSTDEVDRMAGAGLAASPSANVLEEISYGWKEFELELMRDGHDNVVVVCSIN
DPMGVHTGDSVTVAPAMTLTDREYQRMRLGAILREVGVDGTGGCNIQFAVNPRDGR
LI VIEMNPRVSRSSALASKATGFPIAKIAAKLAIGYTLDEIVNDITGETPACFEPTLDYV
VVKAPRFAFEKFPGADPTLTMTMKSVGEAMSLGRNFVEALGKVMRSLETTRAGFWTAPDPDGGI
EEALTRLRTPAEGRLYDIELALRLGATVERVAEASGVDPWFIAQINELVNLRLNELVAAPVL
NAELLRRAKHSGLSHDHQIASLRPELAGEAGVRSRLVRLGIHPVYKTVDTCAAEEFEAQTPY
HYSSYELDPAAETEVAQTERPKVLILGSGPNRIGQGIEFDYSCVHAATTLSQAGFETVMV
NCNPETVSTDYDTADRLYFEPLTFEDVLEVYHAEMESGSGPGVAGVIVQLGGQTPLGLA
HRLADAGVPIVGTPEAIDLAEDRGAFGDLLSAAGLPAPKYGTATTFAQARRIAEEIGYPV
LVRPSYVLGGRGMEIVYDEETLQGYITRATQLSPEHPVLVDRFLEDAVEIDVDALCDGAE
VYIGGIMEHIEEAGIHSAGDSACALPPVTLGRSDIAKVRKATEAIAHGIGVVGLLNQYALK
DDVLYVLEANPRASRTVPFVSKATAVPLAKACARIMLGATIAQLRAEGLLAVTGDGAHA
ARNAPIAVKEAVLPFHRFRRADGAIDSLLGPEMKSTGEVMGIDRDFGSFAKSTAAAYG
SLPAQGTVFVSVANRDKRSLVFPVKRLADLGFRVLATEGTAEMLRNGIPCDDVRKHFE
P AQPGRPTMSAVDAIRAGEVNMVINTPYGNSGPRIDGYEIRSAAVAGNIPCITTVQGASAAV
QGIEAGIRGDIGVRSLQELHRVIGGVER

>sp|F2XG53|CAS3_STRTR CRISPR-associated nuclease/helicase Cas3 OS=Streptococcus thermophilus OX=1308 GN=cas3 PE=1 SV=1
MKHINDYFWAKKTEENSRLWLPLTQHLEDTKNIAGLLWEHWLSEGQKVLIENSINVKS
NIENQGKRLAQFLGAVHDIGKATPAFQTQKGYANSVDLDIQLLEKLERAGFSGISSQLAS
PKKSHHSIAGQYLLSHYGVDEDIATIIGGHHGRPVDLDGLNSQKSYPSNYYQDEKKDSL
VYQKWKSNQEAFLNVALTETGFNSVSQLPKIKQPAQVILSGLLIMSDWIASNEHFFPLLSL
DETVDKNSQRIETGFKKWKKS NLWQPETFVDLVTLYQERFGFSPRNFQLILSQTIEKTTN
PGIVILEAPMGIGKTEAALAVSEQLSSKKGCSGLFFGLPTQATSNGIFKRIEQWTENIKGNN
SDHFSIQLVHGKAALNTDFIELLKGNTINMDDSENGSIFVNEWFSGRKTSALDDFVVGTV

QFLMVALKQKHLALRHLGFSKKVIVIDEVHAYDAYMSQYLLEAIRWMGAYGVPVILSA
TLPAQQREKLIKSYMAGMGVKWRDIENIDQIKIDAYPLITYNDGPDHIVKMFEEKQEQKNI
YIHLRPEEQQLFDIVKEGLDNGGVVGIIVNTVRKSQELARNFSDIFGDDMVDLLHSNFIATER
IRKEKDLLQEIGKKAIRPPKKIIGTQVLEQSLDIDFDVLISDLAPMDLLIQRIGRLHRHKIKR
PQKHEVARFYVLGTFFEEFDFDEGTRLVYGDYLLARTQYFLPKIRLPDDISPLVQKVYNSD
LTITFPKPELHKKYLDKIEHDDKIKNKETKAKSYRIANPVLKKSRRVTRNSLIGWLKNLHP
NDSEEKAYAQVRDIEDTVEVIALKKISDGYGLFIENKDISQNTDPIIAKKVAQNTLRPMS
LSKAYNIDQTINELERYNNSHLSQWQNSSWLKGSGLGIIFDKNNEFILNGFKLLYDEKYGVT
IERLDKNESV

>sp|Q72HA9|ARGB_THET2 Acetylglutamate kinase OS=Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039) OX=262724 GN=argB PE=1 SV=1

MSEALLVKVGGSLRGAEALLDELAAYPGPLVLVHGGGPEIGAWLGRLGYESRFVGGRLV
TPPEQLEVEMALYLTGKRLAEGLSRRGRKALALSGRDALCLKGRALPELGRVGEVVEV
EVGLLQDLLAKGYTPLLAPIALDAEGLNVNADTAAGAVAGALGWPAVFLTDVEGVYR
DPKDPRTFRPRLTPKEVEALKGEGVIQGGMIPKVEAALSALRAGAPWAAIAKGERGVLEA
VLRGEAGTRFTL

>sp|P63727|C562_SALTY Soluble cytochrome b562 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=cybC PE=1 SV=1

MRKSLAILAVSSLVFGSAVFAADLEDNMDILNDNLKVVEKTDSAPELKAALTKMRAAA
LDAQKATPPKLEDKAPDSPKDFRHHGFDILVGQIDGALKLANEGNVKEAKAAAEALKT
TRNTYHKKYR

>sp|Q1JUP5|ARALA_AZOBR L-arabinolactonase OS=Azospirillum brasilense OX=192
GN=araB PE=1 SV=1

MQQIHPAGQATLLADTRNTLGEGATWCDRTRALYWVDIEGAQLWRCRADGSDLTPWPM
PERLACFALTDPPDVLLVGLATHLAFFDLRSGAFTRIVEPELPTRLNDGRCDGSGAFVF
GMKDEGAEPRAVGGFYRLNADLTLERLALPPAAIANSIGFSPDGSKMYFCDSLVRIFVC
DYRPGGEVANVRPFARLTPDGDPDGSIIVDRDGLWNAQWGGRRVVRYGPDGVETDRV
AVPTAQPSCTALDGEGRLYVTSARVGLSDDALADDPHAGGVFVAQTRHAGMATARFAG
TPRG

>sp|Q9X597|C26AA_BACTF Pesticidal crystal protein Cry26Aa OS=Bacillus thuringiensis subsp. finitimus OX=29337 GN=cry26Aa PE=1 SV=1

MNSEEMNHVNPFEISDNNDVSIPSQRYPFANDPADSVFCADDFLQSYGEFNMDNFGGESEPF
IDASGAINAAIGVTGTVLGFLGVPFAGALTTFYQKLFGLFPNNNTKQWEEFMKQVEALID
EKISDAVRNKAISELQGLVNNITLYTEALEEWLENKENPAVRDRVLQRWRILDGFFEQQM
PSFAVKGFVLLL VVYTQAANLHLLSLRDAYIYGAEWGLTPTNIDQNHTRLLRHSAYTD
HCVNWyNTGLKQLENSDAKSWFQYNRFRREMTLSVLDVIALFPAYDVKMYPIPTNFQLT
REVYTDVIGKIGRNDSDHWYSANAPSFNLESTLIRTPHVVDYIKKLIFYATVDYYGIYG
RSGKWVGHIITSATSANTTETRNyGTIVNHDSVELNFEGKNIYKTGSLPQGVPPYQIGYVT
PIYFITRAVNFFT VSGSKTSVEKYYSKKDRYYSEGLPEEQGVFSTEQLPPNSIAEPEHIAysh
RLCHVTfISVSNGNKYSKDLPLFSWTHSSVDFDNYVYPTKITQLPATKGYNVsIVKEPGFIG
GDIGKNNGQILGKYKVNVEDVSQKYRFRVRYATETEGELGIKIDGRTVNLYQYKKTKAP
GDPLTYKAFDYLSFSTPVKFNNASSTIELFLQNKTSGTFYLAGIEIIPVKSnyEEELTLEEAK
KAVSSLFTDARNALKIDVTDYQIDQAANLVECISGDLYAKEKIVLLRAVKFAKQLSQSQN
LLSDPEFNNVNRENSWTASTSVAIIEGDPLYKGRAVQLSSARDENFPTYLYQKIDESTLKP
YTRYQLRGFVEGSENLDVYLIRYGAAHVRMNPYNLEIIDTSSPVNPCEEVDGLSHRSCN
VFDRCKQSISVAPDANTGPDQIDGDPHAFSFIHDTGTVDSTENLGIWVAFKISELDGSAIFG
NLELIEVGPLSGEALAQVQRKEEKWKQVLAKKRETTAQTVCSGEASQLTNSSQILKIRNY
DLIQNFRIFSLRNTLSIKFKIYTITNYPYSRLNYDLFMELNRIQNASLYMTSNILQNGGFKS
DVTSWETTANAeVQQIDGASVLVLSNWNASVAQSVNVQNDHGYVLRVTAKKEGIGNGY

VTILDCANHIDTLTFSACRSDSDTSSNELTAYVTKTLEIFPDTEQIRIEIGETEGMIFYVESVEL
IRMEN

>sp|Q05582|CAS2_STRC2 Clavaminate synthase 2 OS=Streptomyces clavuligerus (strain ATCC
27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602)
OX=443255 GN=cs2 PE=1 SV=3

MASPIVDCTPYRDELLALASELPEVPRADLHGFLDEAKTLAARLPEGLAAALDTFNAVGS
EDGYLLLRGLPVDDSELPETPTSTPAPLDRKRLVMEAMRALAGRRLGLHTGYQELRSGTV
YHDVYPSPGAHYLSSETSETLLEFHTMAYHILQPNYVMLACSRADHENRAETLVGSVRK
ALPLLDEKTRARLFDRKVPCCVDVAFRGGVDDPGAIAINVKPLYGDANDPFLGYDRELLA
PEDPADKEAVAHLSQLDDVTVGVKLVPGDVLIIDNFRTHARTPFSPRWGDKDRWLHR
VYIRTDNRNGELSGGERAGDTISFSPRR

>sp|Q8VPF2|CATJ_PSEKB 3-oxoadipate CoA-transferase subunit B OS=Pseudomonas
knackmussii (strain DSM 6978 / LMG 23759 / B13) OX=1301098 GN=catJ PE=1 SV=1
MSAYSTNEMMTVAAARRLKNGAVCFVGIGLPSKAANLARLTSSPDVLIYESGPIGAKPT
VLPLSIGDGELAETADTVVPTGEIFRYWLQGGRIDVGFLGAAQVDRFGNINTTVIGDYNKP
KVRLPGAGGAPEIAGSAKEVLILKQSHRTFVDKLAFITSVGHGEGGDHRKQLGLPGKGPV
AIITDLCIMEPEAGSNEFIVTSLHPGVTREQVIENTGWAIRFAEQVKETAAPTEVELEALRA
LEARTAAAHGQQGGEE

>sp|P9WPX5|ASPG_MYCTU Probable L-asparaginase OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) OX=83332 GN=ansA PE=1 SV=1
MARLTVITTGGTISTTAGPDGVLRPHTCGATLIAGLDMDSIEVVDLMALDSSKLTPADW
DRIGAAVQEAFRGGADGVVITHGTDLTLEETALWDLTYAGSRPVVLTGAMLSADAPGAD
GPANLRDALAVAADPAARDLGVLVSFGGRVLQPLGLHKVANPDLCGFAGESLGFTSGGV
RLTRTKTRPYLGDLGAAVAPRVDIVAVYPGSDAVAMDACVAAGARAVVLEALGSGNAG
AAVIEGVRRHCRDGSDDPVVIAVSTRVAGARVGAGYGPGHDLVEAGAVMVPRLPPSQARV
LLMAALAANSPVADVIDRWG

>sp|Q4H4E9|BTRH_BACCI Ribostamycin:4-(gamma-L-glutamylamino)-(S)-2-hydroxybutanoyl-
[BtrI acyl-carrier protein] 4-(gamma-L-glutamylamino)-(S)-2-hydroxybutanoate transferase
OS=Bacillus circulans OX=1397 GN=btrH PE=1 SV=1
MCLTRYDEKFFDCRKSQIIAYLDSQQVPVIPLFYNSYQSTAEIYRQIFIENKSKWKYSEPSFS
DDDLLRKGIRPVRAFSPDFSQASDCLKDLLARHKLVFVWGDEYCLPYRKEAFQAIHSTHS
LVVTGYDGENKAYYVEDWDGLYGYLPAVHLEAAFDLSLRQMRTLLVLELNDEEMRENK
QEDTDLFRKWLQAFEDDYIFYDRVLLDMRDYEENRLISMDHGLRLIAASRHVFSKFLHYI
DDAPEEVGLLIRNHQLANHIAAIVRRYIIAKQIDWDGAACKIRQLREQEDDFMRKLKSRY
G

>sp|P00888|AROF_ECOLI Phospho-2-dehydro-3-deoxyheptonate aldolase, Tyr-sensitive
OS=Escherichia coli (strain K12) OX=83333 GN=aroF PE=1 SV=1
MQKDALNNVHITDEQVLMTPQLKAAFPPLSLQQEAQIADSRKSISDIIAGRDPRLLVVCGP
CSIHDPETALEYARRFKALAAEVSDSLYLVMRVYFEKPRTTVGWKGLINDPHMDGSFDVE
AGLQIARKLLELVNMGLPLATEALDPNSPQYLGDLSWSAIGARTTESQTHREMASGLS
MPVGFKNGTDGSLATAINAMRAAAQPHRFVGINQAGQVALLQTQGNPDGHVILRGGKAP
NYSADVAQCEKEMEQAQLRPSLMVDCSHGNSNKDYRRQPAVAESVVAQIKDGNRSIIG
LMIESNIHEGNQSSEQPRSEMKYGVSVDACISWEMTDALLREIHQDLNGQLTARVA

>sp|P00864|CAPP_ECOLI Phosphoenolpyruvate carboxylase OS=Escherichia coli (strain K12)
OX=83333 GN=ppc PE=1 SV=1
MNEQYSALRSNVSMGLKVLGETIKDALGEHILERVETIRKLSKSSSRAGNDANRQELLTTL
QNLSNDELPLVARAFSQFLNLANTAQYHSISPKEAASNPVIARTLRKLKNQPELSEDTI
KKAVESLSLELVLTAHPTEITRRTLHKMVEVNACLKQLDNKDIADYEHNQLMRRLRQLI
AQSWHTDEIRKLRPSPVDEAKWGFVAVVENSLSWQGVPNYLRELNEQLEENLGYPVEFV
PVRFTSWMGGDRDGPNPVTADITRHVLLLSRWKATDLFLKDIQVLVSELSMVEATPELLA

LVGEEGAAEPYRYLMKNLRSRLMATQAWLEARLKGEELPKPEGLLTQNEELWEPLYACY
 QSLQACGMGIIANGDLLDTLRRVKCFGVPLVRIDIRQESTRHTREALGELTRYLGIGDYESW
 SEADKQAFILRELNSKRPLLPRNWQPSAETREVLDTCQVIAEAPQGSIAAYVISMATPSD
 VLAVHLLLKEAGIGFAMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGY
 SDSAKDAGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAAALLSQP
 PGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPPEPKESWRRIMDELSVI
 SCDVYRGYVRENKDFVPYFRSATPEQELGKLPLGSRPAKRRPTGGVESLRAIPWIFAWTQ
 NRLMLPAWLGAAGTALQKVVEDGKQSELEAMCRDWPFFSTRLGMLEMVFAKADLWLAE
 YYDQRLVDKALWPLGKELRNLQEEDIKVVLAIANDSLHLMADLPWIAESIQLRNIYTDPLN
 VLQAELLHRSRQAEKEGQEPDPRVEQALMVTIAGIAAGMRNTG

>sp|P25718|AMY1_ECOLI Periplasmic alpha-amylase OS=Escherichia coli (strain K12)

OX=83333 GN=malS PE=1 SV=1

MKLAACFLTLLPGFAVAASWTSPGFAFSEQGTGTFVSHAQLPKGTRPLTLNFDQQCWQP
 ADAIKLNQMLSLQPCSNTPPQWRLFRDGEYTLQIDTRSGTPTLMISIQNAEPVASLVREC
 PKWDGLPLTVDVSAFPEGAAVRDYYSQQIAIVKNGQIMLQPAATSNGLLLLERAETDTS
 APFDWHNATVYFVLTDREFNGDPSNDQSYGRHKDGMAEIGTFHGGDLRGLTNKLDYLQ
 QLGVNALWISAPFEQIHGWVGGGKGDFFHYAYHGYTQDWTNLDANMGNEADLRTL
 VDSAHQRGIRILFDVVMNHTGYATLADMQEYQFGALYLSGDEVKKSGLGERWSDWKPA
 GQTWHSFNDYINFSDKTGWDKWWGKNWIRTDIGDYDNPGFDDLTMSLAFLPDIKTESTT
 ASGLPVFYKNKMDTHAKAIDGYTPRDYLTHWLSQWVRDYGIDGFRVDTAKHVELPAWQ
 QLKTEASAALREWKKANPDKALDDKPFWMTGEAWGHGVMQSDYYRHGFDAMINFDY
 QEQAAKAVDCLAQMDTTWQQMAEKLQGFNVLSYLSSHDTLRFREGGDKAAELLLLAPG
 AVQIFYGDESSRPFGPTGSDPLQGTRSDMNWQDVSGKSAASVAHWQKISQFRARHPAIGA
 GKQTTLLLKQGYGFVREHGDDKVLVWVAGQQ

>sp|Q92PC8|BLUB_RHIME 5,6-dimethylbenzimidazole synthase OS=Rhizobium meliloti (strain 1021) OX=266834 GN=bluB PE=1 SV=1

MLPDPNGCLTAAGAFSSDERAAVYRAIETRRDVRDEFLPEPLSEELIARLLGAAHQAPSVG
 FMQPWNFVLVRQDETREKVWQAFQRANDEAAEMFSGERQAKYRSLKLEGIRKAPLSICV
 TCDRTRGGAVVLGRTHNPQMDLYSTVCAVQNLWLAARAEGVGVGWVSIFHESEIKAILG
 IPDHVEIVAWLCLGFVDRLYQEPELAAKGWRQRLPLEDLVFEEGWGVR

>sp|P9WQP7|3BHS_MYCTU 3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase

OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv1106c PE=1 SV=1

MLRRMGDASLTTELGRVLVTGGAGFVGANLVTTLDRGHVRSFDRAPSLPAAHPQLEV
 LQGDITDADVCAAVDGIDTIFHTAAIHELMGGASVTDEYRQRSFAVNVGGTENLLHAGQ
 RAGVQRFVYTSSNSVVMGGQNIAGGDETLPTYTDRFNDLYTETKVVAERFVLAQNGVDG
 MLTCAIRPSGIWNGDQTMFRKLFESVLKGHVKVLVGRKSARLDNSYVHNLIHGFILAAA
 HLVPDGTAPGQAYFINDAEPINMFEFARPVLEACGQRWPKMRISGPAVRWVMTGWQRLH
 FRFGFPAPLLEPLAVERLYLDNYFSIAKARRDLGYEPLFTTQQALTECLPYVVSLEQMK
 N EARA EKTAATVKP

>sp|P9WQ91|AAT_MYCTU Probable aspartate aminotransferase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=aspC PE=1 SV=1

MDNDGTIVDVTTTHQLPWHTASHQRQRAFAQSAKLQDVLYEIRGPVHQHAARLEAEGHRI
 LKLNIGNPAPFGFEAPDVIMRDIIQALPYAQGYSDSQGILSARRAVVTRYELVPGFPRFDVD
 DVYLGNGVSELITMTLQALLDNGDQVLIPSPDYPLWTASTSLAGGTPVHYLCDETQGWQP
 DIADLESKITERTKALVVINPNPTGAVYSCEILTQMVDLARKHQLLLLDADEIYDKILYDD
 AKHISLASIAPDMLCLTFNGLSKAYRVAGYRAGWLAITGPKEHASSFIEGIGLLANMRLCP
 NVPAQHAIQVALGGHQSIEDLVLPGGRILLEQRDIAWTKLNEIPGVSCVKPAGALYAFPR
 LDPEVYDIDDDEQLVLDLLLSEKILVTQGTGFNWPAPDHLRLVTLPWSRDLAAAIERLGNFL
 VSYRQ

>sp|P39758|ABH_BACSU Putative transition state regulator Abh OS=Bacillus subtilis (strain 168)
OX=224308 GN=abh PE=1 SV=1
MKSIGVVRKVDELGRIVMPIELRRALDIAIKDSIEFFVDGDKIILKKYKPHGVCLMTGEITSE
NKEYGNGKITLSPEGAQLLLEEIQAAALKE

>sp|P0A042|BLAI_STAAU Penicillinase repressor OS=Staphylococcus aureus OX=1280
GN=blaI PE=1 SV=1
MANKQVEISMAEWDVMNIIWGKKSVSANEIVVEIQKYKEVSDKTIRTLITRLYKKEIHKRY
KSENIYFYSSNIKEDDIKMKTAKTFLNKLYGGDMKSLVLNFAKNEELNNKEIEELRDILND
ISKK

>sp|O05391|BOFC_BACSU Protein BofC OS=Bacillus subtilis (strain 168) OX=224308
GN=bofC PE=1 SV=1
MKRFSTAYLLLGLCSAAVFLIGAPSRALGAEEHYEPLQVHVQLEKVYLDGDVSIHKKH
EKVFSMDDFWAAYAGWTLVEQKKGYVLFKQMDDISPLSKVNGYIGVSDNGVISTFHGR
PEPASEPIQSFFQIDLERLESHMQKNLLKGIPFRTKAEFEDVIEHMKTYSG

>sp|Q9ZCH9|ACP_RICPR Acyl carrier protein OS=Rickettsia prowazekii (strain Madrid E)
OX=272947 GN=acpP PE=1 SV=1
MEFKIMSTTDKIEQKVIEMVAEKLNDKAIITDSRFIEDLKADSLDTVELMMAIEVEYCID
IPDDEATKIKTVSDVIKIKERQS

>sp|Q9HY69|ALG44_PSEAE Mannuronan synthase OS=Pseudomonas aeruginosa (strain ATCC
15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)
OX=208964 GN=alg44 PE=1 SV=1
MNTAVNVNVVHESEAQRQFARVKLPARIRYIGANREGVDARLLDLSAGGFAFTASGAPIQ
PGDLYKGKLLFQVDSISFSLEVEFQVRSVDPASRRVGCEFNKPREVAALRYLITSYLAG
EVIGVGDMLNTLQRENFTKARKQGGGNGGMGFFGRVRAVTLSTAIFVVGVGAFILNQ
MYNLYFVTHADSGVSVPNQQITMPREGTVQSLLGPNAEVAKGAPIATFSANLLDMLKG
NLTEEQLNPGNIEKLFGHQMKGTLTSPCDCRVVQQLVADGQYANKGQVIFTLAPRDSVAS
IEARFPYRNAAELAPGTRVNFQVAGDGVNRSGRIVNTAPVDGDLSEIRVQIQPDQPLDAQ
YAGRPAEVSIGGLPGRITLLNKAVTLATAR

>sp|P10932|AMIR_PSEAE Aliphatic amidase regulator OS=Pseudomonas aeruginosa (strain
ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)
OX=208964 GN=amiR PE=1 SV=2
MSANSLGSLRELQVLVLNPPGEVSDALVLQLIRIGCSVRQCWPPESFDVPVDVVFTSIFQ
NRHHDEIAALLAAGTPRTTLVALVEYESPAVLSQIIIELECHGVITQPLDAHRVLPVLVSARR
ISEEMAKLKQKTEQLQERIAAGQARINQAKALLMQRHGWDEREAHQYLSREAMKRREPIL
KIAQELLGNEPSA

>sp|O85673|ANTDA_ACIAD Anthranilate 1,2-dioxygenase large subunit OS=Acinetobacter
baylyi (strain ATCC 33305 / BD413 / ADP1) OX=62977 GN=antA PE=1 SV=1
MTARNLAEWQNFVQGCIDFRPNDGVYRIARDMFTEPELFELEMELIFEKVWIYACHESEIP
NNNDFVTVQIGRQPMIVSRDGKGELHAMVNACEHRGATLTRVAKGNQSVFTCPFHAWC
YKSDGRLVKVKAPGEYCEDFDKSSRGLKQGRIASRGFVFSVSLDTQATDSLEDLGDGAKV
FLDLMVDQSPTGELEVLQGKSAYTFAGNWKLQNENGLDGYHVSTVHYNYVSTVQHRQQ
VNAAKGDELDTLDYSKLGAGDSETDDGWFSFKNGHSVLFSDMPNPTVRPGYNTVMPLYL
VEKFGEKRAEWAMHRLRNLYPSLFFMDQISSQLRIIRPVAWNKTEVISQCIGVKGESSE
ARRNRIRQFEDFFNVSGLGTPDDLVEFREQQKGFGRIERWSDISRGYHQWYTGPTQNSQ
DLGIEPVITGREFTHEGLYVNQHGWQRLILDGLNKKALKMHDVTFDNQSVMDDEV

>sp|P63883|AMIC_ECOLI N-acetylmuramoyl-L-alanine amidase AmiC OS=Escherichia coli
(strain K12) OX=83333 GN=amiC PE=1 SV=1
MSGSNTAISRRRLQGAGAMWLLSVSQVSLAAVSQVAVRVWPASSYTRVTVESNRQLK
YKQFALSNERVVVDIEDVNLNSVLKGMAAQIRADDPFIKSARVGQFDPQTVRMVFEKQ
NVKPQLFALAPVAGFKERLVMDLYPANAQDMQDPLLALLEDYNGKDLEKQVPPAQSGP

QPGKAGRDRPIVIMLDPGHGGEDSGAVGKYKTREKDVVLQIARRRLSLIEKEGNMKVYM
 TRNEDIFIPLQVRVAKAQKQRADLFVSIHADFTSRQPSGSSVFALSTKGATSTAAKYLAQ
 TQNASDLIGGVSKSGDRYVDHTMFDMVQSLTIADSLKFGKAVLNKLGKINKLHKNQVEQ
 AGFAVLKAPDIPSILVETAFISNVEEERKLKTATFQQEVAESILAGIKAYFADGATLARRG
 >sp|P23793|ARCA_MYCAR Arginine deiminase OS=Mycoplasma arginini OX=2094 GN=arcA
 PE=1 SV=4
 MSVFDSKFKGIHVYSEIGELESVLVHEPGREIDYITPARLDELLFSAILESHDARKEHKQFV
 AELKANDINVVELIDLVAETYDLASQEAKDKLIEEFLEDSEPVLSEEHKVVVRNFLKAKKT
 SRELVEIMMAGITKYDLGIEADHELIVDPMPLNYFTRDPFASVGNGVTIHYMRYKVRQRE
 TLFSRFVFSNHPKLINTPWYYDPSLKLSIEGGDVFIYNNDTLVVGVSERTDLQTVTLAKNI
 VANKECEFKRIVAINVPKWNTNLMHLDTWLTMLDKDKFLYSPIANDVFKFWDYDLVNGG
 AEPQPVENGLPLEGLLQSIINKKPVLIPIAGEGASQMEIERETHFDGTNYLAIRPGVVIGYSR
 NEKTNAALEAAGIKVLPFHGNQLSLGMGNARCMSMPLSRKDVKW
 >sp|B2FKA7|ABP_STRMK Actin-binding protein Smlt3054 OS=Stenotrophomonas maltophilia
 (strain K279a) OX=522373 GN=Smlt3054 PE=1 SV=1
 MEMDIQESLLRLLRPLGLQRAEALAGALAREAGASKGLHDSQVLARAHALSVAPVEGRL
 GDLVWQVRQREHDGAPQVDLRWGLHRLGLDAPSRASRDLDVRAYERRADRNEPMVYS
 TLAERVAGSMAEHTSLFQGMAMAVEEARARRSDANRLRENAPWQGWLVGASRAGHEA
 ALLACIGMGADARLPDASGNTPLHHAARFGHFSLVTPLEAGADVAALNAHWAPLHL
 AALHKHARACLHLMAHGANPEQPGWRGRTPTRMHRHEQTQAL
 >sp|Q7SIF4|AIOA_ALCFA Arsenite oxidase subunit AioA OS=Alcaligenes faecalis OX=511
 GN=aioA PE=1 SV=2
 MSRPNDRLTLPPANAQRTNMTCHFCIVGCGYHVYKWPELQEGGRAPEQNALGLDFRKQL
 PPLAVTLTPAMTNVVTEHNGRRYNIMVVPDKACVVNSGLSSTRGGKMASYMYTPTGDG
 KQRLKAPRLYAADQWVDTTWDHAMALYAGLIKKTLDDKDGPPQGVFFSCFDHGGAGGGF
 ENTWGTGKLMFSAIQTPMVRIHNRPAYNSECHATREMGIGELNNAYEDAQLADVIWSIG
 NNPYESQTNYFLNHWLPNLQGATTSKKKERFPNENFPQARIIFVDPRETPSVAIARHVAGN
 DRVLHLAIEPGTDTALFNGLFYVVEQGWIDKPFIEAHTKGFDDAVKTNRLSLDECSNITG
 VPVDMLKRAAEWSYKPKASGQAPRTMHAYEKGIWGNNDNYVIQSALLDLVIATHNVGRR
 GTGCVRMGGHQEGYTRPPYPGDKKIYIDQELIKGKGRIMTWWGCNNFQTSNNAQALREA
 ILQRSIVKQAMQKARGATTEEMVDVIYEATQNGGLFVTSINLYPTKLAEAAHMLPAAH
 PGEMNLTSMNERRIRLSEKFMDPPGTAMADCLIAARIANALRDMYQKDGAEMAAQFE
 GFDWKTEEDAFNDGFRRAGQPGAPIDSQGGSTGHLVTYDRLRKSGNNGVQLPVVSWD
 ESKGLVGTEMLYTEGKFDTDGKAHFKPAPWNGLPATVQQQKDKYRFWLNNGRNNEV
 WQTAYHDQYNSLMQERYPMAYIEMNPDDCKQLDVTGGDIVEVYNDFGSTFAMVYPVAE
 IKRGQTFMLFGYVNGIQGDVTTDWTDRNIPIYYKGTWGDIRKVGSMEEFKRTVSFKSRRF
 A
 >sp|A9AE46|BIOF_BURM1 8-amino-7-oxononanoate synthase OS=Burkholderia multivorans
 (strain ATCC 17616 / 249) OX=395019 GN=bioF PE=1 SV=1
 MNLLDTLQRGLADLDAQGLRRVRRTADSACDAHMTVNGREIVGFASNDYLGAAHPKL
 VAAFAEGAQRYGSGSGSHLLGGHSRAHAKLEDELAFAGGFSDAPRALYFSTGYMANL
 AAVTALAGKDATIFSDALNHASLIDGTRLSRATVQVYPHADTATLGALLEACTSQTKLIVT
 DTVFSMDGDIAPLAELLALAERHGAWLVVDDAHGFGVLGPQGRGALAAAALRSPHLVY
 VGTLGKAAGVAGAFVVAHETVIEWLIQRARSYIFTTAAPPAVAHAVSASLKVIAGDEGDA
 RRAHLAALIERTRALLRRTRWQPVDSTAVQPLVIGSNEATLAAMRALDAHGLWVPAIRP
 PTVPAGTSRLRISLSAAHSFDDLARLETALLRASEEAA
 >sp|P77256|AKRMG_ECOLI NADH-specific methylglyoxal reductase OS=Escherichia coli
 (strain K12) OX=83333 GN=ydjG PE=1 SV=1
 MKKIPLGTTDITLSRMGLGTWAIGGGPAWNGDLDRQICIDTILEAHRCGINLIDTAPGYNF
 GNSEVIVGQALKKLPREQVVVETKCGIVWERKGSLEFNKVGDRQLYKNLSPESIREEVAAS

LQRLGIDYIDIYMTHWQSVPPFFTPIAETVAVLNELKSEGKIRAIGAANVDADHIREYLQY
GELDIIQAKYSILDRAMENELLPLCRDNGIVVQVYSPLEQGLLTGTITRDYVPGGARANKV
WFQRENMLKVIDMLEQWQPLCARYQCTIPTLALAWILKQSDLISILSGATAPEQVRENV
ALNINLSADATLMREMAEALER
>sp|Q9KWS2|AMND_PSESP 2-aminomuconate deaminase OS=Pseudomonas sp. OX=306
GN=amnD PE=1 SV=1
MVSKADNSAKLVEGKAKPMGSFPHVKRAGDFLFVSGTSSRRPDNTFVGAEPDDTGRPRP
NIELQTREVISNIRDILQSVGADLGDVVEVCSYLVNMNDFAAYNKVYAEFFDATGPARTT
VAVHQLPHQPQLVIEIKVVAYKPL
>sp|P06720|AGAL_ECOLI Alpha-galactosidase OS=Escherichia coli (strain K12) OX=83333
GN=melA PE=1 SV=1
MMSAPKITFIGAGSTIFVKNILGDVVFHREALKTAHIALMDIDPTRLEESHIVVRKLMDSAGA
SGKITCHTQQKEALEDADFFVVFQIGGYEPCVTDFEVCKRHGLEQTIADTLGPGGIMR
ALRTIPHLWQICEDMTEVCPDATMLNYVNPMAMNTWAMYARYPHIKQVGLCHSVQGTA
EELARDLNIDPATLRYRCAGINHMAFYLELERKTAADGSYVNLYPELLAAYEAGQAPKPNI
HGNTRCQNIVRYEMFKKLG YFVTESSEHFAEYTPWFIKPGREDLIERYKVPLDEYPKRCVE
QLANWHKELEEYKKASRIDIKPSREYASTIMNAIWTGEP SVIYGNVRNDGLIDNLPQGCCV
EVACLVDANGIQPTKVGTLP SHLAALMQTNINVQTLTEAILTENRDRVYHAAMMDPHT
AAVLGIDEIYALVDDLIAAHGDWLPGLWHR
>sp|P9WPQ7|BIOB_MYCTU Biotin synthase OS=Mycobacterium tuberculosis (strain ATCC
25618 / H37Rv) OX=83332 GN=bioB PE=1 SV=1
MTQAATRPTNDAGQDGGNNSDILVVARQQVLQRGEGLNQDQVLAVLQLPDDRLEELLA
LAHEVRMRWCGPEVEVEGIISLKTGGCPEDCHFCSQSGLFASPVRSAWLDIPSLVEAAKQT
AKSGATEFCIVA AVRGPDERLMAQVAAGIEAIRNEVEINIACSLGMLTAEQVDQLAARGV
HRYNHNLETARSFFANVVTHTTWEERWQTL SMVRDAGMEVCCGGILGMGETLQQRAEF
AAELAE LGPDEVPLNFLNPRPGTFADLEVMPVGDALKAVAAFR LALPRTMLRFAGGREI
TLGDLGAKRGILGGINAVIVGNYLTTLGRPAEADLELLDELQMP LKALNASL
>sp|G4T4R7|AGASK_RUMGN Bifunctional alpha-galactosidase/sucrose kinase AgaSK
OS=Ruminococcus gnavus OX=33038 GN=agaSK PE=1 SV=1
MAIIYNPNKKIFTLHTAHTTYQM QVDPLGYLLHLYYGEKTNSSMDYVLT YADRGFSGNP
YAAGMDRTYSLDALPQEYPSLGTGDYRNIALNIKNEKGVESADLLFKSYEIRNGKYRLQG
LPAVWADEKEAQ TLEIVLADENAQVEVHLLYGVLEENDVITRSVRIKNTGTGQITIEKAA
AACLD FVQGEFDVLR FYGKHAMERNLERTPLGHGTIAFGSRRGTSSHQYNPAVILA EKGT
TETAGSCYGM L FVYSGNFSCEAEKDQFNQTRLLLGLNEELFSYPLASGETFTVPEVILSYS
AEGLSALSQQYHNCIRNHVCRSKYVHMQR PVLINSWEAA YFDFTGDTIVDLAKEAASLGI
DMVVMDDGWFGKRND DNSSLGDWQVNETKLGGSLAELITRVHEQGMKFGIWIPEMIN
EDSDLYRAHPDWAIRIQGKKPVRSRNQLLLDFSRKEVRDCVFDQICV VLDQGKIDYVKW
DMNRSMADVYAGNLSYDYVLGVYDFMERLCSRYPDLLLEGCSGGGGRFDAGMLYYSPQ
IWCSDNTDAINRTRI QYGT SFFYPVSAMGAHVSAVPNHQTGRVTSFHTRGVTAMAGTFGY
ELNPALLSDEEKQQIREQIKTYKKYETLINEGTYWRLSDPFTDEIAAWMSVSEEQDHALVS
VVRLMAEANQATVYVRLRGLKPD AVYLEEQSGRQYSGAALMHAGIPLPPFTEEYEA YQF
AFTELKEAGRLYEKVQKWCDGNAENRVVISIYGGSGSGKTTLATALQQYFLNDGTECYL
LSGDDYPHRIPKRND EERM RVYKEAGEDGLRGYLGTKKEIDFDRINEVLAAFHEGKDSIT
LRHMGREDGEISLEETDFSGISVLLLEWTHGGSDDLHGVDLPVFLESSPGETRERRIRNR
DENAASPFICRVVELEQE KLEVQRKNAGLIVGKDGSVYEQ
>sp|Q2YIQ1|ERYA_BRUA2 Erythritol kinase OS=Brucella abortus (strain 2308) OX=359391
GN=eryA PE=1 SV=2
MSAMREKGDIIIIGIDAGTSVLKAVAFDFSGRQIESAAVRNTYVTGDHGA V TQSLAQTWQD
CARALRDLGAKLPGLAQRTAAIAVTGQGDGTWL VGKDNRPVGD AWIWL DARAAS TVTR
LAAGPMNRARFEATGTGLNTCQQGAQMAHMDTIAPELLDNAE AALHCKDWLYLNL TG V

RATDPSEASFTFGNFRTRQYDDVVIEALGLQKRRNLLPEIIDGSQSQHPLSAEAAAATGLL
AGTPVSLGYVDMAMTALGAGVCGGTAGAGCSTIGSTGVHMRAPVADIHLNKEGTGYV
IALPIPGIVTQVQTNMGATINIDWILQVAADLMSTPEKPVSLGDLIPRLDDWFNASRPGAIL
YHPYISEAGERGPFVNANARAGFIGLSSRDRFPELVRSVVEGLGMATRDCYAAMGEMPAE
LRITGGAARSKALRGTLAAVNAPVRVSAREEAGAAGAAMMAAVAIGAYPAMDDCIAE
WVEPLLGAASEAPDAARAHQYEELFVAYREARLALAPVWDKLSGK

>sp|P0AEJ6|EUTB_ECOLI Ethanolamine ammonia-lyase heavy chain OS=Escherichia coli (strain K12) OX=83333 GN=eutB PE=1 SV=1

MKLKTTLFGNVYQFKDVKEVLAKANELRSGDVLGVAASSQERVAAKQVLSEMTVAD
IRNNPVIA YEDDCVTRLIQDDVNETAYNQIKNWSISELREYVLSDETSVDIAFTRKGLTSE
VVA AVAKICSNADLIYGAKKMPVIKKANTTIGIPGTFSARLQPNDRDDVQSIAAQIYEG
SFGVGDAVIGVNPVTDDVENLSRVLDTIYGVIDKFNIPTQGCVLAVHTTQIEAIRRGAPGG
LIFQSICGSEKGLKEFGVELAMLDEARAVGAEFNRIAGENCLYFETGQGSALSAGANFGA
DQVTMEARNYGLARHYDPFIVNTVVGFIGPEYLYNDRQIIRAGLEDHFMGKLSGISMGC
CCYTNHADADQNLNENLMILLATAGCNYIMGMP LGDDIMLNYQTAFHDTATVRQLLN
LRPSPEFERWLESMGIMANGRLTKRAGDPSLFF

>sp|P80506|G3P1_NOSS1 Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Nostoc sp. (strain PCC 7120 / SAG 25.82 / UTEX 2576) OX=103690 GN=gap1 PE=1 SV=3

MAKLKVGINGFGRIGRLVLRAGINNPNIIEFVGINDLVPPDNLAYLLKYDSTHGRLRSQVET
KDDGIVIDGHFIPCVSVRNPAELPWGKLGADYVVESTGLFTDSEGASKHLQAGARRVIISA
PTKDPDRVRTLLVGVNHDLFDPSKDLIVSNASCTTNCLAPIAKVINDNFGLTEGLMTTVHA
MTATQPTVDGPSKKDWRGGRGAAQNIIPSTGAAKAVALVPELKGKLTGMAFRVPTPD
VSVVDLTFKTAKATSYKEICAAMKQASEGSLAGILGYTDEEVVSTDFQGDTHSSIFDAGA
GIELNSNFFKVVAWYDNEWGYSNRVVDLMLSMVQKEQLAAV

>sp|P0CY93|FPRA_RHOCA Type A flavoprotein fprA OS=Rhodobacter capsulatus OX=1061 GN=fprA PE=1 SV=1

MSVPPFTIRPAAPRLDGPTGPVAVAPGVHWVGALDPGLRNFDVILKTANGTTYNAYAVR
GSEGVAVIDTVKA EFAGDFFARLEAVARYDEIRLIVLNHLEPDHTGAVPELLRRAPQAQV
RLSPRGLPMLRALLKDDFERYDIKGVTTGQSVSLGDRICSFFTTPFVHWPDTQCTWLAAE
RVLFTCDLFGSHYCDGRLFNDLVGDFRFSFEYYFDRIMRPFRSFVAQVLDLIEPLDFGIIAP
AHGPILRSHPRDYLTHTRRLISSWLAAETGSEKTLIFYVSAYRATAQLAQAIHDGAAESP
DVRVSLFDLEGGEITPFLDLIEEADGIALGTPTINGDAVRTIWEMLAALVDIETRGLGAAF
GSYGWSGEAVRLVETRLQGLKMRLPEPGLRVKLHPSAAELEEGRAFGRRLLADHLTGRAR
PREVDFAEIAAR

>sp|P45543|FRLD_ECOLI Fructoselysine 6-kinase OS=Escherichia coli (strain K12) OX=83333 GN=frlD PE=1 SV=1

MKTLATIGDNCVDIYPQLNKA FSGGNAVNVAVYCTRYGIQPGCITWVGDDDDYGTKLKQD
LARMGVDISHVHTKHGVT AQTQVELHDNDRVFGDYTEGVMADFALSEEDYAWLAQYDI
VHAAIWGHAEDAFPQLHAAGKLTAFDFSDKWDSP LWQTLVPHLDFAFASAPQEDELRL
KMKAIVARGAGTVIVTLGENGSI AWDGAQFWRQAPEPVTVIDTMGAGDSFIAGFLCGWS
AGMTLPQAIAQGTACA AKTIQYHGAW

>sp|Q45694|DNTAB_BURSR 2,4-dinitrotoluene dioxygenase system, ferredoxin component OS=Burkholderia sp. (strain RASC) OX=69003 GN=dntAb PE=1 SV=1

MSENWIDAAARDEVPRGRRDRHQYRRQGDCLYE VAGEIYATDNTCTHGAARMSDGFLE
GREIECPLHQGRFDVCTGKALCTPLTQDIKTYPVKIENMRVMLKLD

>sp|O69668|EGTE_MYCTU Probable hercynylcysteine sulfoxide lyase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=egtE PE=1 SV=3

MRRSGANSPAGDSLADRWRAARPPVAGLHLD SAACSRQSFAALDAAAQHARHEAEVGG
YVAAEAAA AVLDAGRAAVAALSGLPDAEVVFTTGS LHALDLLLGSWPGENRTLACLPGE
YGPNLAVMAAHGFDVRPLPTLQDGRVALDDAAFMLADDPDLVHLTVVASHRGVAQPL

AMVAQLCTELKLPLVVDAAQGLGHVDCAVGADVITYASSRKWIAGPRGVGVLA VRPELM
ERLRARLPAPDWMPLTVAQQLGFGEANVAARVGFVSVALGEHLACGPQAIRARLAE LGD
IARTVLADVSGWRVVEAVDEPSAITTLAPIDGADPAAVRAWLLSQRRIVTTYAGVERAPL
ELPAPVLRISPHVDNTADDLDAFAEALVAATAATSGER

>sp|Q8FKL3|ECPD_ECOL6 Fimbria adhesin EcpD OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) OX=199310 GN=ecpD PE=1 SV=1

MRVNLLIAMIIIFALIWPATALRAAVSKTTWADAPAREFV FVENNSDDNFFVTPGGALDPR
LTGANRW TGLKYNGSGTIYQQSLGYIDNGYNTGLYTNWKFDMWLENSPVSSPLTGLRCI
N WYAGCNMTTSLILPQT TDASGFYGATVTSGGAKWMHGM LSDAFYQYLQQMPVGSSFT
MTINACQTSVNYDASSGARCKDQASGNWYVRNVTHTKAANLRLINTHSLAEVFINS DGV
PTLGEGNADCRTQTIGSRSLCKMVNYTLQTNGLSNTSIHIFPAIANSSLASAVGAYDMQ
FSLNGSSWKPVSN TAYYYTFNEMKSADSIYVFFSSNFFKQMVNLGISDINTKDLFNFRFQN
TTSPEGWYEFSTSN TLIKPRDFSISIISDEYTQTPSREGYVGSGESALDFGYIVTTSGKTAA
DEVLIKVTGPAQVIGGRSYCVFSSDDGKAKVPFPATLSFITRNGATKTYDAGCDDSWRDM
TDALWLTTPWTDISGEVGQMDKTTVKFSIPMDNAISLRTVDDNGWFGESASGEIHVQAT
WRNIN

>sp|P9WNB9|END8A_MYCTU Endonuclease 8 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=nei1 PE=1 SV=1

MPEGHTLHRLARLHQRRFAGAPVSVSSPQGRFADSASALNGRVLRRASAWGKHLFHHYV
GGPVVHVHLGLYGTFTWARPTDGWLPEPAGQVRMRMVGA EFGTDLRGPTVCESIDDG
EVADVVARLGPDPLRSDANPSSAWSRITKSRRPIGALLMDQTVIAGVGNVYRNELLFRHRI
DPQRPGRGIGEPEFDAAWNDLVSLMKVGLRRGKIIVVRPEHDHGLPSYLPDRPRTYVYRR
AGEPCRVC GGVIRTALLEGRNVFWCPVCQT

>sp|P94527|G1PDH_BACSU Glycerol-1-phosphate dehydrogenase [NAD(P)+] OS=Bacillus subtilis (strain 168) OX=224308 GN=egsA PE=1 SV=1

MNRIAADVQRAFENAGEKTLPIKVEEIVLGKQAADSLLDYVKRKNNQHIVLVCDANTHRI
AGIDLENRLNQEGFQAECLIIPENEAGDVTADERSLIHVL IHTKQPTDVMIAVGS GTIHDIV
RFAAFQRDLPFISYPTAPSV DGFTSAGAPIILYGT KTTIQT KAPSALFADLDLLKAAPQSMV
AAGFGDMLGKITSLADWEISRHLAGEPYSPAGAKIVQEALACIEHTEDIAMKTETGIRVL
MESLLVSGLVMLALDHSRPASGGEHHISHWIEMELMEKKRPQILHGAKVGCAAVLLTDT
YRKLAQDDGLNEFSPSRREAIQSAYQTLPRGEVLADW LRSAGGPAYFDEIGVGQDSVKNA
FRHAHTLRDRCTGLRIINENKTLINHGLYE

>sp|P74070|EFTS_SYNY3 Elongation factor Ts OS=Synechocystis sp. (strain PCC 6803 / Kazusa) OX=1111708 GN=tsf PE=1 SV=3

MAEITAQLVKELREKTGAGMMDCKKALKENEGDLEKSIEWLRQKGIASADKKSGRTAAE
GLVHSYIHFGGRIGVLVEVNCETDFVARGDRFKDLVNDVAMQIAACPNVEYVSVADIPQE
MVAKEKEIEMGRDDL GKKPANIKEKIVQGRIDKRLKELSLLDQPYIKDQNL TIEELVKQAI
AELGENIQVRRFIRFNLGEGIEKAETNFAEEVAAA AAKG

>sp|P0AC73|EBGC_ECOLI Evolved beta-galactosidase subunit beta OS=Escherichia coli (strain K12) OX=83333 GN=ebgC PE=1 SV=1

MRIIDNLEQFRQIYASGKKWQRCVEAIENIDNIQPGVAHSIGDSLTYRVETDSATDALFTG
HRRYFEVHYLYLQGQQKIEYAPKETLQVVEYYRDET DREYLKGCGETVEVHEGQIVICDIH
EAYRFICNNAVKKVVLKVTIEDGYFHNK

>sp|O83047|DNAA_TREPA Chromosomal replication initiator protein DnaA OS=Treponema pallidum (strain Nichols) OX=243276 GN=dnaA PE=1 SV=1

MDAVGYEVFWNETLSQIRSESTEAEFNMWFAHLFFIASFENAIEIAVPSDFFRIQFSQKYQE
KLERKFLELSGHPIKLLFAVKKGT PHGNTAPPKHVHTYLEKNSPA EVPSKKS FHPDLNRDY
TFENFVSGEETKF SHSAAISVSKNPGTSYNPLLIYGGVGLGKTHLMQAIGHEIYKTTDLNVI
YVTAENFGNEFISTLLNKK TQDFKKKYRYTADVLLIDDIHFFENKDGLQEELFYTFNELFE
KKKQIIFTCDRPVQELKNLSSRLRSRCSRGLSTD LNMPCFETRCAILIKKIQNYNSTYPHKAI

HISDDVVRLVSENISSNIRDLEGALTKIIAFIEVSGSITIDIVPSLLKEFFLSARPKHITVETILH
VVADHFNISYSDLKGKKRNKSVVYPRQIAMFLSKELTELSTTELGIEFGGRDHSTVIYGCQ
KIEGEILTNPQLQANLDDLKSKVQDSIR
>sp|P18776|DMSB_ECOLI Anaerobic dimethyl sulfoxide reductase chain B OS=Escherichia coli
(strain K12) OX=83333 GN=dmsB PE=1 SV=4
MTTQYGFFIDSSRCTGCKTCELACKDYKDLTPEVSFRRIYIYAGGDWQEDNGVWHQNVF
AYYLSISCNHCEDPACTKVCPSGAMHKREDGFVVVDEEDVCIGCRYCHMACPYGAPQYNE
TKGHMTKCDGCYDRVAEGKKPICVESCPLRALDFGPIDELRKKHGDLA AVAPLPRAHFTK
PNIVIKPNANSRPTGDTTGYLANPKEV
>sp|Q03131|ERYA1_SACER 6-deoxyerythronolide-B synthase EryA1, modules 1 and 2
OS=Saccharopolyspora erythraea OX=1836 GN=eryA PE=1 SV=1
MSGPRSRTTSRRTPVRIGAVVVASSTSELLDGLAAVADGRPHASVVRGVARPSAPVVVFV
PGQGAQWAGMAGELLGESRVFAAAMDACARAFEPVTDWTLAQVLDSPEQSRRVEVVQP
ALFVQTSALWRSFGVTPDAVVGHSIGELAAAHVCGAAGAADAARAAALWSREMIP
LVGNGDMAAVALSADEIEPRIARWDDDVVLAVNGPRSVLLTGSPEPVARRVQELSAEG
VRAQVINVSMAAHSQAQVDDIAEGMRSALAWFAPGGSEVPFYASLTGGAVDTRELVADY
WRRSFRLPVRFDEAIRSALEVGPSTFVEASPHVLAAALQQTLD AEGSSAAVVPTLQRGQ
GGMRRFLAAQAFTGGVAVDWTAAYDDVGPNPALCRSSRRPRRKT SRPSPASTGTRHR
TCCERLLAVVNGETAALAGREADAEATFRELGLDSVLAAQLRAKVSA AIGREVNIALLYD
HPTPRALAEALAAGTEVAQRETRARTNEAAPGEPVAVVAMACRLPGGVSTPEEFWELLS
EGRDAVAGLPTDRGWDLSL FHPDPTRSGTAHQ RGGGFLTEATAFDPAFFGMSPREALA
VDPQQRLMLELSWEVLERAGIPPTSLQASPTGVFVGLIPQEYGPRLAEGGEGVEGYLMTG
TTTSVASGRIAYTLGLEGPAISVDTACSSSLVAVHLACQSLRRGESSLAMAGGVTVMPTPG
MLVDFSRMNSLAPDGRCKAFSAGANGFGMAEGAGMLLLERLS DARRNGHPVLAVLRGT
AVNSDGASNGLSAPNGRAQVRVIQQALAESGLGPADIDAVEAHGTGTRLGDPIEARALFE
AYGRDREQPLHLG SVKSNLGHTQAAAGVAGVIK MVLAMRAGTLPRTLHASERSKEIDWS
SGAISLLDEPEPWPAGARPRRAGVSSFGISGTNAHAIIIEEAPQVVEGERVEAGDVVAPWVL
SASSAEG LRAQAARLA AHLREHPGQDPRDIAYSLATGRAALPHRAAFAPVDESAALRVLD
GLATGNADGA AVGTSRAQQRAVFVFPQGQWQWAGMAVDLLDTSPVFAAALRECADAL
EPHLDFEVIPFLRAEAARREQDAALSTERV DVVQPVMFVVMVSLASMWRAHGVEPAAVI
GHSQGEIAAACVAGALSLDDAARVVALRSRV IATMPGNKGMA SIAAPAGEVRARIGDRV
EIAAVNGPRSVV VAGDSDELDRLVASCTTECIRAKRLAVDYASHSSHVETIRDALHAELG
EDFHPLPGFVPFFSTVTGRWTQ PDELDAGYWYRNLRRTVRFADAVRALAEQGYRTFLEV
SAHPILTAAIEEIGDGS GADLSAIHSLRRGDGSLADFG EALSRAFAAGVAVDWESVHLGTG
ARRVPLPTYPFQ RERVWLEPKPVARRSTEVDEVSALRYRIEWRPTGAGEPARLDGTWLVA
KYAGTADETSTAAREALESAGARVREL VVDARCGRDELAERLSVGEVAGVLSLLAVDE
AEPEEAPLALASLADTL SLVQAMVSAELGCPLWTVTESAVATGPFERVRNAAHGALWGV
GRVIALENPAVWGGLVDVPAGSVAELARHLAAVVSGGAGEDQLALRADGVYGRRWVR
AAPATDDEWKPTGTVLVTGGTGGVGGQIARWLARRGAPHL LLSRSGPDADGAGELV
AELEALGARTTVAACDVTDRESVRELLGGIGDDVPLSAVFHAAATLDDGTVDTLTGERIE
RASRAKVLGARNLHELTRELDLTA FVLFSSFASAFGAPGLGGYAPGNAYLDGLAQQRSD
GLPATAVAWGTWAGSGMAEGAVADRFR RHGVIEMPPE TACRALQNALDRAEVCPIVIDV
RWDRFLLAYTAQRPTRLFDEIDDARRAAPQAPAEPRVGALASLPAPEREEALFELVRSHA
AAVLGHASAERV PADQAF AELGVDSL SALELRNRLGAATGVRLPTTTVFDHPDVRTLAA
HLAAELGGATGAEQAAPATTAPVDEPIAIVGMACRLPGEVDS PERLWELITSGRDSAAEV
PDDRGWVPDEL MASDAAGTRAHGNFMAGAGDFDA AFFGISPREALAMDPQQRQALET
WEALESAGIPPETLRGSDTG VFGVGM SHQGYATGRPRPEDGVDGYLLTGNTASVASGRIAY
VLGLEGPALTVD TACSSSLVALHTACGSLRDGDCGLAVAGGV SVMAGPEVFTEFSRQGA
LSPDGRCKPFSDEADG FGLGEGSAFVVLQRLSDARREGRRVLGVVAGSAVNQDGASNGL
SAPSGVAQQRVIRRAWARAGITGADVAVVEAHGTGTR LGDPVEASALLATY GKSRGSSG

PVLLGSVKSNIHAQAAAGVAGVIKVLLGLERGVVPPMLCRGERSGLIDWSSGEIELADG
VREWSPAADGVRRAGVSAFGVSGTNAHVIIAEPPEPEPVQP RRMLPATGVVPVLSART
GAALRAQAGRLADHLAAHPGIAPADVSWTMARARQHFEERA AVLADTAEAVHRLRAV
ADGAVVPGVVTGSASDGGSVFVFPQGGAQWEGMARELLPVPVFAESIAECD AVLSEVAG
FSVSEVLEPRPDAPSLERVDVVQPVLFAVMVSLARLWRACGAVPSAVIGHSQGEIAAAVV
AGALSLEDGMRVVARRSRVRAVAGRGSM LSVRGGRSDVEKLLADDSWTGRLEVA AV
NGPD AVVVAGDAQAAREFLEYCEGVGIRARAIPVDYASHTAHVEPVRDEL VQALAGITPR
RAEVPFFSTLTGDFLDGTELDAGYWYRNLRHPVEFHSAVQALTDQGYATFIEVSPHPVLA
SSVQETLDDAESDA AVLGTLERDAGDADRFLTALADAHTRGVAVDWEAVLGRAGLVDL
PGYFPQGKRFWLLPDRTTPRDEL DGWFYRVDWTEVPRSEPAALRGRWL VVVPEGHEEDG
WTVEVRSALAEAGAEPEVTRGVGGLVGDCAGVVSL LALEGDGAVQTLVLVRELD AEGID
APLWTVTFGAVDAGSPVARPDQAKLWGLGQVASLERGPRWTGLVDLPHMPDPELRGRL
TAVLAGSEDQVAVRADAVRARRLSPAHTATSEYAVPGGTILVTGGTAGLGA EVARWL
AGRGAEHLALVSRGPDTEGVGDLTAELTRLGARVSVHACDVSSREPVREL VHGLIEQGD
VVRGVVHAAGLPQQVAINDMDEAA FDEVVAAKAGGAVHLDELCSDAELFLLFSSGAGV
WGSARQGAYAAGNAFLDAFARHRRGRGLPATSVAWGLWAAGGMTGDEEAVSFLRERG
VRAMPVPRALAALDRVLASGETAVVVTDVDWPAFAESYTAARPRLLDRIVTTAP SERA
GEPETESLRDRLAGLPRAERTAE LVRVLTSTATVLGHDDPKAVRATTPFKELGFD SLAA
VRLRNLLNAATGLRLPSTLVFDHPNASAVAGFLDAELGTEVRGEAPSALAGLDALEGALP
EVPATEREELVQRLERMLAALRPVAQAADASGTGANPSGDDLGEAGVDELLEALGRELD
GD

>sp|P37957|ESTA_BACSU Lipase EstA OS=Bacillus subtilis (strain 168) OX=224308 GN=estA
PE=1 SV=2

MKFVKRRRIALVTILMLSVTSLFALQPSAKAAEHNPVVMVHGIGGASFNFAGIKSYLVSQG
WSRDKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTLYYIK
NLDGGNKVANVVTLGGANRLTTGKALPGTDPNQKILYTSIYSSADMIVMNYLSRLD GAR
NVQIHGVGHIGLLYSSQVNSLIKEGLNGGGQNTN

>sp|P00380|DYR_ENTFC Dihydrofolate reductase OS=Enterococcus faecium OX=1352
GN=folA PE=1 SV=1

MFISMWAQDKNGLIGKDGLLPWRLPNDMRFFREHTMDKILVMGRKTYEGMGKLSLPYR
HIIVLTQKDFKVEKNAEVLHSIDELLAYAKDIPEDIYVSGGSRIQALLPETKIIWRTLIDA
EFEGDTFIGEIDFTSFELVEEHEGIVNQENQYPHRFQKWQKMSKV

>sp|E1VA04|ECTD_HALED Ectoine dioxygenase OS=Halomonas elongata (strain ATCC 33173 /
DSM 2581 / NBRC 15536 / NCIMB 2198 / 1H9) OX=768066 GN=ectD PE=1 SV=1

MSVQTSSNRPLPQANLHIATETPEADSRIRSAPRPGQDPYPTRLSEPLDLPWLNRRREP VVK
GEEADGPLSAAQLDTERQGFIFEPDFLKGEELALRHELNALLARDDFRGRDFAITEPQG
NEIRSLFAVHYLSRVFSRLANDERLMGRARQILGGEPYVHQSRINYKPGFEGKGFNWHSD
FETWHAEDGMPAMHAVSASIVLTDNHTFNGLMLVPGSHRVFVPCLGETPEDHHRQSLK
TQEFVPSRQALRELIDRHGIEAPTGAAGGLLLFDCNTLHGSNANMSPDPRSNAFFVYNRR
DNRCVEPYAASKRRPRFLAHEPDEAWSPDG

>sp|P06575|BINA1_LYSSH 41.9 kDa insecticidal toxin OS=Lysinibacillus sphaericus OX=1421
GN=binA PE=1 SV=1

MRNLDFIDSFIPTEGKYIRVMDFYNSEYPFCIHAPSAPNGDIMTEICSRENNQYFIFPTDDG
RVIIANRHNGSVFTGEATSVVSDIYTGSP LQFFREVKRTMATYYLAIQN PESATDVRALEP
HSHELPSRLYYTNNIENNSNILISNKEQIYLTPLSPENEQYPKTPVLSGIDDIGPNQSEKSIIG
STLIPCIMVSDFISLGERMKTPYYYVKHTQYWQSMWSALFPPGSKETKTEKSGITDTSQIS
MTDGINVSIGADFGLRFGNKTFGIKGGFTYDTKTQITNTSQLLIETTYTREYTN TENFPVRY
TGYVLASEFTLHRSDGTQVNTIPWVALNDNYTTIARYPHFASEPLLGN TKIITDDQN

>sp|P17725|CITE_KLEPN Citrate lyase subunit beta OS=Klebsiella pneumoniae OX=573
GN=citE PE=1 SV=2

MKPRRSMLFIPGANAMLSTSFVYGADAVMFDLEDAVSLREKDTARLLVYQALQHPLYQ
 DIETVVRINPLNTPFGLADLEAVVRAGVDMVRLPKTDSKEDIHELEAHVERIERECGREVG
 STKLMAAIESALGVVNAVEIARASPRLAALAAFDYVMDMGTSRGDGTSELFYARCAVL
 HAARVAGIAAYDVVWSDINNEEGFLAEANLAKNLGFNGKSLVNPRQIELLHQVYAPTRK
 EVDHALEVIAAAEEAETRGLGVVSLNGKMGIDGPIIDHARKVVALSASGIRD
 >sp|D5E3H2|CP107_BACMQ Cytochrome P450 CYP107DY1 OS=Bacillus megaterium (strain
 ATCC 12872 / QMB1551) OX=545693 GN=BMQ_pBM50008 PE=1 SV=1
 MKKVTVDDFSSPENMHDVIGFYKKLTEHQEPLRLDDYYGLGPAWVALRHDDVVITILKN
 PRFLKDVRKFTPLQDKKDSIDDSTSASKLFEWMMNMPNMLTVDPPDHTRLRLRLASKAFTP
 RMENLRPRIQQITNELLDSEVGKRNMDLVADFSFPLPIIVISEMLGIPPLDQKRFRDWTDK
 LIKAAMDPSQGAVVMETLKEFIDYIKKMLVEKRNHPDDDDVMSALLQAHEQEDKLSANEL
 LSTIWLLITAGHETTAHLISNGVLALLKHPEQMRLLRDNPSSLPSAVEELLRYAGPVMIGG
 RFAGEDIIMHGKMIPKGEMVLFSLVAANIDSQKFSYPEGLDITRENEHLTFGKGIHHCLG
 APLARMEAHIAFGTLLQRFPLRLAIESEQLVYNNSTLRSLSKSLPVIF
 >sp|P32400|CSH_ARTSP N-carbamoylsarcosine amidase OS=Arthrobacter sp. OX=1667 PE=1
 SV=1
 MTETSGTFNDIEARLAAVLEEAFEAGTSIYNERGFKRRIGYGNRPAAVHIDLANAWTQPGH
 PFSCPGMETIIPNVQRINEAARAKGVVPFYTTNVYRNRDASSGTNDMGLWYSKIPTETLPA
 DSYWAQIDDRIAPADGEVVIEKNRASAFPGTNLELFLTSNRIDTLIVTGATAAGCVRHTVE
 DAIKAGFRPIIPRETIGDRVPGVVQWNLYDIDNKFQDVESTDSVVQYLDALPQFEDTVPKT
 LSDPQPEVEAPADPVFAEQH
 >sp|J7T0S1|CSXB_CLOS1 Exosporium protein B OS=Clostridium sporogenes (strain ATCC
 15579) OX=471871 GN=csxB PE=1 SV=1
 MSKSSEEKMEKEVLNINSFNISEFCNAEEGSNFIHFKPCEICKRAILDPINVADTSRLLQVN
 VALRNVICIGKELTVGCILIDRTGTVLAFKSQTFTVGHGGSGCGCSEDKHGSPCTNTSRFS
 FILPTRDLCSSMDLKVKIIANYTHPCN
 >sp|P33752|CTFA_CLOAB Butyrate--acetoacetate CoA-transferase subunit A OS=Clostridium
 acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787)
 OX=272562 GN=ctfA PE=1 SV=1
 MNSKIIRFENLRSFFKDGMTIMIGGFLNCGTPTKLIDFLVNLNIKNLTIISNDTCYPNTGIGK
 LISNNQVKKLIASYIGSNPDTGKKLFNNELEVELSPQGTIVERIRAGGSGLGGLVLTGTGLG
 TLIEKGKKKISINGTEYLLELPLTADVALIKGSIVDEAGNTFYKGTTKNFNPYMAMAAKT
 IVEAENLVSCEKLEKEKAMTPGVLINIVKEPA
 >sp|P40138|CYAB_STIAU Adenylate cyclase 2 OS=Stigmatella aurantiaca OX=41 GN=cyaB
 PE=1 SV=3
 MLQGHHRVMVVDSDPLACDFVKEGLEALGLGYEVMCFQDPYEALQVGVQPAIVLSD
 LDMPGIDGLELCWRLKESPSRQVPVIILTANDSEAERVKGLRAGADDYVNSASMAELSA
 RIESVMRRTSETERMRKLFARYTSDAVVEEILKSPDTVVLTKGKPEVTVLFAIRNFTGLA
 ESLPPEQVVGVLNQVLGRLSDAVLTCGGTLDKFLGDGLMAVWGAPVHRTDDALRALQA
 AKMMMTAMVELRQAAQAEWAANERLGRPLVLELGIGINSGLA VAGNIGGSMRTEYTCI
 GDAVNVAARLCALAGPGEILAGERTRELVSHREMPFEDLPPVRLKGKQQPVPLYRVL
 >sp|P9WHP3|CRTB_MYCTU Phytoene synthase OS=Mycobacterium tuberculosis (strain ATCC
 25618 / H37Rv) OX=83332 GN=crtB PE=1 SV=1
 MTEIEQAYRITESITRTAARNFYYGIRLLPREKRAALSAVYALGRRIDDVADGELAPETKIT
 ELDAIRKSLDNIDDSSDPVLVALADAARRFPVPIAMFAELIDGARMEIDWTGCRDFDELIV
 YCRRGAGTIGKLCLSIFGPVSTATSRYAEQLGIALQQTNILRDVREDFLNGRIYLPDELDR
 LGVRLRLDDTGALDDPDGRLAALLRFSADRAADWYSLGLRLPHLDRRSAACCAAMSGI
 YRRQLALIRASPAVVYDRRISLSGLKKAQVAAAALASSVTCGPAHGPLPADLGSHPSH
 >sp|O32213|CYSI_BACSU Sulfite reductase [NADPH] hemoprotein beta-component
 OS=Bacillus subtilis (strain 168) OX=224308 GN=cysI PE=1 SV=1

MVTKILKAPDGSPSDVERIKKESDYLRGTLKEVMLDRISAGIPDDDNRLMKHHGSYLQDD
RDLRNERQKQKLEPAYQFMLRVRMPGGVSTPEQWLVMDDLSQKYGNGLTKLTTRETFQ
MHGILKWNMKKTIQTIHSALLDTIAACGDVNRNVMCASNPYQSEIHSEVYEWSSKKLSDD
LLPRTRAYHEIWLDEERVAGTPEEEVEPMPYGPLYLPRKFKGIAVPPSNDIDVFSQDLGFIAI
VEDGKLIGFNVAIGGGMGMTHTGDTATYPQLAKVIGFCRPEQMYDVAEKTITIQRDYGNRS
VRKNARFKYTVDRGLGLENVKEELENRLGWSLEEAKPYHFDHNGDRYGWVEGIEDKWHF
TLFVEGGRITDYDDYKLMTGLREIAKVHTGEFRLTANQNLMIANVSSDKKEEISALIEQYG
LTDGKHYSALRRSSMACVALPTCGLAMAEAEERYLPTLLDKIEEIIDENGLRDQEITIRMTG
CPNGCARHALGEIGFIGKAPGKYNMYLGAAFDGSRLSKMYRENIGEADILSELRIILSRYA
KEREAGEHFGDFVIRAGIIKATTDGTNFHD

>sp|P09928|CSMA_CHLAA Bacteriochlorophyll c-binding protein OS=Chloroflexus aurantiacus
(strain ATCC 29366 / DSM 635 / J-10-fl) OX=324602 GN=cmsA PE=1 SV=3

MATRGWFSESSAQVAQIGDIMFQGHWQWVSNALQATAAAVDNINRNAYPGVSRSGSGE
GAFSSSPSNGFRPKRIRSRFNR

>sp|Q2RN15|COWN_RHORT N(2)-fixation sustaining protein CowN OS=Rhodospirillum rubrum
(strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIB 8255 / S1) OX=269796
GN=cowN PE=1 SV=1

MTMDGPAHMPRRYVTFQGVNVEGLSQQLIARILFHVADPAKSNAFWEHFKAKLADADK
TLARTADSLCLLCGAIGYIDELFEDNDDEEGLTILRRLEDEL

>sp|Q02861|CRTI_MYXXA All-trans-zeta-carotene desaturase OS=Myxococcus xanthus OX=34
GN=carC PE=1 SV=1

MASEGGSVRHVIVVGAGPGGLSAAINLAGQGFRVTVVEKDAVPGGRMKGLTLGASGEY
AVDTGPSILQLPGVLEQIFRRAARRLEDYVKLLPLDVNTRVHFWDGTHLDTTRHLDRMEA
ELAKFGPRQASALRQWMEDGREKYGIAYQKFICTSADNLGYYAPWRLAPTLRFPKWQTL
YRQLDGGFFHDDRVTYALAYPSKYLGLHPTTCSSVFSVIPFLELAFGVWHVEGGFRELSRG
MMRCARDLGATFRMGTPVEKVRVDAGRAVGKLVGGEVLDADAVVNNADLAYAARS
LIPAEAREGSRLTDAALERAKYSCSTFMAYYGLDTVYADLPHHLIYLSESARRTDRDALE
DRHVDLEDPPFYVCNPGVTDPSGAPAGHSTLYVLVPTPNTGRPVDWVKTEQALRERIPAM
LEKVGLKGVREHIREERYFTAETWRDDFNVFRGAVFNLSHTWLQLGPLRPKVKNRDIEGL
YFVGGGTHPGSGLLTIMESANIAADYLTREAGKGPLPGWPYPVPLEPESPVQARAG

>sp|P39778|CLPY_BACSU ATP-dependent protease ATPase subunit ClpY OS=Bacillus subtilis
(strain 168) OX=224308 GN=clpY PE=1 SV=1

MEKKPLTPRQIVDRLDQYIVGQQNAKKAVAVALRNRYRRSLLDEKLKDEVVPKNILMMG
PTGVGKTEIARRIAKLSGAPFIKIEATKFTEVGYVGRDVESMVRDLVETSVRLIKEEKMNE
VKEQAEENANKRIVRLLVPGKKKQSGVKNPFEMFFGGSQPNGEDEAESQEEANIEEKRRK
MAHQLALGELEDYVYVTEVEVEEQQPSMFDMLQGSGMEQMGMNMQDALSGLMPKKKKR
RKMTVREARKVLTNEEASKLIDMDEVGQEAVQRAEESGIIFIDEIDKIAKNGGASSSADVS
REGVQRDILPIVEGSTVVTKYGSVKTDHVLFAAGAFHMAKPSDLIPELQGRFPPIRVELNKL
TVDDFVRILVEPDNALLKQYQALLQTEGISLEFSDEAIIHKIAEVAYHVNQDQTDNIGARRLH
TILERLLEDLSFEAPDVTMEKITITPQYVEEKLGTIAKNKDLSQFIL

>sp|Q9X1A7|COAE_THEMA Dephospho-CoA kinase OS=Thermotoga maritima (strain ATCC
43589 / MSB8 / DSM 3109 / JCM 10099) OX=243274 GN=coaE PE=1 SV=1

MVIGVTGKIGTGKSTVCEILKNKYGAHVNNVDRIGHEVLEEVEKEKLVELFGGSVLEDGKV
NRKKLAGIVFESRENKKLELLVHPLMKKRVQEIINKTSGLIVIEAALLKRMGLDQLCDHV
ITVVASRETILKRNREADRRLKFQEDIVPQGIVVANNSTLEDLEKKVEEVMKLVWEKRE

>sp|Q01330|CRTX_ESCVU Zeaxanthin glucosyltransferase OS=Escherichia vulneris OX=566
GN=crtX PE=1 SV=1

MSHFAIVAPPLYSHAVALHALALEMAQRGHRVTFLTGNVASLAEQETERVAFYPLPASVQ
QAQRNVQQQSNGNLLRLIAAMSSLTDVLCQQLPAILQRLAVDALIVDEMEPAGSLVAEAL
GLPFISIAACALPVNREPGLPLPVMPPHYAEDKRALRRFQVSERIYDALMYPHGQTILRHAQ

RFGLPERRRLDECLSPLAQISQSVPALDFPRRALPNCFHVYGALRYQPPPQVERSPPRSTPRIF
ASLGTLLQGHRLRLFQKIARACASVGA EVTIAHCDGLTPAQADSLYACGATEVVVSFVDQPR
YVAEANLVITHGGLNTVLDALAAATPVLA VPLSFDQPAVAARLVYNGLGRRVSRFARQQ
TLADEIAQLLGDETLHQRLATARQQNDAGGTPRAATLIEQAIAGSESVS

>sp|Q59750|BGAL_RHIML Beta-galactosidase OS=Rhizobium meliloti OX=382 GN=lacZ PE=1
SV=1

MRSVTSFNDSWVFSEASTRDAERSGRVSRSA CRTNAVELPFNYFDERCYQRAFTYQRVLA
WRPDFSQGSRSSSTRQWPMRSCISTAKRSSRIRDGYTPFEARLTDRLLLEGDNLITVKIDGSE
NPEIPFGAGIDYLT YAGIYRDVWLKVTD PVSIANIKIETRDLSDHKAVSLRCDLSNPQGL
SFSGTISALLKNAAGEVLA EVAGETT GQSLAFEMDGLRGLSLWDIDDPVLYVIEVELRTGQ
GFRLLRRAFR LPHGEFTTEGFRLNGRPLKIRGLNRHQSFYVGLRMGR TAKGSAHADIMN
AHLHCNLV R TSHYPQSKWFLDHCDRIGLLVFARNPRLAAYRWGGMETGGNPERPPHRS
SATGTTRLSYIWGVRINESQDSHDFYAETNRLARELDPTRQTGGVRYITDSEFLEDVYTMN
DFILGNEELPGANRPGTALRPQ QECTGLPRKVPYLITEFGGHMYPTKIYDQEQRAEHVRR
HLEVLNAA YARNPGISGAIGWCMFDYNTTRISAPATGSAITASWTCSASPKFAAYVYASQ
CDPSEEIVMKPVTFWARGDDDIGGVLPLIVLTNCDEIELKYGSLTKRVGPDRENFP HLPHP
PVVIDHRHFTKDELGVWGMKWESA EFTGFIAGKPVADLRMAADPVPTTLQVEADSKTLR
REG RDTVRLILRALDQAGNVLPFLNDAVDIEIHGPARLVGPARIVLQGGSGFLAGVHGRR
RHASSRSRRRGSA AAKLDLVALADGAASA

>sp|P96855|CHSE3_MYCTU Acyl-CoA dehydrogenase FadE34 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) OX=83332 GN=fadE34 PE=1 SV=2

MVATVTDEQSAARELVRGWARTAASGAAATAAVRDM EYGFEEGNADAWRPVFAGLAG
LGLFGVAVPEDCGGAGGSIEDLCAMVDEAARALVPGPVATTAVATLVVSDPKLRSALAS
GERFAGVAIDGGVQVDPKTSTASGTVGRVLGGAPGGVVLLPADGNWLLVDTACDEVVV
EPLRATDFSLPLARMVLTSAPVTVLEVSGERVEDLAATVLAEEAAGVARWTLDTAVAYA
KVREQFGKPIGSFQAVKHLCAQMLCRAEQADVA AADAARAAADSDGTQLSIAAAVAASI
GIDAAKANAKDCIQVLGGIGCTWEHDAHLYLRRAHGIGGFLGGSGRWLRRVTALTQAGV
RRRLGVDLAEVAGLRPEIAAAVAEVAALPEEK RQVALADTGLLAPHWPAPYGRGASPAE
QLLIDQELAAAKVERPDLVIGWWAAPTILEHGTPEQIERFVPATMRGEFLWCQLFSEPGAG
SDLASLRTKAVRADGGWLLTGQKVWTSAAHKARWGVCLARTDPDAPKHKGITYFLVD
MTTPGIEIRPLREITGDSL FNEVFLDNVFPDEM VVGAVNDGWRLARTTLANERVAMATG
TALGNPMEELLKVLGDMELDVAQQDRLGRLILLAQAGALLDRRIAELAVGGQDPGAQSS
VRKLIGVRYRQALAEYLMEVSDGGGLVENRAVYDFL NTRCLTIAGGTEQILLTVAAERLL
GLPR

>sp|Q54518|CPSB_STREE Tyrosine-protein phosphatase CpsB OS=Streptococcus pneumoniae
OX=1313 GN=cpsB PE=1 SV=1

MIDIHSHIVFDVDDGPKSREESKALLAESYRQGVRTIVSTSHRRKG MFETPEEKIAENFLQV
REIAKEVADDLVIAYGAEIYYTLDALEKLEKKEIPTLND SRYALIEFSMHTSYRQIHTGLSN
ILMLGITPVIAHIERYDALENNEKRVRELIDMGCYTQINSYHVSKPKFFGEKYKFMKKRAR
YFLERDLVHVVASDMHNLDSRPPYMQQAYDIIAKKYGAKKAKELFVDNPRKIIMDQLI

>sp|P9WJB7|ESPR_MYCTU Nucleoid-associated protein EspR OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) OX=83332 GN=espR PE=1 SV=1

MSTTFAARLNRLFDTVYPPGRGPHTSAEVIAALKAEGITMSAPYLSQLRSGNRTNPSGAT
MAALANFFRIKAA YFTDDEYYEKLDKELQWLCTMRDDGVRRIAQRAHGLPSAAQQKVL
DRIDELRRAEGIDA

>sp|P0A953|FABB_ECOLI 3-oxoacyl-[acyl-carrier-protein] synthase 1 OS=Escherichia coli
(strain K12) OX=83333 GN=fabB PE=1 SV=1

MKRAVITGLGIVSSIGNNQEVLASLREGRSGITFSQELKDSGMRSHVWGNVKLDTTGLID
RKVVRFMSDASIYAFLSMEQAIADAGLSPEAYQNNPRVGLIAGSGGGSPRFQVFGADAMR
GPRGLKAVGPYVVTKAMASGVSACLATPFKIHGVNYSISSACATSAHCIGNAVEQIQLGK

QDIVFAGGGEEELCWEMACEFDAMGALSTKYNDTPEKASRTYDAHRDGFVIAGGGGMVV
VEELEHALARGAHIYAEIVGYGATSDGADMVAPSGEGAVRCMKMAMHGVDTPIDYLS
HGTSTPVGDVKELAAIREVFGDKSPAISATKAMTGHSLGAAGVQEAIYSLLMLEHGFIAPS
INIEELDEQAAGLNIVTETTDRELTTVMSNSFGFGGTNATLVMRKLKD
>sp|P85148|ETC50_ENTFC Bacteriocin E50-52 OS=Enterococcus faecium OX=1352 PE=1
SV=1
TTKNYGNVCNSNVNWCQCGNVWASCNLATGCAAWLCKLA
>sp|Q9FA38|FAE_METEA 5,6,7,8-tetrahydromethanopterin hydro-lyase OS=Methylobacterium
extorquens (strain ATCC 14718 / DSM 1338 / JCM 2805 / NCIMB 9133 / AM1) OX=272630
GN=fae PE=1 SV=3
MAKITKVQVGEALVGDGNEVAHIDLIIGPRGSPAETAFCNGLVNNKHGFTSLLAVIAPNLP
CKPNTLMFNKVTINDARQAVQMFGPAQHGVAMAVQDAVAEGIIPADEADDLVVLVGVFI
HWEAADDAAKIQKYNYEATKLSIQRAVNGEPKASVVTEQRKSATHPFAANA
>sp|P85147|ETC76_ENTSX Enterocin E-760 OS=Enterococcus sp. OX=35783 PE=1 SV=1
NRWYCNSAAGGVGGAAVCGLAGYVGEAKENIAGEVRKKGWGMAGGFTHNKACKSFPGS
GWASG
>sp|Q0S7V5|FAD3_RHOJR 3-[(3aS,4S,7aS)-7a-methyl-1,5-dioxo-octahydro-1H-inden-4-
yl]propanoyl:CoA ligase OS=Rhodococcus jostii (strain RHA1) OX=101510 GN=fadD3 PE=1
SV=1
MTEQPTTTPSALKRAAREFGELTAVADGDVRLTFTQLHDRVRDFAAALSSQDVRPGDHV
AVWSPNTYHWVVAALGIHYAGATLVPINTRYTATEALDILERTKTTALVVAGNFLGTDR
YASLRDESSTFDLPTVVRVPVDGGDAELPGVDFDFFLALADEDTRAEADARAAAVSPD
DVSDVMFTSGTTGRSKGVMSAHRQSVGIAQAWGECAEVTSDDNYLIINPFFHTFGYKAGF
LVCLLNGATVVPMAVFDVPKVMATVHDEQITVLPGAPTIFQSILDHPDRPKYDLSSLRVAI
TGAAAVPVALVERMQSELSFDAVLTA YGQTEAVVVTMCRTDDDPVTVSTTSGRAIPGME
VRIGDQGEILVRGENVMLGYLDDPESTAKTIDADGWLHTGDVGTLD DRGYVDITDRLKD
MYISGGFNVYPAEVENALARLDGVAESA VIGVPDERMGEVGRAYVVAKP GVT LAEDDV
VAFCKERLANFKVPRSVRFVDSLPRNPSGKVMKNVLREEKK
>sp|P9WN69|G6PI_MYCTU Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) OX=83332 GN=pgi PE=1 SV=1
MTSAPIPDITATPAWDALRRHHDQIGNTHLRQFFADDPGRGRELTVSVGDLYIDYSKHRV
TRETALLIDLARTAHLEERRDQMFAGVHINTSEDRAVLHTALRLPRDAELVVDGQDVVT
DVHAVLDAMGAFTDRLRSGEWGTATGKRISTVVNIGIGGSDLGPMVYQALRHYADAGI
SARFVSNVDPADLIATLADLDPATTLFIVASKTFSTLETLTNATAARRWLTDALGDAAVSR
HFVAVSTNKRVLDDFGINTDNMFGFWDWVGGRYSVDSAIGLSLMTVIGRDAFADFLAGF
HIIDRFATAPLESNAPVLLGLIGLWYSNFFGAQSRTVLPYSNDLSRFPAYLQQLTMESNG
KSTRADGSPVSADTGEIFWGEPTNGQHAFYQLLHQGTRLVPADFIGFAQPLDDLPTAEG
TGSMHDLLMSNFFAQTVLAFGKTAEEIAADGTPAHVVAHKVMPGNRPSTSILASRLTPS
VLGQLIALYEHQVFTEGVVWGIDSFDQWGVELGKTQAKALLPVITGAGSPPPQSDSSTDG
LVRRYRTERGRAG
>sp|P20657|FMI_MORBO Fimbrial protein 1 OS=Moraxella bovis OX=476 PE=1 SV=1
MNAQKGFTLIELMIVIAIIGILAAIALPAYQDYISKSQTTRVSGELAAGKTA VDAALFEGKT
PVLSEESSTSKENIGLTSSETSTKPRSNLMASVELTG FADNGAGTISATLG NKANKDIAKTV
ITQERTTDGVWTCKIDGSQA AKYKEKFNPTGCVKK
>sp|I6XHI4|FADA5_MYCTU Steroid 3-ketoacyl-CoA thiolase OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) OX=83332 GN=fadA5 PE=1 SV=1
MGYPVIVEATRSPIGKRNGWLSGLHATELLGAVQKAVVDKAGIQSGLHAGDVEQVIGGC
VTQFGEQSNNISRVAWLTAGLPEHVGATTVDCQCGSGQQANHLIAGLIAAG AIDVGIACG
IEAMSRVGLGANAGPDRSLIRAQSWDIDLPNQFEAAERIAKRRGITREDVDVFGLESQRRRA
QRAWAEGRFDRDISPIQAPVLDEQNQPTGERRLVFRDQGLRETTMAGLGELKPVLEGGIH

TAGTSSQISDGAAAVLWMDEAVARAHGLTPRARIVAQALVGAEPYYHLDGPVQSTAKVL
EKAGMKIGDIDIVEINEAFASVVLWARVHEPDMDRVNVNGGAIALGHPVGCTGSRLITT
ALHELERTDQSLALITMCAGGALSTGTIIERI

>sp|Q44501|FESII_AZOVI Protein FeSII OS=Azotobacter vinelandii OX=354 GN=fesII PE=1
SV=1

MATIIYFSSPLMPHNKKVQAVAGKRSTLLGVAQENGVKIPFECQDGNCGSCLVKITHLDGE
RIKGMLLTDKERNVLKSVGKLPKSEEERA AVRDLPTTYRLACQTIVTDEDLLVEFTGEPGG
A

>sp|C5B137|FHCA_METEA Formyltransferase/hydrolase complex Fhc subunit A
OS=Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / JCM 2805 / NCIMB 9133 /
AM1) OX=272630 GN=fhcA PE=1 SV=1

MLTRIHGGRVVDPTAGRDAVGDVWIEDGRVVAPSERAPDQTIDATGCVVMAGGVEVHS
HIAGGNVMSRLLLPDLVSESA PNGHPFAHAGGSGSWGANYARMGYTTAVEPALPPS
NALATHLELADIPLDRGGLAVLGNDDHLLQLLRDGEKGQAVRDLVQQT LAHSRGLGVK
CINAGGASAFKDGVLKLSLDDEIPCYGLSTRKIMSALLDAVEEIGVPHPLHVHCNNLGLPG
ADDSLVATLEAAEGRRIFHAHAQFYAYGVVDPENPMTGGFRSAAERINAAMEAHPNATY
DVGQVVFGQTVTISLDILRQFGGRKGAKPKKWVISAGDAEGGGVVPFLYRPRGPVSSLQ
WAIGLELMLLSSNPERTILTTDHPNGGVFTEYPRIIHLMDAEERAKEIATLPAIVGERSGLP
KIEREYSFSEIAQLTRSGPAKLLGLTDRGHLREGAKADVAIYRDDKDRTAMFSRAKLVLK
DGQPIVEDGEVVAWFSGKTLSLDVEADAGMEKRAESYLQDRFGAGLDTFAVPDAAFPEN
TGTFEDVACRA

>sp|Q5HG25|DAPA_STAAC 4-hydroxy-tetrahydrodipicolinate synthase OS=Staphylococcus
aureus (strain COL) OX=93062 GN=dapA PE=1 SV=1

MTHLFEGVGVALTTPFTNNKVNIEALKTHVNFLLENNQAIIVNGTTAESPTLT TDEKERI
LKTVIDLVDKRVPVIAGTGTNDTEKSIQASIQA KALGADAIMLITPYYNKTNQRGLVKHFE
AIADAVKLPVVLVYNVPSRTNMTIEPETVEILSQHPYIVALKDATNDFEYLEEVKKRIDTNSF
ALYSGNDDNVVEYYQRGGQGVISVIANVIPKEFQALYDAQQSGLDIQDQFKPIGTLLSALS
VDINPIPIKALTSYLGFGNYELRLPLVSLEDTDTKVLRETYDTFKAGENE

>sp|Q9WZY5|COAX_THEMA Type III pantothenate kinase OS=Thermotoga maritima (strain
ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) OX=243274 GN=coaX PE=1 SV=1

MYLLVDVGNTHSVFSITEDGKTFRRWRLSTGVFQTEDELFSHLHPLLGDAMREIKGIGVA
SVVPTQNTVIERFSQKYFHISPIWVKAKNGCVKWNVKNPSEVGADRVANVVAFVKEYGK
NGIIIDMGTTATTVDLVVNGSYEGGAILPGFFMMVHSLFRGTAKLPLVEVKPADFVVGKDT
EENIRLGVVNGSVYALEGIIGRIKEVYGDLPVVLTTGGQSKIVKDMIKHEIFDEDLTIKGVYH
FCFGD

>sp|Q5SME3|CY552_THET8 Cytochrome c-552 OS=Thermus thermophilus (strain HB8 / ATCC
27634 / DSM 579) OX=300852 GN=cycA PE=1 SV=1

MKRTLMAFLLLGG LALAQAADGAKIYAQCAGCHQQNGQGIPGAFPPLAGHVAEILAKEGG
REYLILVLLYGLQGQIEVKGMKYNGVMSSFAQLKDEEIAAVLNHIATAWGDAAKKVKGFK
PFTAEVVKLRKKLTPQQVLAERKKLGLK

>sp|Q9F8T9|COUO_STRRH C-methyltransferase CouO OS=Streptomyces rishiriensis OX=68264
GN=couO PE=1 SV=1

MKIEPITGSEAEAFHRMGSRAFERYNFVDLLVGAGIADGQTVVDLCCGSGELEIILTSRFP
SLNLVGVDLSEDMVRIARDYAAEQGKELEFRHGDAQSPAGMEDLLGKADLVVSRHAFH
RLTRL PAGFDTMLRLVKPGGAILNVSFLHLSDFDEPGFRTWVRFLKERPWDAEMQVAVA
LAHYYPRLQDYRDALAQAADETPVSEQRIWVDDQGYGVATVKCFARRAAA

>sp|P67825|CUTC_SHIFL Copper homeostasis protein CutC OS=Shigella flexneri OX=623
GN=cutC PE=1 SV=1

MALLEICCYSMECALTAQQNGADRVELCAAPKEGGLTPSLGVLSVRQRVTIPVHPIIRPR
GGDFCYS DGEFAAILEDVRTVRELGFPGLVGTGVLVDGNVDMPRMEKIMAAAGPLAVTF

HRAFDMCANPLYTLNNLAELGIARVLTSGQKSDALQGLSKIMELIAHRDAPIMAGAGVR
AENLHHFLDAGVLEVHSSAGAWQASPMRYRNQGLSMSSDEHADEYSRYIVDGAAVAEM
KGIIRHQAK

>sp|P9WPN9|CP126_MYCTU Putative cytochrome P450 126 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) OX=83332 GN=cyp126 PE=1 SV=1

MTTAAGLSGIDLTDLNFDAGFPFHLFAIHRREAPVYWHRPTEHTPDGEGFWSVATYAET
LEVLRDPVTYSSVTGGQRRFGGTVLQDLPVAGQVLNMMDDPRHTRIRRLVSSGLTPRMIR
RVEDDLRRRARGLLDGVPEGAPFDFVVEIAAELPMQMICILLGVPETDRHWLFEAVEPGF
DFRGSRRATMPRLNVEDAGSRLTYALELIAGKRAEPADDMLSVMANATIDDPDAPALSD
AELYLFFHLLFSAGAETTRNSIAGLLALAENPDQLQTLRSDFELLPTAIEEIVRWTSPPSK
RRTASRAVSLGGQPIEAGQKVWWEGSANRDPVSFDRADEFDITRKPNPHLGFQGVHY
CLGANLARLELRVLFEELLSRFGSVRVVEPAEWTRS NRHTGIRHLVVELRGG

>sp|P9WPL1|CP144_MYCTU Cytochrome P450 144 OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) OX=83332 GN=cyp144 PE=1 SV=1

MRRSPKSGPGLVLDLQRRVDQAVSADHAELMTIAKDANTFFGAESVQDPYPLYERMRAA
GSVHRIANSDFYAVCGWDAVNEAIGRPEDFSSNLATMTYTAEGTAKPFEMDPLGGPTH
VLATADDPAAHVHRKLVLRHLAAKRIRVMEQFTVQAADRLWVDGMQDGCIEWMGAM
ANRLPMMVVAELIGLPDPDIAQLVKWGYAATQLLEGLVENDQLVAAGVALMELSGYIFE
QFDRAAADPRDNLGELATACASGELDTLTAQVMVTLFAAGGESTAALLGSAVWILAT
RPDIQQQVRANPELLGAFIEETLRYEPPFRGHYRHVRNATTLDTGTELPADSHLLLLWGAA
NRDPAQFEAPGEFRLDRAGGKGHISFGKGAHFCVGAALARLEARIVLRLLLDRTSVIEAA
DVGGWLPSILVRRIERLELAVQ

>sp|P33673|CHIS_BACCI Chitosanase OS=Bacillus circulans OX=1397 GN=csn PE=1 SV=2

MHMSNARPSKSR TKFLLAFLCFTLMASLFGATALFGPSKAAAASPDDNFSPETLQFLRN
TGLDGEQWNNIMKLINKPEQDDLWIKYYGYCEDIEDERGYTIGLFGATTGGSRDTHPDG
PDLFKAYDAAKGASNPADGALKRLGINGKMKGSILEIKDSEKVFCEGKIKKLQNDAAWR
KAMWETFYNVYIRYSVEQARQRGFTSAVTIGSFVDTALNQGATGGSDTLQGLLARSGSS
NEKTFMKNFHA KRTL VVD TNKYNKPPNGKNRVKQWDTLVDMGKMNLKNVDSEIAQVT
DWEMK

>sp|Q47840|COPZ_ENTHA Copper chaperone CopZ OS=Enterococcus hirae (strain ATCC 9790
/ DSM 20160 / JCM 8729 / LMG 6399 / NBRC 3181 / NCIMB 6459 / NCDO 1258) OX=768486
GN=copZ PE=1 SV=1

MKQEFVSKGMSCNHCVARIEEAVGRISGVKKVKVQLKKEKAVVKFDEANVQATEICQAI
NELGYQAEVI

>sp|P0C2B2|DSBA_PSEAE Thiol:disulfide interchange protein DsbA OS=Pseudomonas
aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C /
PRS 101 / PAO1) OX=208964 GN=dsbA PE=1 SV=1

MRNLILTAMLAMASLFGMAAQADDYTAGKEYVELSSPVVPSQPGKIEVVELFWYGCPHC
YAFEPTIVPWSEKLPADVHFVRLPALFGGIWNVHGMFLTLESMGVEHDVHNAVFEAIHK
EHKKLATPEEMADFLAGKGV DKEKFLSTYNSFAIKGQMEKAKKLAMAYQVTGVPTMVV
NGKYRFDIGSAGGPEETLKLADYLIEKERA AAKK

>sp|P9WNT3|DPO41_MYCTU DNA polymerase IV 1 OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) OX=83332 GN=dinB1 PE=1 SV=1

MESRWVLHLDMDAFFASVEQLTRPTLRGRPVLVGGLGGRGVVAGASYEARAYGARSAM
PMHQARRLIGVTAVVLP RGVVYGIASRRVFDTVRGLVPVVEQLSFDEAF AEPQLAGAV
AEDVETFCERLRRRVRDETGLIASVGAGSGKQIAKIASGLAKPDGIRVVRHAEEQALLSGL
PVRRLWGIGPVAEEKLHRLGIETIGQLAALSDAEAANILGATIGPALHRLARGIDDRPVVE
RAEAKQISAESTFAVDLT TMEQLHEAIDSIAEHAHQRLLRDGRGARTITVKLKKSDMSTLT
RSATMPYPPTTDAGALFTVARLLPDPLQIGPIRLLGVGFSGLSDIRQESLFADSDLTQETAA

AHYVETPGAVVPAAHDATMWRVGDDVAHPELGHGWVQAGAGHGVVTVRFETRGS GPGS
ARTFPVDTGDISNASPLDSLDPDYIGQLSVEGSAGASAPTVDVDR

>sp|M1V9Q0|DTCYA_STRSQ Diterpene cyclase DtcycA OS=Streptomyces sp. OX=1931
GN=dtcycA PE=1 SV=1

MTDPAVTPLAFSIPQLYCPFPTAIHPEVDTLTRAGMDFMTHHGFCNTEADRLVVANIDAG
AIVARWYPNPDFPVDRLQMVTDFLYLYFLIDDLRFEVINS DTGLAGPIALFAQHLDLWEYP
QAHRR EELDLFHQAIHDLASRMAELTTPTKAARMRRSINGWFLALLREIALFNDDHAVM
AEEYLP IRVVTVASRLMIDVNGFICPAEVP GDEWYSLKVQAAAEAAMSVCLYDNELYSA
GKEQWLKSRATAHRRPRNLVALIQAQTGGSTEHALQEVAEYRNRTVCLYLNLR SQLEK
TASPALLAYLSVLDGVISGNLDAHATSSRYHNPDGHHPHAI AFTPLRTTDECSARAHTPIA
PPIAWWWEQLDQ

>sp|A6QG57|FLIPR_STAAE FPRL1 inhibitory protein OS=Staphylococcus aureus (strain
Newman) OX=426430 GN=flr PE=1 SV=1

MKKNITKTHIASTVIAAGLLTQTNDAKAFFSYEWKGLEIAKNLADQAKKDDERIDKLMKE
SDKNLTPYKAETVNDLYLIVKKLSQGDVKKAVVRIKDDGPRDY YTFDLTRPLEENRKNIK
VVKNGEIDSITWY

>sp|P15931|FLGJ_SALTY Peptidoglycan hydrolase FlgJ OS=Salmonella typhimurium (strain
LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=flgJ PE=1 SV=1

MIGDGKLLASAAWDAQSLNELKAKAGQDPAANIRPVARQVEGMFVQMMLKSMREALP
KDGLFSSDQTRLYTSMYDQQIAQQMTAGKGLGLADMMVKQMTSGQTMPADDAPQVPL
KFSLETVNSYQNQALTQLVRKAIPKTPDSSDAPLSGDSKDFLARLSLPARLASEQSGVPHH
LILAQA ALESGWGQRQILRENGEPSYNVFGVKATASWKGPVTEITTTTEYENGEAKKV KAK
FRVYSSYLEALSDYVALLTRNPRYAAVTTAATAEQGAVALQNAGYATDPNYARKLTSMI
QQLKAMSEKVS KTYSANLDNLF

>sp|P26416|FLIK_SALTY Flagellar hook-length control protein OS=Salmonella typhimurium
(strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=fliK PE=1 SV=2

MITLPQLITTD TDMTAGLTSGKTTGSAEDFLALLAGALGADGAQ GKDARITLADLQAAGG
KLSKELLTQHGE PGQAVKLADLLAQKANATDETLDLTQAQHLLSTLTPSLKTSALAALS
KTAQHDEKTPALSDEDLASLSALFAMLPGQP VATPVAGETPAENHIALPSLLRGDMPSAP
QEETH TLSFSEHEKGKTEASLARASDDRATGPALTPLVVAAAATS AKVEVDSP PAPVTHG
AAMPTLSSATAQPLPVASAPVLSAPLGSHEWQQTF SQQVMLFTRQGQQAQLRLHPEELG
QVHISLKLDDNQAQLQMVS PSHVRAALEAALPMLRTQLAESGIQLGQSSISSESFAGQQ
QSSSQQSSRAQHTDAFGAEDDIALAAPASLQAAARGNGAVDIFA

>sp|Q99QV3|DRP35_STAAM Lactonase drp35 OS=Staphylococcus aureus (strain Mu50 / ATCC
700699) OX=158878 GN=drp35 PE=1 SV=1

MMSQQDLPTLFYSGKSNSAVPIISESELQTITAEPWLEISKKGLQLEGLNFDRQGQLFLLDV
FEGNIFKINPETKEIKRPFVSHKANPAAIKIHKDGRLFVCYLGDFKSTGGIFAATENGDNLQ
DIIEDLSTAYCIDDMVFDSKGGFYFTDFRGYSTNPLGGVYYVSPDFRTVTPHQNISVANGIA
LSTDEKVLWVTETTANRLHRIALED DGVTIQPF GATIPYYFTGHEGPDSCCIDSDDNLYVA
MYGQGRVLVFNKRGYP IGPQILIPGRDEGHMLRSTHPQFIPGTNQLIICSNDIEMGGGSMLY
TVNGFAKGHQSFQFQ

>sp|P06710|DPO3X_ECOLI DNA polymerase III subunit tau OS=Escherichia coli (strain K12)
OX=83333 GN=dnaX PE=1 SV=1

MSYQVLARKWRPQTFADVVGQEHVLTALANGLSLGRIHHAYLFSGTRGVGKTSIARLLA
KGLNCETGITATPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPARGRF
KVYLIDEVHMLSRHSFNALLKTLEEPPEHV KFLLATTPDQKLPVTILSRCLQFHLKALDVE
QIRHQLEHILNEEHIAHEPRALQLLARA AEGSLRDALSLTDQAIASGDGQVSTQAVSAMLG
TLDDDQALSLVEAMVEANGERVMALINEAAARGIEWEALLVEMLG LLLHRIAMVQLSPAA
LGNDMAAIELRMRELARTIPPTDIQLYYQTL LIGRKELPYAPDRRMGVEMTLLRALAFHPR
MPLPEPEVPRQSFAPVAPTAVMTPTQVPPQPQSAPQQAPT VPLPETTSQVLAARQQLQRV

QGATKAKKSEPAAATRARPVNNAALERLASVTDRVQARPVPSALEKAPAKKEAYRWKA
TTPVMQQKEVVATPKALKKALEHEKTPELAAKLAAEAIERDPWAAQVSQSLPKLVEQV
ALNAWKEESDNAVCLHLRSSQRHLNNRGAQQKLAEALSMLKGSTVELTIVEDDNPAVRT
PLEWRQAIYEEKLAQARESIIADNNIQTLLRRFFDAELDEESIRPI

>sp|C2M262|DPP7_CAPGI Dipeptidyl-peptidase 7 OS=Capnocytophaga gingivalis OX=553178
GN=dpp7 PE=1 SV=1

MRKLIFSLVTSFLLLPVIRADEGMWFLMFIKRLNERDMQKKGLQLTAEEIYSINNNSLK
NAIVQFNGGCTASIISPDGLVITNHHCGYGAIAGLSTPEHNYLKDGYWAKDRSQELPPKSL
YVRRFFVRMDNVTDRMLSVMNSSMSEKERQDALNREMEKIQKENSEGGKYVVSVRPFFQG
NEYYYFVYQDFKDVRVFGTTPPENVGKFGGDTDNWEWPRHTGDFSFRVYTDKDGNPAP
YSPNNIPMKAKKYLVNVTGKGVQENDFAMILGYPGRTNRWVSSHVVDQQVKYGYPAWV
EASKTAMDAMKAHMDKDKAVRLKYASRYASLANYWKNRQGMIDALTAHKTADLKRA
AEKKFAVWANKPENKAHEYGNVLSDLATYFEKTNQEAANHNYLLFFRASRIVPQANGYV
KQLNTYLNSSSDQEKQQIRERIAKELDAYYESYLP AEIDLFADNLKLYADKATDIPQEIQAQ
IKSQYNGDFRKF AA EVFARSIFTTKENFENFMNNPSSDALQSDPIAQIARVMIDKYNSQSE
ALKDGYEKA FRKYVKGM RDSKVSLILYPDANSTLRLTYGSVKS LPKDKRNHDV KRNYT
TFKTMLEKYKPGDAEFDMPKKFVEMYEEKDFGRYLDKDGTMHVCFLTNDITGGNSGS
PVMNGKGELIGLAFDGNIEAMAGDVIFDKKLQRTIVVDIRYVLWCIDTFGGAKHIVDEMTI
IQ

>sp|Q47155|DPO4_ECOLI DNA polymerase IV OS=Escherichia coli (strain K12) OX=83333
GN=dinB PE=1 SV=1

MRKIIHVDMDCFFAAVEMRDNPALRDIPIAIGGSRRERG VISTANYPARKFGVRSAMPTG
MALKLCPHLTLLPGRFDAYKEASNHIREIFSRYSRIEPLSLDEAYLDVTD SVHCHGSATLI
AQEIRQTIFNELQLTASAGVAPVKFLAKIASDMNKPNGQFVITPAEVP AFLQTLPLAKIPGV
GKVSAAKLEAMGLR TCGDVQKCDLVMLLKRFGKFGRLWERSQGIDERDVNSERLRKSV
GVERTMAEDIHHWSECEAIERLYPELERRLAKVKPDL LIARQGVKLKFDDFQQTTEHV
WPRLNKADLIATARKTWDERRGGRGVRLVGLHVTL LDPQMERQLVLGL

>sp|Q04810|DPAB_BACSU Dipicolinate synthase subunit B OS=Bacillus subtilis (strain 168)
OX=224308 GN=dpaB PE=1 SV=1

MSSLKGKRIGFGLTGSHCTYEAVFPQIEELVNEGAEVRPVVTFNVKSTNTRFGEGA EWVK
KIEDLTGYEAIDSIVKAEPLGPKLPLDCMVIAPLTGNSMSKLANAMTDS PVLMAAKATIRN
NRPVVLGISTNDALGLNGTNLMRLMSTKNIFFIPFGQDDP FKKPNSMVAKMDLLPQTIEKA
LMHQQLQPILVENYQGND

>sp|B0NAQ4|BAIN_CLOS5 3-dehydro-bile acid delta(4,6)-reductase OS=Clostridium scindens
(strain ATCC 35704 / DSM 5676 / VPI 13733 / 19) OX=411468 GN=baiN PE=1 SV=1

MNRIGIIGGGASGIVAAIAAARS DGD AQVFILEQKENIGKKILATGN GRCNLTNEAMDASC
YHGEDPEFARNVLKQFGYGETLEFFASLGLFTKSRGGYIYPRSDQAASVLELLE MELRRQ
KVKIYTGVRVEALKLSAKGFVIRADGQRFPADR VILACGGKASKSLGSDGSGYALARSMG
HTLSPVVPALVQLKVKKHPFAKAAGVRTDAKVAALLGRQVLAEDTGEMQITAYGISGIPV
FQISRHIAGGLYEGKEMKVRVDFLP EMEASQVRKAFNTHLDKCPYATCQEFLT GIFPKKLI
PRLLELSHIRQNFPASELKPAQWEDLIRACKQTLLTIEDTNGFDNAQVCAGGVRTGEVYPD
TLESRYADGLYLTGELL DVEGICGGYNLQWAWATGYLAGRAAAERP

>sp|D5CBA0|CDIA_ENTCC 16S rRNA endonuclease CdiA OS=Enterobacter cloacae subsp.
cloacae (strain ATCC 13047 / DSM 30054 / NBRC 13535 / NCDC 279-56) OX=716541
GN=cdiA PE=1 SV=1

MMKQDQVRFSQRALSALLSVLLATQPLLPAVAASITPSGNTQMDKAANGVPVVNIATPN
QSGISHNKYNDYNVGKEGLILNNATGQLNQTQLGGLIQNNPNLKAGQEAKGIINEVTGAN
RSNLQGYTEVAGKAANVIVANPYGITCNGCGFINTPNVTLTTGKPVLDASGKLQSLDVTQ
GAVTIEGAGLNGSQSDAVSIISRATEINVQLHAKDLRVVAGANRVAADG SVSALKGEGTA
PKVAVDTGALGGMYANRIRLVSSETGVGVNLGNLNARQGDIALSSAGKVVLKNTLASGS

TTVSAADVTLRGDHKAGGNVTVSGQTALTLQAHVAADNNLQLTTRGTLTQNGGAFTA
 ANDATLAATTLIQSVDAQASAGRHLAVNAEKNAALNGSVVAGQQLSVKGGELVQQGNL
 SASEIALNAQTLTQESRSTTNASGNITLTTSQHSQLKGSTTAGQSLAVSAGSLANHGALAA
 VADTRINTGIFSNTGTVQGNSLTVSGTDITSSGALKSASTLDIRADNATLSGETGAKGKTTV
 TASGNLNNSGTLISDDTLTLNAAQIVNSGTLSGVRGLTTSKFTTASATSVTQSDGDVALN
 NTDTTLAGETSAGGAVTVQGRSLNTTATAQTQGNVGVAVQNAKLEGTQAAKGNMTLK
 ADSSLNHTGKSSASGLKVETGHLNSNGTLTASALVIDSPEVINGGLIHAGQTLVTRLLDN
 RSSGVLYSPSALSLSLSELNNAGIITSDAALSLSGSNLTNSGELSGTSLAIDYETLKNSAEGM
 LLAQGANRITAQSVSSAGSMVGNTLTLNADRLESAGLLQGDSALSLTAGILNLLTGSRTLT
 GGALGLSGTTLTLAGQLQGQDVSRSHDWTNRGSSLATGSLDVTTAGTSLNTGELMSQG
 NGTLNAVTTVNSGNMLSAGDLSLNGKTLRNSGTLQGNRVTAHQDTITNSGTLTGIAALM
 LAARLEMAAPLLTLVNDASGSLTAGELSVTGGDLRNAGQWQGKRVLIHAQALTNGGAI
 QAENLLDAQIDSTLTGTAGSKITSNGELALSALTLANSGQWIAKHLTLGASTLNNSGEITG
 VVALSVALTQLNNQAGGKLLSAGALTLDVENATNAGQIQGKATTVTAGQLINSGRLOGE
 ALTNLASGALNNTASGVLLSENALTVSTATLNNQGTLOGGGESSVKATTRVQNDGKMLS
 GGKLTLTAPELANSSSGLVQAVRLLLDVVKAVNGGNVLATTRAELRGSSLDNSGTLQGA
 DLQANYQSVTNSGTVLGTSLTINGDALDNTEGKLYSGDKLLLDVRNYSRGRGDVVSLG
 DTTLKLVNALVNTGTLAASKTSLVSSQNAMTNSGVMQGNALALSAGGAFTNNGTLTTGN
 GSSTFNAQSLLLNASGSLQAGGDVQLTSRENITVNGFTGTAGSLTMTAAGTLLNTALIYA
 GNNISLFAARIHNIYGDILADNSLWMQKNAVGEANAEEVNRSGTIETTRGDITVNTGHLL
 NEADGLTVSQSEREYPDAIPAADDEHYFSYDLNGRRSDFVLLLEDWKNDGSKVVYDWYEQ
 CLGSGANGSGQCRDRVDYRLTGEDIRQFLLSESVVSATGSSARIAAGRDITINAGTLDN
 RASHILAGRNAVLGGTLNLSAEGGRRVTYVQAEYRCEWFYRDCSDSKWEPLTQYPDG
 SWGWFEDEDYGWYGWVPYILGERTTEFVADGGVYRSVISAGGNVSANFTSDISNTNVTAN
 SGEFSNTIDAPTLNLTLSPEAIGKGLNSESQAQGSADIRFPEQLGNITDALKDISGGSSLSQ
 NGSSGNYPLPSGNNGYFVPSTDPDPSYLITVNPKLDELGNMDDSLFNGLYDLLGITPGATP
 RETNSAYTDRNQFLGSSYFLDRLGLNPDRDYRFLGDAAFDTRYVSNAILNQTGSRYINGIG
 SDLDQMRYLMDSAAEQKTLGLKFGVALTAEQVAALDKSMLWWESATINGQTMIPKV
 YLSPKDVTVHSGSVISGNVQLAGGNVINSGSTIAAQNGLSIDSSNSLSNLNAGLLSAGGG
 LNLSALGDINNIGSTISGKTVGLESVAGSINNITRAQQWNVDAGNVHFSGTDVGKTASITA
 TDGLTMRAGQDINVTGANVSAGGSLGMAAGNDINITANEIVTSEGRAGRNRATTETASVT
 HQGSTLSAGDDLTLQAGNDVNARAAAIAAEGDVGIIQAGRDVDLLAEASMERSSSQAKKK
 TAIDESVRQQGTEIASGGNTVILAGRDVTAQAADVTAQGDIGVAAGRDVNLTATATESDYR
 YREQTKTSSGFLSKKTHTHIEESATREKGSLLSGDNVTVSAGNNLRVLGSAVAGDGDVA
 LSAGNNVDIVAATNTDTAWRFKETKKSGLMGTGGIGFTIGSSKSTHDLREQGTTQSESFST
 VGSTGGNVSIAAGKQAHIGGADIIAQKDISLTGDSVVIPEGHDKRTRDEKFEQKSSGLTVA
 LSGAAGSAVNNAVTTAQSAKQSSDSRLAALQGTQAALSGVQAGQAVALDQVKGDSDKR
 NNNTIGVSASIGSQSSKSSSHMESETTTGSTLSAGNNVTIKATGSDITVAGSQIKAGKDVT
 DAARDVNLIASQDTQQTGKNSSSGSLGVGVGVGSGGAGISISANANSSKGHEKNGV
 WQNETTVDAGNRVTINTGRDATIAGAQVSGETTVADIGRDLTIASQSDSHYNSKQNSVS
 GGAGYTFGAGGFGSGSINVS RDKMTSDYDSVQEQSGLFAGNGGFDVTVGNHTQLDSGVIA
 STATADKNRLDTGTLGFSDIHNQADFKTEHQGAGISSGGSIGKQFAGNMANALLAGGGNS
 GHAE GTTQAAVSEGTLIIRDKENQKQDVADLSRDAEHANGSISPIFDKEKEQQRLQEVQLI
 GEIGSQVVDIANTQGEINGLNAGRKELADKGITEPGADASDEVKAAAYQNALRETDAYKTT
 TAKYGTGSDLQRGIQAATAALQGLAGSDLTAALAGASAPELAYRIGHGMGIDNNTAAKTI
 AHAILGGAVAALQGN SAAAGAAGAATGELAAKAIAGMLYPDVKDLSTLSEEQKQTVSAL
 ATISAGMAGGLAGDSTGSAVAGGQAGKNAENNSLALVARGCAVAAPCRTKVAEQLLLEI
 GAKAGIAGLAGAAVKDMADKMTSDELEHLVTLEMMGNDEIIAKYVSLLDHDKYAPSHTG
 GNLLPETLPGHTGNNTGSVD TGPNHTGNTNRQNDSGSNNTGNTGAPNTGGNTTITPIP

GPSKDDIAYLALKGKEAQEAASN LGFDRRIPPQKAPFNSHGQPVFYDGKNYITPDIDSHNV
TNGWKMFSK GK RIGTYDSGLNRIKD

>sp|P19413|BAIF_CLOSV Bile acid-CoA transferase OS=Clostridium scindens (strain JCM
10418 / VPI 12708) OX=29347 GN=baiF PE=1 SV=3

MAGIKDFPKFGALAGLKILDSGSNIAGPLGGGLLAECGATVIHFEGPKKPDNQRGWYGYP
QNHRNQLSMVADIKSEEGRKIFLDLIKWADIWVESSKGGQYDRLGLSDEVIWEVNP KIAIV
HVSGYGQTGDPSYVTRASYDAVGQA FSGYMSLNGTTEALKINPYLSDFVCGLTTCWAML
ACYVSTILT GKGESVDVAQYEALARIMDGRMIQYATDGVKMPRTGNKDAQAALFSFYTC
KDGR TIFIGMTGAEVCKRGFP IIGLPVPGTGDPDFEGFTG WMIYTPVGQRMEKAMEKYV
SEHTMEEVEAEMQA HQIPCQRVYELEDCLNDPHWKARGTITEWDDPMMGHITGLGLINK
FKRNPSEIWRGAPLFGMDNRDILKDLGYDDAKIDELYEQGIVNEFDLDTTIKRYRLDEVIP
HMRKKEE

>sp|N0DKX5|BCID_CHLLM Bacteriochlorophyllide c C-7(1)-hydroxylase OS=Chlorobaculum
limnaeum OX=274537 GN=bcid PE=1 SV=1

MSTKR VITKEDIHLKARLLSEGA KVTVNKPPASGFNPFRAMVLNGSDLATLVRQEPYTRL
EVQVNGDDVEFYDCGQHLASGRMQEAFSWRSGKLSNGRPVDA AVIGMNQDIINIHYSYS
CDNNNTGRSCRFCFFADQHIGVGKELAKMPFSKIEELAKEQAEAVKIATDAGWRGTLVII
GGLVDPSRRAQVADLVELVMAPLREQVSPEVLNELHITANLYPPDDFKEMEKWKASGLN
STEFDLEVTHPDYFKAICPGKSATYPLEYWLEAQEASVKIFGPGRGTTSFILMGLEPMNIM
LEGVEERMSKGVYPNMLVYQVPVGADMFRMPPPNADWLVEASEKVADLYIKYQDRFDM
PLAKDHRPGYTRMGRSQYIILAGDMLAYKLQEQQGYELPEAYPVC

>sp|F8JJ27|BESE_STREN L-gamma-glutamyl-L-propargylglycine hydroxylase OS=Streptomyces
cattlea (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057)
OX=1003195 GN=besE PE=1 SV=1

MSGTTHHHATFPAVEAAAFTRRHLD DLAAGLLGTVRVPGFFGRPALDTMLTSLHRVPVV
SFDLDRMHHPMARFGTALNDYRTPELALDADRYWHDADTARRQWAGIGMTPDPLELAL
DALGRAWGV RPAPATIGGRPAFVGMLREVNDGTFIHYDDINREYRGGLFDQKIVAQLAF
NAWLAAPREGGTTTVWRHRWEPADENRRHGYGFQPTAVADDPYVTVAPAAGDALLFN
ANNYHV VHPGAPGQRRIALACFLGVTAGGELVVWS

>sp|Q74C76|CIMA_GEOSL (R)-citramalate synthase OS=Geobacter sulfurreducens (strain ATCC
51573 / DSM 12127 / PCA) OX=243231 GN=cimA PE=1 SV=1

MSLVKLYDTTLRDGTQAEDISFLVEDKIRIAHKLDEIGIHYIEGGWPGSNPKDVAFFKDIKK
EKLSQAKIAAFGSTRRAKVTPDKDHN LKTLQAEPDVCTIFGKTWDFHVHEALRISLEENL
ELIFDSLEYLKANVPEVFYDAEHFFDGYKANPDYAIKTLKAAQDAKADCIVLCDTNGGTM
PFELVEIIREVRKHITAPLGIH THNDSECAVANSLHAVSEGIVQVQGTINGFGERC GNANLC
SIIPALKLKMKRECIGDDQLRKLRDLSRFVYELANLSPNKHQAYVGNSAFAHKGGVHVSA
IQRHPETYEHLRPELVGNMTRVLVSDLSGRSNILAKAEFNIKMDSKDPVTLEILENIKEME
NRGYQFEGAEASFELLMKRALGTHRKF FSVIGFRVIDEK RHEDQKPLSEATIMVKVGGKIE
HTAAEGNGPVNALDNALRKALEKFY PRLKEVKLLDYKVRVLPAGQGTASSIRVLIESGDK
ESRWGTVGVSENIVDASYQALLDSVEYKLHKSEEIEGSKK

>sp|H1ZV38|GEOA_CASDE Geraniol dehydrogenase OS=Castellaniella defragrans OX=75697
GN=geoA PE=1 SV=1

MNDTQDFISAQA AAVLRQVGGPLAVEPVRISMPKGDEV LIRIAGVGVCHTDLVCRDGFVPV
LPIVLGHEGSGTVEAVGEQVRTLKPGDRVVL SFNSCGHCGNCHDGHPSNCLQMLPLNFG
GAQRVDGGQVLDGAGHPVQSMFFGQSSFGTHAVAREINAVKVGD DLPLELLGPLGCGIQ
TGAGAAINSLGIGPGQSLAIFGGGGVGLSALLGARAVGADR VVVIEPNAAARRALALELGA
SHALDPHAEGDLVAAIKAATGGGATHSLDTTGLPPVIGSAI ACTLPGGTVGMVGLPAPDA
PVPATLLDLLSKSVTLRPITEGDADPQRFIPRMLDFHRAGKFPFDR LITRYRFDQINEALHA
TEKG EAIKPVLVF

>sp|H1ZV37|GEOB_CASDE Geranial dehydrogenase OS=Castellaniella defragrans OX=75697
GN=geoB PE=1 SV=1
MTIDHQHIFVGGQWIAPKSTQRSNILNASTEELVGSVPKCNEDMDRAVAAAREAMRSL
AWAGLDGKGRAQHLRRFADAVERRGQQLARSVSLQNGMPINVADQLESAFVVSLRLYY
ASLAENLVEEEARPSPTGSTTLVRRDPVGVVGAIPWNFPVALSIFKIAPALAAGCAVVVKP
SSGTVLDSYVLAEEAAAEAGLPPGVINWVPGDRGIGSHLVSHPGVDKVAFTGSTSAGRIIE
ACARLLRPVTLELGGKSAAIVLEDADLDALIRSLPMSSVLNNGQACFSCTRILAPAGRYDE
VVDAIAGAVSAYSVDALDRATVVGPMASAAHRDSVQRYIELGTGEARLVVGGGRTSQ
DRGWVFVQPTVFADVDNRSRIAREEIFGPVLSIIRYEGEDEAVEIANDSEYGLGGTVWSTDH
DHAVTIARRMETGTVGINGYMPDLNAPFGGVKSSGMGRELGPESIGAYQRYKSVYLLG
>sp|P37921|FIMA1_SALTY Type-1 fimbrial protein, A chain OS=Salmonella typhimurium
(strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=fimA PE=1 SV=2
MKHKLMTSTIASLMFVAGAAVAADPTPVSVSGGTIHFEGKLVNAACAVSTKSADQTVTL
GQYRTASFTAIGNTTAQVPFSIVLNDGDPKVAANAFAVSGQADNTNPNLLAVSSADNST
TATGVGIEILDNTSSPLKPDGATFSAKQSLVEGTNLTARTARYKATAAATTPGQANADATF
IMKYE
>sp|P9WNE7|FER_MYCTU Ferredoxin OS=Mycobacterium tuberculosis (strain ATCC 25618 /
H37Rv) OX=83332 GN=fdxA PE=1 SV=1
MTYVIGSECVDVMDKSCVQCEPVDICIYEGARMLYINPDECVDGACKPACRVEAIYWEG
DLPDDQHQLGDNAFFHQVLPGRVAPLGSPGGAAAVGPIGVDTPLVAAIPVECP
>sp|P31697|FIMC_ECOLI Chaperone protein FimC OS=Escherichia coli (strain K12) OX=83333
GN=fimC PE=1 SV=3
MSNKNVNRKSQEITFCLLAGILMFAMMMVAGRAEAGVALGATRVIYPAGQKQEQQLAV
TNNDENSTYLIQSWVENADGVKDGRFIVTPPLFAMKGGKENTLRILDATNNQLPQDRESL
FWMNVKAIPSMDSKLTENTLQLAISRIKLYRPAKLALPPDQAAEKLRFRRSANSITLIN
PTPYLTVTELNAGTRVLENALVPPMGESTVKLPSDAGSNITYRTINDYGALTPKMTGVM
E
>sp|P0DPQ7|GCOA_AMYS7 Aromatic O-demethylase, cytochrome P450 subunit
OS=Amycolatopsis sp. (strain ATCC 39116 / 75iv2) OX=385957 GN=gcoA PE=1 SV=1
MTTTERPDALWLDEVTMTQLERNPYEVYERLRAEAPLAFVPVLGSYVASTAEVCREVAT
SPDFEAVITPAGGRTFGHPAIIGVNGDIHADLRSMVEPALQPAEVDRWIDDLVRPIARRYLE
RFENDGHAELVAQYCEPVSVRSLGDLGLQEVDSDKLREWFALNRSFTNAAVDENGFE
ANPEGFAEGDQAKAEIRAVVDPLIDKWIEHPDDSAISHWLHDGMPPGQTRDREYIYPTIYV
YLLGAMQEPGHGMASITLVGLFSRPEQLEEVDDPTLIPRAIAEGLRWTSPIWSATARISTK
PVTIAGVDLPAGTPVMLSYSANHDTGKYEAPSQYDLHRPPLPHLAFGAGNHACAGIYFA
NHVMRIALEELFEAIPNLERDTRREGVEFWGWGFRGPTSLHVTWEV
>sp|Q9L6V3|FENR_RHOCA Flavodoxin/ferredoxin--NADP reductase OS=Rhodobacter
capsulatus OX=1061 GN=fpr PE=1 SV=2
MNETTPIAPAKVLPDAQTVTSVRHWTDTLFSFRVTRPQTLRFRSGEFVMIGLLDDNGKPI
RAYSIASPAWDEELEFYSIKVPDGLTSRLQHIKVGEEQILRPKPVGTLLVIDALLPGKRLWFL
ATGTGIAPFASLMREPEAYEKFDEVIMMHACRTVAELEYGRQLVEALQEDPLIGELVEGK
LKYYPTTTREEFHMMGRITDNLASGKVFEDLGIAPMNPETDRAMVCGSLAFNVDVMKVL
ESYGLREGANSEPREFVVEKAFVGEI
>sp|P9WN77|GPDA_MYCTU Glycerol-3-phosphate dehydrogenase [NAD(P)+]
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=gpsA PE=1
SV=1
MAGIASTVAVMGAGAWGTALAKVLADAGGEVTLWARRAEVADQINTTRYNPDYLPGA
LLPSSIATADAEALGGASTVLLGVPAQTMANLERWAPLLPEGATLVSLAKGIELGTL
MRMSQVIISVTGAEPQVAVISGPNLASEIAECQPAATVVACSDSGRAVALQRALNSGYFR
PYTNADVVGTEIGGACKNIIALACGMAVGIGLGENTAAAIITRGLAEIIRLGTALGANGAT

LAGLAGVGDLVATCTSPRSRNRSFGERLGRGETLQSAGKACHVVEGVTSCEVLALASSY
DVEMPLTDAVHRVCHKGLSVDEAITLLLGRRTKPE
>sp|H2A7G5|LANA_STRMD Lantibiotic macedovicin OS=Streptococcus macedonicus (strain
ACA-DC 198) OX=1116231 GN=SMA_1409 PE=1 SV=1
MMNATENQIFVETVSDQELEMLIGGADRGWIKTLTKDCPNVISSICAGTIITACKNCA
>sp|B5GRC8|LATES_STRC2 Labda-7,13(16),14-triene synthase OS=Streptomyces clavuligerus
(strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 /
VKM Ac-602) OX=443255 GN=SCLAV_p0491 PE=1 SV=1
MGRRARARSFGVSPLWGGVSVRSRSGDRGEAAVGGLEWVPDFWGLFPSRISPLAGEVESG
TRVWLDGWRLVEEAGPGERLKASKVGRLVALAYPDAPADLLRWAADLFAWLTAFFDDV
HVEAPGVTTAELGPHMASFVGVLETGTAPGAAPTFFPAALAEELDRARELLTPLQEERVR
ARLGKVFVAMLWEITTRERTVSTAEYETMRPHTFFSAVGAALVEPCAGLDLSHGVRADP
GVRRLTQALATLWERTNDLYSFAYEQRALGSVPRTLPLWLIAQERGLPLDAAFAEAGRWC
EEEAVLAHRLIGELSASAREGVPEYAGAVAHAIGGTRRLYEVS DRWREE
>sp|O05306|LOGH_MYCTU Cytokinin riboside 5'-monophosphate phosphoribohydrolase
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=log PE=1 SV=1
MSAKIDITGDWTVAVYCAASPTHAELLELAEEVGAAIAGRGWTLVWGGGHVSAMGAVA
SAARACGGWTVGVIPKMLVYRELADHDADELIVTDTMWERKQIMEDRSDAFIVLPGGVG
TLDELFDWTDGYLGTHDKPIVMVDPWGHFDGLRAWLNGLLDTGYVSPTAMERLVVVD
NVKDALRACAPS
>sp|Q2G278|LDP_STAA8 Probable autolysin LDP OS=Staphylococcus aureus (strain NCTC
8325) OX=93061 GN=SAOUHSC_00773 PE=1 SV=1
MKKSLTVTVSSVLAFLALNNAHAHQHGTQVKTPVQHNYVSNVQAQTQSPTTYTVVAG
DSLYKIALEHHLTLNQLYSYNGVTPLIFFPGDVISLVPQNKVKQTKAVKSPVRKASQAKK
VVKQPQQASKKVVKQAPKQAVTKTVNVAYKPAQVQKSVPTVPVAHNYNKSANRG
NLYAYGNCTYYAFDRRAQLGRSIGSLWGNANNWNYAAKVAGFKVDKTPEVGAIQTAA
GPYGHVGVVESVNPNGTITVSEMNYAGFNVKSSRTILNPGKYNIIH
>sp|Q9KWL3|LIGC_SPHSK 4-carboxy-2-hydroxy muconate-6-semialdehyde dehydrogenase
OS=Sphingobium sp. (strain NBRC 103272 / SYK-6) OX=627192 GN=ligC PE=1 SV=1
MRIALAGAGAFGEKHL DGLKNIDGVEIVSIISRKAEEQAEEVA AKYGA KHSGTDLSEALAR
DDVDAVILCTPTQMHA EQAIACMNAGKHVQVEIPLADSWADAEAVMKKSQETGLVCMV
GHTRRFNPSHQYIHNKIVAGELAIQQMDVQTYFFRRKNMNAKGEPRSWTDHLLWHHAA
HTVDLFAYQAGKIVQANAVQGPIHPELG IAMDMSIQLKSETGAICTLSLSFNNDGPLGTFF
RYICDNGTWIARYDDLVTGKEEPVDVSKVDVSMNGIELQDREFIAAIREGREPNSSVARVL
DCYRVLGELEVQLEKQG
>sp|Q07251|LDH_CUPNH L-lactate dehydrogenase OS=Cupriavidus necator (strain ATCC 17699
/ H16 / DSM 428 / Stanier 337) OX=381666 GN=ldh PE=1 SV=1
MKISLTSARQLARDILAAQQVPADIADDVAEHLVESDRCGYISHGLSILPNYRTALDGHSV
NPQGRAKCVLDQGTLMVFDGDGGFGQHV GKSVMQAAIERVRQHGHCIVTLRRSHHLGR
MGHYGEMAAAAGFVLLSFTNVINRAPVVAPFGGRVARLTTNPLCFAGPMPNGRPPLVVD
IATSAIAINKARVLA EKGEPAPEGSII GADGNPTTDASTMFGEHPGALLPFGGHKGYALGV
VAELLAGVLSGGGTIQPDNPRGGVATNNLFAVLLNPALDLGLDWQSAEVEAFVRYLHDT
PPAPGVDRVQYPGEYEAANRAQASDTLNINPAIWRNLERLAQSLNVAVPTA
>sp|P24484|LIP2_MORS1 Lipase 2 OS=Moraxella sp. (strain TA144) OX=77152 GN=lip2 PE=1
SV=1
MPILPVPALNALLTKTIKTIKTGA AKNAHQHHVLHHTLKGLDNLPAPVLERINRRLKASTA
EQYPLADAHRLILAISNKLKRPLAIDKLPKLRQKFGTDAVSLQAPSVWQQNADASGSTE
NAVSWQDKTIANADGGDMTVRCYQKSTQNSERKSTDEAAMLFFHGGGFCIGDIDTHHEF
CHTVCAQTGWAVVSVDYRMAPEYPAPTALKDCLAA YAWLAEHSQSLGASPSRIVLSGDS
AGGCLAALVAQQVIKPIDALWQDNNQAPAADKKVNDTFKNSLADLPRPLAQLPLYPVTD

YEA EYPSWEL YGEGLLLDHND AEVFNSAYTQHSGLPQSHPLISVMHGDNTQLCPSYIVVA
ELDILRDEGLAYAE LLQKEGVQVQTYTVLGAPHGFINLMSVHQGLGNQTTYIINEFACLV
QNLLTSEGD KPNLRA

>sp|D9XD61|EAES_STRVT 7-epi-alpha-eudesmol synthase ((2E,6E)-farnesyl diphosphate
cyclizing) OS=Streptomyces viridochromogenes (strain DSM 40736 / JCM 4977 / BCRC 1201 /
Tue 494) OX=591159 GN=SSQG_07226 PE=1 SV=1
MPQDVRFDL PFETPVSKHLESARARHLRWVWEMRLVHSREGFEEYRSWDLPQAAARTYP
HASADDMVVL MNWFLAFLFDDQFDASRPDRADRIA EVARELIVTPLRPAGTPPRVACPI
TLAWTEVWKHL SHGMSLTWQSRFAASWGRFLEAHCEEVDLAARGLEGTLGLVEFTEFR
RRTVGIHHSIDAGERSRGFEVPAQAMAHVMERMRLAADTIGFMNDIHSFEREKRRGDG
HNLIAVLR RERGCSWQEATDEAYRMTIARLDEYLELQERVPMCMDELRLDEAQRDGVRL
GVEAIQHWINGNYEWALTSGRYAAAKEGAVATAELAGRGSVDDLLTV

>sp|Q47013|ELAD_ECOLI Protease ElaD OS=Escherichia coli (strain K12) OX=83333 GN=elaD
PE=1 SV=3
MMVTVVSNYCQLSQTQLSQTFAEKFTVTEELLQSLKKTALSGDEESI ELLHNIALGYDKFG
KEAEDILYHIVRTP TNETLSIIRLIKNACLKLYNLAHIA TNSPLKSHDSDDL FKKLFSPSKL
MTIIGDEIPLISEKQSLSKVLLNDENNELSDGTNFWDKNRQLTTDEIACYLQKIAANAKNT
QVNYPTGLYVPYSTRTHLEDALNENIKSDPSWPNEVQLFPINTGGHWILVSLQKIVNKK
NKLQIKCVIFNSLRALGYDKENSLKRVINSFNSELMGEMSNNNIKVHLNEPEIIFLHADLQQ
YLSQSCGAFVCMAAQEVIEQRESNSDSAPYTLLKNHADRFKKYSAEEQYEIDFQHRLANR
NCYLDKYGDANINHYYRNLEIKHSQPKNRASGKRVS

>sp|Q9WXE6|LINE_SPHJU Chlorohydroquinone/hydroquinone 1,2-dioxygenase
OS=Sphingobium japonicum (strain DSM 16413 / CCM 7287 / MTCC 6362 / UT26 / NBRC
101211 / UT26S) OX=452662 GN=linE PE=1 SV=1
MMQLPERVEGLHHITVATGSAQGDVDLLVKT LGQRLVKKTMFYD GARPVYHLYFGNEL
GEPGTLTYTTFPVRQAGYTGKRGAGQISAVSYNAPVGTLSWWQEHLIKRAVTVSEVRERF
GQKYLSEHPDCGVGFIEEQDTDGQFEPWDSPPYVPKEVALRGFHSWTATLNRNEEMDSF
MRNAWNLPKQGRDGN YQRYAFGNNGGAAKVLDVYIDEDERPGT WALGEGQVHHAAFEV
ADLDVQAALKFDVEGLGYTDFSDRKHRGYFESIYVRTPGGVLF EASVTLGFTHDESPEKL
GSEVKVAPQLEGVKDELLRTMNDPIV

>sp|P9WKE9|KGUA_MYCTU Guanylate kinase OS=Mycobacterium tuberculosis (strain ATCC
25618 / H37Rv) OX=83332 GN=gmk PE=1 SV=1
MSVGEGPDTPKPTARGQPA AVGRVVVLSGPSAVGKSTVVRCLRERIPNLHFSVSATTRAPR
PGEVDGVDYHFIDPTRFQQLIDQGELLEWAEIHGGLHRS GTLAQPVRAAAATGVPVLIEV
DLAGARAIKKTMP EAVTVFLAPPSWQDLQARLIGRGTTETADV IQRRLDTARIELAAQGDF
DKVVVNRRLESACAELVSLLVGTAPGSP

>sp|O67648|LPXC_AQUAE UDP-3-O-acyl-N-acetylglucosamine deacetylase OS=Aquifex
aeolicus (strain VF5) OX=224324 GN=lpxC PE=1 SV=1
MGLEKTVKEKLSFEGVGIHTGEYSKLIHPEKEGTGIRFFKNGVYIPARHEFVVHTNHSTDL
GFKGQRIKTVEHILSVLHLL EITNVTIEVIGNEIPILDGSGWEFYEAIRKNILNQNREIDYFVV
EPIIIVEDEGR LIKAEPSTLEVTYEGEFKNFLGRQKFTFVEGN EEEIVLARTFCFDWEIEHI
KKVGLGKGGSLKNTLV LGKDKVYNPEGLRYENEPVRHKVFDLIGDLYLLGSPVKGKFYS
FRGGHSLNVKLVKELAKKQKLTRDLPHLPSVQAL

>sp|P28269|OAPT_PSEPU Omega-amino acid--pyruvate aminotransferase OS=Pseudomonas
putida OX=303 PE=1 SV=1
NMPEHAGASLASQLKLD AHWMPYTANRNFLRDPRLIVAAEGSWLVDDKGRKVYDSLGS
LWTCGAGHTRKEIQEAVAKQLSTLDYSPGFQYGHPLSFQLAEKITDLTPGNLNHVFFTDS
GSECALTAVKMVRAYWRLKGQATKTKMIGRARGYHGVNIAGTSLGGVNGNRKLFQGP
MQDVDHLPHTLLASNAYSRGMPKEGGIALADELLKLIELHDASNIAAVFVEPLAGSAGVL
VPPEGYLKR NREICNQHNILLVFDEVITGFGRTGSMFGADSGVTPDLMCIAKQVTNGAIP

MGAVIASTEIYQTFMNQPTPEYAVEFPHGYTYSAHPVACAAGLAALCLLQKENLVQSVAE
VAPHFEKALHGIKGAKNVIDIRNFLAGAIQIAPRDGDAIVRPFEAGMALWKAGFYVRFG
GDTLQFGPTFNSKPQDLDRLFDAVGEVLNKLDD

>sp|O34777|OHRR_BACSU Organic hydroperoxide resistance transcriptional regulator

OS=Bacillus subtilis (strain 168) OX=224308 GN=ohrR PE=1 SV=1

MENKFDHMKLENQLCFLLYASSREMTKQYKPLLDKLNITYPQYLALLLLWEHETLTVKK
MGEQLYLDSTLTPMLKRMEQQGLITRKSEEDERSVLISLTEDGALLKEKAVDIPGTILG
LSKQSGEDLKQLKSALYTLLETTLHQKN

>sp|P0AA16|OMPR_ECOLI Transcriptional regulatory protein OmpR OS=Escherichia coli (strain K12) OX=83333 GN=ompR PE=1 SV=1

MQENYKILVVDDDMRLRALLERYLTEQGFQVRSVANAEQMDRLLTRESFHLMVLDLML
PGEDGLSICRRLRSQSNPMPIMVTAKGEEVDRIVGLEIGADDYIPKPFNPPELLARIRAVLR
RQANELPGAPSQEEAVIAFGKFKNLGTREMFREDEPMPLTSGEFAVLKALVSHPREPLSR
DKLMNLARGREYSAMERSIDVQISRLRMVEEDPAHPRIYQTVWGLGYVFVDPGSKA

>sp|A0A0H3C7V4|MREB_CAUVN Cell shape-determining protein MreB OS=Caulobacter vibrioides (strain NA1000 / CB15N) OX=565050 GN=mreB PE=1 SV=1

MFSSLFGVISNDIAIDLGTANTLIYQKGKIVLNPSVVALRNVGGRKVVHAVGIEAKQML
GRTPGHMEAIRPMRDGVIADEFVAEEMIKYFIRKVNHRKGFVNPKVIVCVPSGATAVERR
AINDSCLNAGARRVGLIDEPMAAAIGAGLPIHEPTGSMVVDIGGGTTEVAVLSLSGIVYSR
SVRVGGDKMDEAIISYMRHHNLLIGETTAERIKKEIGTARAPADGEGLSIDVKGRDLMQ
GVPREVRISSEKQAADALAEPVGQIVEAVKVALEATPPELASDIADKGIMLTGGGALLRGL
DAEIRDHTGLPVTVADDPLSCVALGCGKIVLEHPKWMKGVLESTLA

>sp|P0A223|MXIH_SHIFL Protein MxiH OS=Shigella flexneri OX=623 GN=mxih PE=1 SV=1
MSVTVPNDDWTLSSLSETFDDGTQTLQGELTLALDKLAKNPSNPQLLAEYQSKLSEYTLY
RNAQSNTVKVIKDVDAAIIQNFR

>sp|P61496|PHR_THET2 Deoxyribodipyrimidine photo-lyase OS=Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039) OX=262724 GN=phr PE=1 SV=1

MGPLLVWHRGDLRLHDHPALLEALARGPVVGLVLDPNNLKTTPRRRWFLNVRLR
EAYRARGGALWVLEGLPWEKVPEAARLKAHAVYALTSYTPYGRYDAKVQEALPVPL
HLLPAPHLLPPDLPRAYRVYTPFARRFLGVEAPLPAPEALPKGPEEGEIPREDPGLPLPEPGE
EAALAGLRAFLEAKLPRYAEERDRLDGEGRSLSPYFALGVLSPLAAWEAERRGGEGA
RKWVAELLWRDFSYHLLYHFPWMAERPLDPRFQALPWQEDEALFRAWYEGRTGVPLVD
AAMRELHATGFLSNRARMNAAQFAVKHLLLPWKRCEEAFRHLLLDGDRAVNLQGWQW
AGGLGVDAAPYFRVFNPLVQGERHDPEGRWLKRWAPPEYPSYAPKDPVVDLEEARRRYL
RLARDLARG

>sp|O34767|OXDD_BACSU Oxalate decarboxylase OxdD OS=Bacillus subtilis (strain 168) OX=224308 GN=oxdD PE=1 SV=1

MLLEQQPINHEDRNVPPQPIRSDGAGAITGPRNIIRDIQNPNIFFVPPVTDEGMIPNLRFSFSD
APMKLDHGGWSREITVRQLPISTAIAGVNMSLTAGGVRELHWHKQAEWAYMMLLGRARIT
AVDQDGRNFIADVGPDLWYFPAGIPHSIQGLEHCEFLVFDDGNFSEFSTLTISDWLAHT
PKDVLSANFGVPENAFNSLPSEQVYIYQGNVPGSVASEDIQSPYGKVPMTFKHELLNQMPI
QMPGGSVRIVDSSNFPISKTIAAALVQIEPGAMRELHWHPNSEDEWQYYLTGQGRMTVFIG
NGTARTFDYRAGDVGYVPSNAGHYIQNTGTETLWFLEMFKSNRYADVSLNQWMALTPK
ELVQSNLNAGSVMLDSLRRKKKVPVVKYPGT

>sp|P0AFD1|NUOE_ECOLI NADH-quinone oxidoreductase subunit E OS=Escherichia coli (strain K12) OX=83333 GN=nuoE PE=1 SV=1

MHENQQPQTEAFELSAAEREAIEHEMHYEDPRAASIEALKIVQKQRGWVPDGAIHAIAD
VLGIPASDVEGVATFYSQIFRQPVGRHVIRYCDSSVCHINGYQGIQAALKKLNKPGQTT
FDGRFTLLPTCCLGNCDKGPNMMIDEDTHAHLTPEAIPPELLERYK

>sp|P37562|PKN1_BACSU Probable serine/threonine-protein kinase YabT OS=Bacillus subtilis (strain 168) OX=224308 GN=yabT PE=1 SV=2
MMNDALTSACSLKPGTTIKGKWNGNTYTLRKQLGKGANGIVYLAETSDGHVALKVSD
DSLSITSEVNVLSFSKAQSVTMGPSFFDTHDAYIPSANTKVSFYAMEYIKGPLLLKYVSD
KGAEWIPVLMIQLLSSLSVLHQGWIFGDLKPDNLIVTGPPARIRCIDVGGTTKEGRAIKEY
TEFYDRGYWGYGTRKAEPSYDLFAVAMIMINSVHKKEFKKTNPKEQLRSLIEGNPLLQK
YKKALFSALNGDYQSADEMKKDMLDAGQKAAQRKQPIKASPQPATRQRQQKPRQGKIT
KTRYTPKQKPAKSGGLFETTLIVISVLALYFAYIIFLI

>sp|Q99U74|ODO1_STAAN 2-oxoglutarate dehydrogenase E1 component OS=Staphylococcus aureus (strain N315) OX=158879 GN=odhA PE=1 SV=1
MTNERKEVSEAPVNFGANLGLMLDLYDDFLQDPSSVPEDLQVLFSTIKRVMRLIDNIRQY
GHLKADIYPVNPVKRKHVPKLEIEDFDLDQQTLEGISAGIVSDHFADIYDNAYEAILRMEK
RYKGPIAFEYTHINNTERGWLKRRIETPYKVTLNNNEKRALFKQLAYVEGFEEKYLHKNF
VGAKRFSIEGVDALVPMLQRTITIAAKEGIKNIQIGMAHRGRLNVLTHVLEKPYEMMISEF
MHTDPMKFLPEDGSLQLTAGWTGDVKYHLGGIKTTDSYGTMQRIALANNPISHLEIVAPV
VEGRTRAAQDDTQRAGAPTTDHHKAMPIIIHGDAAYPGQGINFETMNLGNLKGYSTGGSL
HIITNNRIGFTTEPIDARSTTYSTDVAKGYDVPIFHVNADDVEATIEAIDIAMEFRKEFHKDV
VIDLVGYRRFGHNEMDEPSITNPVYQNIKHDSEVEYVFGKKLVNEGVISEDEMHSFIEQV
QKELRQAHDKINKADKMDNPDMEKPAELALPLQADEQSFTFDHLKEINDALLTYPDGFNI
LKLNKLVLEKRHEPFNKEDGLVDWAQAEQLAFATILQDGTPIRLTGQDSERGTFSHRHAV
LHDEQTGETYTPLHHVPDQKATFDIHNSPLSEAAVVGFEYGYNVENKKSFNWEAQYQYD
ANMSQMIFDNFLFSSRSKWGERSGLTFLPHAYEGQGPEHSSARLERFLQLAAENNCTVV
NLSSSSNYFHLLRAQAASLDSEQMRPLVVMSPKSLLRNKTVAKPIDEFTSGGFEPILTESYQ
ADKVTKVILATGKMFIDLKEALAKNPDESLLVAIERLYPFEEEEIEALLAQLPKLEEVSW
VQEEPKNQGAWLYVYPYVKVLVADKYDLSYHGRIQRAAPAEGDGEIHKLVQNKIENAL
KNN

>sp|Q92G53|PLD_RICCN Phospholipase D OS=Rickettsia conorii (strain ATCC VR-613 / Malish 7) OX=272944 GN=pld PE=1 SV=1
MKRKNNKFIEISIAFILGIALGLYGQNPDYFTNLISQKSLALSALQIKHYNISELSRSKVSTCF
TPPAGCTKFIANQIDKAEESIYMQAYGMSDALITTALINAQARGVKVRILLDRSNLKQKFS
KLHELQRAKIDVDIDKVPGLAHNKVIIDKKKVITGSFNFTAAADKRNAENVIIEDQELAES
YLQNWLNLRKASN

>sp|Q48708|NRDH_LACLM Glutaredoxin-like protein NrdH OS=Lactococcus lactis subsp. cremoris (strain MG1363) OX=416870 GN=nrdH PE=1 SV=1
MVTVYSKNNCMQCKMVKKWLSEHEIAFNEINIDEQPEFVEKVIEMGFRAAPVITKDDFAF
SGFRPSELAKLA

>sp|P73390|PHAC_SYNY3 Poly(3-hydroxyalkanoate) polymerase subunit PhaC
OS=Synechocystis sp. (strain PCC 6803 / Kazusa) OX=1111708 GN=phaC PE=1 SV=1
MFLFFIVHWLKIPLPFFAQVGLEENLHETLDFTEKFLSGLNLQGLNEDDIQVGFTPKEA
VYQEDKVILYRFQPVVENPLPIPVLVYALVNRPYMVDLQEGRSLVANLLKLGLDVYLID
WGYPSTRGDRWLTLEDYLSGYLNNCVDIICQRSQQEKITLLGVCQGGTFSLCYASLFPDKV
KNLVVMVAPVDFEQPGTLLNARGGCTLGAEAVDIDLMVDAMGNIPGDYLNLEFLMLKPL
QLGYQKYLDVPDIMGDEAKLLNFLRMEKWIFDSPDQAGETYRQFLKDFYQQNKLIKGEV
MIGDRLVDLHNLTPILNLYAEKDHLVAPASSLALGDYLPENCYTVQSFVGHIGMYVS
GKVQRDLPPAIAHWLSERQ

>sp|P9WJI5|NAT_MYCTU Arylamine N-acetyltransferase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=nat PE=1 SV=1
MALDLTAYFDRINYRGATDPTLDVLQDLVTVHSRTIPFENLDPLLGVVDDLSQALADK
LVLRRRGGYCFEHNGLMGYVLAELGYRVRRAARVVWKLAPDAPLPQTHTLLGVTFPG
SGGCYLVVDVGFGGQTPTSPLRLETGAVQPTTHEPYRLEDVRVDGFLQAMVRDTWQTLYE

FTTQTRPQIDLKVASWYASTHPASKFVTGLTAAVITDDARWNLSGRDLAVHRAGGTEKIR
LADAAAVVDTLSEFNGINVADIGERGALETRIDELLARQPGADAP
>sp|D9XF45|PHPC_STRVT Phosphonoacetaldehyde reductase OS=Streptomyces
viridochromogenes (strain DSM 40736 / JCM 4977 / BCRC 1201 / Tue 494) OX=591159
GN=phpC PE=1 SV=1
MTAVFPGELLAEIHEIARVTALLSGPLRRAPRVAQVVGPFGAGRPWAPRLTDALRPLD
PTVVVHDGPTTPDSVAALARQLRAIRADVAVAIGGGTVMDAAKAAAALADGGPPDADR
VRQACAAGPAAGDTPPAVRVAVPTTAGTGAEATPFATLWDLKHRRKLSLTGPRVRPSA
AVLAPELLAGLGRRALATGILDALCQGAESWSIRSTPESIRWGTSAVTLAAEALDQVQD
DAPDAAARLALQRAAHHSGRAIALAQTSCHASISYPLTLRLGLAHGHACGVTGLRLLRYN
HAVPAGDCADPRGTGHVRRVLDALAAPLGGTPARAALRVERFITACGLTPYDALDVDHR
SLAAEAITYPRCHDNPRLDRESLGRLLGERSEMEETCG
>sp|Q9X113|OXPB_THEMA Oxalate-binding protein OS=Thermotoga maritima (strain ATCC
43589 / MSB8 / DSM 3109 / JCM 10099) OX=243274 GN=TM_1287 PE=1 SV=1
MKEGTGMVVRSEITPERISNMRGGKGEVEMAHLLSKEAMHNKARLFARMKLPPGSSVG
LHKHEGEFEIYYILLGEGVFHDNGKDVPIKAGDVCFTDSGESHSIENTGNTDLEFLAVIILL
>sp|Q51793|PHZG_PSEFL Phenazine biosynthesis protein PhzG OS=Pseudomonas fluorescens
OX=294 GN=phzG PE=1 SV=1
MNGSIQGGKPLLKGMSSESLTGTLDAFPPEYQTLPADPMSVLHNWLERARRVGIREPRALA
LATADSQGRPSTRIVVISEISDAGVVFSTHAGSQKGRELLHNPWASGVLYWRETSQQIILN
GQAVRLPNAKADDAWLKRPYATHPMSSVSRQSEELQDVQAMRNAARQLAELQGGLPRP
EGYCVFELRLESLEFWGNGQERLHERLRYDRSDTGWNVRRLLQ
>sp|P0ADI0|PINR_ECOLI Serine recombinase PinR OS=Escherichia coli (strain K12) OX=83333
GN=pinR PE=1 SV=1
MSRIFAYCRISTLDQTTENQRREIESAGFKIKPQQIIEEHISGSAATSERPGFNRLRLARLKCG
DQLIVTKLDRLGCNAMDIRKTVEQLTETGIRVHCLALGGIDLTSPGKMMMQVISAVAEF
ERDLLLERTHSGIVRARGAGKRFRGPPVLNEEQKQVVFERIKSGVSISAIAREFKTSRQTIL
RAKAKLQTPDI
>sp|Q02L47|PHZB2_PSEAB Phenazine biosynthesis protein PhzB 2 OS=Pseudomonas
aeruginosa (strain UCBPP-PA14) OX=208963 GN=phzB2 PE=1 SV=1
MLDNAIPQGFEDAVELRRKNRETVVKYMNKTKGQDRLRRHELFVEDGCGGLWTTDTGSPI
VIRGKDKLAEHAVWSLKCFPDWEWYNIKFETDDPNHFWVECDGHGKILFPGYPEGYE
NHFLHSFELDDGKIKRNFEMNVFQQLRALSIPVPQIKREGIPT
>sp|Q9WYW0|NPD_THEMA NAD-dependent protein deacetylase OS=Thermotoga maritima
(strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) OX=243274 GN=cobB PE=1 SV=1
MKMKEFLDLLNESRLTVTLTGAGISTPSGIPDFRGPNGIYKKYSQNVFDIDFFYSHPEEFYR
FAKEGIFPMLQAKPNLAHVLLAKLEEKGLIEAVITQNIDRLHQRAGSKKVIELHGNVEEYY
CVRCEKKYTVEDVIKKLESSDVPLCDDCNLSLRPNIVFFGENLPQDALREAIGLSSRASLMI
VLGSSLVVYPAAELPLITVRSGGKLIVVNLGETPFDDIATLKYNMDVVEFARRVMEEGGIS
>sp|L0T864|FPG2_MYCTU Uncharacterized formamidopyrimidine-DNA glycosylase-like protein
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=fpg2 PE=1 SV=1
MAGTPQPRALGPDALDVSTDDLGLLAGNTGRIKTVITDQKVIAGIGNAYSDEILHVAKIS
PFATAGKLSGAQLTCLHEAMASVLSDAVRRSVGQGAAMLKGEKRSGLRVHARTGLPCPV
CGDTVREVSFADKSFQYCPTCQTGGKALADRRMSRLK
>sp|P73245|HEMW_SYNY3 Heme chaperone HemW OS=Synechocystis sp. (strain PCC 6803 /
Kazusa) OX=1111708 GN=hemW PE=1 SV=1
MNTGTYLMPATAAYIHIPFCRQRCFYCDFPIAVTGFQSLTLDGWVGEYVEAVCREIAGQQH
QQQPLQTVFFGGGTPSLLPITGLEKILLAVDQYLGIAPDAAEISIEIDPGTFDQVQLQGYKNLG
INRFSLGVAQFDNLLALCGRHRRRDIDQALTAIAKENIENWSLDLITGLPEQTAADWHS
SLTLALAAGPKHISCYDLVLEPQTVFDKWEQRGKLAVPPERSADFYRHGQEVLTQAGFH

HYEISNYGRPGHQCRHNQIYWRNLPYYGLGMGATSYIDGKRFGPRPRTRNGYYQWLESW
 LNQGCPPIGERVSLENLLESMLGLRLTAGVTWAQLPSVNQTEKAKILATLTSFGDRRW
 LEFYGEDNQMLAPNQTTTETVQRFCTDPEGILYSNQILSALFAALEEDF
 >sp|P9WML7|HIS8_MYCTU Histidinol-phosphate aminotransferase OS=Mycobacterium
 tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=hisC PE=1 SV=1
 MTRSGHPVTLDLPLRADLRGKAPYGAPQLAVPVRLNTNENPHPPTRALVDDVVRVRE
 AAIDLHRYPDRAVALRADLAGYLTAQTGIQLGVENIWAANGSNEILQQLQAFGGPGRS
 AIGFVPSYSMHPIISDGTHTIEWIEASRANDFGLDVDVAVAAVVDKPDVVFIA SPNNPSGQ
 SVSLPDLCKLLDVAPGIAIVDEAYGEFSSQPSAVSLVEEYPSKLVVTRTMSKAFAGGRL
 GYLIATPAVIDAMLLVRLPYHLSSVTQAAARAALRHSDDTLSSVAALIAERERVTTSLND
 MGFRVIPSDANFVLFGEFADAPAAWRRYLEAGILIRDVGIPGYLRATTGLAEENDAFLRAS
 ARIATDLVPVTRSPVGAP
 >sp|Q5F881|FITA_NEIG1 Antitoxin FitA OS=Neisseria gonorrhoeae (strain ATCC 700825 / FA
 1090) OX=242231 GN=fitA PE=1 SV=1
 MASVVIRNLSEATHNAIKFRARAAGRSTEA EIRLILDNIAKAQQTVRLGSMLASIGQEIGGV
 ELEDVRGRNTDNEVSL
 >sp|P9WNF1|FDHD_MYCTU Sulfur carrier protein FdhD OS=Mycobacterium tuberculosis
 (strain ATCC 25618 / H37Rv) OX=83332 GN=fhdD PE=1 SV=1
 MGYATAHRRVRHLSADQVITRPETLAVEEPLEIRVNGTPVTVTMRTPGSDFELVQGFLLA
 EGVVAHREDVLTVS YCGRRVEGNATGASTYNVLDVALAPGVKPPDVDVTRTFYTTSSCG
 VCGKASLQAVSQVSRFAPGGDPATVAADTLKAMPDQLRRAQKV FARTGGLHAAALFGV
 DGAMLAVREDIGRHNAVDK VIGWAFERDRIPLGASVLLVSGRAS FELTQKALMAGIPVLA
 AVSAPSSLAVSLADASGITLVAFLRGDSMN VYTRADRT
 >sp|B1VTI5|GRIF_STRGG Grixazone synthase OS=Streptomyces griseus subsp. griseus (strain
 JCM 4626 / NBRC 13350) OX=455632 GN=grIF PE=1 SV=1
 MVHVRKNHLTMTAEKRRFVHAVLEIKRRGIYDRFVKLHIQINSTDYLDKETGKRLGHV
 NPGFLPWHRQYLLKFEQALQKVDPRVTLPYWDWTTDHGENSPLWSDTFMGGNGRPGDR
 RVMTGPFARRNGWKL NISVIPEGPEDPALNGNYTHDDRDLVRDFGTLTPDLPTPQELEQ
 TLDLTVYDCPPWNHTSGGTPPYESFRNHLEGYTKFAWEPRLGKLGAAHVWTGGHMMY
 IGSPNDPVFFLNHC MIDRCWALWQARHPDVPHYLPTVPTQDVPDLNTP LGPWHTKTPAD
 LLDHTRFYTYDQ
 >sp|P22319|HOXY_CUPNH NAD-reducing hydrogenase HoxS subunit delta OS=Cupriavidus
 necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) OX=381666 GN=hoxY PE=1 SV=1
 MRAPHKDEIASHEL PATPMDPALAANREGKIKVATIGLCGCWGCTLSFLDM DERLLPLLE
 KVTLLRSSLTDIKRIPERCAIGFVEGGVSSEENIETLEHFRENC DILISVGACAVWGGVPAM
 RNVFELKDCLAEAYVNSATAVPGAKAVVPFHPDIPRITTKVYPCHEVVKMDYFIPGCPPD
 GDAIFKVLDL VNGRPFDLPSINRYD
 >sp|P37728|KDGR_DICCH Pectin degradation repressor protein KdgR OS=Dickeya
 chrysanthemi OX=556 GN=kdgR PE=1 SV=2
 MIFNRSVTYSNARLPYSKRSLYTKTRVLFFLKQKILSRVTTKMAIADLDKQPD SVSSVLKV
 FGILQALGEEREIGITELSQRVMMMSKSTVYRFLQTMKSLGYVAQEGESEKYS LTLKLFELG
 AKALQNVDLIRSADIQMRELSALTRETIHLGALDEDSIVYIHKIDSMYNLRMYSRIGRRNPL
 HSTAIGKVLLAWRDREEVKEILSQVEFKRTTVHTIGSTEELLPQLDLVRQQGYGEDNEEQE
 EGLRCIAVPVDFDRFGVVIAGLSISFPTIRFSEDNKHEYVAMLHTAARNISDQMGYHDYPF
 >sp|B1N1A2|HSPA_PSEPU 6-hydroxy-3-succinoylpyridine 3-monooxygenase HspA
 OS=Pseudomonas putida OX=303 GN=nicB PE=1 SV=1
 MQRKLDSEPLRTRIYIDGYNFYYGCLRGTPYKWLDLLPLFEKHILPSILVTDNHGQIRAWR
 LLESPSIKYFTAKIIESVARAGDSVSSQARYHTALRKLHDGRIELIEGYAVNKMVKIVDP
 ENPDKAPRECREIQAWKVEEKQSDVNLA LQAYHDSITGQVDHAVIVTNDTDIAPALQMIR
 AHTDVRIGVVVPTSGQNRSANTDLIKFAHWKREHINS GELAACQLPRVIPGRKPTIKPESW

YGQPELLQEILDLAIPVRGSRAAAFKWMEQPNQFLSGERPIELVETAEGATRVLQYIHSWI
 AQQEELP
 >sp|P00553|KKA4_BACCI Aminoglycoside 3'-phosphotransferase OS=Bacillus circulans
 OX=1397 GN=aphA4 PE=1 SV=1
 MNESTRNWPEELLELLGQTELTVNKIGYSGDHVYHVKEYRGTPAFLKIAPSVWWRTLRLPE
 IEALAWLDGKLPVPKILYTAEHGGMDYLLMEALGGKDGSHETIQAKRKLFVKLYAEGLR
 SVHGLDIRECPLSNGLEKKLRDAKRIVDESLVDPADIKKEEYDCTPEELYGLLLESKPVTEDL
 VFAHGDYCAPNLIIDGEKLSGFIDLGRAGVADRYQDISLAIRSLRHDYGDDRYKALFLELY
 GLDGLDEDKVRYYIRLDEFF
 >sp|Q1Q0T4|HZSB_KUEST Hydrazine synthase subunit beta OS=Kuenenia stuttgartiensis
 OX=174633 GN=kuste2859 PE=1 SV=1
 MVIRRKMNKMIRKGMIGAVMLGAAVAISGGVATAGYIQGTHVKTDLPGPFHITMSPDGS
 TLFISNQSGHSVTFVDARTQKVTGEVAVRVQPEASAVTPDGAFLYVCNAESDSVSVVDIQ
 RKQEIKEIKVGDWPSGIKISPDGKTAYVACSGCMWNAIDVIDTGRMEKVRISIYTSYDYGPR
 MVEISPDGKTLVAILDTVGSINRSVDFIDIASGRVVENRVIHESSNLRDVVYTPDGKYIAVT
 HQTPKNWLPVCEAENGQVFTNNVTIETKAGGKVARLPLDDLNNYDGNPNYGMAMDPKG
 KYLYIGVRGMHRVTILDMDKVLGLVRSSTQEELDYLRDDLGLVRDYLVARVPTGLGPSS
 VCLSPDGKFCYAANYFSNNVTVIRTAVD
 >sp|P80064|HPPD_PSEUJ 4-hydroxyphenylpyruvate dioxygenase OS=Pseudomonas sp. (strain
 P.J. 874) OX=72587 GN=hpd PE=1 SV=1
 ADLYENPMGLMGFEFIELASPTNTLEPIFEIMGFTKVATHRSKDVHLYRQGAINLILNNEP
 HSVASYFAAEHGSPVCGMAFRVKDSQKAYKRALELGAQPIHIETGPMELNLPAIKGIGGA
 PLYLIDRFEGEGSSIYDIDFVFLEGVDRHPVGAGLKIIDLHNLHNVYRGRMAYWANFYEKLFN
 FREIRYFDIKGEYTGLTSKAMTAPDGMIRIPLNEESSKGAGQIEEFLMQFNGEGIQHVAFLS
 DDLIKTWDHLKSIGMRFMTAPPDTYYEMLEGRLPNHGEPVGELQARGILLDGSSSESGDKR
 LLLQIFSETLMGPVFFEFIQRKGDDGFGEGNFKALFESIERDQVRRGVLSTD
 >sp|O25560|HYPB_HELPY Hydrogenase/urease maturation factor HypB OS=Helicobacter pylori
 (strain ATCC 700392 / 26695) OX=85962 GN=hypB PE=1 SV=1
 MSEQRQESLQNNPNLSKKDKVIVEKILSKNDIKAAEMKERYLKEGLYVLNFMSSPGSGKT
 TMLLENLADFKDFKFCVVEGDLQTNRDADRLRKKGVSAHQITTGEACHLEASMIEGAFDL
 LKDEGALEKSDFLIENVGNLVCPSSYNLGAAMNIVLLSVPEGDDKVLYPTMFMCADAV
 IISKADMVEVFNFRVSQVKEDMQKLKPEAPIFLMSSKDPKSLEDFKNFLLEKKRENYQSTH
 SF
 >sp|P9WJ95|INIC_MYCTU Isoniazid-induced protein IniC OS=Mycobacterium tuberculosis
 (strain ATCC 25618 / H37Rv) OX=83332 GN=iniC PE=1 SV=1
 MSTSDRVRAILHATIQAIRGAPAYRQRGDVFCQLDRIGARLAEPLRIALAGTLKAGKSTL
 VNALVGDDIAPTDATRIVTWFRHGPTPRVTANHRGGRRANVPITRRGGLSFDLRRINP
 AELIDLEVEWPAAELIDATIVDTPGTSSLACDASERTLRLLPADGVPRVDAVVFLRLTLN
 AADVALLKQIGGLVGGSVGALGIIGVASRADEIGAGRIDAMLSANDVAKRFTRELNQMG
 CQAVVPVSGLLALTARTLRQTEFIALRKLAGAERTELNRALLSVDRFVRRDSPLPVDAGIR
 AQLLERFGMFGIRMSIAVLAAGVTDSTGLAAELLERSGLVALRNVIDQQFAQRSDMLKAH
 TALVSLRRFVQTHPVATPYVIADIDPLLADTHAFEELRMLSLPSRATTLNDDEIASLRRII
 GSGGTSAAARLGLDPANSREAPRAALAAQHWRRRAAHPLNDPFTTRACRAAVRSAEA
 MVAEFSARR
 >sp|P0C0L9|ISCX_ECOLI Protein IscX OS=Escherichia coli (strain K12) OX=83333 GN=iscX
 PE=1 SV=1
 MGLKWTDSREIGEALYDAYPDLPKTVRFTDMHQWICDLEDFDDDPQASNEKILEAILLV
 WLDEAE
 >sp|A0A0D4BSN8|IND2_STRGR Beta-methylindole-3-pyruvate reductase OS=Streptomyces
 griseus OX=1911 GN=ind2 PE=1 SV=1

MKLDDKRILIIIGAGEVGTAVAEDLVNRS DPTEIIIHTSRQQTM DMRVGH LKEMAGPRTLLT
GSWGDIFAPYELTHRSRSEINDRNVRLALAEFFLQPSGEAQLRRTTIYELISRHRPHIVIDAV
NSASVCTYTEDPHQTCGELLDLARGTGGPRTAEAPAELPAVTPDIADVATDALLSLSTPIL
HRYVDSLRRAMADFQVERFIKVSTTGLGGMGYNCPYTHGVSVEFGLSDALVGKIGSAGV
LHQLLWNLHHTAGCDVRLVIPAALIGWESVRHGAYTSRGRPVALQDCSRPLPLHLDRPLG
EHAAASSVAEPAAEDEPSAEMVHVPAGDNSTYSRAEMSLSTALGQFESVTREEVAAAVL
DTLLGSTRFDLFTAMDTASLQSSYLAAQMRTSTLTSMRQLEKAYDRPSIVSGNLGPTISKD
LLELHVLCTAAGSLEQARTMSTTVLASSASALVREDVYLRQQALSIGLAVLLPDDQWLAG
PRLSVPSRIDPEAKVTRADIDDSRQGWVDLRPARILHWQENLRRIEQDASAGKTA FALD
DTAYDVGEVLAYHYKLTGQARRIKGL

>sp|Q936S7|IPUF_PSESP Gamma-glutamyl-L-1-hydroxyisopropylamide hydrolase

OS=Pseudomonas sp. OX=306 GN=ipuF PE=1 SV=1

MEKLRILICDGNTEADRASFKKFVGCAPSKQFESLLKNYNSQIRTEIAFPADPGPLMTLPLG
AYDGILITGSNSHIYEAQPGNLRQIEFAQKAFASGTPMFGVCWGMQLAVVAAGGEVLPSR
VADCSCETPFATGVELTSYGSGHPMHHSRTSGFDVFSFHSDEVTRLPGGAVVTARNRNF
QAVEIKHGRSTFWGVQYHPELSGWDQAGFLRESARSLVEDGSYETLNHVEHAAQAISMF
KAGAQISEENLVHFEGVDTN SFEFRPLEILNWL DHLVIPTAKRKFGWGGGWLQK

>sp|P74921|ILVE_THEMA Probable branched-chain-amino-acid aminotransferase

OS=Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) OX=243274
GN=ilvE PE=1 SV=2

MLIWWRGKFRRADEISLDFSLFEKSLQGAVYETLRTYSRAPFAAYKH YTRLKRSADFFNL
PLSLSFDEFTKVLKAGADEFKQEVRIKVYLF PDSGEVLFVFSPLNIPDLETGVEVKISNVRR
PDLSTPPALKITGRTDIVLARREIVDCYDVILLGLNGQVCEGSFSNVFLVKEGKLITPSLDSG
ILDGITRENVIKLAKSLEIPVEERVVWVWELFEADEMFLTHTSAGVVPVRRRLNEHSFFEEEP
GPVTATLMENFEPFVLNLEENWVGI

>sp|Q03961|KPSD1_ECOLX Polysialic acid transport protein KpsD OS=Escherichia coli

OX=562 GN=kpsD PE=1 SV=2

MKLFKSILLIAACHAAQASAAIDINADPNLTGAAPLTGILNGQQSDTQNM SFGDNTPPPSP
VVM SRMFGAQLFNGTSADSGATVGFPNDYILNPGDSIQVRLWGAFTFDGALQVDPKGNIF
LPNVGPVKVAGVSNSQLNALVTSKVKEVYQSNVNVYASLLQAQPVKVYVTGFVRNPGL
YGGVTSDSLNLIKAGGVDPERGSYVDIVVKRGNRVRSNVNLYDFLLNGKLGLSQFAD
GDTIIVGPRQHTFSVQGDVFNSYDFEFRESSIPVTEALSWARPKPGATHITIMRKQGLQKRS
EYYPISAPGRMLQNGDTLIVSTDYAGTIQVRVEGAHSGEHAMVLPYGSTMRAVLEKVR
PNSMSQMNAVQLYRPSVAQRQKEMLNLSLQKLEEASLSAQSS TKEEASLRMQEAQLISRF
VAKARTVVPKGEVILNESNIDSVLLEDGDVINIPEKTS LVMVHGEVLF PNAVSWQKGMTT
EDYIEKCGGLTQKSGNARIIVIRQNGAAVNAEDVDSLKPGDEIMVLPKYESKNIEVTRGIST
ILYQLAVGAKVILSL

>sp|P0ACE7|HINT_ECOLI Purine nucleoside phosphoramidase OS=Escherichia coli (strain K12)

OX=83333 GN=hinT PE=1 SV=1

MAEETIFSKIIRREIPSDIVYQDDLVTAFRDISPQAPTHILIIPNILIPTVNDVSAEHEQALGRM
ITVAAKIAEQEGIAEDGYRLIMNTNRHGGQEVYHIHMHLLGGRPLGPMLAHKGL

>sp|Q84F16|HPDL_CLODI 4-hydroxyphenylacetate decarboxylase large subunit

OS=Clostridioides difficile OX=1496 GN=hpdB PE=1 SV=1

MSQSKEDKIRSILEAKNIKS NFQNKENLSEFNEKKASKRAEDLLDVYYNTLSTADMEFPY
WYNREYRKSDGDIPVVRRAKALKA AFSHMT PNIPGEKIVMQKTRHYRGSFPMPWVSEF
FVAQGEQMREEAKKLASNTADELTKFGSGGGNVTESFGNVVSIAGKFGMRKEEVPVLVK
MAKEWVGKSVEDLGFHYEKMPDYLKENLMSTLICMFDSGYTLPQGREVINYFYPLN
YGLDGIIEMAKECKKAVAGNASGDGLIGMDRLYFYEA VIVQVIEGLQTWILNYAKHAKYL
ESIETDLEAKKEYSDLVEILEHIAHKQPRTFREALQLTYTIHIASVNED AISGMSIGRFGQIL
YPWYEQDIEKGLITKEEVIELLELYRIKITCIDCFASAGVNGGVLSGNTFNTLSIGGLKEDGS

TGANELEELLLEASMRCTPQPSLTMLYDEKLPEDFLMKAAECTKLGSGYPAWVNNSNG
TTFMMKQFADEGMTVEEARAFALGGCLETSPGCWKQLTLNGKTYSIAGGAGQSAGSGV
HFIANPKILELVLMMNGKDYRMNIQVFEPHNKPLDTYEEVIEVFKDYYKQAINVLERANNIE
LDIWRKFDTSIINSLKPDCLDKGQHIGNMGYRYNATLNVETCGTVMVNSFAALKKLTV
DDKAFTIEEIKDAILNNFGFKDALEVGNYSMADQVKVDKTGKYDAIYKACLDAPKYGNN
DLYADNILKNYEVWLSKVCEEAQSLYAKKMYPCQISVSTHGPQGAATLATPDGRLSGTT
YSDGSVSAYAGTDKNGVYALFESATIWDQAVVQNSQMNLKLHPTTIKGQQGTKKLLDLT
RSYLKGGFHIQYNVVDSETLKDAQKNPDNYRQLMVRVAGFTQYWCELGKPIQDEVIAR
TEYEGV

>sp|Q9KWQ6|HSAD_RHOJR 4,5:9,10-diseco-3-hydroxy-5,9,17-trioxoandrosta-1(10),2-diene-4-
oate hydrolase OS=Rhodococcus jostii (strain RHA1) OX=101510 GN=hsaD PE=1 SV=1
MTTTEEALTFESTSKFAQVRPHLKLHYHEAGVGNDTTIVLLHGGGPGASSWSNFARNIPV
LAEKFHVLAVDQPGYGLSDKPTHEHPQYFVHSASALKDLLDTLGVGGRVHLLGNSLGGGA
AVRFALDYPDRAGRLVLMGPGGLSVNLFAPDPTEGVKNLKGFGYQPTRENLEAFLRIMVF
DQKLITDELIDERFAAASPESLAAAKAMGKSFSSADFELGMLWRDAYKLRQRVLLIWR
EDRVNPLDGLVALKMIPRAQLHVFGGCGHWAQLEKFDEFNRLATDFLLDGGK

>sp|P15623|GLNA3_BACFR Glutamine synthetase OS=Bacteroides fragilis (strain YCH46)
OX=295405 GN=glnA PE=1 SV=2
MSKMRFFALQELSNRKPLEITTPSNKLSDDYYASHVFDRKKMQEYLPKEAYKAVVDATEK
GTPISREMAADLIANGMKSWAKSLNVTHYTHWFQPLTDGTAEKHGDGFIEFGEDGEVIERFS
GKLLIQQEPDASSFPNGGIRNTFEARGYTAWDVSSPAFVVDTTLCIPTIFISYTGEALDYKTP
LLKALAAVDKAATEVCQLFDKNITRVFTNLGWEQEYFLVDTSLYNARPDRLRTGRTLMG
HSSAKDQQLEDHYFGSIPPRVTA FMKELEIECHKLGI PVKTRHNEVAPNQFELAPIFENCNL
ANDHNQLVMDLMKRIARKHHFAVL FHEKPYNGVNGSGKHNNWSLCTDTGINL FAPGKN
PKGNNMLFLTFLVNVLMMVHKNQDLLRASIMSAGNSHRLGANEAPPAILSIFLGSQLSATL
DEIVRQVTNSKMTPEEKTTLKLGIGRIPEILLDTTDRNRTSPFAFTGNRFEFRAAGSSANCA
AAMIAINAAMANQLNEFKASVDKLMEEGIGKDEAIFRILKENIIASEPIRFEGDGYSEEWK
QEAARRGLTNICHVPEALMHYTDNQSRV LIGERIFNETELACRLEVELEKYTMKVQIESR
VLGDLAINHIVPIAVSYQNRLLLENLCRMKEIFSEEEYEVMSADRKELIKEISHRVSAIKVLV
RDMTEARKVANHKENFKEKAFAYEETVRPYLESIRDHIDHLEMEIDDEIWPLPKYRELLFT
K

>sp|P19424|GUN_BACS6 Endoglucanase OS=Bacillus sp. (strain KSM-635) OX=1415 PE=1
SV=1
MKIKQIKQSLSLLLIITLIMSLFVPMASANTNESKSNAPFSDVKKTSWSFPYIKDLYEQEVI
TGTSATTFSPDTSVTRAQFTVMLTRGLGLEASSKDYPFKDRKNWAYKEIQAA YEAGIVTG
KTNGEFAPNENITREQMAAMAVRAYEYLENELSLPEEQREYNDSSSISTFAQDAVQKAYV
LELMEGNTDGYFQPKRNSTREQSAKVISTLLWKVASHDYLYHTEAVKSPSEAGALQLVEL
NGQLTLAGEDGTPVQLRGMSTHGLQWFGEIVNENAFVALSNDWGSNMIRLAM YIGENG
YATNPEVKDLVYEGIELAFEHDMYVIVDWHVHAPGDPRADVYSGAYDFFEEIADHYKDH
PKNHYI IWELANESPNNNGGPGLTNDKKGWEAVKEYAEPIVEMLRKGDNMILVGNPN
WSQRPDLSADNPIDAENIMYSVHFYTGSHGASHIGYPEGTPSSERSNVMANVRYALDNGV
AVFATEWGT SQANGDGGPYFDEADVWLNFLNKHNSWANWSLTNKNEISGAFTPFELGR
TDATDLDPGANQVWAPEELSLSGEYVRARIKGIEYTPIDRTKFTKL VWD FNDGTTQGFQV
NGDSPNKESITLSNNNDALQIEGLNVSNDISEGNYWDNVRLSADGWSENVDILGATELTID
VIVEEPTTVSIAAIPQGPAAGWANPTRAIKVTEDDFESFGDGYKALVTITSEDSPTSLETIATS
PEDNTMSNII L FVGTEADVISLDNITVSGTEIEIEVIHDEKGTATLPSTFEDGTRQGWDWH
TESGVKTALTIEEANGSNALSWEYAYPEVKPSDGWATAPRLDFWKDELVRGTS DYISDFD
YIDAVRASEGAISINAVFQPPANGYWQEVPTT FEIDLTELDSATVTSDELYHYEVKINIRDIE
AITDDTELNRNLLIFADEDSDFAGRVFVDNVRFE

>sp|D2QPE6|HIS7_SPILD Histidine biosynthesis bifunctional protein HisB OS=Spirosoma
linguale (strain ATCC 33905 / DSM 74 / LMG 10896) OX=504472 GN=hisB PE=1 SV=1
MQKIVFIDRDGTLIAEPQPDQQVDSLAKLDFIPKAISAMRKIAEDTTYELVMVTNQDGLGT
GSFPEDTFWPAHNKMMSTFAGENVNFAAVHIDRHFPDHSSTRKPGVGMILTQYFEASYD
LTNSFVIGDRLTDVQLAVNLGAKAILFMPPNGLAAVQSADVSGLTEAMKQAIVLQTGDW
DEIYEFLRLPARTALVERNTKETQIRVELNLDGRGRADMHTGLGFFDHMLDQVAKHSGA
DLAIHVNGDLHIDEHHTIEDTALALGEAYRRALGDKRGISRYGFLPMDEALAQVGIDFSG
RPWLVDAAEFKREKIGDMPTMFYHFFKSFSDTALCNLNKIVEGDNEHHKIEAIFKAFK
AIKMAVRRDINELDNLPSTKGVL

>sp|Q9X0C7|HIS4_THEMA 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]
imidazole-4-carboxamide isomerase OS=Thermotoga maritima (strain ATCC 43589 / MSB8 /
DSM 3109 / JCM 10099) OX=243274 GN=hisA PE=1 SV=1
MLVVPAILDFRGKVARMIKGRKENTIFYEKDPVELVEKLIEEGFTLIHVVDLSNAIENSGEN
LPVLEKLSEFAEHQIGGGIRSLDYAEKLRKLGYYRRQIVSSKVLEDPSFLKSLREIDVEPVFS
LDTRGGRVAFKGWLAEEEIDPVSLKRLKEYGLEEIVHTEIEKDGTQLQEHDFSLTKKIAIEA
EVKVLAAAGGISSENSLKTAQKVHTETNGLLKGVIVGRAFLLEGILTVEVMKRYAR

>sp|P22317|HOXF_CUPNH NAD-reducing hydrogenase HoxS subunit alpha OS=Cupriavidus
necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) OX=381666 GN=hoxF PE=1 SV=1
MDSRITTLERYRSDRTRLIDILWDVQHEYGHIPDAVLPQLGAGLKLSPLDIRETASFYHFF
LDKPSGKYRIYLCNSVIAKINGYQAVREALERETGIRFGETDPNGMFGLFDTPCIGLSQDEP
AMLIDKVVFTRLRPGKITDIIAQLKQGRSPAELANPAGLPSQDIAYVDAMVESNVRTKGPV
FFRGRTDLRSLLDQCLLLKPEQVIETIVDSRLRGRGGAGFSTGLKWRLCRDAESEQKYVIC
NADEGEPGTFKDRVLLTRAPKKVFVGMVIAAYAIGCRKGIVYLRGEYFYLDYLERQLQE
LREDGLLGRAIGGRAGFDFFDIRIQMGAGAYICGDESALIESCEGKRGTPRVKPPFPVQQGY
LGKPTSVNNVETFAAVSRIMEEGADWFRAMGTPDSAGTRLLSVAGDCSKPGIYEVWGV
TLNEVLAMVGARDARAVQISGPSGECVSAKDGERKLAYEDLSCNGAFTIFNCKRDLLEI
VRDHMQFFVEESCGICVPCRAGNVDLHRKVEWVVIAGKACQKDLDDMVSWGALVRRTSR
CGLGATSPKPILTTLEKFPEIYQNKLVREHGPLLPSFDLDTALGGYEKALKDLEEVTR

>sp|P04772|GLNA2_BRADU Glutamine synthetase OS=Bradyrhizobium diazoefficiens (strain
JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110) OX=224911 GN=glnII PE=1 SV=2
MTKYKLEYIWLDGYTPTPNLRGKTQIKEFASFPTLEQLPLWGFDDGSSTQQAEGHSSDCVL
KPVAVFPDAARTNGVLVMCEVMMPDGKTPHASNKRATILDDAGAWFGFEQEYFFYKDG
RPLGFPTSGYPAPQGPYYTGVGFSNVGDVARKIVEEHLDLCLAAGINHEGINAEVAKGQW
EFQIFGKGSKKADEMWMARYLMLRLTEKYGIDIEFHCKPLGDTDWNNGSGMHANFSTEY
MRTVGGKEYFEALMAAFDKNLMDHIAVYGPNDNDKRLTGKHETAPWNKFSYGVADRG
SIRVPHSFVNNGYKGYLEDRRPNSQGDOPYQIASQILKTISSVPTEKKAVA

>sp|P01559|HST1_ECOLX Heat-stable enterotoxin ST-1A/ST-P OS=Escherichia coli OX=562
GN=sta1 PE=1 SV=1
MKKLMLAIFISVLSFSPFSQSTESLDSSKEKITLETKKCDVVKNNSEKKSENMNNTFYCCEL
CCNPACAGCY

>sp|Q9X0Z6|HYDE_THEMA [FeFe] hydrogenase maturase subunit HydE OS=Thermotoga
maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) OX=243274 GN=TM_1269
PE=1 SV=1
MTGREILEKLERREFTREVLKEALSINDRGFNEALFKLADEIRRKYVGDEVHIRAIIFFSNV
CRKNCLYCGLRRDNKNLKRYSMTPEEIVERARLAVQFGAKTIVLQSGEDPYYPMPDVISDI
VKEIKKMGAVALTSLGGEWPREYYEKWKEAGADRYLLRHETANPVLHRKLRPDTSFENRL
NCLLTLKELGYETGAGSMVGLPGQTIDDLVDDLLFLKEHDFDMVGIGPFIPHPDTPANEK
KGDFTLTLKMVALTRILLPDSNIPATTAMGTIVPGGREITLRGANVIMPNWTPSPYRQLY
QLYPGKICVFEDTACIPCVMKMIELLGRKPGRDWGGKRKFVETV

>sp|P9WKL1|IDH_MYCTU Isocitrate dehydrogenase [NADP] OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=icd PE=1 SV=1
MSNAPKIKVSGPVVELDGDDEMTRVIWKLKIDMLILPYLDIRLDYYDLGIEHRDATDDQVTI
DAAYAIKKHGVGVKCATITPDEARVEEFNLKKMWLSPNGTIRNLLGGTIFREPVISNVPR
VPGWTKPIVIGRHAFGDQYRATNFKVDQPGTVTLTFTPADGSAPIVHEMVSIPEDEGGVVL
GMYNFKESIRDFARASFSYGLNAKWPVYLSTKNTILKAYDGMFKDEFERVYEEEFKAQFE
AAGLTIEHRLIDDMVAACLKWEAGGYVWACKNYDGDVQSDTVAQGYGSLGLMTSVLMT
ADGKTVEAEAAHGTVTRHYRQYQAGKPTSTNPIASIFAWTRGLQHRGKLDGTPEVIDFAH
KLESVVIATVESGKMTKDLAILIGPEQDWLNSEEFDAIADNLEKELAN

>sp|P9WNW9|HISX_MYCTU Histidinol dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=hisD PE=1 SV=2
MVYVTAPPPVLTRIDLRGAELTAAELRAALPRGGADVEAVLPTVRPIVAAVAERGAEAL
DFGASFDGVRPHAIRVPDAALDAALAGLDGCDVCEALQVMVERTRAVHSGQRRDVTITL
GPGATVTERWVPVERVGLYVPGGNAVYPSSVVMNVVPAQAAGVDSLVAASPPQAQWD
GMPHPTILAAARLLGVDEVWAVGGAQAVALLAYGGTDDTDGAALTPVDMITGPGNIYVT
AAKRLCSRVRGIDAEAGPTEIAILADHTADPVHVAADLISQAEHDELAASVLVTPSEDLAD
ATDAELAGQLQTTVHRERVTAALTGRQSAIVLVDDVDAAVLVVNAYAAEHLEIQTADAP
QVASRIRSAGAIQVGPWSPVSLGDYCAAGSNHVLPTAGCARHSSGLSVQTFLRGIHVVEYTE
AALKDVSQGHVITLATAEDLPAHGEAVRRRFR

>sp|Q93UJ2|GMHA_BURPS Phosphoheptose isomerase OS=Burkholderia pseudomallei (strain K96243) OX=272560 GN=gmhA PE=1 SV=2
MENRELTYITNSIAEAQRVMAAMLADERLLATVRKVADACIASIAQGGKVLLAGNGGSA
ADAQHIAGEFVSRFAFDRPGLPAVALTTDTSILTAINNDYGYEKLFSRQVQALGNEGDVLI
GYSTSGKSPNILAAFREAKAKGMTCVGFTGNRGEMRELCDLLEVPADTPKIQEGHLV
LGHIVCGLVEHSIFGKQ

>sp|Q05819|HEP1_PEDHE Heparin lyase I OS=Pedobacter heparinus OX=984 PE=1 SV=1
MKKQILYLIVLQQLFLCSAYAQQKKSGNIPYRVNVQADSAKQKAIIDNKWVAVGINKPYA
LQYDDKLRFNKGPSYRFELKAEDNSLEGYAAGETKGRTELSYSYATTNDFKKFPSPVYQN
AQKLKTVYHYGKGICEQGSSRSYTFVYIPSSFPDNATTIFAQWHGAPSRTLVAPEGEIKT
LSIEEFLALYDRMIFKKNIAHDKVEKKDKDGKITYVAGKPNGWKVEQGGYPTLAFGFSKG
YFYIKANSRQWLTDKADRNNANPENSEVMKPYSSEYKTSTIAYKMPFAQFPKDCWITFD
VAIDWTKYGKEANTILKPGKLDVMMTYTKNKKPQKAHIVNQQEILIGRNDDDGYYFKFG
IYRVGNSTVPVTYNLSGYSETAR

>sp|Q9KSX0|HIS5_VIBCH Imidazole glycerol phosphate synthase subunit HisH OS=Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961) OX=243277 GN=hisH PE=1 SV=1
MTQNVVIIDTGCANISSVKFAIERLGAVTISRDPQVVLAADKLFLPGVGTASEAMKNLTE
RDLIELVKRVEKPLLGLICLGMQLLGLKSEEKGQKADEIVQCLGLVDGEVRLQTGDLPLP
HMGWNTVQVKEGHPLFNIEPDAIFYFVHSFAMPVGDYTIAQCEYGPFSAAIQAGNYY
GVQFHPERSSKAGARLIQNLEL

>sp|P99158|HUTG_STAAN Formimidoylglutamase OS=Staphylococcus aureus (strain N315) OX=158879 GN=hutG PE=1 SV=1
MYKQGEPNLWTGRDSETDPKKFRHFQTVTFEDLSKLEKSSMPSGVGILGYAVDKGVAL
NKGRIGAKEGPDAIKQAFAGLPDLNQCETLVYDGNVYHDHEELIDTQKEFAMLAAKSIAN
HRQTFLGGGHDIAYAQYLATRKYPTQSIGVINIDAHFDTRAEQQSTSGTSFRQILEEDEN
TDYLVLGIAQGGNTQSLFDYAKEKKIDYVFADELLSHVSPTIKDMIERFVHEHDVIMFTIC
MDVIDSAFAPGVSAPAVLGLYPHTVLELAKRIIPSDKVSSVSIAEMNPTYDADNRTAKLVA
NLVHHFLK

>sp|P70955|NATR_BACSU Transcriptional regulatory protein NatR OS=Bacillus subtilis (strain 168) OX=224308 GN=natR PE=1 SV=1

MVKVGLVDDYRVDLEKLEAIVSRMQDVEIVFSTDSAKEAYRRVKNGDIDLLLADIEMPH
MSGYELADLIKSHSLDVDVIFVTGHGGYAVHAFDLNVHDYIMKPYYADRLAASFDRYLK
KKTETSLNGRILIKQKSEMHVLQKKDIIFAERTGRSTTIVTTAEVQTYQTLNDIKGDLPEK
DFLRSHRSFIINIHYIKHFSAYTKHSFTVSFEGTSKKAMITKQQLDYFQNYFF
>sp|P30012|NADC_SALTY Nicotinate-nucleotide pyrophosphorylase [carboxylating]
OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=nadC
PE=1 SV=3
MPPRRYNPDDRRDALLERINLDIPAABAQALREDLGGEVDAGNDITAQLLPADTQAHATV
ITREDGVFCGKRWVEEVFIQLAGDDVRLTWHVDDGDIAHANQTVFELNGPARVLLTGER
TALNFVQTLSGVASEVRRYVGLLAGTQTQLLDTRKTLPLGLRTALKYAVLCGGGANHRLG
LTDAFLIKENHIIASGSVRQAVEKAFWLHPDVPVEVEVENLDELDDALKAGADIIMLDNFN
TDQMREAVKRVNGQARLEVSGNVTAETLREFAETGVDFISVGALTKHVRALDLSMRFC
>sp|Q47400|NEUC_ECOLX Polysialic acid biosynthesis protein P7 OS=Escherichia coli OX=562
GN=neuC PE=1 SV=3
MKKILYVTGSRAEYGIVRRLTMLRETPEIQLDLAVTGMHCDNAYGNTIHIIEQDNFNIIKV
VDININTTSHTHILHSMVCLNSFGDFFSNNTYDAVMVLGDRIEYFSVAIAASMHNIPLIHI
HGGEKTLANYDEFIRHSITKMSKLHLTSTEEYKKRVIQLGEKPGSVFNIGSLGAENALSLH
LPNKQELELKYGSLKRYFVVVFHPETLSTQSVNDQIDELLSAISFFKNTHDFIFIGSNADT
GSDIIQRKVKYFCKEYKFRYLISIRSEYDLAMIKYSCGLIGNSSSLGIEVPSLKVATINIGDRQ
KGRVRGASVIDVPVEKNAIVRGINISQDEKFISVVQSSSNPYFKENALINAVRIIKDFIKSKN
KDYKDFYDIPECTTSYD
>sp|Q03202|NISC_LACLL Nisin biosynthesis protein NisC OS=Lactococcus lactis subsp. lactis
OX=1360 GN=nisC PE=1 SV=1
MRIMMNKKNIKRNVEKIIAQWDERTRKNKENFDFGELTLSTGLPGIILMLAELKNKDNSKI
YQKKIDNYIEYIVSKLSTYGLLTGSLYSGAAGIALSILHLREDDEKYKNLLDSLNRYYEYFV
REKIEGFNLENITPPDYDVIEGLSGILSYLLINDEQYDDLKILIINFLSNLTKENGLISLYIK
SENQMSQSESEMYPLGCLNMGLAHGLAGVGCILAYAHIKGYSNEASLSALQKIIFIYEKFE
LERKKQFLWKDGLVADELKKEKVIREASFIRDAWCYGGPGISLLYLYGGLALDNDYFVD
KAEKILESAMQRKLGIDSYMICHGYSGLIEICSLFKRLLNTKKFDSYMEEFNVNSEQILEEY
GDESGTGFLGISGCILVLSKFEYSINFYWRQALLLFDDFLKGGKRK
>sp|B5M9L6|LSD18_STRLS Putative epoxidase LasC OS=Streptomyces lasaliensis OX=324833
GN=lsd18 PE=1 SV=1
MTNTRSAVVLGGGMAGMLVSSMLARHVGSVTVIDRDAPFAGPDLRKGVPQARHAHILW
SGGARIVEELLPGTTDRLLGAGAHRIIPDGQVSYTAYGWQHRFPEAQFMIACSRALLDW
TVREETLREERIALVEKTEVLALLGDAGRVTGVRVRDQESGEEREVPADLVVDTTGRGSP
SKRLLAELGLPAPEEEFVDSGMVYATRLFRAPEAAATNFPLVSVHADHRAGRPGCNAV
MPIEDGRWIVTVSGTRGGEPPADDEGFARFARDGVRHPLVGELIAKAQPLTSVERSRSTVN
RRLHYDRLATWPEGLVVLGDAVAAFNPVYGHGMSAAAHSVLALRSQLGQRAFQPGLAR
AAQRAIAVAVDDAWVLATSHDIGYPGCRTQTRDPRLTRHAGERQVRVTDLVGLTATRNVQV
VNRAAVALNTLSAGMASMQDPAVMAAVRRGPEVPAPTEPPLRPDEVARLVSGAGVTA
>sp|P45028|MLAC_HAEIN Intermembrane phospholipid transport system binding protein MlaC
OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421
GN=mlaC PE=1 SV=1
MNLIQLKKWFTILTFLVLAFLVTRTAIAETSPYVLMQQAADKLFSDIQANQSKIKQDPNYL
RTIVRNDLLPYVNLEYAGSKVLGSYYKSTSAEQREKFFKTFGELIEQKYAQALTNYSNQKI
QIESEKELGDNNFINIRVNIIQANGVAPILLYFKWRKGNKSGEWKVYDMVGAGVSMLED
IKNWVGILNKQGIDTLITKMQQSASQPIIFNQ
>sp|Q2P5V2|MURD2_XANOM UDP-N-acetylmuramoyl-L-alanine--L-glutamate ligase
OS=Xanthomonas oryzae pv. oryzae (strain MAFF 311018) OX=342109 GN=murD2 PE=1 SV=1

MRISQFEGKAVALWGWGREGRGAYRALRAQLPTQSLTMFCNAEEVRELESLADAALHV
ETDASAQALGRFEIVVKSPGISPYRAEALAAAAQGTQFIGGTALWFAEHAQPDGSPGAIC
VTGTKGKSTTTALLAHLRLVAGHRTALVGNIGQPLLEVLPQPPPAYWAIELSSYQTGDV
GRSGARPELAVVLNLFPEHLDWHGDEARYVRDKLSLVTEGRPRIVLLNAADPLLASLQLP
DSEVLWFNHPEGWHLRGDVVYRGEQAIFDSADVPLPGVHNRRNLCAVLAALGLDA
EALAPAALSFRPLPNRLQVLGSDGISYVNDSTTPYASLAALACFAQRRVALLVGGHDR
GLDWHDFARHMAQQAPLEIVTMAANGPRIHALLAPLADAGRFGHLHAANDLEHAMQLAR
DALGGQGGVLLSPGAPSGAYSDYVARGRHFAQLAGFDPAAISAIPLGLGVH

>sp|P81186|NAPA_DESDA Periplasmic nitrate reductase OS=Desulfovibrio desulfuricans (strain ATCC 27774 / DSM 6949) OX=525146 GN=napA PE=1 SV=2

MSTSRDFLKYFAMSAAVAAASGAGFGSLALAADNRPEKWVKGVCRYCGTGCGVLVG
VKDGKAVAIQGDPPNNHAGLLCLKGSLIPVLNSKERVLTQPLVRRHKGGKLEPVSWDEA
LDLMASRFRSSIDMYGPNSVAWYGSQCLTEESYVANKIFKGGFGTNNVDGNPRLCMAS
AVGGYVTSFGKDEPMGTADIDQATCFFIIGSNTSEAHPLFRRIARRKQVEPGVKIIVADP
RRTNTSRIADMHVAFRPGTDLAFMHSMAWVIINEELDNPRFWQRYVNFMDAEGKPSDFE
GYKAFLNRYRPEKVAEICRVPVEQIYGAARAFESAATMSLWCMGINQRVQGVFANNLI
HNLHLITGQICRPGATSFSLTGQPNACGGVRDGGALSHLLPAGRAIPNAKHRAEMEKLWG
LPEGRIAPEPGYHTVALFEALGRGDVKCMII CETNPAHTLPNLNKVHKAMSHPESFIVCIEA
FPDAVTLEYADLVLPAPFWCERDGVYGCGERYSLTEKAVDPPGQCRPTVNTLVEFARR
AGVDPQLVNFNAEDVWNEWRMVSKGTTYDFWGMTRELRERLKRKESGLIWPCPSDHPGTS
LRYVRGQDPCVPADHPDRFFFYGKPDGRAVIWMRPAKGAAEPPDAEYPLYLTSMRVIDH
WHTATMTGKVPPELQKANPIAFVEINEEDAARTGIKHGDSVIVETRRDAMELPAVSDVCR
PGLIAPVFFDPKKLVNKLFLDATDPVSREPEYKICAAVRKA

>sp|P96724|NFI_BACSU Endonuclease V OS=Bacillus subtilis (strain 168) OX=224308 GN=nfi PE=1 SV=2

MKVFDVHKFDMKKEQDFLQVQFNLKNRINLSPTIHPDSINTCAGVDLAYWEQDGEPIYGV
CCIIVIDADTKEVIEKVHSMGRISVPYVSGFLAFRELPLIIEAAKKLETEPDVFLFDGNGYLH
YNHMGVATHAAFFLGKPTIGIAKTYLKIKGCDFTPEIEVGAYTDIIIDGEVYGRALRTRR
DVKPIFLSCGNYIDLSSYQITMSLINQESRLPIPVRLADLETHVLRFTFYQKNHV

>sp|P07328|NIFD_AZOVI Nitrogenase molybdenum-iron protein alpha chain OS=Azotobacter vinelandii OX=354 GN=nifD PE=1 SV=3

MTGMSREEVESLIQEVLEVYPEKARKDRNKHSLAVNDPAVTQSKKCIISNKKSQPGLMTIR
GCAYAGSKGVVWGPDKMIHISHGVPVCGQYSRAGRNNYYIGTTGVNAFVTMNFSTDFQ
EKDIVFGGDKKLAKLIDEVETLPLNKGISVQSECPIGLIGDDIESVSKVKGAELESKTIVPVR
CEGFRGVSQSLGHHIANDAVRDWVLGKRDEDTTFASTPYDVAIIGDYNIGGDAWSSRILL
EEMGLRCVAQWSGDGSISEIELTPKVKLNLVHCYRSMNYISRHMEEKYGIWMEYNFFGP
TKTIESLRAIAAKFDESIQKKCEEVIAKYKPEWEAVVAKYRPRLEGKRVMLYIGGLRPRHV
IGAYEDLGMEVVGTYEFAHNDDYDRMTKEMGDSTLLYDDVTGYEFEEFVKRIKPDIG
SGIKEKFIFQKMGIPIFREMHSWDYSGPYHGFDGFAIFARDMDMTLNNPCWKKLQAPWEA
SEGAEKVAASA

>sp|Q8KC85|NIFB_CHLTE FeMo cofactor biosynthesis protein NifB OS=Chlorobaculum tepidum (strain ATCC 49652 / DSM 12025 / NBRC 103806 / TLS) OX=194439 GN=nifB PE=1 SV=1

MTLNIKNHPCFNDSSRHTYGRIHLPVAPKCNIQCNYCNRKFDKCMNENRPGITSKVLSPRQA
LYYLDNALKLSPNISVVGIAGPGDPFANPEETMETLRLVREKYPEMLLCVATNGLDMLPYI
EELAEQVSHVTLTINAIDPEIGQEIIYAWVRYQKKMYRDRQAAELLENQLAALQKLKRY
GVTAKVNSIIIPGVNDQHVIEVARQVASMADILNALPYNTTETVFENIPEPDPMVRKI
QEEAGKLLPQMKHCARCRADAVGIIIGEINSDEMMAKLAEALMPKNPDEHRPYIAVASL
EGVLINQHLGEADRFLVYALDEEKKSCTLVDSRQAPPPGGGKLRWEALAAKLSDCRAVL

VNSAGDSPQSVLKASGIDVMSIEGVIEEAVYGVFTGQNLKHLMKSSQIHACKTSCGGDGN
GCD

>sp|Q7WZY5|NREB_STACT Oxygen sensor histidine kinase NreB OS=Staphylococcus carnosus
(strain TM300) OX=396513 GN=nreB PE=1 SV=1
MKSISNRDKLQDLLTQYYLNTNEKMVFLNSTGEVIALNEAAEEVFADDNDYSQMTNAV
RRCEGYSNEYDIMSCENCFLEALEIGKGSFQVFIRTKDNKIQPYTASYELIDHEKGIYAFTL
HNVSPQIQRQERMYQRKMMQKTISAQENERKRISRELHDGIVQELINVDVELRLLKYQQD
KDELIDNSKRIEGIMSRLIDDVRNLSVELRPSSLLDDLGLDAAFRSYFKQFEKNYGIHVNYHT
NFSAQRFDNEIETVVYRVVQEALFNALKYAQVDIVEVSLQLNENNIIAEVSDRGVGFKRG
DDPKGTGLGLFGMNERAELVNGTVNIDSQINRGITVTLVPITD

>sp|P13266|NEUA_ECOLX N-acetylneuraminate cytidyltransferase OS=Escherichia coli
OX=562 GN=neuA PE=1 SV=1
MRTKIIAIPARSGSKGLRNKNALMLIDKPLLAYTIEAALQSEMFEKVIVTTDSEQYGAI
AESYGADFLLRPEELATDKASSFEFIKHALSIYTDYESFALLQPTSPFRDSTHII
EAVKLYQTLEKYQCVSVSTRSNKPSQIIRPLDDYSTLSFFDLDDYSKYNRNSIVEYHPNGAIFIAN
KQHLYLHTKHFFGRYSLAYIMDKESSLDIDDRMDFELAITIQKKNRQKIDLYQNIHNRINEKRNEFDSVS
DITLIGHSLFDYWDVKKINDIEVNNLGIAGINSKEYEYIEKELIVNFGEFVFIFFGTNDIVV
SDWKKEDTLWYLKKTCTQYIKKKNAASKIYLLSVPPVFGRIDRDNRINDLNSYLRENVDF
AKFISLDHVLKDSYGNLNKMYTYDGLHFNSNGYTVLENEIAEIVK

>sp|O25758|PARB_HELPY Probable chromosome-partitioning protein ParB OS=Helicobacter
pylori (strain ATCC 700392 / 26695) OX=85962 GN=parB PE=1 SV=1
MAKNKVLGRGLADIFPEINEVYEQGLYERANRVVELGIDEVMPNPYQPRKVFSEDSLEEL
AQSIKEHGLLQPVLVSENGRYHLIAGERRLRASKLAKMPTIKAIVVDIEQEKMR
EVALIENIQREDLNPLELARSYKELLESYQMTQEELSKIVKKSRAHVANIMRLTLSSKVQNALLEE
KITSGHAKVLVGLDGEKQELILNSIIGQKLSVRQTEDLARDFKINANFDNKKHGFKQTQTL
IAGDELERLNQSLWDHYKLKAALKGNKIVLRICYENSLLAEAFMKKMMS

>sp|O31042|PDUE_SALTY Propanediol dehydratase small subunit OS=Salmonella typhimurium
(strain LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=pduE PE=1 SV=1
MNTDAIESMVRDVL SRMNSLQGDAPAAAPAAGGTSRSAKVS DYPLANKHPEWVKTATN
KTLDDFTLENVLSNKVTAQDMRITPETLRLQASIAKDAGRDRLAMNFERAAELTAVPDDR
ILEIYNALRPYRSTKEELLA IADDLENRYQAKICAAFVREAAGLYVERKKLKGDD

>sp|A0A0H3LQK8|PDXA2_BORBR D-threonate 4-phosphate dehydrogenase OS=Bordetella
bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) OX=257310 GN=pxdA2 PE=1
SV=1
MTQDATPSRIPTLAVTLGDVAGIGPEITAKMLLGHDEL RQRARLLVVGDAAVLAQAVQA
VGGD PARVRVIATPAEATNQPGSIEVIQAGPSLAHVPPGQLSAEAGDGSVRYVTTACALA
RDGLIDGIVTAPLNKAAMH MAGHKWPGHTELLAHEFGVKTFSLVLSAGDLYIFHATTHV
SLRQAIEDVNPQRMRAVLR LAGSFARALGRADHPVAVAGLNPHAGENGIFGTEDAEILAP
AVAQANAEGILAAGPIPADALFPQAVRGKWK FVIA CYHDQGHAPFKSVYGGDDGVNITVG
LPVVRVSVDHGTAFDIAGKGIAREDSLVLAAERAAQLAPGWHQVWETARSTTGG

>sp|P22346|PEPX_LACLC Xaa-Pro dipeptidyl-peptidase OS=Lactococcus lactis subsp. cremoris
OX=1359 GN=pepX PE=1 SV=1
MRFNHFSIVDKNFDEQLAELDQLGFRWSVFWDEKKILKDFLIQSPSDMTALQATAELDVI
EFLKSSIELDWEIFWNIALQLLDFVPNDFEIGKA FEYAKNSNLPQIEAEMTTENIISAFYYL
LCTRRKTGMILVEHWVSEGLPLDNHYHFFNDKSLATFDSSLLEREVLWVESPVDSEQRG
ENDLIQIQIRPKSTELPVVMTASPYHLGINDKANDLALHDMNVELEEKTSHEIHVEQKLP
QKLSAKAKELPIVDKAPYRFTHGWTYSLNDYFLTRGFASIYVAGVGTRSSDGFQTS GDYQ
QIYSMTAVIDWLN GRARAYTSRKKTHEIKASWANGKVAMTGKSYLGT MAYGAATTGVE
GLELILAEAGISSWYNYRENGLVRSPGGFPGEDLDVLAALTYSRNLDGADFLKGNAEYE
KRLAEMTAALDRKSGDYNQFWHDRNYLINTDKVKADVLIVHGLQDWNVTPEQAYNFW

KALPEGHAKHAFLHRGAHIYMNSWQSIDFSETINAYFVAKLLDRDLNLDLPPVILQENSK
DQVWTMMNDFGANTQIKLPLGKTAVSFAQFDNNYDDETFKKYSKDFNVFKKDLFENKA
NEAVIDLELPSMLTINGPVELELRLKLNNDTKGFLSAQILDFGQKKRLEDKVRVKDFKVLDR
GRNFMLDDLVELPLVESPYQLVTKGFTNLQNQSLTVDLKADEWFTIKFELQPTIYHLEK
ADKLRVILYSTDFEHTVRDNRKVTYEIDLSQSKLIPIESVKN

>sp|Q59485|PEPX_LACHE Xaa-Pro dipeptidyl-peptidase OS=Lactobacillus helveticus OX=1587
GN=pepX PE=1 SV=1

MKYNQYAYVETDFQQQVKELIDINFLPKNYQVWDFSSLLAKLVKNAIAEAKTDAAKNAK
LAEFAVSDHQTLADFLKEKPTEIGTKQFYNVALQLLGYHVHYDYDFADPTGFMQRNALP
FLQDISDNQKLISAFYRLLNTRAKNGQILLDVMAGKGYFTQFWGQNKFKFFNGKSIPVFD
TNKVIREVVYVETDLDTDHDGKSDLIQVTVFRPEETNKGLKVPALYTASPYFGGIIANEKR
NHNVDENLSDSTEWNDPQYVHSPIVKAKEKPDGSSRPATEEAVHKSSYPLNEYMLARGFAS
VFAGAIGTRGSDGVRITGAPEETESAAAVIEWLHGDRVAYTDRTRTVQTTADWCNGNIG
MTGRSYLGTQLQIAIATTGVKGLKTVVSEAAISSWYDYREHGLVIAPEACQGEDDLLAE
TCQSNLWDAGSYLKIKPEYDKMQKQLREKEDRNTGQYSDFWEARNYRHHADGIKCSWI
SVHGLNDWNVKKPNVYKIWQLVKKMPMKHHLFLHQGPHYMNMLVSDFTDLMNLWF
VHELLGIENNAYNQWPTVMIQDNLQADKWHEEPDWSNDLGQEKIYYPTDEGELFQDGN
GKAQKSFTDVGGIEFKKAGISESDWQYKFCGDEKWAKPSLRFETDEFTHPTTIVGRPEVK
VRVSASLPKGEISVALVELGERQRLTATPKFLMHGGQELGYRFGTDTLQEFVPDKKTKAK
LITKAHMNLQNFKDMKKPEAIDADKFYDLDFLLQPTYYTIPSGSKLALIIYSTDQGMTKRP
LEDETYTIDLANTAIKFYEK

>sp|P0ACC1|PRMC_ECOLI Release factor glutamine methyltransferase OS=Escherichia coli
(strain K12) OX=83333 GN=prmC PE=1 SV=1

MEYQHWLREAI SQLQASESPRRDAEILLEHVTGRGRTFILAFGETQLTDEQCQQLDALLTR
RRDGEPIAHLTG VREFWSLPLFVSPATLIPRPDTECLVEQALARLPEQPCRILDLGTGTGAI
ALALASERPDC EIIAVDRMPDAVSLAQRNAQH LAIKNIHILQSDWFSALAGQQFAMIVSNP
PYIDEQDPHLQQGDVRFEPLTALVAADSGMADIVHIEQSRNALVSGGFLLEHGWQQGE
AVRQAFILAGYHDTVETCRDYGDNERVTLGRYYQ

>sp|P13398|NYLA_FLASK 6-aminohexanoate-cyclic-dimer hydrolase OS=Flavobacterium sp.
(strain K172) OX=261 GN=nylA PE=1 SV=2

MSKVDLWQDATAQAELVRSGEISRTELLEATIAHVQAVNPEINAVIPLFEKARRESELAS
GPFAGVPYLLKDLTVVSQGDINTSSIKGMKESGYRADHDA YFVQRMRAAGFVLLGKTNT
PEMGNQVTTEPEAWGATRNPWNLGRSVGGSSGSGSAAVAAALSPVAHGNDAAAGSVRIP
ASVCGVVGKPTRGRISPGPLVTDSDNVAGAAHEGLFARSVRDIAALLDVVSGHRPGDTF
CAPTASRPYAQGISENPGSLRVGVLTHNPVGDFALDPECAAAAARGAAAALAALGHDVND
AYPEALGDRSFLKDYSTICDVAIAREIERNGELIGRPLTEDDVEWTSWEMVKRADQVTGR
AFAACVDELRY YAGKVERWWEAGWDLILPTVTRQTPEIGELMLAKGTDLEGRQSAFIS
GSLQMLAFTVPFNVSGQPAISLPIMSSDGMPIGVQIVAA YGREDLLLQVAAQLEGALPW
VARRPQLLNPSRKIPAA

>sp|P77165|PAOA_ECOLI Aldehyde oxidoreductase iron-sulfur-binding subunit PaoA
OS=Escherichia coli (strain K12) OX=83333 GN=paoA PE=1 SV=1

MSNQGEYPEDNRVGKHEPHDLSLTRRDLIKVSAATAATAVVYPHSTLAASVPAATPAPEI
MPLTLKVNGKTEQLEVDTRTLLDTRLNLHLIGTKKGC DHGQC GACTVLVNGRRLNAC
LTLAVMHQGA EITIEGLGSPDNLHPMQAAFIKHDGFQCGYCTSGQICSSVAVLKEIQDGI
PSHVTVDLVSAPETTADEIRERMSGNICRCGAYANILAAIEDAAGEIKS

>sp|Q9RX25|PCP_DEIRA Pyrrolidone-carboxylate peptidase OS=Deinococcus radiodurans
(strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 /
VKM B-1422) OX=243230 GN=pcp PE=1 SV=1

MPTLLLTGFEPFH THPDNPSAQAAQELHGLELPGGWGVHSALLPVEPHAAGAALTRLLSE
QDPGAVLLTGLAAGRPQVTLERVGVGVMDFQIPDNAGQTYRDQPIEPDAPAAAYLATLPLR

AILAAWREAEIPGDISNSAGLYVCNFVLYHALHWLREHGRGAVPCGFLHVPANAAVALA
 VPADRPPLPYLPQSEITRAVRVAAEAITAQSSVLQMGKM
 >sp|P9WMQ9|PRIA_MYCTU Probable primosomal protein N' OS=Mycobacterium tuberculosis
 (strain ATCC 25618 / H37Rv) OX=83332 GN=priA PE=1 SV=1
 MLSVPHLDRDFDYLVPAEHSDDAQPGVRVRVRFHGRLVDGFLERRSDSDHHGKLGWL
 DRVVSPEPVLTTTEIRRLVDAVAARYAGTRQDVLRLAVPARHARVEREITTAPGRPVVAPV
 DPSGWAAYGRGRQFLAALADSRAARAVWQALPGELWADRFAEAAAQTVRAGRVLAI
 VPDQRDLDTLWQAATALVDEHSVVALSAGLGPEARYRRWLAALRGSARLVIGTRSAVFA
 PLSELGLVMVWADADDSLAEPAPYPHAREVAMLRHAHQARCAALIGGYARTAEHALV
 RSGWAHDVVAPRPEVRARSPRVVALDDSGYDDARDPAARTARLPSIALRAARSALQSGA
 PVLVQVPRRGYIPSLACGRCRAIARCSCTGPLSLQGAGSPGAVCRWCGRVDPTLRCVRC
 GSDVVRAVVVGARRTAEELGRAFPGTAVITSAGDTLVPQLDAGPALVVATPGAEPRAPG
 GYGALLLDLWALLGRQDLRAAEDALWRWMTAAALVRPRGAGGVTVVAESSIPTVQS
 LIRWDPVGHAEAEELAAARTEVGLPPSVHIAALDGPAGTVTALLEAARLPDPDRLQADLLGP
 VDLPPGVRRPAGIPADAPVIRMLLRVCREQGLELAASLRRGIGVLSARQTRQTRSLVRVQI
 DPLHIG
 >sp|P0C5D2|PTPA_STAAU Low molecular weight protein-tyrosine-phosphatase PtpA
 OS=Staphylococcus aureus OX=1280 GN=ptpA PE=1 SV=1
 MVDVAFVCLGNICRSPMAEAIMRQRLKDRNIHDIKVHSRGTGSWNLGEPPEHGTQKILNK
 HNIPFDGMISELFEATDDFDYIVAMDQSNVDNIKSINPNLKGQLFKLLEFSNMEESDVPDP
 YYTNNFEGVYDMVLSSCDNLIDYIVKDANLKEG
 >sp|Q9RQJ2|PAD_PORGI Peptidylarginine deiminase OS=Porphyromonas gingivalis (strain
 ATCC BAA-308 / W83) OX=242619 GN=PG_1424 PE=1 SV=1
 MKKLLQAKALILALGLFQLPAIAQTQMADRTNGQFATEEMQRAFQETNPPAGPVRAIAE
 YERSAAVLVRYPFGIPMELIKELAKNDKVITIVASESQKNTVITQYTQSGVNLSNCDFIK
 TDSYWTRDYGTFWAMYDTNKVGLVDFIYNRPRPNDDEFKYEAYQLGIEMFGMKLKQT
 GGNMTDGYGSAVQSHIAYTENSLSQAQVNQKMKDYLGITHHDVVQDPNGEYINHVD
 CWGKYLA PNKILIRKVPDNHPQHQALEDMAAYFAAQTCAWGTKYEVYRALATNEQPYT
 NSLILNNRVFVPVNGPASVDNDALNVYKTAMPGYEIIGVKGASGTPWLGTDALHCRTHE
 VADKGYLYIKHYPIGEQAGPDYKIEADVSCANATISPVQCYYRINGSGSFKAADMTME
 STGHYTYSTGLNKNKDKVEYYISAADNSGRKETYPFIGEPDPFKFTCMNETNTCTVTGAA
 KALRAWFNAGRSELAVSVSLNIAGTYRIKLYNTAGEEVAAMTKELVAGTSVFSMDVYSQ
 APGTYVLVVEGNGIRETMKILK
 >sp|P25889|PREA_ECOLI NAD-dependent dihydropyrimidine dehydrogenase subunit PreA
 OS=Escherichia coli (strain K12) OX=83333 GN=preA PE=1 SV=3
 MLTKDLSITFCGVKFPNPFCLSSSPVGNCYEMCAKAYDTGWGGVVFKTIGFFIANEVSPRF
 DHLVKEDTGFIGFKNMEQIAEHPLEENLAALRRLKEDYDPKVLIASIMGENEQQWEELAR
 LVQEAGADMIECNFSCPQMTSHAMGSDVGQSPELVEKYCRAVKRGSTLPMLAKMTPNIG
 DMCEVALAAKRGGADGIAAINTVKSITNIDLNQKIGMPIVNGKSSISGYSGKAVKPIALRFI
 QQMRTHPELRDFPISGIGGIETWEDAAEFLLGAATLQVTTGIMQYGYRIVEDMASGLSHY
 LADQGFDLQEMVGLANNIVPAEDLDRSYIVYPRINLDKCVGCGRCYISCYDGGHQAM
 EWSEKTRTPHCNTEKCVGCLLCGHVCPVGCIELGEVKFKKGEKEHPVTL
 >sp|P20041|PGLR_RALSL Polygalacturonase OS=Ralstonia solanacearum OX=305 GN=pglA
 PE=1 SV=1
 MNHRYTLLALAAAALSAGAHATGTSVTAPWGEVAEPSLPADSAVCKTLSASITPIKGSVD
 SVDGNPANSQPDASRIQSAIDNCPAGQAVKLVKGSAGESGFLSGSLKLKSGVTLWIDTGV
 TLFASRNPA DYDNLGTCGTATTSDNDKSCNALIVARDTAGSGIVGAGAI DGRGGS LVTSG
 PNANRLTWWDIA YLNKTKGLNQNPRLIQTYNGSAFTLYGVTVQNSPNFHVITTTGTS GVT
 AWGIKIVTPSLAYAVAGYKCPSGSTPDKVTPATCFPTETVKNTDGFDPGQSTNVVLAYS YI
 NTGDDHVAVKASSGPTRNLLFAHNHFYYGHGLSIGSETNTGVSNMLVTDLTMDGNDSSA

GNGLRIKSDASRGGKVTNIVYDGICMRNVKEPLVFDPFYSSVKGSLYPNFTNIVVKNFHDL
 GSAKSIKRTMTFLGYKANKQKNPLTITLDNVVFDGTLPAFEGSHYGGPASPNGVHFTFGG
 TGPVSFADAIVTSSTTDVTVTGTPGTAAAVDCSKAFVPLKSVAPTSP
 >sp|Q59589|PILA_MYXXD Fimbrial protein OS=Myxococcus xanthus (strain DK 1622)
 OX=246197 GN=pilA PE=1 SV=1
 MRVSRFNPRNRGFTLIELMIVVAIIGILAAIAIPNFIKFQARSKQSEAKTNLKALYTAQKSFF
 SEKDRYSDFANEIGFAPERGNRYGYRVSAAGDCEVRNAADLPVPAAGVPCISNDSFRFG
 ANSAIDDPVVARFVPQGAAGWNTTLGVQPTIADCPNCNFFAGARGNADNEATFDDWV
 IAGFEGSGQVGPCSEAGNVASGTPYNTRNDVACDGAAQ
 >sp|Q6N140|PK21_RHOPA Polyphosphate:ADP phosphotransferase OS=Rhodopseudomonas
 palustris (strain ATCC BAA-98 / CGA009) OX=258594 GN=RPA4569 PE=1 SV=1
 MKIKTKQFRVGEKEKVDLGKWPTKVDPFYESKEHYHELLRTQVERLSDLQQLLYASNRH
 AVLLIFQAMDAAGKDGVRHVLSGINPQGCQVFSFKHPSATELQHDFLWRTTRDLPERGRI
 GVFNRSYYEEVLIVRVHPDILQSEAVPNGENFGKSFWHKRYRSIRNLEQHLHANGTRIVKF
 FLHLSKDEQRKRFLARIDEPEKNWKFSAADLEERQYWDDYMDAYEKCLSETSSDSPWY
 AVPADDKENARLIVSQVIAETMESLKMSYPETTPARRKELLQMRQQLK
 >sp|P08179|PUR3_ECOLI Phosphoribosylglycinamide formyltransferase OS=Escherichia coli
 (strain K12) OX=83333 GN=purN PE=1 SV=1
 MNIVVLISGNGSNLQAIIDACKTNKIKGTVRVAVFSNKADAFGLERARQAGIATHTLIASAF
 DSREAYDRELIHEIDMYAPDVVVLGFMRLSPAFVSHYAGRLLNIHPSLLPKYPGLHTHR
 QALENGDEEHGTSVHFVTDELDDGGPVILQAKVPVFAGDSEDDITARVQTQEHAIIYPLVIS
 WFADGRLKMHENAAWLDGQRLPPQGYAADE
 >sp|P67675|PRIB_BORPA Primosomal replication protein N OS=Bordetella parapertussis (strain
 12822 / ATCC BAA-587 / NCTC 13253) OX=257311 GN=priB PE=1 SV=1
 MNTLELSARVLECGAMRHTPAGLPALLLLHVESEVVEAGHPRRVELTISAVALGDLALL
 LADTPLGTEMQVQGFLAPARKDSVKVKLHLQARRIAGSMGRDPLVG
 >sp|P15640|PUR2_ECOLI Phosphoribosylamine--glycine ligase OS=Escherichia coli (strain K12)
 OX=83333 GN=purD PE=1 SV=2
 MKVLVIGNGGREHALAWKAAQSPLVETVVFVAPGNAGTALEPALQNVAIGVTDIPALLDF
 AQNEKIDLTIVGPEAPLVKGVVDTFRAAGLKIFGPTAGAAQLEGSKAFTKDFLARHKKIPTA
 EYQNFTEVEPALAYLREKGAPIVIKADGLAAGKGVIVAMTLEEAEEAAVHDMLAGNAFGD
 AGHRIVIEEFLDGEEASFIVMVDGEHVLPMATSQDHKRVGDKDTGPNTGGMGAYSPAPV
 VTDDVHQRTERIHWPTVKGMAAEGNTYTGFYAGLMIDKQGNPKVIEFNCRFGDPETQ
 PIMLRMKSDLVELCLAACESKLDEKTSEWDERASLGVVMAAGGYPGDYRTGDVIHGLPL
 EEVAGGKVFHAGTKLADDEQVVTNGGRVLCVTALGHTVAAEQKRAYALMTDIHWDDC
 FCRKDIGWRAIEREQN
 >sp|O34779|PRPC_BACSU Protein phosphatase PrpC OS=Bacillus subtilis (strain 168)
 OX=224308 GN=prpC PE=1 SV=1
 MLTALKTDTGKIRQHNEDDAGIFKKGKDEFILAVVADGMGGHLAGDVASKMAVKAMGEK
 WNEAETIPTAPSECEKWLEIEQILSVNSKIYDHAQAHEECQGMGTIVCALFTGKTVSVAHI
 GDSRCYLLQDDDFVQVTEDHSLVNELVRTGEISREDAEHHPRKNVLTALGTDQLVSIDT
 RSFDIEPGDKLLLCSDGLTNKVEGTELKDILQSDSAPQEKVNLLVDKANQNGGEDNITAVL
 LELALQVEEGEDQC
 >sp|Q609I3|PFP_METCA Pyrophosphate--fructose 6-phosphate 1-phosphotransferase
 OS=Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) OX=243233 GN=pfp
 PE=1 SV=1
 MAARNAFYAQSGGVTAVINASACGVLETARQYPDRIGTVYAGRNGIVGALTEDLIDTGQ
 ESAEIAIALRHTPSGAFGSCRYKLKGLEENRAQYERLIEVFRAHDIGYFFYNGGGDSADTC
 LKVSQSEKLGYPQLQAVHIPKTVNDLPITDCCPGFGSVAKYIAVSVREASFDVRSMAATS
 TCIFVLEVMGRHAGWIAAAGGLASDERHELALVILFPEQVFDPERFLRAVDEKVRSHGYC

SVVVSEGIRGADGRFVAESGSRDVFGHARLGGVAPVIADLIKERLGKYHWA VADYLQR
AARHIASRTDVEQAYAVGKAGVEMALKGLSAVMPAIVRTSDSPYRWEITAASLAEVANV
EKKMPLEFISADGFGITEACRRYLRLIEGEDYPPYAGGLPDYVTL CNVAVPKKLAASFVS
>sp|Q0P8U5|PSEG_CAMJE UDP-2,4-diacetamido-2,4,6-trideoxy-beta-L-altropyranose hydrolase
OS=Campylobacter jejuni subsp. jejuni serotype O:2 (strain ATCC 700819 / NCTC 11168)
OX=192222 GN=pseG PE=1 SV=1
MKVLFRRSDSSSQIGFGHIKRDVLAKQYSDVSFACLPLEGLSIDEIPYPVYELSSSESIYELINL
IKEEFELLIIDHYGISVDDEKLIKLETGVKILSFDDEIKPHHCDILLNVNAYAKASDYEGLV
PFKCEVRCGFSYALIREEFYQEAKENREKKYDFFICMGGTDIKNLSLQIASELPKTKIISIAT
SSSNPNLKKLQKFAKLHNNIRLFIDHENIAKLMNESNKLIISASSLVNEALLKANFKAICY
VKNQESTATWLAKKGYEVEYKY
>sp|Q9RUB7|PSPA_DEIRA Phage shock protein A homolog OS=Deinococcus radiodurans (strain
ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM
B-1422) OX=243230 GN=DR_1473 PE=1 SV=1
MSIFDRLSRLLRANVNDMISKAEDPAKIIDQALRDMRSAYADARNEVAGAMAQAAKLER
EAGTNSKLAAEYKKAEEALRGGSDDLAREALRR AQNHKDLAKGFDEQRTVQQSTVDQ
LKTQLRALEAKIDEMESKKTLLAARQKTAQAGETLDRVSGFSKAGGAMDAFNEME QKV
AGMEDRNKAMGELRNDQDFDAQKDLGRDKDVDDALAALKAKVQSSNQ
>sp|Q59702|PCHA_PSEPU 4-hydroxybenzaldehyde dehydrogenase (NADP(+))
OS=Pseudomonas putida OX=303 GN=pchA PE=1 SV=2
MSQRLAAYENMSLQLIAGEWRVVGKAGRDLVDLPFTQEKLLQIPLANREDLDEAYRSAR
QAQVAWAACGPSERAQVMLNAVRI FDERRDEIIDWIRESGSTRIKAQIEWGAARAITQES
ASLPSRVHGRILASDVP GKESRVYREPLGVIGIISPWNFPLHLTARSLAPALALGNACVIKP
ASDTPVTGGLLLAHIFEEAGLPKGVLSVVVGSGSEIGDAFVEHEVPGFISFTGSTQVGRNIG
RIAAGGEHLKHVALELGGNSPFVVLADADLDQAVNAAVVGKFLHQGQICMAINRIIVEDS
VYDEFVNRYAERVKSLPYGDPSKPETVVGVPVINAQQLAGLQDKIATAKSEGARVMVEGE
AQGNVLP PHVFADVTADMEIAREEIFGPLVGIQRARDEAHALELANSS EYGLSSAVFTSSL
ERGVKFARGIRAGMTHINDIPVNDEPNAPFGGEKNSGLGRFNGDWAIEEFTTDHWITVQH
APRRYPF
>sp|Q8L3B2|PADF_AZOEV NADH-dependent phenylglyoxylate dehydrogenase subunit delta
OS=Azoarcus evansii OX=59406 GN=padF PE=1 SV=1
MSRHQSYPLFNLEQAGVPDDLCPVATVVS PMLPGDWRSMPVVD RDKCVKCAVCWLYC
PVQCVEEHA AWFDFNLKTCKGCGICANECPQRRSR
>sp|Q55434|PHY2_SYNY3 Phytochrome-like protein cph2 OS=Synechocystis sp. (strain PCC
6803 / Kazusa) OX=1111708 GN=cph2 PE=1 SV=1
MNPNRSLEDFLRNVINKFHRALTLRET LQVIVEEARIFLGVD RVKIYKFASDGSGEVLAEA
VNRAALPSLLGLHFPVEDIPPQAREELGNQRKMIAVDVAHRRKKSHEL SGRISPTEHSNGH
YTTVDSCHIQYLLAMGVLSSLTPVPMQDQQLWGIMAVHHSKPRRFTEQEWETMALLSKE
VSLAITQS QLSRQVHQQQVQEALVQRLETTVAQYGDRPETWQYALETVGQAVEADGAV
LYIAPDLTGSAQHYQWNLRFDWGNWLETSLWQELMRGQPSAAMEPMAAVQSTWEKP
RPFTSVAPLPPTNCVPHGYTLGELEQRSDWIAPPESLSAENFQSFLIVPLAADQQWVGS LIL
LRKEKSLVKHWAGKRGIDRRNIPRLSFEAWEETQKL VPTWNRSERKLAQVASTQLYMA
ITQQFVTRLITQQTAYDPLTQLPNWIIFN RQLTLALLDALYEGKMVGVLVIAMDRFKRINE
SFGHKTGDGLLQEVADRLNQKLSPLAAYSPLLSRW HGDGFTILLTQISDNQEMIPLCERLL
STFQEPFFLQGQPIYLTASMGISTAPYDGETAESLLKFAEIALTRAKCQGKNTYQFYRPQDS
APMLDRLTLES DLRQALTNQEFVLYFQPQVALDTGKLLGVEALVRWQHPRLGQVAPDVF
IPLAEELGLINHLGQWVLETACATHQHFFRETGRRLMAVNISARQFQDEKWLNSVLECL
KRTGMPPEDLELEITESLMMEDIKGT VVLLHRLREEGVQVAIDDFGTGYSSLSILKQLPIHR
LKIDKSFVNDLLNEGADTAIIQYVIDLANGLNLETVAEGIESEAQLQRLQKMGCHLGQGYF
LTRPLPAEAMMTYLYYPQILD FGTPPLPKVALPETET EAGQGNVGDRPLPNSLNRENPW

TEKLHDYVLLKERLQQRNVKEKLVVKIANKIRASLNINDILYSTVTEVRQFLNTDRVVLFK
FNSQWSGQVVTESHNDFCRSIINDEIDDPCKGHYLRLYREGRVRAVSDIEKADLADCHK
ELLRHYQVKANLVVPVVFNENLWGLLIAHECKTPRYWQEEDLQLLMELATQVAIAIHQG
ELYEQLETANIRLQQISSLDALTQVGNRYLFDSTLEREWQRLQRIREPLALLLCDVDFFKG
FNDNYGHPAGDRCLKKIADAMAKVAKRPTDLVARYGGEEFAILLSETSLEGAINVTEALQ
VEVANLAIPHTVSGTGHVTLSIGIAVYTPERHINPNALVKAADLALYEAKAKGRNQWLAY
EGSQLPHVDGEV

>sp|P67318|NRDR_STRPN Transcriptional repressor NrdR OS=Streptococcus pneumoniae
serotype 4 (strain ATCC BAA-334 / TIGR4) OX=170187 GN=nrdR PE=1 SV=1
MRCPKCGATKSSVIDSRQAEEGNTIRRRRECDECQHRFTTYERVEERTLVVVKKDGTREQ
FSRDKIFNGIIRSAQKRPVSSDEINMVVNRIEQKLGRNENEIQSEDIGSLVMEELAELEIT
YVRFASVYRSFKDVSELESLLQQITQSSKKKKER

>sp|Q51947|NAHE1_PSEPU Trans-O-hydroxybenzylidenepyruvate hydratase-aldolase
OS=Pseudomonas putida OX=303 GN=nahE PE=1 SV=1
MLNKVIKTTRLTAEDINGAWTIMPTSTPDASDWRSTNTVDLDETARIVEELIAAGVNGIL
SMGTFGECATLTWEEKRDYVSTVVETIRGRVPYFCGTTALNTREVIRQTRELIDIGANGTM
LGVPMWVKMDLPTAVQFYRDVAGAVPEAAIAIYANPEAFKFDPRPFWAEMSKIPQVVT
AKYLGIGMLDLDLKLAPNIRFLPHEDDYAAARINPERITAFWSSGAMCGPATAIMLRDE
VERAKSTGDWIKAKAISDDMRAADSTLFPRGDFSEFSKYNIGLEKARMDAAGWLKAGPC
RPPYNLVPEDYLVGAQKSGKAWAALHAKYSK

>sp|O31156|PHNX_BACCE Phosphonoacetaldehyde hydrolase OS=Bacillus cereus OX=1396
GN=phnX PE=1 SV=3
MKIEAVIFDWAGTTVDYGCFAPLEVFMEIFHKRGVAITAEEARKPMGLLKIDHVRALTEM
PRIASEWNRVFRQLPTEADIQEMYEEFEEILFAILPRYASPINGVKEVIASLRERGIKIGSTTG
YTREMMDIVAKEAALQGYKPDFLVTDDVPAGRPYPWMCYKNAMELGVPYPMNHMIKV
GDTVSDMKEGRNAGMWTVGVLGSSELGLTEEEVENMDSVELREKIEVVRNRFVENGAAH
FTIETMQELESVMEHIEKQELIIS

>sp|P9WIA3|PHOL_MYCTU PhoH-like protein OS=Mycobacterium tuberculosis (strain ATCC
25618 / H37Rv) OX=83332 GN=Rv2368c PE=1 SV=1
MTSRETRAADAAGARQADAQVRSSIDVPPDLVVGLLSADENLRALERTLSADLHVVRGN
AVTLCGEPADVALAERVISELIAIVASGQSLTPEVVRHSVAMLVGTGNESPAEVLTLTDILSR
RGKTIRPKTLNQKRYVDAIDANTIVFGIGPAGTGKTYLAMAKAVHALQTKQVTRIILTRPA
VEAGERLGFLPGTLSEKIDPYLRPLYDALYDMMDPPELIPKLMSAGVIEVAPLAYMRGRTL
NDAFIVLDEAQNTTAEQMKMFLTRLGFGSKVVVTGDVTQIDLPGGARSLRAAVDILEDI
DDIHIAELTSVDVVRHRLVSEIVDAYARYEEPGSGLNRAARRASGARGRR

>sp|P16687|PHNI_ECOLI Alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit
PhnI OS=Escherichia coli (strain K12) OX=83333 GN=phnI PE=1 SV=2
MYVAVKGGEKAIDAAHALQESRRRGDTDLPELSVAQIEQQLNLAVDRVMTEGGIADREL
AALALKQASGDNVEAIFLLRAYRTTLAKLAVSEPLDTTGMRLERRISAVYKDIPGGQLLGP
TYDYTHRLLDFTLLANGEAPTTLTADSEQQPSPHVFSLLARQGLAKFEEDSGAQPDITRT
PPVYPCSRSSRLQQLMRGDEGYLLALAYSTQRGYGRNHPFAGEIRSGYIDVSIVPEELGFA
VNVGELLMTECEMVNGFIDPPGEPHFTRGYGLVFGMSERKAMAMALVDRALQAPEYG
EHATGPAQDEEFVLAHADNVEAAGFVSHLKLPHYVDFQAELELLKRLQQEQNHG

>sp|P16684|PHNF_ECOLI Probable transcriptional regulator PhnF OS=Escherichia coli (strain
K12) OX=83333 GN=phnF PE=1 SV=1
MHLSTHPTSYPTRYQEIAAKLEQELRQHYRCGDYLPAEQQLAARFEVNRHTLRRRAIDQLV
EKGWVQRRQGVGVVLVLMRPFDYPLNAQARFSQNLDDQGSHTSEKLLSVLRPASGHVAD
ALGITEGENVIHLRTRLRRVNGVALCLIDHYFADLTLWPTLQRFDSGSLHDFLREQTGIALR
RSQTRISARRAQAKECQRLEIPNMSPLLCVRTLNRDGESSPAEYSVSLTRADMIEFTMEH

>sp|Q9X9S0|PYRDA_STRPN Probable dihydroorotate dehydrogenase A (fumarate)
OS=Streptococcus pneumoniae serotype 4 (strain ATCC BAA-334 / TIGR4) OX=170187
GN=pyrDA PE=1 SV=2
MVSTKTQIAGFEFDNCLMNAAGVACMTIEELEE VKNSAAGTFVTKTATLDFRQGNPEPRY
QDVPLGSINSMGLPNNGLDYYLDYLLDLQEKESNRTFFLSLVGMSPEETHILKKVQESDF
RGLTELNLSCPNVPGKPQIAYDFETTDRLAEVFAYFTKPLGIKLPYFDIVHFDQAAAFN
KYPLKFVNCVNSIGNGLYIEDES VVIRPKNGFGGIGGEYIKPTALANVHAFYQRLNPQIQII
GTGGVLTGRDAFEHILCGASMVQVGTTLHKEGVSAFDRITNELKAIMVEKGYESLEDFRG
KLRYID

>sp|P78061|PUUA_ECOLI Gamma-glutamylputrescine synthetase PuaA OS=Escherichia coli
(strain K12) OX=83333 GN=puaA PE=1 SV=2
METNIVEVENFVQQSEERRGSAFTQEVKRYLERYPNTQYVDVLLTDLNGCFRGKRIPVSS
LKKLEKGCYFPASVFAMDILGNVVEEAGLGQEMGEPDRTCVPVLGSLTPSAADPEFIGQM
LLTMVDEDGAPFDVEPRNVNLRLWQQLRQGLFPVVAVELEFYLLDRQRDAEGYLQPPC
APGTDDRNTQSQVYSVDNLNHFADVLNDIDELAQLQLIPADGAVAEASPGQFEINLYHTD
NVLEACDDALALKRLVRLMAEKHKMHATFMAKPYEEHAGSGMHIHISMQNNRGENVLS
DAEGEDSPLLKMLAGMIDLMPSSMALLAPNVNSYRRFQPGMYVPTQASWGHNNRTVA
LRPCGDRHNHRVEYRVAGADANPYLVMAAIFAGILHGLDNELPLQEEVEGNGLEQEGLP
FPIRQSDALGEFIENDHLRRYLGERFCHVYHACKNDELLQFERLITETIEWMLKNA

>sp|P10577|NTRC_RHIME DNA-binding transcriptional regulator NtrC OS=Rhizobium meliloti
(strain 1021) OX=266834 GN=ntrC PE=1 SV=2
MTGATILVADDDAAIRTVLNQALS RAGYDVRITSNAATLWRWIAAGDGD LVVTDVVM P
DENAFDLLPRIKKARPDLPVLVMSAQNTFMTAIKASEKGAYDYLPKPFDLTELIGIIGRAL
AEPKRRPSKLEDDSDQGMPLVGRSAAMQEYRVLARLMQTDLTLMITGESGTGKELVAR
ALHDYGKRRNGPFVAINMAAIPRDLIESELFGEKGAFTGAQTRSTGRFEQAEGGTFLFDE
IGDMPMDAQTRLLRVLQQGEYTTVGGRTPIRSDVRIVAATNKDLKQSINQGLFREDLYYR
LNVVPLRLPLRDRAEDIPDLVRHFVQQA EKEGLDVKRFDQEAELMKAHPWP GNVREL
ENLVRRLTALYPQDVITREIENELRSEIPDSPIEKAAARSGSLSISQAVEENMRQYFASFGD
ALPPSGLYDRVLAEMEYPLILAALTATRGNQIKAADLLGLNRNTLRKKIRELGVS VYRSSR
SA

>sp|P12041|PURQ_BACSU Phosphoribosylformylglycinamide synthase subunit PurQ
OS=Bacillus subtilis (strain 168) OX=224308 GN=purQ PE=1 SV=1
MKFAVIVLPGSNCDIDMYHAVKDELGHEVEYVWHEETSLDGF DGVLP GGFSYGDYLR C
GAJARFANIMPAVKQAAAEKGKPV LGVCNGFQILQELGLLP GAMRRNKDLKFICRPVELIV
QNDET LFTASYEKGESITIPVAHGEGNFYCDDETLATLKENNQIAFTYGSNINGSVSDIAGV
VNEKGNVLGMMMPHERAVDELLGSADGLKLFQSIVKNWRETHVTTA

>sp|P96917|VAPC5_MYCTU Ribonuclease VapC5 OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) OX=83332 GN=vapC5 PE=1 SV=2
MSTTPAAGVLDTSVFIATESGRQLDEALIPDRVATTVVTLAELRVGVLA AATTDIRAQRLA
TLESVADMETLPVDDDAARMWARLRIHLAESGRRVRINDLWIAAVAASRALPVITQDDD
FAALDGAASVEIIRV

>sp|O31562|YFIT_BACSU Putative metal-dependent hydrolase YfiT OS=Bacillus subtilis (strain
168) OX=224308 GN=yfiT PE=1 SV=1
MTSVNLSYPIGEYKPRE SISKQKDKWIQVLEE VPAKLKQAVEVMTDSQLDTPYRDGGW
TVRQVVHHLADSHMNSYIRFKLSLTEETPAIRPYDEKAWSELKDSKTADPSGSLALLQEL
HGRWTALLRTLTDQQFKRGFYHPDTKEITLENALGLYVWVSHHHIAHITELSRRMGWS

>sp|P64382|YHIT_HELPY Uncharacterized HIT-like protein HP_0404 OS=Helicobacter pylori
(strain ATCC 700392 / 26695) OX=85962 GN=HP_0404 PE=1 SV=1
MNVFEKIIQGEIPCSKILENERFLSFYDINPKAKVHALVIPKQSIQDFNGITPELMAQMTSFIF
EVVEKLGIKEKGYKLLTNVGKNAGQEV MHLHFHILSGDKH

>sp|P31808|YCIK_ECOLI Uncharacterized oxidoreductase YciK OS=Escherichia coli (strain K12)
OX=83333 GN=yciK PE=1 SV=3

MHYQPKQDLLNDRIILVTGASDGIGREAAMTYARYGATVILLGRNEEKLRQVASHINEET
GRQPQWFILDLTCTSENCQQLAQRIAVNYPRLDGVHLNAGLLGDVCPMSEQNPQVWQD
VMQVNVNATFMLTQALLPLLLKSDAGSLVFTSSSVGRQGRANWGAYAASKFATEGMMQ
VLADEYQQRLRVNCINPGGTRTAMRASAFPTEDPQKLKTPADIMPLYLWLMGDDSRRT
GMTFDAQPGRKPGISQ

>sp|G3XD01|WBPD_PSEAE UDP-2-acetamido-3-amino-2,3-dideoxy-D-glucuronate N-
acetyltransferase OS=Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 /
JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1) OX=208964 GN=wbpD PE=1 SV=1
MSYYQHPSAIVDDGAQIGSDSRVWHFVHCAGARIGAGVSLGQNVFVGNKVVGDRCKIQ
NNVSVYDNTLEEGVFCGSPMVFTNVYNPRSLIERKDQYRNTLVKKGATLGANCTIVCG
VTIGEYAFVGAGAVINKNVPSYALMVGVPARQIGWMSEFGEQLQLNEQGEAVCSHSGAR
YVLNGKILSKVDV

>sp|P9WF39|WHIB4_MYCTU Transcriptional regulator WhiB4 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) OX=83332 GN=whiB4 PE=1 SV=1
MSGTRPAARRTNLTAAQNVVRSVDAEERIAWVSKALCRTTDPDEL FVRGAAQRKAAVIC
RHCPVMQECAADALDNKVEFGVWGGMTERQRRALLKQHPEVVSWSDDYLEKRKRRTGT
AG

>sp|O25386|XERH_HELPY Tyrosine recombinase XerH OS=Helicobacter pylori (strain ATCC
700392 / 26695) OX=85962 GN=xerH PE=1 SV=1
MKHPLEELKDPTENLLLWIGRFLRYKCTSLSNSQVKDQNKVFECLNELNQACSSSQLEKV
CKKARNAGLLGINTYALPLLKFHEYFSKARLITERLAFNSLKNIDEVMLAEFLSVYTGGLS
LATKKNYRIALLGLFSYIDKQNQDENEKSYIYNITLKNISGVNQSAGNKLPTHLNNEELEK
FLESIDKIEMSAKVRARNRLLIKIIIVFTGMRSNEALQLKIKDFTLENGCYTILIKGKGDKYR
AVMLKAFHIESLLKEWLIERELYPVKNDLLFCNQKGSALTQAYLYKQVERIINFAGLRREK
NGAHMLRHSFATLLYQKRHDLLVQEALGHASLNTSRIYTHFDKQRLEEAASIWEEN

>sp|P54327|XKDG_BACSU Phage-like element PBSX protein XkdG OS=Bacillus subtilis (strain
168) OX=224308 GN=xkdG PE=1 SV=1
MRNQEIRKAEMSLSALKSGGLMNPAQASAFIRMVQNTPTIFSESRIQMENDSQKFEKIG
FGQRILRAAQEGKALSNDLTVPTTSTVQLNTKEVIAEINITYDTLENNIEKDGLQQTIMQI
LAERAAVDIEELIVNGDTASADPYLAQLDGIRKQAVSHIVDMNGEELSRAFKKGLKAVP
PKYLRI PQEFRFYTSHGLEVEWKDRVADRQTNLGDQAVQGGGLSTAFGVPVKGVSNIQPYT
VGEGDAQYDASDIILTHPKNIILGFSRNIRIEVDKDIRSRKFIIVLTAKLDSKFEEEDACAKLI
NVKE

>sp|Q45070|XYNC_BACSU Glucuronoxylanase XynC OS=Bacillus subtilis (strain 168)
OX=224308 GN=xynC PE=1 SV=1
MIPRIKKTICVLLVCFTMLSVMLGPGATEVLAASDVTNVNSAEKQVIRGFGGMNHPAWA
GDLTAAQRETAFGNGQNQLGFSILRIHVDENRRNNWYKEVETAKSAVKHGAIVFASPWNP
PSDMVETFNRRNGDTSARLKYNKYAAAYAQHLNDFVTFMKNNGVNLYAISVQNEPDYAH
EWTWWTPQEILRFMRENAGSINARVIAPESFYQLKNLSDPILNDPQALANMDILGTHLYG
TQVSQFPYPLFKQKGAGKDLWMTEVYYPNSDTNSADRWPEALDVSQHIHNAMVEGDFQ
AYVWWYIRRSYGPMKEDGTISKRGYNMAHFSKFVRPGYVRIDATKNPNANVYVSAYKG
DNKVIVIVAINKSNTGVNQNFVLQNGSASNVSRWITSSSNLQPGTNLTVSGNHFWAHLPA
QSVTTTFVVR

>sp|Q2G260|Y094_STAA8 Uncharacterized protein SAOUHSC_00094 OS=Staphylococcus
aureus (strain NCTC 8325) OX=93061 GN=SAOUHSC_00094 PE=1 SV=1
MKKLATVGSLIVTSTLVFSSMPFQNAHADTTSMNVSNKQSQNVQNHPRPYGGVVPQGMT
QAQYTELEKALPQLSAGSNMQDYNMKLYDATQNIADKYNVIITTNVGVFKPHAVRDMN

GHALPLTKDGNFYQTNVDANGVNHGGSEMVQNKTGHMSQQGHMNQNTHEPTATHATR
SYAIKPSNDESKSKYAFIKSSNEPK

>sp|O31699|YKUV_BACSU Thiol-disulfide oxidoreductase YkuV OS=Bacillus subtilis (strain
168) OX=224308 GN=ykuV PE=1 SV=2

MKLRQPMPELTGEKAWLNGETREQLIGEKP TLHFWSISCHLCKEAMPQVNEFRDKYQD
QLNVVAVHMPRSEDDLDPGKIKETAAEHDITQPIFVDSHALTDAFENEYVPAYYVFDKT
GQLRHFQAGGSGMKMLEKRVNRVLAETE

>sp|O86237|Y138A_HAEIN Uncharacterized protein HI_1388.1 OS=Haemophilus influenzae
(strain ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=HI_1388.1 PE=1 SV=1

MITVFGLKSKLAPRREKLA EVIYNSLHLGLDIPKGKHAIRFLCLEKEDFYYPFDRSDDYTVI
EINLMAGRMEGTKKRLIKMLFSELEYKLGIRAH DVEITIKEQPAHCWGFRGMTGDEARDL
DYDIYV

>sp|O31945|YONO_BACSU DNA-directed RNA polymerase YonO OS=Bacillus subtilis (strain
168) OX=224308 GN=yonO PE=1 SV=1

MKGKKDGLNKQVHIYSIDTS AFYNDQENKLHNKILKSYRYRDHLRKLEHV DKKHKKYIT
QRIISLKEKLYNAFNDHNQIRTLRTDSLKDNNVISLFD SVLTRLGIKENSLS EIMVVQTY
HFQILRDIIDKGFIHNNEKYVYFTSSAGQIRTKKSCFIKQSTLDKYQNALTCGLSVEHINAQ
GGSSINKWNSYMA LSNASSSWEIDIDKAIVVNDLETNVSSLVDYIDRDTYEITRKIMDPIE
HTDGCGMMLPSLSQKSFMVRLPWVKGLLPFD FRKFAEKHSSFIVKDVYGKEWDI IKDDI
QIIFTKSQFKMWKY YDSWDDYRYKFKKYGCLGAKLNEEDPSVEGKLT YQMLQTLTDITD
EELKQISSKT VSEITQLGTDKETMMKVLGATEKNKHKTSLQEALLIYPELLNDDHTKEI IK
NKKKSMIKDAKSGKLLVSDARYTYLCPDLYAF CERLFLGIESPKGLLSGSDVHCSLYDEG
YIDILRSPHLFREHGV RWNKKNEEYEWFITPGVYTSIHDPISKLLQFDNDGDKALIISDELI
VNIAKRNMADIVPLY YEMSVAQKQEINSRNIYEAL TLAYGINIGEYSNNITKIWN SDNINL
DVIKWLCMENNFTIDFAKTLFMPTRPDH VDEKIKDYIKNKVP HFFINAKDKEEHSVESINE
STVNKLD SIIPSDRINF AAVAGKFDYRFL LKNKEIKLNEAVINEYKRLDRNKKWLMNDEE
AKPGQKLYVYKIIKQK LLEIHND DGFITDVLVKHLYKKKSKYKSTLWECFGDIVLENIKH N
LKTFKGCCICGKAFKPTS NKA KYCQSCGKKKERD KYKKYNKKRINHR

>sp|P9WLX3|Y1486_MYCTU Uncharacterized protein Rv1486c OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv1486c PE=1 SV=1

MWCPSVSLSIWANAWLAGKAAPDDVLDALSLWAPTQSVAAYDAVAAGHTGLPWPDPVH
DAGTVSLLQTLRAAVGRRRLRG TINVVL PVPGDVRGLAAGTQFEHDALAAGEAVIVANP
EDPGSAVGLVPEFSYGDVDEAAQSEPLTPELCALSWMVYSLPGAPVLEHYELGDAEYALR
SAVRSAEALSTIGLGSSDVAKPRGLVEQLLESSRQHRVPDHAPS RALRVLENAAHVDAII
AVSAGLSRLPIGTQSLSDAQRATDALRPLTAVVRSARMSAVTAILHSAWPD

>sp|P77475|YQAB_ECOLI Fructose-1-phosphate phosphatase YqaB OS=Escherichia coli (strain
K12) OX=83333 GN=yqaB PE=1 SV=1

MYERYAGLIFDMDGTILDTEP THRKA WREVLGHYGLQYDIQAMIALNGSPTWRIAQAII E
LNQADLD PHALAREKTEAVRSMLLDSVEPLPLVDVVKSWHGRRPMAVGTGSESAIAEAL
LAHLGLRHYFDAVVAADHV KHHKPAPDTFLLCAQRMGVQPTQCVVFEDADFGIQAARA
AGMDAVDVRL

>sp|Q8NQ03|Y1651_CORGL Uncharacterized protein Cgl1651/cg1859 OS=Corynebacterium
glutamicum (strain ATCC 13032 / DSM 20300 / JCM 1318 / LMG 3730 / NCIMB 10025)
OX=196627 GN=Cgl1651 PE=1 SV=1

MKLFSRTSLVALGTAAAITLSGVTAPAF ADEDSNAAVSALKTAEDNTPEAPGASTPLKLE
QPGTITGVPGKAITPVT VKV VAGEAESFTSDNLPSGLLIDNTGKITGTPKKEFTGSAKIIAKN
EAGVEAEVYVNFDFNEEPSSEEPSSGSSD TDNIENWIKIITAVIGALT TILTFSTKLDSFLK

>sp|P9WFX9|TRPB_MYCTU Tryptophan synthase beta chain OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) OX=83332 GN=trpB PE=1 SV=1

MMTDLSTPDLPRMSAAIAEPTSHDPDSGGHFGGPSGWGGRYVPEALMAVIEEVTAAYQK
ERVSQDFLDDLDRLQANYAGRPSPLEYATRSLQSHAGSARIFLKREDLNHTGSHKINNVLG
QALLARRMGKTRVIAETGAGQHGVATATACALLGLDCVIYMGIDTARQALNVARMRL
LGAEVVAVQTGSKTLKDAINEAFRDWVANADNTYYCFGTAAGPHFPPTMVRDFQRIIGM
EARVQIQGQAGRLPDVAVACVGGGSNAIGIFHAFLDDPGVRLVGFEAAGDGVETGRHAA
TFTAGSPGAFHGSFSYLLQDEDGQTIESHSISAGLDYPGVGPEHAWLKEAGRVDYRPITDS
EAMDAFGLLCRMEGIIPAIESAHAVAGALKLGVELGRGAVIVVNLSGRGDKDVETA AKW
FLLGND

>sp|Q9A0T3|UCDH_STRP1 Unsaturated chondroitin disaccharide hydrolase OS=Streptococcus
pyogenes serotype M1 OX=301447 GN=ugl PE=1 SV=1

MARPLKTIALEPIKQPERFTKEDFLSQEDITQALDLALKQVRLNMDYFKEDFPTPATKDNQ
YAIMDNTEWTNAFWTGCLWLAYEYSGDDAIKALAQANDLSFLDRVTRDIELDHHDLGFL
YTPSCMAEWKLLKTPESREAALKAADKLVQRYQDKGGFIQAWGELGKKEDYRLIIDCLL
NIQLFFASQETGDNRYRDMANHFYASANHVIRDDASAYHTFYFDPETGDPVKGVTRQG
YSDDSAWARGQAWGIYGIPLTYRFLKEPELIQLFKGMTHYFLNRLPKDQVSYWDLIFGDG
SEQSRDSSATAIAVCGIHEMLKTLDPHDPPDKKTYEAMHSMMLRALIKDYANKDLKPGAPL
LLHGVYSWHSKGKGVDEGNIWGDYYYLEALLRFYKDWNPYW

>sp|P64455|YDCY_ECOLI Uncharacterized protein YdcY OS=Escherichia coli (strain K12)
OX=83333 GN=ydcY PE=1 SV=1

MSHLDEVIARVDAAIEESVIAHMNELLIALSDDAELSREDRYTQQQRLRTAIAHHGRKHK
EDMEARHEQLTKGGTIL

>sp|P0A8A2|YEEN_ECOLI Probable transcriptional regulatory protein YeeN OS=Escherichia
coli (strain K12) OX=83333 GN=yeeN PE=1 SV=1

MGRKWANIVAKKTAKDGATSKIYAKFGVEIYAAAKQGEPPPELNTSLKFVIERAKQAQV
PKHVIDKAIDKAKGGGDETFVQGRYEGFGPNGSMIAETLTSNVNRTIANVRTIFNKKGGN
IGAAGSVSYMFDNTGVIVFKGTDPDHIFEILLEAEVDVRDVTEEEGNIVIYTEPTDLHKGIA
ALKAAGITEFSTTELEMIAQSEVELSPEDLEIFEGLVDALEDDDDVQKVYHNVANL

>sp|P0A9E9|YEIL_ECOLI Regulatory protein YeiL OS=Escherichia coli (strain K12) OX=83333
GN=yeiL PE=1 SV=1

MSESAFKDCFLTDVSADTRLFHFLARDYIVQEGQQPSWLFYLTRGRARLYATLANGRVSL
IDFFAAPCFIGEIELIDKDHEPRAVQAIEECWCLALPMKHYPRLNNDTLFLRKLCVTLSHK
NYRNIVSLTQNQSFPVLNRLAAFILLSQEGDLYHEKHTQAAEYLGVSRYHLLYVLAQFIHD
GLLIKSKKGYLIKNRKQLSGLALEMDPENKFSGMMQ

>sp|P31490|YERA_YERE8 YopE regulator OS=Yersinia enterocolitica serotype O:8 / biotype 1B
(strain NCTC 13174 / 8081) OX=393305 GN=yerA PE=1 SV=1

MYSFEQAITQLFQQLSLSIPDTIEPVIGVKVGEFACHITEHPVGQILMFTLPSLDNNNEKETL
LSHNIFSQDILKPILSWDEVGGHPVLWNRQPLNNLDNNSLYTQLEMLVQGAERLQTSSLIS
PPRSFS

>sp|Q9KZX7|VGB_STRCO Virginiamycin B lyase OS=Streptomyces coelicolor (strain ATCC
BAA-471 / A3(2) / M145) OX=100226 GN=vgb PE=1 SV=1

MNEINESYDTSVREFTVSDADAGPYALAEAGPDGALWFTLVHRGAVARRDPDDGRVTV
HPVGDGPTVIAPGPDGALWFTEYRAHRIGRITPEGHYASFAPLTPEGGPFGITAGPDGAMW
FTLSSADRVGRVTMDGEVTEHPAPGAFPSALTAGPDGALWCTLNQGNAIGRLTPDGHGT
AYPLPTPGAAPVGIAAGPDGALWFTEIGAGRIGRITVTGDLTEYPLSDPAARPHAVTAGPN
GALWFTEWGSGRVGRITVDGRVTSYPLSRTDCEPHGIAVHDGALWCALETGSLARIQVPA

>sp|P07166|VIRC2_AGRFC Protein virC2 OS=Agrobacterium fabrum (strain C58 / ATCC 33970)
OX=176299 GN=virC2 PE=1 SV=1

MGIRKPALSVGEARRLAAARPEIVHPSLPVATQNSTLPQPPENLDEEDRRPAPATAKRCHS
SDQQSMLTVDALSSTTAPEKIQVFLSARPPAPEVSKIYDNLILQYSPSKSLQMILRRALGDF

ENMLADGSFRAAPKSYPIPHATAFEKSIIVQTSRMFPVSLIEAARNHFDPLGLETARAFGHKL
ATAALACFFAREKATNS

>sp|O31511|YESE_BACSU Uncharacterized protein YesE OS=Bacillus subtilis (strain 168)

OX=224308 GN=yesE PE=1 SV=1

MLMNEFEKACETLRKFMA YM LEKDMKSWTELWDENAVFEFPYAPEGSPKRIEGKAAIY
DYIKDYPKQIHLSSFTAPT VYRSADSNTVIAEFQCDGHVIETGLPYRQSYISVIETRDGRIVR
YRDYWNPLVVKEAFGG SFLQTEESGK

>sp|P39358|YJHG_ECOLI D-xylonate dehydratase YjhG OS=Escherichia coli (strain K12)

OX=83333 GN=yjhG PE=1 SV=2

MSVRNIFADESHDIYTVRTHADGPDGELPLTAEMLINRPSGDLFGMTMNAGMGWSPDEL
DRDGILLSTLGG LR GADGKPVALALHQGHYELDIQMKA AAEVIKANHALPYAVYVSDP
CDGRTQGTTGMFDSL PYRNDASVMRRLIRSLPDAKAVIGVASCDKGLPATMMALAAQ
HNIATVLPVGGATLPAKDGEDNGKVQTIGARFANGELSLQDARRAGCKACASSGGGCQF
LG TAGTSQVVAEGLGLAIPHSALAPSGEPVWREIARASARAALNLSQKGITTREILTDKAIE
NAMTVHAAFGGSTNLLLHIPAIAHQAGCHIPTVDDWIRINKRVPRLVSVLPNGPVYHPTV
NAFMAGGVPEVMLHLRSLGLLHEDVMTVTGSTLKENLDWWEHSERRQRFKQLLLDQEQ
INADEVIMSPQQA KARGLTSTITFPVGNIAPEGSVIKSTAIDPSMIDEQGIYYHKGVAKVYL
SEKSAIYDIKHDKIKAGDILVIIGVGPSGTGMEETYQVTSALKHLSYGKHVSLITDARFSGV
STGACIGHVGPEALAGGP IGLRTGDLIEIKIDCRELHGEVNFLGTRSDEQLPSQEEATAILN
ARPSHQDLLPDPELPDDTRLWAMLQAVSGGTWTGCIYDVNKIGAALRDFMNKN

>sp|P9WMD5|Y1255_MYCTU Uncharacterized HTH-type transcriptional regulator Rv1255c

OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv1255c PE=1
SV=1

MAGTDWLSARRTELAADRILDAAERLFTQRDPASIGMNEIAKAAGCSRATLYRYFDSREA
LRTAYVHRETRRLGREIMVKIADVVEPAERLLVSITTTLRMVRDNPALAAWFTTTRPPIGG
EMAGRSEVIAALAA AFLNSLGPDDPTTVERRARWVVRMLTSLLMFPGRDEADERAMIAE
FVVPITPASAAARKAGHPGPE

>sp|P9WM37|Y1289_MYCTU Uncharacterized protein Rv1289 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) OX=83332 GN=Rv1289 PE=1 SV=1

MCVSVGESVAQSLQQWDRKLWDVAMLHACNAVDETGRKRYPTLGVGTRFRTALRDSL
DIYGVMATPGVDLEKTRFPVGVRSDLLPDKRPDIADVLYGIHRWLHGHADESSVEFEVSP
YVNASAAALRIANDGKIQLPKSAILGLLAVAVFAPENKGEVIPPDYQLSWYDHVFFISVWW
GWQDHFREIVNVDRASLVALDFGDLWNGWTPVG

>sp|P0DPP2|YOAL_ECOLI Protein YoaL OS=Escherichia coli (strain K12) OX=83333

GN=yoaL PE=1 SV=2

MDRHRHHSIRPFNACLSGTLCRTFRLHFVVTPALFLASNSYSLSRSLSWNS

>sp|P54865|XYND_CELFI Bifunctional xylanase/deacetylase OS=Cellulomonas fimi OX=1708

GN=xynD PE=1 SV=1

MSDSFEATRTRRRRPLQALTGLLAAGALVAGALAAASPA AAVTSNTTGTHDGYFYSF
WTDSPGSVSMDLNSGGGYTRWSNTGNFVAGKGWSTGGRKTVSYSGQFNPSRNAYLTLY
GWTQSPLVEYYIVDSWGT YRPTGT FMGT VTS DGGTYDIYRTQRVNKPSIEGDSSTFYQYW
SVRQQKRTGGTITSGNHFDAWASKGMNLGRHNYMIMATEGYQSSGSSSITVSESGGGG
GGDTGGGGGSTGCSVTATRAEEWSDRFNVTYSVSGSSAWTVNLALNGSQTIQASWNAN
VTGSGSTRVTVPNGSGNTFGVTVMKNGSSTTPAATCAGSGGGTATPTPTPTPTPQSCSA
GYVGLTFDDGPNTGTTNQILSTLTQYGATATVFPTGQNAQGNPSLMQAYKNAGVQIGNH
SWDHPHLVNMSQSDMQSQLTRTQQAIQQTAGVTPTLFRPPYGESNATLRQVESSLGLREII
WDVDSQDWNNASASQIRQAASRLTNGQILMHDWPAATVQALPGILQDLRSRNLCTGHIS
SSTGRAVAPSSAGGGGGGGGGGTGSCSVSAVRGEEWADRFNVTYSVSGSSSWVTLGLNG
GQSVQSSWNAALTGSSGTVTARPNNGSGNSFGVTFYKNGSSATPGATCATG

>sp|O31639|YJCQ_BACSU Uncharacterized protein YjcQ OS=Bacillus subtilis (strain 168)
OX=224308 GN=yjcQ PE=1 SV=1
MNKDKLRYAILKEIFEGNTPLSENDIGVTEDQFDDAVNFLKREGYIIGVHYSDDRPHLYKL
GPELTEKGENYLNKENGTSKAYKTIKEIKDWIK

>sp|P67330|Y095_STRPN UPF0176 protein SP_0095 OS=Streptococcus pneumoniae serotype 4
(strain ATCC BAA-334 / TIGR4) OX=170187 GN=SP_0095 PE=1 SV=1
MAKDIRVLLYYLYTPIENAEQFAADHLAFCKSIGLKGRILVADEGINGTVSGDYETTQKY
MDYVHSLPGMEELWFKIDEENEQAFKKMFVRYKKEIVHLGLEDNDFDNDINPLETTGAY
LSPKEFKEALLDKDTRNDYEDLGHFRGAIRPDIRNFRELQWVRDNKEKFMMDK
RVVVYCTGGVRCEKFSGWMVREGYKDVGQLHGGIATYGKDPEVQGELWDGKMYVFDE
RIAVDVNHVNPTIVGKDWFDGTPCERYVNCGNPFCNRRILTSEENEDKYLRGCSHECRVH
PRNRYVSKNELTQAEVIERLAAIGESLDQAATV

>sp|O31947|YONK_BACSU SPbeta prophage-derived uncharacterized protein YonK
OS=Bacillus subtilis (strain 168) OX=224308 GN=yonK PE=1 SV=1
MASKKVHQINVKGFFDMDVMEVTEQTKEAEYTYDFKEILSEFNGKNVSITVKEENELPVK
GVE

>sp|P44276|Y1624_HAEIN Uncharacterized protein HI_1624 OS=Haemophilus influenzae (strain
ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=HI_1624 PE=1 SV=1
MELKKIAVGLTALLGMSVANAHNVWLEPASSQDEYVVKFGHEQTETYPESKLKSIQALN
SQGKLTAVDYQFRNGEAYLMPKSDLVVFHFDNGVWSKLPSPGKYVEKTKREEPTAEFSTN
PVKFGKAILKWDAESFKSHQQAAYELIPQEKAAQANKPLSILVLHNGKPVQGIKVGVSSEAPF
NLTNEKGIAQFTPTKGFNKVWAEFEEKVTNNADYDRRTVEYMLTFDAQ

>sp|P67049|TYSY_STRPN Thymidylate synthase OS=Streptococcus pneumoniae serotype 4
(strain ATCC BAA-334 / TIGR4) OX=170187 GN=thyA PE=1 SV=1
MTKADTIFKENIERILKEGVFSEQARPKYKDGTVANSKYVTGAFSEYDLSKGEFPITTLRPI
AIKSAIKEVLWIYQDQSNSLEVLNDKYNVHYWNDWEVGDGTIGERYGAVVKKHDIINK
LLKQLETNPWNRRNIISLWDYQAFEETDGLLPCAFQTMFDVRRVDGEIYLDATLTQRSND
MLVAHHINAMQYVALQMMIAKHFGWKVGKFFYFINNLHIYDNQFEQAQELLRREPSNCQ
PRLVLNVPDGTNFFDIKAEDFELVDYDPVKPQLKFDLAI

>sp|P27836|WECG_ECOLI UDP-N-acetyl-D-mannosaminuronic acid transferase OS=Escherichia
coli (strain K12) OX=83333 GN=wecG PE=1 SV=2
MNNNTTAPTYTLRGLQLIGWRDMQHALDYLFADGQLKQGTLVAINAEKMLTIEDNAEV
RELINAAEFKYADGISVVRSVRKKYPQAQVSRVAGADLWEELMARAGKEGTPVFLVGGK
PEVLAQTEAKLRNQWNVNIVGSQDGYFKPEQRQALFERIHASGAQIVTVAMGSPKQEIM
RDCRLVHPDALYMGVGGTYDVFTGHVKRAPKIWQTLGLEWLYRLLSQPSRIKRQLRLLR
YLRWHYTGNL

>sp|P44290|Y1681_HAEIN UPF0319 protein HI_1681 OS=Haemophilus influenzae (strain
ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=HI_1681 PE=1 SV=1
MKLRVAVLGLATLCTSTATFAGMVSTSSNLEFLAIDGQKASKSLGKAKTFTVDDTQNHQ
VVVRLNEIVGSGSNQSLFESNPVIVTFQGNAEDLVISAPVIRNLDSDGDFNQMNPITVKTGS
GNAISAKVDVLKQEGLFPSGNVLNDLAEYNASGAAASVSKFAATTVASSVAVAPAGNAK
ANKGKVVVQGENVAEQQLQYWFQQADKETQTRFLNWAKSHK

>sp|A3DHB8|Y2143_CLOTH Nucleoid-associated protein Cthe_2143 OS=Clostridium
thermocellum (strain ATCC 27405 / DSM 1237 / NBRC 103400 / NCIMB 10682 / NRRL B-4536
/ VPI 7372) OX=203119 GN=Cthe_2143 PE=1 SV=1
MAKGGFPGFGGNINNLVKQAQKMQRDMERVQEELKEKTVEASAGGGAVTVVATGRKDI
KEITIKPEVDPDDVEMLQDLILAAVNEALRKADEMVTAEISKITGGLGGIPGLF

>sp|P76084|PAAI_ECOLI Acyl-coenzyme A thioesterase PaaI OS=Escherichia coli (strain K12)
OX=83333 GN=paaI PE=1 SV=1

MSHKAWQNAHAMYENDACAKALGIDIISMDEGFAVVTMTVTAQMLNGHQSCHGGQLF
SLADTAFAAYACNSQGLAAVASACTIDFLRPGFAGDTLTATAQVRHQGKQTGVYDIEIVNQ
QQKTVALFRGKSHRIGGTITGEA

>sp|P37646|PDEH_ECOLI Cyclic di-GMP phosphodiesterase PdeH OS=Escherichia coli (strain K12) OX=83333 GN=pdeH PE=1 SV=3

MIRQVIQRISNPEASIESLQERRFWLQCERAYTWQPIYQTCGRLMAVELLTVVTHPLNPSQ
RLPPDRYFTEITVSHRMEVVKEQIDLLAQKADFFIEHGLLASVNIDGPTLIALRQQPKILRQI
ERLPWLRFELVEHIRLPKDSTFASMCEFGPLWLDDFGTGMANFSALSEVRYDYIKIARELF
VMLRQSPEGRTLFSQLLHLMNRYCRGVIVEGVETPEEWRDVQNSPAFAAQGWFLSRPAPI
ETLNTAVLAL

>sp|Q82IY9|PTLF_STRAW 1-deoxy-11-beta-hydroxypentalenate dehydrogenase
OS=Streptomyces avermitilis (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 /
NCIMB 12804 / NRRL 8165 / MA-4680) OX=227882 GN=ptlF PE=1 SV=1

MHLQPSTAVVTGAASGIGFALSARLAQAGARVVMTDIAGDGLAGAVEELAAHGADVTA
VVADLTDPAAVQELADTAFGRLGDIDVVCNNAGVVGPMPLWSVPLDEMHAHVFDVN
YWAHVHVARAFVPRLLDSGRPSHLVQTASMSAFVVGAGTASYAASKHADLAAARSLRA
DLDGTPVRVSVLCPGRVDTPMTRGLVAPRNATGNTTISADEAADA VWNALGSDRFYIFT
NADAQTRLGDQFNDVWRHLAREKYWTESSSPSVNSSRP

>sp|Q9PN58|PDXA_CAMJE 4-hydroxythreonine-4-phosphate dehydrogenase OS=Campylobacter
jejuni subsp. jejuni serotype O:2 (strain ATCC 700819 / NCTC 11168) OX=192222 GN=pdxA
PE=1 SV=1

MKKLAISIGDINSIGLEILVRSHEELSKICTPFYFIHESLLNKALKLLNLKLFNAKIVAFKDDK
DYEFNFIKKENSLEIYSFCLPLGFKVDENFEIQAGEIDAKSGLYGFLSFKAASYFVYEKHAH
ALLTLPIHKKAWEDAGLKYKGHTDALRDFFKKNAMMLGCKELFVGLFSEHIPLAKVSKK
ITFKNLSIFLKDFYKETHFKKMGLLGFNPHAGDYG VIGGEEEEKIMEKAIAFVNAFLHKKD
EKFFKKALKDENLQKELLNFKGKGVYLPYPLVADTAFTKTGLKNCNRLVAMYHDLAL
APLKALYFDKSINVSINLPIIRVSVDHGTAFDKAYKNAKINTKSYFEAAKFAINLHASKA

>sp|O50461|RELE_MYCTU Toxin RelE OS=Mycobacterium tuberculosis (strain ATCC 25618 /
H37Rv) OX=83332 GN=rele PE=1 SV=1

MSDDHPYHVAITATAARDLQRLPEKIAAACVEFVFGPLLNNPHRLGKPLRNDLEGLHSAR
RGDYRVVYAIDDGHHRVEIIHIARRSASYRMNPCRPR

>sp|P25026|PRXC_BURPY Non-heme chloroperoxidase OS=Burkholderia pyrocinia OX=60550
GN=cpo PE=1 SV=3

MPYVTTKDNVEIFYKDWGPKDAQPIVFHHGWPLSGDDWDAQMLFFVQKGYRVIAHRRR
GHGRSAQVSDGHDMDHYAADAFAVVEALDLRNAVHIGHSTGGGEVARYVANDGQPAG
RVAKAVLVSAVPPLMLKTESNPEGLPIEVFDGFRKALADNRAQFFLDVPTGPFYGFNRAG
ATVHQGVIRNWWRQGMESAKAHYDGIKAFSETDQTEDLKSITVPTLVLHGEDDQIVPIA
DAALKSIKLLQNGTLKTPGYSHGMLTVNADVLNADLLAFVQA

>sp|Q9X0X1|PURS_THEMA Phosphoribosylformylglycinamide synthase subunit PurS
OS=Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) OX=243274
GN=purS PE=1 SV=1

MPLFKFAIDVQYRSNVRDPRGETIERVLREEKGLPVKKLRLGKSIHLEVEAENKEKAYEIV
KKACEELLVNPVVEEYEVREL

>sp|P0A7F9|QUEA_ECOLI S-adenosylmethionine:tRNA ribosyltransferase-isomerase
OS=Escherichia coli (strain K12) OX=83333 GN=queA PE=1 SV=1

MRVTDFFSFPESLIAHYPMPESSCRLSLDGPTGALTHGTFTDLLDKLNPGDLLVFNNNT
RVIPARLFGRKASGGKIEVLVERMLDDKRILAHIRASKAPKPGAELLGDDDESINATMTAR
HGALFEVEFNDRSVLDILNSIGHMPLPPYIDRPDEDADRELYQTVYSEKPGAVAAPTAGL
HFDEPLLEKLRAKGVEMAFVTLHVGAGTFQPVVRVDTIEDHIMHSEYAEVPQDVVDAVLA

AKARGNRVIAVGTTSVRSLESAAQAAKNDLIEPFFDDTQIFIYPGFQYKVVDALVTNFHLP
ESTLIMLVSAFAGYQHTMNAYKAAVEEKYRFFSYGDAMFITYNPQAINERVGE
>sp|Q54304|RAPL_STRRN L-lysine cyclodeaminase OS=Streptomyces rapamycinicus (strain
ATCC 29253 / DSM 41530 / NRRL 5491 / AYB-994) OX=1343740 GN=rapL PE=1 SV=2
MQTKVLCQRDIKRILSVVGRDVMMMDRLISEVHAGFARLGRGETDEPPPRGTGFARGGDPVPG
VIEFMPHRASGIGVTMKTVSYSYPQNFERFNLPTIVGTVSRLDDDSGSMVALADAATITAMR
TGAVAAVATRLLARPGSTTLALIGAGAQAQAVTQAHALSRVLPLERILISDIKAEHAESFAGR
VAFLELPVEVTDAATAMATADVLTCTVTSVPVGGGPVPAEPRQAHLHVNGIGADEQGKT
ELPKALLDDAFICVDHPGQARAEGEFQQLPDRELGPSLADLCAAPEIAAPHPERLSVFDST
GSAFADHIALDVLLGFADELGLGHKMSIESTPEDVLDPYSL
>sp|Q9X1X4|PYRKH_THEMA Dihydroorotate dehydrogenase B (NAD(+)), electron transfer
subunit homolog OS=Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM
10099) OX=243274 GN=TM_1639 PE=1 SV=1
MGGTALNEIVKKVKIAEDVDFWVHSPSVSKEARPGQFVVIRLHEKGERIPLTVADTKPEE
GLFRMVVKVVGKTTHELKKEGDTILDVVGPLGNPSEIENYGNVLLVGGGVGIATLYPI
AKALKEAGNNITTVLGARTKDYLMVDEFKEISDVLLVTDDGSAGMKGVVTDAMDKLFR
ERKFDICWAVGPTIMMKFCTLKAREFGVPIWVSLNPIMVDGTGMCGACRVTVSGQIKFAC
VDGPEFRGEEVDWDELLKRLAQYREQEKISYERFLKTAGESE
>sp|Q6N4R7|RL10_RHOPA 50S ribosomal protein L10 OS=Rhodopseudomonas palustris (strain
ATCC BAA-98 / CGA009) OX=258594 GN=rplJ PE=1 SV=3
MVLLAGTANRRELAVERAAKKEAVESLNGLFQTTSAIVAHYSGLTVAQMQLRQQMK
QAGASVKVSKNRLAKIALEGTDVAAIGPLLKGPTVIATSSDPVAAPKVAVEFAKANEFVI
LGGSMGTTVLNVLDGVKALASLPSLDELRAKLVGLVQAPATKIAQVTTAPAAKLARVVQA
YASKSEAA
>sp|P40869|SP5AD_BACSU Stage V sporulation protein AD OS=Bacillus subtilis (strain 168)
OX=224308 GN=spoVAD PE=1 SV=1
MKLTGKQTWVFEHPIFVNSAGTAAGPKEKDGPLGSLFDKTYDEMHCNQKSWEMAERQL
MEDAVNVALQKNLTKDDIDLLLAGDLLNQNVNTANYVARHLKIPFLCMFGACSTSMETV
AVASALVDGGFAKRALAATSSHNATAERQFRYPTEYGGQKPDTATSTVTGSGAVVISQTP
GDIQITSATVGKVSIDLGITDPFDMGSAMAPAAADTIKQHFKDLNRTADDYDLITGDLSG
VGSPIVKDILKEDGYPVGTHDDCGLLIYTPDQQVFAGGSGCACSAVVITYSHIFKQLREG
KLNRFVVFVATGALLSPTMIQQKETIPTIAHGTVFERAGGAS
>sp|P37956|SPL_BACSU Spore photoproduct lyase OS=Bacillus subtilis (strain 168) OX=224308
GN=splB PE=1 SV=1
MQNPFVPLVYIEPRALEYPLGQELQDKFENMGIEIRETTSHNQVRNIPGKNHLQQYRNA
KSTLVIGVRKTLKFDSSKPSAEYAIPFATGCMGHCHYCYLQTTMGSKPYIRTYVNVEEILD
QADKYMKERAPEFTRFEASCTSDIVGIDHLTHTLKRAIEHFQSDLGKLRFTKHHVDHL
LDAKHNGKTRFRFSINADYVIKNFEPGTSPLDKRIEAAVKVAKAGYPLGFIVAPIYIHEGW
EEGYRHLFEKLDALPQDVRHDITFELIQHRFTKPAKRVIKKNYPKTKLELDEEKRRYKW
GRYGIGKYIYQKDEEHALREALESYIDTFPPNAKIEYFT
>sp|Q59495|SUCP_LEUME Sucrose phosphorylase OS=Leuconostoc mesenteroides OX=1245
PE=1 SV=1
MEIQNKAMLITYADSLGKNLKDVBHQLKEDIGDAIGGVHLLPFFPSTGDRGFAPADYTRV
DAAFGDWADVEALGEEYYLMFDFMINHISRESVMYQDFKKNHDDSKYKDFFIRWEKFW
AKAGENRPTQADVLDLIYKRKDKAPTQEITFDDGTENLWNTFGEEQIDIDVNSAIAKEFIK
TTLEDMVKHGANLIRLDAFAYAVKKVDTNDFVVEPIWDTLNEVREILTPLKAEILPEIHE
HYSIPKKINDHGYFTYDFALPMTTLYTLYSGKTNQLAKWLKMSPMKQFTTLDTHDGIGV
VDARDILTDDEIDYASEQLYKVGANVKKTYSSASYNNDIYQINSTYYALGNDDAAYLL
SRVFQVFAPGIPQIYYVGLLAGENDIALLESTKEGRNINRHYYTREEVKSEVKRPVVANLL

KLLSWRNESPAFDLAGSITVDTPDTTIVVTRQDENGQNKAVLTADAANKTFEIVENGQT
VMSSDNLTON

>sp|P52097|TILS_ECOLI tRNA(Ile)-lysine synthase OS=Escherichia coli (strain K12)
OX=83333 GN=tilS PE=1 SV=1
MTLTLNRQLLTSRQILVAFSGGLDSTVLLHQLVQWRTEPGVALRAIHVHHGLSANADA
WVTHCENVVCQQWQVPLVVERVQLAQEGLGIEAQARQARYQAFARTLLPGEVLVTAQHL
DDQCETFLALALRGSGPAGLSAMA EVSEFAGTRLIRPLLARTRGELVQWARQYDLRWIED
ESNQDDSYDRNFLRLRVVPLLQQRWPHFAEATARSAALCAEQESLLDELLADDLAHCQSP
QGTLQIVPMLAMS DARRAAIIRRWLAGQNAPMPSRDALVRIWQEVALAREDASPCRLRG
AFEIRRYQSQLWWIKSVTGQSENIVPWQTLWQPLELPAGLGSVQLNAGGDIRPPRADEAV
SVRFKAPGLLHIVGRNGGRKLKKIWQELGVPPWLRDTPLLFYGETLIAAAGVFVTQEGV
AEGENGVSFVWQKTLS

>sp|P47480|TIG_MYCGE Trigger factor OS=Mycoplasma genitalium (strain ATCC 33530 / G-37 / NCTC 10195) OX=243273 GN=tig PE=1 SV=1
MKLYKVLNSKTTDKSLCLEVEIDPNYWQATQKKLVGEMAKSIKIKGFRPGKIPPNLASQSI
NKAELMQKSAQNVMNSIYESVQQUEIVASNDNVIDDYPTIDFKTITEQNCVLLFYFDLIPNF
QLPDYKKIKDLTPLTKLTEAEFNNEIEKLA KTKSTMVDVSDKKLANGDIAIIDFTGIVDNK
KLASASAQNYELTIGSNSFIKGFETGLIAMKVNQKKTLALTFPSDYHV KELQSKPVTFEVV
LKA IKKLEFTPMDETNFKSFLPEQFQSFTSLKAFKSYFHKLMENKKQETILQENNQKIRQFL
LTNTKLPFLPEALIKLEANRLLKLQQSQA EQYKIPFEKLLSASNITLTELQDRNIKEAKENV
TFALVMKKIADIEKIKVDNNKIKAEIENVIAVEYPFASDEM KKQLFFNMEQQKEFVESIIIN
RLTTTKIVSYSTH

>sp|P39153|SUA5_BACSU Threonylcarbamoyl-AMP synthase OS=Bacillus subtilis (strain 168)
OX=224308 GN=ywlC PE=1 SV=1
MKTKRWFVDVTDELSTNDPQIAQAAALLRENEVVAFP TETVYGLGANAKNTDAVKKIYE
AKGRPSDNPLIVHIADISQLEDLTGPAP EKAKATLMKRFWPGALTILPCKPDALSPRV TAGL
ETVAIRMPDHPLALALIRESGLP IAAPSANLSGKPSPTKAEHVAHDLDGRIAGIVDGGPTGI
GVESTVLSCADDIPVLLRPGGITKEQIEAVIGPIHVDKGLSDQNEKPISPGMKYTHYAPTAP
LAICEGSPERIQHLIQEYQQGGRRVGVL TTEEKAGVYSADYVKSCGRRAQLETVAAGLYD
ALRSFDENKVDFIIAESFPDTGVGLAIMNRLMKAAGGRVIR

>sp|P9WG75|THIE_MYCTU Thiamine-phosphate synthase OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) OX=83332 GN=thiE PE=1 SV=1
MHESRLASARLYLCTDARRERGD LAQFAEAALAGGVDIIQLRDKGSPGELRFGPLQARDE
LAACEILADAAHRYGALFAVND RADIAARAAGADVLHLGQRDLPNVVARQILAPDTLIGRS
THDPDQVAAAAAGDADYFCVGPCWPTPTKPGRAAPGLGLVRVAAELGGDDKPWF AIGG
INAQRLPAVL DAGARRIVVRAITSADDPRAAAEQLRSALTAAN

>sp|P23395|SYM_THET8 Methionine--tRNA ligase OS=Thermus thermophilus (strain HB8 /
ATCC 27634 / DSM 579) OX=300852 GN=metG PE=1 SV=2
MEKVIFYVTTPIIYYVNAEPHLGHAYTTVVADFLARWHRLDGYRTFFLTGTDEHGETVYRA
AQAAGEDPKAFVDRVSGRFRKRAWDL LGIAYDDFIRTTEERHKKVVQLVLKKVYEAGDIY
YGEYEGLYCVSCERFYTEKELVEGLCPIHGRPVERRKEGNYFFRMEKYRPWLQEYIQENP
DLIRPEGYRNEVLAMLAEPIGDLSISRPKSRVPWGIPLPDENHVTYVWFDALLNYVSAL
DYPEGEAYRTFWPHAWHLIGKDILKPHAVFWPTMLKAAGIPMYRHLNVGGFLLGPDGRK
MSKTLGNVVDPFALLEKYGRDALRY YLLREIPYQDTPVSEEALRTRYEADLADDLGNL
VQRTRAMLFRFAEGRIPEPVAGEELAE GTGLAGRLRPLVRELKFHVALEEAMAYVKALN
RYINEKKPWELFKKEPEEARAVLYRVVEGLRIASILLTPAMPDKMAELRRALGLKEEVRL
EEAERWGLAEPRPIPEEAPVLF PKKEAKVEAKPKEEAWIGIEDFAKVELRVAEVLAAEKHP
NADRLVLRLSLGNEERTVVS GIAKWYRPEELVGKKVVLVANLKPALRGIESQGMILAA
QEGEALALVTVEGEVPPGAVVK

>sp|P23191|T2M2_MORBO Type-2 restriction enzyme MboII OS=Moraxella bovis OX=476
GN=mboIIR PE=1 SV=1
MKNYVSNINLGNSSLKFIDERLQSENYRGIHLSQHNRYDLPKLIDILTLLNKHAPNQSLMQI
RTTDISKRPQNIPEEQSYAEFCNEAKSLTNIGTQDAMRKNLFVDFARMGLINRYNDKKVLT
DPFKRGVTKYVALSDMGVVKLIDPKLDILSKNLIFSLSLNKLLTGTFVEDVLSLLTNSDLKEIS
FDEFMLFVSAMNCNFNFSISTEQCESLIKEYRLLSRVQKNAVIDTLKSELIPDNFNNGDKKDK
RDYHNWANENQQIWTLFENIPFFIMEKDSRKLILITSDVDLSKYSKSKMKRSQQAKNDYF
KHHKVNKIKGYELDHIPLLEAESVDEYRYLDNWLNLIDYIDGKTHAIKSQSGSKYYIFTFD
DNDYNQIYFLDTQGDKLSINDDTALFDKNKVPKIYEYNQNFNAKTS

>sp|P10026|TRAM1_ECOLI Relaxosome protein TraM OS=Escherichia coli (strain K12)
OX=83333 GN=traM PE=1 SV=1
MAKVNLISNDAYEKINAIIEKRRQEGAREKDVFSFASATASMLLELGLRVHEAQMERKESA
FNQTEFNKLLLECVVKTQSSVAKILGIESLSPHVSGNSKFHEYANMVEDIREKVSSEMERFFP
KNDDE

>sp|Q9RX51|TREZ_DEIRA Malto-oligosyltrehalose trehalohydrolase OS=Deinococcus
radiatorum (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 /
NCIMB 9279 / R1 / VKM B-1422) OX=243230 GN=treZ PE=1 SV=1
MTQTQPVTPPPASFQTQHDPRTRLGATPLPGGAGTRFRLWTSTARTVAVRVNGTEHVM
TSLGGGIYELELPVGPARYLVLDGVPTDPYARFLPDGVHGEAEVDFGTFDWDAD
WHGIKLADCVFYEVHVGTFTEPGTYRAAAEKLPYLKELGVTAIQVMPLAAFDQGQRGWG
YDGAIFYAPYAPYGRPEDLMALVDAAHRLGLGVFLDVVYNHFGPSGNLSSYAPSYFTD
RFSSAWGMGLDYAEPHMRRYVTGNARMWLRDYHFDGLRLDATPYMTDDSETHILTELA
QEIHELGGTHLLAEDHRNLPDLVTVNHLDDGIWTDDFHHETRVTLTGEQEGYYAGYRGG
AEALAYTIRRGWRYEGQFWAVKGEEHERGHPSDALEAPNFVYCIQNHQIGNRPLGERL
HQSDGVTLEHYRGAAALLPMTPLLFQGGQEWAASTPFQFFSDHAGELGQAVSEGRKKEF
GGFSGFSGEDVPDPQAEQTFLNSKLNWAEREGGEHARTLRLYRDLLRLRREDPVLHNRQ
RENLTGHDGDVWVRTVTGAGERVLLWNLGQDTRAVAEVKLPFTVPRRLLHTEGRE
DLTLGAGEAVLVG

>sp|P07118|SYV_ECOLI Valine--tRNA ligase OS=Escherichia coli (strain K12) OX=83333
GN=valS PE=1 SV=2
MEKTYNPQDIEQPLYEHWEKQGYFKPNGDESQESFCIMIPPPNVTGSLHMGHAFQQTIMD
TMIRYQRMQGKNTLWQVGTDHAGIATQMVVERKIAAEEGKTRHDYGREAFIDKIWEWK
AESGGTITRQMRRLGNSVDWERERFTMDEGLSNAVKEVFVRLYKEDLIYRGKRLVNWD
KLRTAISDLEVENRESKGSMDWHIRYPLADGAKTADGKDYLVAATTRPETLLGDTGVAVN
PEDPRYKDLIGKYVILPLVNRRIPIVGDEHADMEKGTGCVKITPAHDFNDYEVGKRHALP
MINILTFDGDIRESAQVFDTKGNESDVYSSEIPAEFQKLERFAARKAVVAVDALGLLEEI
KPHDLTVPYGDRGGVIEPMLTDQWYVRADVLAKPAVEAVENGDIQFVVPKQYENMYFS
WMRDIQDWCSRQLWWGHRIPAWYDEAGNVYVGRNEDEVKRNENLGDVVLQRQDEDV
LDTWFSSALWTFSTLGWPENTDALRQFHPTSMVSGFDIIFWIARMIMMTMHFIKDENG
KPQVPFHTVYMTGLIRDDEGQKMSKSKGNVIDPLDMVDGISLPELLEKRTGNMMQPPQA
DKIRKRTEKQFPNGIEPHGTDALRFTLAALASTGRDINWDMKRLEGYRNFCNKLWNASRF
VLMNTEGQDCGFNGGEMTSLADRWLAEFNQTIKAYREALDSFRFDIAAGILYEFTWNQ
FCDWYLELTKPVMNGGTEAELRGTRHTLVTVLEGLRLAHPIIPFITETIWQRVKVLCGIT
ADTIMLQFPQYDASQVDEAALADTEWLKQAIIVARNIRAEMNIAPGKPLELLLRGCSAD
AERRVNENRGFLQTLARLESITVLPADDKGPVSVTKIIDGAELLIPMAGLINKEDELARLAK
EVAKIEGEISRIENKLANEGFVARAPEAVIAKEREKLEGYAEAKAKLIEQQAVIAAL

>sp|P31032|T2M4_NEIGO Type-2 restriction enzyme NgoMIV OS=Neisseria gonorrhoeae
OX=485 GN=ngoMIVR PE=1 SV=1
MNPLFTQERRIFHKLLDGNILATNNRGVVSNAADGSNTRSFNIAKGIADLLHSETVSRPLP
GQTSGNAFEAICSEFVQSAFEKLQHIRPGDWNVKQVGSRRNRLEIARYQQYAHLTALAKAA

EENPELAAALGSDYTITPDIIIVTRNLIADAEINRNEFLVDENIATYASLRAGNGNMPLHASI
SCKWTIRSDRAQNARSEGLNLVRNRKGRLPHIVVVTAEPTPSRISSIALGTGEIDCVYHFAL
YELEQILQSLNYEDALDLFYIMVNGKRLKDISDLPLDLAV
>sp|P43870|T2D3_HAEIN Type-2 restriction enzyme HindIII OS=Haemophilus influenzae (strain
ATCC 51907 / DSM 11121 / KW20 / Rd) OX=71421 GN=hindIII PE=1 SV=1
MKKSALEKLLSLIENLTNQEFKQATNSLISFIYKLNREVIELVRSIGILPEAIKPSSTQEKLF
SKAGDIVLAKAFQLLNLNSKPLEQQRGNAGDVIALSKEFNYGLVADAKSFRLSRTAKNQKD
FKVKALSEWREDKDYAVLTAPFFQYPTTKSQIFKQSLDENVLLFSWEHLAILLQLDLEETN
IFSFEQLWNFPKKQSKKTSVSDAENNFMRFNKFMDLFDKIDKDTLNQLLQKEINFIEERS
LIEKEYWKKQINIKNFTREEAIEALLKDINMSSKIETIDFSIKGIKSNDRLYL
>sp|O66552|RSME_AQUAE Ribosomal RNA small subunit methyltransferase E OS=Aquifex
aeolicus (strain VF5) OX=224324 GN=rsmE PE=1 SV=1
MHVFYSEERRGNLLILREGEVKHFRVRRIEKDEEFGVIHEGKIYVCKVRREDKREISCEIVE
ELETKLPPKDITLYQSVTVDLKTMDTIVRQATELGVLTFVPIISERSFQKEEAILKKTEKWK
RIVIEAMKQSRPPIEIKKPVRLSDLIPESEENIILDNFYEGVKPKDVNLEAKTYSVVVGPE
GGFSKRESQILREKGFKSVLLEPYTLRTETAVVSIVSILMNF
>sp|A0R550|RS14_MYCS2 30S ribosomal protein S14 OS=Mycobacterium smegmatis (strain
ATCC 700084 / mc(2)155) OX=246196 GN=rpsN PE=1 SV=1
MAKKSKIVKNEQRRELVQRYAERRAELKRTIRDPASSPERRAAAVSALQRLPRDSSPVRL
RNRDVVDGRPRGHLRKFGLSRVVRVREMAHRGELPGVRKASW
>sp|P46350|RXL7_BACSU Ribosome-associated protein L7Ae-like OS=Bacillus subtilis (strain
168) OX=224308 GN=rplGB PE=1 SV=3
MSYDKVSQAKSIIGTKQTVKALKRGSVKEVVVAKDADPILTSSVVSLAEDQGISVSMVES
MKKLKGKACGIEVGAAVAIIL
>sp|Q7A3K0|SARU_STAAN HTH-type transcriptional regulator SarU OS=Staphylococcus
aureus (strain N315) OX=158879 GN=sarU PE=1 SV=1
MDYQTFEKVNKFINVEAYIFFLTQELKQQYKLSLKELLILAYFYKNEHSISLKEIIGDILYK
QSDVVKNIKSLSKKGFINKSRNEADERRIFVSVTPIQRKKIACVINELDKIIGFNKERDYIK
YQWAPKYSKEFFILFMNIMYSKDFLKYRFNLTFDLDSILYVISSRKNEILNLKDLFESIRFM
YPQIVRSVNRLNNGMLIKERSLADERIVLIKINKIQYNTIKSIFTDTSKILKPRKFFF
>sp|P72077|RSMJ_NEIGO Ribosomal RNA small subunit methyltransferase J OS=Neisseria
gonorrhoeae OX=485 GN=rsmJ PE=1 SV=1
MTDILIDDTATEAVRTLIRAFPLVPVSQPPEQGSYLLAEHDTVSLRLVGEKSNVIVDFTSGA
AQYRRTKGGGELIAKAVNHTAHTPVWDATAGLGRDSFVLASLGLTVTAFEQHPAVACLL
SDGIRRALLNPETQDTAARINLHFGNAAEQMPALVKTQGKPDIVYLDPMYPERRKSAAVK
KEMAYFHRLVGEAQDEVVLLHTARQTAKKRVVVKRPRLGEHLAQAPAYQYTGKSTRF
DVYLPYGADKG
>sp|Q99SU7|SAK_STAAN Staphylokinase OS=Staphylococcus aureus (strain N315) OX=158879
GN=sak PE=1 SV=1
MLKRSLLFLTLLLLFSFSITNEVSASSSFDKGKYKKGDDASYFEPTGPYLMVNVTGVDS
KGNELLSPHYVEFPIKPGTTLTKEKIEYYVEWALDATAYKEFRVVELDPSAKIEVTTYDKN
KKKEETKSPITEKGFFVPDLSEHIKNPGFNLITKVVEKK
>sp|O32062|SAFA_BACSU SpoIVD-associated factor A OS=Bacillus subtilis (strain 168)
OX=224308 GN=safA PE=1 SV=1
MKIHIVQKGDLSWKIAEKYGVDEEVKKLNTQLSNPDLIMPGMKIKVPSEGVPRKEPKA
GKSPAAGSVKQEHPIAKEPKSVVDVEDTKPKEKKSMPYVPPMPNLQENVYPEADVND
YYDMKQLFQPWSPPKPEEPKKHHDGNMDHMYHMQDQFPQQEAMSNMENANYPNMPN
MPKAPEVGGIEEENVHHTVPNMPMPAVQPYHYPAHFVPCVPVSPILPGSGLCYPYPA
QAYPMHPMHGYQPGFVSPQYDPGYENQHHENSHHGHYGSYGAPQYASPAYGSPYGHMP

YGPYYGTPQVMGAYQPAAAHGYMPYKDHDDCGCDGDHQPYFSAPGHSGMGAYGSPN
 MPYGTANPNPNPYSAGVSMPTNQPSVNQMFRPEEENE
 >sp|O66186|SCNB_THITI Thiocyanate hydrolase subunit beta OS=Thiobacillus thioarus
 OX=931 GN=scnB PE=1 SV=3
 MSSSIREEVHRHLGTVALMQPALHQQTHAPAPTEITHTLFRAYTRVPHDVGGEADVPIEY
 HEKEEEIWELNTFATCECLAWRGVWTAEEERRRKQNCDEVGQTVYLGMPYYGRWLLTAAR
 ILVDKQFVTLTELHNKIVEMRERVASGQGLGEYLPPKAK
 >sp|P75897|RUTB_ECOLI Peroxyureidoacrylate/ureidoacrylate amidohydrolase RutB
 OS=Escherichia coli (strain K12) OX=83333 GN=rutB PE=1 SV=2
 MTTLTARPEAITFDPQQSALIVVDMQNAYATPGGYLDLAGFDVSTTRPVIANIQTAVTAA
 RAAGMLIWFQNGWDEQYVEAGGPGSPNFHKSNAKLTMRKQPQLQGKLLAKGSWDYQL
 VDELVPQPGDIVLPKPRYSGFFNTPLDSILRSRGIRHLVFTGIATNVCVESTLRDGGFFLEYFG
 VVLEDATHQAGPKFAQKAALFNIETFFGWVSDVETFCDALSPSTFAHIA
 >sp|P37610|TAUD_ECOLI Alpha-ketoglutarate-dependent taurine dioxygenase OS=Escherichia
 coli (strain K12) OX=83333 GN=tauD PE=1 SV=3
 MSERLSITPLGPYIGAQISGADLTRPLSDNQFEQLYHAVLRHQVVFLRDQAITPQQQRALA
 QRFGEHLIHPVYPHAEGVDEIIVLDTHNDNPPDNDNWHTDVTFIETPPAGAILAAKELPST
 GGDTLWTSGIAAYEALSVPFRQLLSGLRAEHDFRKSFPYKYRKTEEEHQRWREAVAKNP
 PLLHPVVRTHPVSGKQALFVNEGFTTRIVDVSEKESEALLSFLFAHITKPEFQVRWRWQPN
 DIAIWDNRVTQHYANADYLPQRRIMHRATILGDKPFYRAG
 >sp|P09333|SLAPO_BREBN Outer cell wall protein OS=Brevibacillus brevis (strain 47 / JCM
 6285 / NBRC 100599) OX=358681 GN=BBR47_54150 PE=1 SV=1
 MNKKVVLSTTLVASVAASAFAAPKDGIIYIGGNIKKYYSTDVLFEMTPQAKATYASEL
 NAMASDFNNVVFVDYKKGKASIEELFTKGSKVALGEPLKKEDFADLYKVVNKDGSSTAT
 EDARAKVDPTPTGDLNVESVSANNLKEVVVTFDKAVDADTAGDKAYYTFTANKLAVDK
 VTVSGKTVVLTAAKAENQASYELNVDGIGLVLKTTKEVKFFDNTTPTVAAVAAGPKQ
 VKVTFSEPLSAKPSFSVNNGAIAVVADNFVEGTKEVILTLGAQPTASTNTVTVEGGADYAS
 YKVEKVTKDFTTVVADTTPTTVSVKKASAKQVVLEFSEDVQNVQDKNVVIFYHTTKGHEG
 YKGTILGVDGKEVTISFVNPLPEGQFKIFVDYVVDNGTQISDLWGNKLPEQVITGTFAADT
 TPPTVTKVEAKTNTTEIHVTFSETVNGADNKANFTLKGVTGNVIPLTKAEVVDAAKNIYKV
 VTTEPLNGGSYYLTVKGIEDASKNKLVEYTATVAVADTVPPNVKDLDPATPGTDAQLISP
 TKVKIAFTEPMDKASIENKNNYMFNGFNLDKSVTLTATDSNTAVVVDFTNVVGFNGFKN
 GDAISVGRVLDTAGNPKTEMQTKVNLPSVSAPLFDKAEVTGKNTVKLYFKELIINAKAD
 DFAVDNGEGYKAVNSISNDVVENKSVITLTGNDLPTTAAGVKVKTVEVDKAKNQYGV
 AVALTDVPADDKIGPNWLKAETVDTNNNGKIDQFKLTFSEALYVASVQDSDFRIEGYTIA
 GVETKGEVVTIKVTELDIDDSATPTVAVIGSVEDLKRNASGPFEPQKAIDGVSAPDKEAP
 VVTGVEAGKTYNTAVTPDSADKDIKTVVLKKGKELAGYALKTPISENGSYELVVTDNA
 GNTTTVKFKVDIPAEDKKAPEIKTVTDDKVAVADAPKWEAPKATATDDVDGDISDKIAV
 TYSSSEDAGSKVTDLASAQTHLGTAGNTVKVTYNVTDKAGNPATAVSATFTAI
 >sp|Q6F9F7|TGNC_ACIAD (Z)-2-((N-methylformamido)methylene)-5-hydroxybutyrolactone
 dehydrogenase OS=Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) OX=62977
 GN=tnnC PE=1 SV=1
 MQQFQLYINGKFEDGAAQFDSINPATGEIWAKMPEARTDQVNRAVDAAEQAFYDSSWSG
 LTASQRGKLLYKLADLVEKSAPRLAALETTDTGKIIRETSSQIAVVAEYYRYAGLADKIE
 GSFIPVDKPDMAWLVRPVGVAIAIVPWNSQLFLSAVKVGPALAAAGCTVVLKASEEAP
 APLEFAKLIDEAGFPAGVVNVITGFGPECAGVLSAHPKVAHIAFTGGPETAKHIVRNSAE
 NLAKVSLELGKSPFIVFADTDINSALNAQIAAIFAATGQSCVAGSRLLIEESIKDEFLQRLA
 ERVQSIKMGLPDDMQTEYGPLCTLKQREKIQQVVQRSVEQGAKLITGGQVCDGAGYYYP
 PTILDCSGVSDAQSIHTELFGPVLSVDTFSTEAEAIQKANSTPYGLASGVFTSNLTRAHRMT

RAIRSGIVWLNTYRVVSPLAPFGGYGLSGHGREGGLSAALEYTTTCTVWLRMSDQPIDDP
FVMR

>sp|Q9WZF8|TIG_THEMEA Trigger factor OS=Thermotoga maritima (strain ATCC 43589 /
MSB8 / DSM 3109 / JCM 10099) OX=243274 GN=tig PE=1 SV=1
MEVKELERDKNRVVLEYVFGAEEIAQAEDKAVRYLNQRVEIPGFRKGRIPKNVLKMKLG
EEFQEYTLDFLMDLIPDTLKDRKLILSPIVTERELKDVTARVVVEVHEEPEVRIGDISKIEVE
KVDEEKVLEKYVERRIEDLRESHALLEPKEGPAEAGDLVRVNMEVYNEEGKKLTSREYE
YVISEDDEPRFVKDLVGKKKGDVVEIEREYEGKKYTYKLEVEEVYKRTLPEIGDELAHSV
NNEFETLEQLKESLKKEGKEIYDVEMKESMREQLLEKLPEIVEIEISDRTLEILVNEAINRLK
REGRYEQIVSSYESEEKFREEKERILDDIKRDRVIEVLAQEKGISVNDEELEKEAEELAPF
WGISPDRAKSLVKARQDLREELRWAILKRKVLDLLQEVKVKVVEPKGEGDDSEGKEDN

>sp|Q6FAX7|STIP_ACIAAD Cysteine protease StiP OS=Acinetobacter baylyi (strain ATCC 33305
/ BD413 / ADP1) OX=62977 GN=stiP PE=1 SV=1
MAIINKDKATELILKQGFSGSYQSEQVTFLLRTHIEPTDTAEKERLIQSGEKHYSQMISLE
NAPTARHLELFEQAMQQGQQLAQEVQQLAQTLVVEFNEPIVLVSFVRAGVPLGVLLYH
AIQDLGRDCVHYGISIIRDRGIDFAALETIIARHGHASIVFVDGWTGKGAIRQELQRS LGND
TRFIGKPLPLVVLSDIAGCAWLAASGDDWLIPSGILGSTISGLISRSICEGETLSADEITAENI
DQWHRCIEYHHLKEFDISQQFIQRINQIRLKLNPQSNAVWAETQQQAQQDQSQQVVHKL
QEQYDIQNINRIKPSIAEATRAILRRVPDLVLLRDADDEDTRLLRHLTQITKTPVQVVG DQIA
PYRAITLIQKLKGK

>sp|Q8ZP57|STEC_SALTY Secreted effector kinase SteC OS=Salmonella typhimurium (strain
LT2 / SGSC1412 / ATCC 700720) OX=99287 GN=steC PE=1 SV=1
MPFTFQIGNHSCQISERYLRDIIDNKREHVFSTCEKFIDFFRNIFTRRSLISDYREIYNLLCQK
KEHPDIKGPFSPGPFSCRDEDCRWRPLLGYIKLIDASRPETIDKYTVEVLAHQENMLLQ
MFYDGVLVTTETECSERCVDFLKETMFNYNNGEITLAALGNDNLPPSEAGSNGIYEAFEQR
LIDFLTTPATASGYESGAIDQTDASQPAEAFINSPEFQKNIRMRDIEKNKIGSGSYGTVYR
LHDDFVVKIPVNERGIKVDVNSPEHRNCHPDRVSKYLNMANDDKNFSRS AIMNINGKDV
TVLVSKYIQGQEFDEVEDENYRMAEALLKSRGVYMH DINILGNILVKEGVLFVVDGDQIV
LSQESRQQRSVSLATRQLEEQIKAHMIMKLKRAETEGNTEDVEYYKSLITDL DALIGEEEQ
TPAPGRRFKLAAP EEGTLVAKVLKDELKK

>sp|Q9S1H0|SERA_THASE Selenate reductase subunit alpha OS=Thauera selenatis OX=33058
GN=serA PE=1 SV=1
MRKVMNSPDDGNGRRRFLQFSMAALASAAAPSSVWAFSKIQPIEDPLKSYPYRDWEDLY
RKEWTWDSTGFITHSNGCVAGCAWRVVFVKNGVPMREEQVSEYPQLPGVPDMNPRGCQK
GAVYCSWSKQPDFLKYPLKRVGERGERKWKRI SWDEAFTEIADKIIDTTVKRGP GNVCM
KRPFAVITSAGYSRLANLIGAIPDVSSMTGDLYPGIQTVRMPARTVSTFDDWFTSDLILM
WHKNPIVTRIPDAHFLTEARYNGARLVNISPDYNPSSVHADLHLPVTTGTDSHLAAI VNV
LIADKKYKADYLKEQTDL PFLVRTDNGKFLREKDFNKGDSDEVFYIWDSKSGKAVLAPG
SMGSKDKTLKLGAVEPALEGTFDANGIEVTTVFARLKA EIAPYTPEATHKTTGIHPSVVRQ
LAGWIGDCKALRILDGYNQKHFDGFGCGRLLKILITLIGHHGTGTSIDTTYEGWVLEGN
KALGGVKGRPGRSVSMVLAQWVWGEQYRRSKAYFDDTELREQIGFGVDEMEALRKESE
ANGWMPNWQSIKDPVYINAGINTFATSTGYQHLRENFLKRCELYVVVDFRLNSGAMYA
DIVLPAATNLEKLDIRETSSTRFIHAFGQPIKPMYDRRTDWQISVGLARKIQERARARGITR
VDDPEIKSFIDFDKVYDEFTMNGAVEKDEDALRFVMEKSKALGPGSYEEVLKRGFVG VGP
SAGKTGPVPADKPYRPFTVNVSEKVPYKTLTGRLQFYIDHDWYQRFGATVPKPQYGGGV
LGPKKYFPVYNTPHTRWGVHSFARTDQWMLRHQRGEPDVR LNPAAMARKGIKDG DQV
RIFNSSGEFFAMAKAWPGLPENMLFSEHGWEQYLYKNMTHYNSVNAELINPLELVGGYG
HVKFAAGGFNPNRIFHETTVDVEKA

>sp|Q46338|SOXG_CORIS1 Sarcosine oxidase subunit gamma OS=Corynebacterium sp. (strain P-
1) OX=69006 GN=soxG PE=1 SV=1

MASNTLIESTSVRRSPAHLAEAMAQGSTAGTVQLREIAFATQVGVRAVPGSGGFAALAE
 AVGTGLPQQVGVVAGSVEGTAVLWLGPDFLAIAPEGAELAAELVAALGDEPGQVLDLS
 ANRSVLELSGPAAPLVLRKSCPADLHPRAFGVNLAITTTLANIPVLLWRTGEQSWYILPRA
 SFTEHTVHWLIDAMSEFASEPVA
 >sp|Q8KES3|SPRE_CHLTE Sepiapterin reductase OS=Chlorobaculum tepidum (strain ATCC
 49652 / DSM 12025 / NBRC 103806 / TLS) OX=194439 GN=CT0609 PE=1 SV=1
 MKHILLITGAGKGIGRAIALEFARAARHHPDFEPVLVLSSRTAADLEKISLECRAGALTDIT
 ITADISDMADVRLTTHIVERYGHIDCLVNNAGVGRFGALSDLTEEDFDYTMNTNLKGT
 FLTQALFALMERQHSGHIFITSVAATKAFRHSSICYMSKFGQRLVETMRLYARKCNVRI
 TDVQPGAVYTPMWGKVDDDEMQUALMMMPEDIAAPVVQAYLQPSRTVVEEILRPTSGDIQ
 DD
 >sp|P9WGG7|SIGE_MYCTU ECF RNA polymerase sigma factor SigE OS=Mycobacterium
 tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=sigE PE=1 SV=1
 MELLGGPRVGNTEQLCVADGDDLPTYCSANSEDLNITTITLSPTSMSPQQRDDQWV
 EPSDQLQGTAVFDATGDKATMPSWDELVRQHADRVRRLAYRLSGNQHDAEDLTQETFIR
 VFRSVQNYQPGTFEGWLHRITTNLFLDMVRRRARIRMEALPEDYDRVPADEPNPEQIYHD
 ARLGPDQLAALASLPPEFRAAVVLCIDIEGLSYEEIGATLGVKLGTVRSRIHRGRQALRDYL
 AAHPEHGECAVHVNPVR
 >sp|O69730|TCRX_MYCTU Probable transcriptional regulatory protein TerX
 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=trcX PE=1 SV=3
 MRRADGQPVTVLVVDDEPVLAEMVSMALRYEGWNITTAGDGSSAIAAARRQRPDVVVL
 DVMLPDMSGLDVLHKLRSNPGLPVLLLTAKDAVEDRIAGLTAGGDDYVTKPFSIEEVVL
 RLRALLRRTGVTTVDSGAQLVVGDLVLDEDSHEVMRAGEPVSLTSTEFELLRFMMHNSK
 RVLSCAQILDRVWSYDFGGRSNIVELYISYLRKKIDNGREPMIHTLRGAGYVLKPAR
 >sp|Q8NKX2|SPEC_STRP8 Exotoxin type C OS=Streptococcus pyogenes serotype M18 (strain
 MGAS8232) OX=186103 GN=speC PE=1 SV=1
 MKKINIIVFIITVILISTISPIIKSDSKKDISNVKSDLLYAYTITPYDYKDCRVNFSTHTLNI
 DTQKYRGKDYISSEMSYEASQKFKRDDHVDVFGFLFYILNSHTGEYIYGGITPAQNNKVN
 HKLLGNLFISGESQQNLNNKIILEKDIVTFQEIDFKIRKYLMDNYKIYDATSPYVSGRIEIGT
 KDGKHEQIDLFDSNEGTRSDIFAKYKDNRIINMKNFSHFIDYLEK
 >sp|P75948|THIK_ECOLI Thiamine kinase OS=Escherichia coli (strain K12) OX=83333
 GN=thiK PE=1 SV=1
 MPFRSNNPITRDELRSRFFPQYHPVTTFNSGLSGGSFLIEHQGQRFVVRQPHDPDAPQSAFL
 RQYRALSQLPACIAPKPHLYLRDWMVVDYLPGAVKTYLPDTNELAGLLYYLHQQPRFG
 WRITLLPLLELYWQQSDPARRTVGWLRMLKRLRKAREPRPLRLSPLHMDVHAGNLVHSA
 SGLKLIDWEYAGDGDIALELAADVVENTEQHRQLVNDYATRAKIYPAQLWRQVRRWFP
 WLLMLKAGWFEYRWRQTGDQQFIRLADDTWRQLLIKQ
 >sp|A0QVM0|SYP_MYCS2 Proline--tRNA ligase OS=Mycobacterium smegmatis (strain ATCC
 700084 / mc(2)155) OX=246196 GN=proS PE=1 SV=1
 MITRMSSELFLRTLRRDDPADAEPVPSHKLIRAGYVRAVGPGLYSWLPLGLRVLRKIENVVRS
 EMNAIGAQEILLPALLPRGPYETTNRWTEYGDTLFRLQDRRNNDYLLGPTHEELFTLTVK
 GEYSSYKDFPVILYQIQTKYRDEARPRAGILRGREFVMKDSYSFDVDDDDGLKNAYYQHRE
 AYQRIFARLGVRYVIVSAVSGAMGGSASEEFLAESEVGEDTFVRCVESGYAANVEAVITR
 APEAQPTGLPEAKVYDTPDTPTIATLVEWANSASLPQFEGRTVTAADTLKNVLLKTREP
 GGEWELLAVGVPGDREVDEKRLGAALPAEFALLDDADFAANPFLVKGYVGPALQDN
 GVRYLVDPRVVHGSSWITGADAPNRHVGLVAGRDFTPDGTIEAAEVRDGDPSPDGAGV
 LTSARGIEIGHIFQLGRKYTDAFSADVLGEDGKPLRLTMGSYGIGVSRLVAVIAEQQHDQL
 GLRWPSVAPFDVHVHVANKDAGARAGAAELVADLRLGHEVLFDQRQASPGVKFKDA
 ELLGMPWIVVVGRGWADGVVELNRFTGETREIAADGAAAEISSVLG

>sp|Q9RUW4|SYP_DEIRA Proline--tRNA ligase OS=Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422) OX=243230 GN=proS PE=1 SV=1
MTKDGGKKDNQGQDKKAQQYGVTPQSVDFNDWYNEVVKKADLADNSPVAGAMVVRP
YGSALWENIQRWLDDRKFASGHESLIFPTLIPMNFIMKEADHVEGFAPELFTVNKIGTEEL
AEPYVMRPTSETIIGHMWSGWLNSYRDLPLFLHYQWGSVFRAELRTKAFLRTSEFFWHEG
HTAHADAEAEARAQQLDLYHEFCRDVLALPVVRGEKTASERFAGAVATYSIEGMMR
DGKALQSGTSHYLGQNFSRAFDVKYQTREQKEEFAHTTSWAISSRIIGAIIMTHGDDSGLM
MPPRIAPIQVVVIPVGRKDNFDQMVQEGEKLAAELRAQGLRVKVDGRDGVNTNGFKYND
WELKGVVPVRIELGPRDLESGVLVVKNRHSEDKETLPRAEAVSGMSARLDTIHDFLMKRAT
DFLLANTAQVDSYDAFQREIEAGHWVRAYHCGEPACEKSIKEDTKATARNVPFDDAEFFA
ERGEGQCVKCGQPSAYGKRVLFGRQY

>sp|P0ACX9|YDIE_ECOLI Uncharacterized protein YdiE OS=Escherichia coli (strain K12)
OX=83333 GN=ydiE PE=1 SV=1
MRYTDSRKLTPETDANHKTASPQPIRRISSTLLGPDGKLIIDHDGQEYLLRKTQAGKLL
TK

>sp|P0A8B5|YBAB_ECOLI Nucleoid-associated protein YbaB OS=Escherichia coli (strain K12)
OX=83333 GN=ybaB PE=1 SV=1
MFGKGGGLGNLMKQAQMQEKMQKMQUEEIAQLEVTGESGAGLVKVTINGAHNCRRVEID
PSLLEDDKEMLEDLVAAAFNDAARRIETQKEKMASVSSGMQLPPGFKMPF

>sp|P41039|YBIIECOLI Uncharacterized protein YbiI OS=Escherichia coli (strain K12)
OX=83333 GN=ybiI PE=1 SV=1
MASGWANDDAVNEQINSTIEDAIARARGEIPRGESLDECEECGAPIQARREAIIPGVRLCIH
CQQEKDLQKPAYTGYNRRGSKDSQLR

>sp|Q9JZJ6|TTCA_NEIMB tRNA-cytidine(32) 2-sulfurtransferase OS=Neisseria meningitidis serogroup B (strain MC58) OX=122586 GN=ttcA PE=1 SV=1
MSKKTQKQELNNKLSKRLRHAVGDAINDFNMIPEDDKIMVCLSGGKDSYALLDILRQLQA
SAPIDFQLVAVNLDQKQPGFPEEVLPITYLESIGVPYKIVEEDTYSTVKRVLDEGKTTCSLCS
RLRRGILYRTAKELGCTKIALGHHRDDILATLFLNMFYGGKCLKAMPKLVSDNGEHIVIRP
LAYVKEKDLIKYAEKQFPIPCNLCSQPNLQRQVIGDMLRDWDKRFPGRIESMFSAQN
VVPShLADTELDFVGLERGQSLKHGGDLAFDSEKMPERFSDGSEEDSEIKIEPQKAERK
VINILANKPKTCGS

>sp|Q83DN9|Y658_COXBU Uncharacterized protein CBU_0658 OS=Coxiella burnetii (strain RSA 493 / Nine Mile phase I) OX=227377 GN=CBU_0658 PE=1 SV=1
MSAILPTEADRRLLSDIKESITDMQQQMAYTYSNLADLKLVGESHDKTVRITMTATYNFE
DIEFDERALQGGVKEFKWIREAWKNLCETIQKTTQSKTIELLQSMRIPEDIRNLSVEEEGG
EGGEGGQGTRGMIGNPIASGG

>sp|Q8XDI5|ULAE_ECO57 L-ribulose-5-phosphate 3-epimerase UlaE OS=Escherichia coli O157:H7 OX=83334 GN=ulaE PE=1 SV=1
MLSKQIPLGIYEKALPAGECWLERLQLAKTLGFDFVEMSVDDETDERLSRLDWSREQRLAL
VNAIVETGVRVPSMCLSAHRRFPLGSEDDAVRAQGLEIMRKAQFAQDVGIRVIQLAGYD
VYYQEANNETRRRFRDGLKESVEMASRAQVTLAMEIMDYPLMNSISKALGYAHYLNPNP
WFQLYPDIGNLSAWDNDVQMEQLQAGIGHIVAVHVKDTKPGVFKNPVFGEGVVDFFERCFE
TLKQSGYCGPYLIEMWSETAEDPAAEVAKARDWVKARMAKAGMVEAA

>sp|Q9XCW4|VIOA_ECOLX dTDP-4-amino-4,6-dideoxy-D-glucose transaminase
OS=Escherichia coli OX=562 GN=vioA PE=1 SV=1
MNDKTIPVTQPSLPelaEFMPYLEKIWKKNKWLTNNGPFHQELEEKLCEFLGVQHISLFNN
ATIALITALQALRITGEVITTPYSFVATSHAILWNLTPVFVDIENDGYNIDYRKIEQAITPK
TSAILPVHCYSTPCEVEEIQKIADNYGLKVIYDAAHAFGVNFKGGKVYLTMVYQFLVSM
RRKSSINFEGGAISPDAKTKLRIDRLKNFGIADELTVTAPGINGKMSEINAAFGVLVQLKHIE

GSISKRKIIDSLYRNLLKGTPGITIFPGNINTNSNYSYFPIIDDDGFHMSRDQAYELLKKNIL
 SRKYFYPLISNMPMYRGLISASVDNLPIANSVADKVLCLPIYTDLNEEIVVKITKLLLGKM
 >sp|E6Z0R3|VBHT_BARS Protein adenylyltransferase VbhT OS=Bartonella schoenbuchensis
 (strain DSM 13525 / NCTC 13165 / R1) OX=687861 GN=vbhT PE=1 SV=1
 MRKYEGSNDPYTDPETGVMYNLLGIKDQARLERVESAFAYIRSFELGRTSISGKFDLDHM
 KKIHKKLFGDVYEWAGKTRLVDIVKDNSKFAHYTQIESYAPQITQQLAREQHRLRGDANE
 FSQRAGYYMGELNALHPFREGNGRTLREFIWQLAREAGYHIDWDRVERQEMTRASIESY
 YGNSDLMSALIRRNLTFTVNRRVDVSQGINERVLSHIDIDKEWPQKGFNIAIQTQQAPY
 LSSYTDTSNLEEKAAQNALRNEQSYVDTFKELNDHLKTIYKDPQAAALKIEQITILAGKGDK
 LPDILAKAPNKVGE LRGS DRLIDKLKSAGKERKAALYNVPLAISTIRRLQSFYKNSYEKHM
 DKLTREREQLKVEVPSLSQEAVAYMKNVEVGRNNYSKIPENINKEFVQLESALNRRFGKD
 VIYKRNFNLSKEIASKQTYDKKLVELQTAIKFLQQRHIQKQNNLAITRTPSKGITR
 >sp|P33128|YADV_ECOLI Probable fimbrial chaperone YadV OS=Escherichia coli (strain K12)
 OX=83333 GN=yadV PE=1 SV=2
 MFFNTKHTTALCFVTCMAFSSSSIADIVISGTRVIYKSDQKSVNVRLNKGNNPLLVSQWL
 DTGDDNAEPGSITVPFTATPPVSRIDAKRGQTIKLMYTASTSLPKDRESVFWFNVLEVPPKP
 DAEKVANQSLQLAFRTRIKLFYRPDGLKGNPSEAPLALKWFWGSEGKASLRVTNPTPY
 YVSFSSGDLEASGKRYPIDVKMIAPFSDEVMKVNLNGKANSKAVHFYAINDFGGAIEGN
 ARL
 >sp|P37574|YACP_BACSU Uncharacterized protein YacP OS=Bacillus subtilis (strain 168)
 OX=224308 GN=yacP PE=1 SV=1
 MDILLVDGYNMIGAWPQLKDLKANSFEEARDVLIQKMAEYQSYTGNRVIVVFD AHLVKG
 LEKKQTNHRVEVIFTKENETADERIEKLAQALNNIATQIHVATSDYTEQW AIFGQGALRKS
 ARELLREVETIERRIERRVRKITSEKPAGKIALSEEVLKTFEKWRRGDLD
 >sp|Q39BA7|UGL_BURL3 Ureidoglycolate lyase OS=Burkholderia lata (strain ATCC 17760 /
 DSM 23089 / LMG 22485 / NCIMB 9086 / R18194 / 383) OX=482957 GN=Bcep18194_B0137
 PE=1 SV=1
 MKLLRYGPSGQEKPGILDADGRIRDLSAHVPDLSGDVLS DAGLARLR AIDPATLPLVSGEP
 RIGACVGHVKGKFIGIGLNYADHAAEAGMPVPKEPVVFGKWTSSICGPNDGIDIPKGSVKTD
 WEVELGVVIGATCKDVDEARALDYVAGYCVVNDVSEREWQIERGGQWDKGKGFDTFGP
 IGPWLVTREVPDPQRLDLWLEIDGHRYQNGNTRTMVFTVAQLIAYLSSCMTLQPGDVIT
 TGTPPGVGMGIKPSPVFLKAGQMVR LGVEGLGEQLQHTRDAR
 >sp|A0A0H3CCP8|SOCA_CAUVN Antitoxin SocA OS=Caulobacter vibrioides (strain NA1000 /
 CB15N) OX=565050 GN=socA PE=1 SV=1
 MPPLTQDPQSVDARAVANLLLDKAAALDIPISNLALQKLLYFAHGRFLVDKGRPLVNGFF
 EAWKFGPVHPVYRCFSANGPKYIINRAIKKDILSGLHIIVSPPRDQDIHEGIERVLLTMGR
 MSASQLVAVSHASGGPWDVIANGPGTNLGLGLRICDKVIKDRFRFQKVS SVSVPGLGDTL
 EEAPPS
 >sp|Q06517|SMP_SERME Extracellular minor metalloprotease OS=Serratia marcescens (strain
 ATCC 21074 / E-15) OX=617 GN=smp PE=1 SV=1
 MPAQRMRSVIPPYMLRALLTRYAPQRDCALHTLNHVQSLLGNKPLRSPTEKNARAGERS
 AISTTPERHPTARQTGAQGGAQQPRRAVDEAYDHLGVTYDFFWQAYRRNSVDNKGLPL
 VQRALRQGLPEQLSGTASRWSETATARSSTVSPSPSTLVGHEALTHGSDRERSRLIYYQQS
 GALNESLSDVFGSLVKQFHLQQTADKADWLIGAGLLAKGIKKGKLRMSAPGTAYDDPL
 LGKDPQPASKMDYIQTKE DNGGVHLNSGIPNRAFYLAATVLGGFAGKKPVTS GMTRCAT
 KRCRKTPSDHLRPRHGETRAGLRTRGDKVQQAWASGWQWSNETAADAQSGYGH
 >sp|Q9KNX6|SLYD_VIBCH FKBP-type peptidyl-prolyl cis-trans isomerase SlyD OS=Vibrio
 cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961) OX=243277 GN=slyD PE=1
 SV=1

MKIEKNTVASLAYQLTIEDGVVVDQSTVDAPLDYLGHNHNLITGLERELEGKVAGDKFTV
TIAPEDAYGEHNEDLVQRPADVFGVDELEVGMRFADTDQGPIPEITEVDGDEVVVD
GNHMLAGQSLTFTVEVVAVRAATEDEIAHGHIHQAGGCGHDHDHDHEGGCCGGEGH
GHDHHGHGKKEGGCCGGGGCGSH

>sp|P29480|TCPT_VIBCH Toxin coregulated pilus biosynthesis protein T OS=Vibrio cholerae
serotype O1 (strain ATCC 39315 / El Tor Inaba N16961) OX=243277 GN=tcpT PE=1 SV=2
MSIDIKYLSRIDIDREEFFKDSRLMCKKFDEEREVLTLLEFDTKFRVNLLKKDKVYKYFL
VSDANHKLLIANLVTEQQAKDLSFIEKDIMKIIASSATAYGASDIHFIREDRICKIKFRVNGT
MIDYREILSSEADALMFVLYNVMATTKETTWNRLPQDANIILVINEKAYRFRYAHMPLF
GEGGKNYHAVVRIIYPSNNFVCTNYQDIGYNEADTDAIARILNTSYGLFIVSGTTGSGKSTS
LKKYIELLFFNKYKKGKCFVTVEDPVEYLISGAQQSSIVADNDDKTKNPFADAVRSAMRR
DPDVIMIGEIRDKPTVEALSSAVESGHYCLTTIHAGSVVSVLQRLSGLGMKADKIASPGFL
AGITSQKLIPELCPSCKVSFVDERYQRAVFSANENGCEACNHSFGKGRLLLLLETLVPTVED
LELVASENWVSLYRKYRERRFIKTGKKGLGEGFSIKDKAYYNVLKGKVCHEYFMLHFGQ
LDHEDENIIYENYLQEV

>sp|O34321|SLTSR_BACSU Salt stress-responsive protein YocM OS=Bacillus subtilis (strain
168) OX=224308 GN=yocM PE=1 SV=1
MDFEKMKGWMEFAQQMYGGDFWKQVFDEDEDQKTPFMTNGQSPFPFAQQDQRGKGDASF
PSMDIVDTVAEVQFLIYLPGYRKQDVHILSYGDYLVVKGQRFSYFNEQDFRQKEGKYGSF
EKKIPLSDHLHGKMNAIFKDGILYITIKDEGQAKTIVIDD

>sp|P73817|SLAP_SYNY3 S-layer protein OS=Synechocystis sp. (strain PCC 6803 / Kazusa)
OX=1111708 GN=sll1951 PE=1 SV=1
MALSPNVIAALQIMYTGRGVSASDLNWWATDGANITYAEAVALFASSPDAAIKYPFFQAP
QTADKRQYVAQVFANLYNIDINDTSLVPTEELDYWINWLSLSPDNYLDFPNALNNASAAA
GLTDRLEALTNKADVLSYTEALSTAGVNTFTEAQYAEAAGIATVDDTNASVLAAEAQI
VEIAASLSVFTIAQAQATPNLPPAYTISDTADNLIAGADDPVVTGANNVIANQSPAAPLSVE
DANILLATADELAAGVTWDILDTAADVLGGAASVGAASVGITDIVDVATASQLLALGN
FDGVYAIADTSANIVADPGVSGGATAITLSDPDVPVSVASATFLQGLGIPVGPSYIVEDTSA
NILAALSTPAIVNAAEVIVNNTDVPLSVAQAEDLLSLPNLNAGFTYIIADTLDNLSAAPSTL
LDGAVSYSLTNTNPDLGVITEAEAVIVNGATNASDFNFLVADVILTPQADIRSGNSFLSVA
VVEGGSIFNTLNSNDRLTGTGEDPTLSLTWQEATFGNINTIFPVLGDIETLVATLIENDLTLV
SNDFDVVGQGFITGLKNVAASGTKGGDLELINLQTALETVSVTNYFFGDDVSFSIADPELA
GDNDLLLLTVDQVTEDGPDVTSIKISDFSGNGGYETLGLTSGVTTSSKGNTNTVDIEGIVA
VESIGITGIENLTLSTSLIGSVVKVDATGSALIFEFEGRVFTGDLKAFFDDRPGGDITFLSGS
GNDEISIARDAFTLSEDLKDVISKGHILDGGAGNDELITGDAFSDTDAGHTVIGGEGNDSI
LLTGVAEGPIAGHVNSFDLINEVGGAGDDINISGDAIGDSAGHVVFEGGAGEDDIFIGFD
KTLAVSGNGAALGVDLAGHVVFAGDDDDTVRITGDSFTSDSANGSGHSVEGGTGDDLIEI
SGDALTAADPDSETIANPFFDDSEPSDLDFIAADQPIPTTEEYQYVLLAQLGLPADYNPRNFI
RGVAAISGAHTVRGGEGNDVILFGPIAGEPGNGDGQHLAFGDEGDDFIEMTGIGSVEFNG
GAGDDTLVGGDGDPILGFGNDILNGDEGNDFLFGGKGNDNLQGGEGDDIMSGGEGDDFF
FVDAGFDVIEDLGDANSETGDQFQVSEDAEAEIRVVQDWEATGLTFNLGIATLTIENTPGGG
SVDLSASNPNTNGYTVIGNIGDDEIIGSRDDDSIFGGRGEDSIAGLGGDDIIEGNDDDDFI
SGDSLLLPLPLEEILPFGNDDIDAGSGNDVIAGDLLVVTGDDIDLNLFNNGKDTIEAGLGS
DITVGDWSIGAFGDIDLNASLERTAIGGDDTITTKQGDNGIVFPIGQVAIDNFLVGDAAA
DGVGNDIFLTETLTVIGGDDTMTGADGLDVIVGDVGLFGFEFNDSEINLTNFKLGQVNGST
VSAGDDSIITGEGGNDILVGDLFVGVINNGIIIDGGKGFQLGKDGTTSFIGGDDSISSGGDN
DFLAGDFVLVDQLSAPFDPLDPNDWTFVNPYATLQGGAGDSKAQAAQAAINLAQLRLEF
RAVGGDDELVGGRGNDTFYGGGLGADTIDIGNDVTVGGVGVNGANEIWMNGAFENAA
VNGANVDNITGFNVNNDKFVFAAGANNFLSGDATSGLA VQRVLNLQAGNTVFNLNDPIL

NASANNINDVFLAVNADNSVGASLSFSLLPGLPSLVEMQQINVSSGALAGREFLFINNGVA
AVSSQDDFLVELTGISGTFGLDLTPNFVREFYA

>sp|P14081|SELB_ECOLI Selenocysteine-specific elongation factor OS=Escherichia coli (strain K12) OX=83333 GN=selB PE=1 SV=3

MIATAGHVDHGKTTLLQAITGVNADRLPEEKKRGMTIDLGYAYWPQPDGRVPGFIDVPG
HEKFLSNMLAGVGGIDHALLVVACDDGVMAQTREHLAILQLTGNPMLTVALTKADRVD
EARVDEVERQVKEVLREYGFAEAKLFITAATEGRGMDALREHLLQLPEREHASQHSFRLA
IDRAFTVKGAGLVVTGTALSGEVKVGDLSLWLTGVNKPMPRVRLHAQNQPTETANAGQRI
ALNIAGDAEKEQINRGDWLLADVPPEPFTRVIVELQTHPLTQWQPLHIHHAASHVTGRV
SLEDNLAELVFDTPWLADNDRLVLRDISARNTLAGARVVMLNPPRRGKRKPEYLQWL
ASLARAQSDADALSVHLERGAVNLAFAWARQLNGEGMRELLQQPGYIQAGYSLLNAP
VAARWQRKILDTLATYHEQHRDEPGPGRERLRMALPMEDEALVLLLIEKMRESGDIHSH
HGWLHLPDHKAGFSEEQQAIWQKAEPFLGDEPWWVRDLAKETGTDEQAMRLTLRQAAQ
QGIITAIVKDRYYRNDRIVEFANMIRDLQCEGSTCAADFRDRLGVGRKLAIQILEYFDRIG
FTRRRGNDHLLRDALLFPEK

>sp|P9WGV7|YQGF_MYCTU Putative pre-16S rRNA nuclease OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv2554c PE=1 SV=1

MVPAQHRPPDRPGDPAHDPGRGRRLGIDVGAARIGVACSDPDAILATPVETVRRDRSGKH
LRLAALAAELEAVEVIVGLPRTLADRIGRSAQDAIELAEALARRVSPTPVRLADERLTTV
SAQRSLRQAGVRASEQRAVIDQAAAVAILQSWLDERLAAMAGTQEGSDA

>sp|O34960|YJGB_BACSU Uncharacterized protein YjgB OS=Bacillus subtilis (strain 168) OX=224308 GN=yjgB PE=1 SV=1

MKKTMSAITAAAAVTSCFTGFGAASFSAKAAAQNTLSENTNQSAELVKNLYNTAY
KGEMPQQAQGLTINKSTKGDVHAAFGEPPERPVGGDNRFDLYHWNMGQPGYGFSYHKD
MTISEIRYFGTGVERQLNLGGVTPEVLQKQLGPVNRVLTVPFTDEIDYVYDTGRYELHFVI
GTDQQTADHVNLKAK

>sp|Q9L082|Y2771_STRCO Uncharacterized phosphatase SCO2771 OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) OX=100226 GN=SCO2771 PE=1 SV=1

MPIPGTPSRAELAEHLVRTRIAGDVATPRENNLSHYRKLANGDRGFWLGLELGDRWSDE
QDVLAVMAERVGVNDDPEHRYGQDTIDPELTISALERMAGRRLKAADGGQRVLFATGHP
GGLLDVHRATAAALRDAGCEIVVIPEGLTTEEGYVQQFADVSVLEHGASLWHTHSGEPM
KAILTGLEREGRPLPDLVVADHWAGYAAQHGVDSVGYADCNDPALFLAESEGLQVA
VPLDDHVVSPPRYDPMATAYLLTEAGLK

>sp|P54955|YXEP_BACSU Uncharacterized hydrolase YxeP OS=Bacillus subtilis (strain 168) OX=224308 GN=yxeP PE=1 SV=2

MADKAFHTRLINMRRDLHEHPELSFQEVETTKKIRRWLEEEQIEILDVPQLKTGVIAEIKGR
EDGPVIAIRADIDALPIEQTNLPASKVDGTMHACGHDFHTASIIGTAMLLNQRRRAELKG
TVRFIFQPAEEIAAGARKVLEAGVLNGVSAIFGMHNKPDLPVGTIGVKEGPLMASVDRFEI
VIKKGKGHAGIPNNSIDPIAAAGQIISGLQSVVSRNISSLQNAVVSITRVQAGTSWNVIPDQ
AEMEGTVRTFQKEARQAVPEHMRRVAEGIAAGYGAQAEFKWFPYLPVQNDGTFLNAA
SEAAARLGYYQTVHAEQSPGGEDFALYQEKIPGFFVWMGTNGTEEWHHPAFTLDEEALTV
ASQYFAELAVIVLETIK

>sp|P46303|UVEN_MICLC Ultraviolet N-glycosylase/AP lyase OS=Micrococcus luteus (strain ATCC 4698 / DSM 20030 / JCM 1464 / NBRC 3333 / NCIMB 9278 / NCTC 2665 / VKM Ac-2230) OX=465515 GN=pdg PE=1 SV=2

METESTGTPTGETRLALVRRARRIDRILAETYPYAVAELDFETPFELLVATVLSAQTTDVR
VNAATPALFARFPDAHAMAAATEPELQELVRSTGFYRNKASAILRLSQELVGRHDGEVPA
RLEDLVALPGVGRKTAFFVLGNAFGQPGITVDTHFGRLARRLGFTDETDPGKGRARRGRP
VPPARDWTMLSHRLIFHGRRVCHARRPACGRCPARWCPSYAAGETDPERARALLAYEL
KPGREELLELLRAGR TAGAAGPRPRAGGXAPGLPAQPFR

>sp|O32125|YUTF_BACSU Acid sugar phosphatase OS=Bacillus subtilis (strain 168)
OX=224308 GN=yutF PE=1 SV=1
MKTYKGYLIDLDGTMYNNGTEKIEEACEFVRTLKDRGVYPYLFVTNNSRTPKQVADKLVSF
DIPATEEQVFTTSMATAQHIAQQKKDASVYVIGEEGIRQAIEENGLTFGGENADFFVVVGID
RSITYEKFVAVGCLAIRNGARFISTNGDIAIPTERGLLPNGSLTSVLTSTGVQPVFIGKPESI
IMEQAMRVLGTDVSETLMVGDNYATDIMAGINAGMDTLLVHTGVTKREHMTDDMEKPT
HAIDSLTEWIPYI

>sp|O32067|YTZE_BACSU Uncharacterized HTH-type transcriptional regulator YtzE
OS=Bacillus subtilis (strain 168) OX=224308 GN=ytzE PE=1 SV=1
MKPSTNRMLTRIKSVYMFIEKGLVTTQELVDEFGITPRTIQRDLNVLAYNDLVHSPSRGK
WETTRKKVKITS

>sp|O69731|Y3766_MYCTU Uncharacterized protein Rv3766 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) OX=83332 GN=Rv3766 PE=1 SV=2
MTDTLFAADVSEYQVPVNNSYPYRVLSIRVCDGTYRDRNFANHYRWMRSAFDSGRLTFGI
VYTYARNPNWWANANTVRSMIDAAGGLHPRVALMLDVESGGNPPGDGSSWINRLYWNL
ADYAGSPVRIIGYANAYDFFNMWRVRPAGLRVIGAGYGSNPPLPGQVAHQYTDGSGYSP
NLPQGAPPFGRCDMNSANGLTPQQFAAACGVTTTGGPLMALTDDEEQTLLTKVREIWDQ
LRGPNAGAGWPQLGQNEQGQDLTPVDAIAVIKNDVAAMLAE

>sp|P54945|YXEF_BACSU Uncharacterized protein YxeF OS=Bacillus subtilis (strain 168)
OX=224308 GN=yxeF PE=1 SV=1
MVIPLRNKYGILFLIAVCIMVSGCQQQKEETPFYYGTWDEGRAPGPTDGVKSATVTFTED
EVVETEVMGRGEVQLPFMAYKVISQSTDGSIEIQYLGPIYPLKSTLKRGENGTLIWEQNG
QRKTMTRIESKTGREEKDEKSKS

>sp|P9WKS5|Y634A_MYCTU Uncharacterized protein Rv0634A OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv0634A PE=1 SV=1
MGSDCGCGGYLWSMLKRVEIEVDDDLIQKVIRRYRVKGAREAVNLALRTLGEADTAEH
GHDDEYDEFSDPNAWVPRRSRDTG

>sp|P9WLL9|Y2067_MYCTU Uncharacterized protein Rv2067c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) OX=83332 GN=Rv2067c PE=1 SV=1
MTDDHPRADIVSRQYHRWLYPHPIADLEAWTTANWEWFDVPVHSHRILWPDREYRPDLDI
LIAGCGTNQAAIFAFTNRAAKVVAIDISRPALDHQQYLKDKHGLANLELHLLPIEELATLG
RDFDLVVSTGVLHHLADPRAGMKELAHCLRRDGVVAAMLYGKYGRIGVELLGSVFRDL
GLGQDDASIKLAKEAISLLPTYHPLRNYLTKARDLLSDSALVDFTLHGRQRSYTVEECVDL
VTSAGLVFQGWFFHKAPYYPHDFFVPNSEFYAAVNTLPEVKAWSVMERLETNLATHLFMA
CRRDRPKQYITIDFSTVAALDYVPLMRTRCGVSGTDMFWPGWRMAPSPAQLAFLQQVD
GRRRTIREIAGCVARTGEPSGGSLADLEEFGRKLFQSLWRLDFVAVALPASG

>sp|O32036|YRRM_BACSU Putative O-methyltransferase YrrM OS=Bacillus subtilis (strain 168)
OX=224308 GN=yrrM PE=1 SV=1
MTDRYEQINDYIEALLKPRPDNVKRLEAYAEHHVPIMEKAGMEVLLQILSVKQPKKILEI
GTAIGYSAIRMALELPSAEIYTIERNEKRHEEAVNNIKEFQLDDRIHVIFYGDALELADAVH
VTAPYDVIFIDAAKGQYQNFFHLYEPMLSPDGVITDNVLFKGLVAEDYSKIEPKRRRLV
AKIDEYNHWMNHPDYQTAIIPVGDGLAISKKKR

>sp|P9WFY5|Y3579_MYCTU Uncharacterized tRNA/rRNA methyltransferase Rv3579c
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv3579c PE=1
SV=1
MPGNSRRRGAVRKSGTKKGAGVGSGGQRRRGLEGRGPTPPAHLRPHHPAAKRARAQPR
RPVKRADETETVLGRNPVLECLRAGVPATALYVALGTEADERLTECVARAADSGIAIVEL
LRADLDRMTANHLHQGIALQVPPYNYAHPDDLAAALDQPPALLVALDNLSDPRNLGAI
VRSVAAFGGHGVLPQRRSASVTAVAWRTSAGAAARIPVARATNLRTLKGWADRGVVRV

IGLDAGGGTALDDVDGTDLSLVVVVGSEGKGLSRLVRQNCDEVVSIPMAAQAESLNASVA
AGVVLAEIARQRRRPREPREQTQNRMI

>sp|P9WMD9|Y472_MYCTU Uncharacterized HTH-type transcriptional regulator Rv0472c
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv0472c PE=1
SV=1

MAERIPAVTVKTDGRKRWRHQHKVERRNELVDGTIEAIRRHGRFLSMDEIAAEIGVSKTV
LYRYFVDKNDLTTAVMMRFTQTTLIPNMIAALSADMDGFELTREIRVYVETVAAQPEPY
RFVMANSSASKSKVIADSERIARMLAVMLRRRMQEAGMDTGGVEPWAYLIVGGVQLAT
HSWMSDPRMSSDELIDYLTMLSWSALCGIVEAGGSLEKFFREQPHPSPIVPAWGQV

>sp|P75455|Y330_MYCPN Uncharacterized protein MG237 homolog OS=Mycoplasma
pneumoniae (strain ATCC 29342 / M129) OX=272634 GN=MPN_330 PE=1 SV=1

MINKPNQFVNHLKALKHFAASYKELREAFNDYHKHNGDELTTFFLHQFDKVMELVKQKD
FKTAQSRCEEELAAPYLKPLVSFFQSLLQLVNHDLLEQQNAALASLPAAKIHELVLQDYP
NKLNMIHYLLPKTKAFVKPHLLQRLQFVLTDSLELKRFSFFQALNQIPGFQGEQVEYFN
SKLKQKFTLTTLGEFEIAQQPDAKAYFEQLITQIQQLFLKEPVNAEFANEIIDAFLVSYFPLHP
PVPLAQLAAKIYEYVSQIVLNEAVNLKDELIKLVHTLYEQLDRPVGDEN

>sp|Q7A788|Y511_STAAN Uncharacterized epimerase/dehydratase SA0511 OS=Staphylococcus
aureus (strain N315) OX=158879 GN=SA0511 PE=1 SV=1

MKKIMITGALGQIGTEL VVKCREIYGTDNVLATDIREPEADSPVQNGPFEILDVTDRDRMF
ELVRDFEADSLMHMAALLSATAEKNPILAWDLNMGGLMNALEAARTYNLHFFTPSSIGA
FGDSTPKVNTPTQVTIQPTTMYGVNKGAGELLQYYFKRFGVDTRSVRFPGLISHVKEPG
GGTTDYAVEIYFKAVREGHYTSFIDKGTMDMMYMDDAIEAIKLMEADDAKLETRNGY
NLSAMSFDPEMVKEAIQEYYPNFTLDYDVPDPIRQGIANSWPDSIDTSCSRGEWGFDPKYD
LASMTKLMLEAIEQKDTVKNNN

>sp|O32079|YUAD_BACSU Putative metal-sulfur cluster biosynthesis proteins YuaD
OS=Bacillus subtilis (strain 168) OX=224308 GN=yuaD PE=1 SV=1

MWKRMTAKAEGLYIADTKSFVTKQMDKLDYGGIPGDLHFGGLTKKAGAREPMSRGT
EIFNRRQISIVSIEECNEIALKMGVPRILPEWLGANVAVSGMPDLTSLKEGSRIIFPSGAALL
CEGENDPCIQPGVEVIQSYYPDQPKLASAFVRHALGIRGIVCIVERPGAVYTGDEIEVHSYQR
KVKRKAERV

>sp|O34760|YTNP_BACSU Probable quorum-quenching lactonase YtnP OS=Bacillus subtilis
(strain 168) OX=224308 GN=ytnP PE=1 SV=2

METMKIGNITLTWLDGGVTHMDGGAMFGVVPKPLWSKKYPVNEKNQIELRTDPILIQKD
GLNIIDAGIGYGKLTDKQKRNYGVTQESNVKPSLAALGLTVADIDVIAMTHLHFDHACG
LTEYEGERLVSVPNAVITYSAVEWDEMRHPNIRSKNTYWKENWEAVAGQVKTFEDTLT
ITEGITMHHTGGHSDGHSVLICEDAGETAHVHADMPLTHAHRNPLWVLAYDDYPMTSIP
QKQKWQAFAAEKDAWFIFYHDAEYRALQWEEDGSIKKSVMKMR

>sp|P43485|MCRA_STRLA Mitomycin radical oxidase OS=Streptomyces lavendulae OX=1914
GN=mcrA PE=1 SV=2

MSTQWGWALEPDQPGYDDARLGLNRAAESRPAYVVEAADEQEVA AAVRLAAEQKRPV
GVMATGHGPSVSADDAVLVNTRRMEGVSVDAARATAWIEAGARWRKVLEHTAPHGLA
PLNGSSPNVGAVGYLVGGGAGLLGRRFGYAADHVRRLRLVTADGRLRDVTAGTDPDLF
WAVRGGKDNFGLVVGMEVDLFPVTRLYGGGLYFAGEATAEVLHAYA EWVRHVPEEMA
SSVLLVHNPDLPDVPEPLRGRFITHLRIAYSGEPADGEHLVRPLRELGPILLDTVRDMPYAE
VGTIHHEPTSMPIYVAYDRNVLLSDLTDDAVIDIIVALAGPDAGAPFVTELRFHGGAYARPP
KVPNCVGGRDAAFSLTGAVPEAEGLRRRDDLLDRLRPWSTGGTNLNFAGVEDISPASVE
AAYTPADFARLRAVKAQYDPDNMFRVNFNIPPAESWT

>sp|Q5SK48|MQNE_THET8 Aminodeoxyfutasine synthase OS=Thermus thermophilus (strain
HB8 / ATCC 27634 / DSM 579) OX=300852 GN=mqnE PE=1 SV=1

MRGIRDPRLPIAEKVMEGKRLSFEDGLVLYQTKDLPTLMRLANLVRERKHGHKTYFVHS
IRVSQTNICYVGCTFCFAFQRRFGEEGAWDWDVDEVVAWVKERYQPGLTEIHLTAGHHPK
RPFAYYLDLVRALKENFPGVQVKAWTA AEIHHFSKIARLPYREVLKALKEAGLDAMPGG
GAEIFAERVRRKIARAKVSAEGWLEIHRTAHELGIPTNATMLYGHIETLEERLDHMDRLRR
LQDETGGFMSFIPLAFQPDGNQLARELGKKEFTTGLDDLRLNLA VARLYLDNFPHIKGYWA
TLPELAQVSLDWGVTDVDGTLIEERIVHMAGSPTPQGLTKRELARIILMAGRIPVERDAL
YREVRVWDRVEA

>sp|A1A278|MANA_BIFAA Mannan endo-1,4-beta-mannosidase OS=Bifidobacterium
adolescentis (strain ATCC 15703 / DSM 20083 / NCTC 11814 / E194a) OX=367928
GN=BAD_1030 PE=1 SV=1

MKTTVTKLLATVAAASTIFGMSTLPFAAEGKSASNGNSVNISDVNATAETRALFDKLN
SGKGDLRFQQHATDENISSASQGDVYETTGYPAVFGWDAGLALRGAEKPGSGADKN
ANAKALAQNITDADSKGAIVTLSAHWCNPGTGKDFNDTTAVASELLPGGKYSGTFNKEL
DAIAATAQRAKRS DGTLP IIFRPLHENNGSWFWWGATHASASEYKELYRYIVDYLRDVK
DVHNLLEYAYSPGGVFNGDSTDYLATYPGDQWVDVLGYDEYDSDDSADDSSAWINTVVK
DMKMVSDQASQRGKIVALTEFGRSGDRKFESGTGDKDTKFFSELAELAENVPSTAYM
MTWANFGGGGDNFQAYTSWKGSDGEADFKAFADSNKNLMASKDNVDYSNAPAAAMQ
NGSARIVTPVDGNRVTDTKVVVRVKTEGVKYSDLDLNSAIVTTDRGQNVKLKYSCNGYF
TGILDLNAAGINLDQSKLTLTPQVKTKDGKTLAAADGNGSVTVKLGAKPEQTVDNVEDF
DSYDNEAELQSVYSPSHSTKSNLTLVDSPEDNGTKAGNIHYDFVSYPEYNGFQRSHTPKQ
DWSGFSKLNMF LKADGSDHKFVVQVNAGGVTFEAYPKIDGTDGHVVS LNF GDADGNGG
DFAPASWDTAHAGMKLSQKLLSKVGSFALYINDNGGNRPKSGDLT LDSIKLDGKRDAYA
PNTNPTPGNTAKAQSVDDFSGYSDDAAAQSAWGNRGHTEVLSLDEGPTDGSKALRFKYD
FSNGGWYDVAKYLDGANWSGESVLAFQVKGDGSGNAIGLQIGTSDGKYFLASVKLDFTG
WKQIEIPLVDNANLTQSWPEDANKDNPMTEDDLASIKELVFASQQWNSESDGLDSSIADI
KVEPAENTSNEQTPKDESKTEVKADKEQE QSEDT SADVTAQDPATCPISEDESKGSTGNT
TVT VKPTPDTKEPADNTGKDGLSRTGSNIISAIAAVALLGGCAVLIARKRKGGDIE

>sp|P9WQ41|MBTM_MYCTU Long-chain-fatty-acid--[acyl-carrier-protein] ligase MbtM
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=mbtM PE=1
SV=1

MSELA AVLTRSMQASAGDLMVLDRETSLWCRHPWP EVHGLAESVA AWLLD HDRPAAV
GLVGEPTVELVAAIQGAWLAGAAVSILPGPVRGANDQRWADATL TRFLGIGVRTVLSQG
SYLARLRSVDTAGVTIGDLSTAAHTNRSATPVASEGPAVLQGTAGSTGAPRTAILSPGAVL
SNLRGLNQ RVGTDAATDVGCSWLPLYHDMGLAFVLSAALAGAPLWLAPTTAFTASPFR
WLSWLSDSGATMTAAPNFAYNLIGKYARRVSEVDLGALRVTLNGGEPVDCDGLTRFAEA
MAPFGFDAGAVLPSYGLAESTCAVTVPVPGIGLLADRVIDGSGAHKHA VLGNPIPGMEVR
ISCGDQAAGNASREIGEIEIRGASMMAGYLGQQPIDPDDWFATGDLGYLGAGGLVVCGR
AKEVISIAGRNIPTLEVELVAAQVRGVREGAVVALGTGDRSTRPGLVVA AEFRGPDEANA
RAELIQRVASECGIVPSDVVVFSPGSLPRTSSGKLRLRAVRRSLEMAD

>sp|Q3YAT5|MPDC_MYCAO Hydroxyisobutyraldehyde dehydrogenase OS=Mycolicibacterium
austroafricanum OX=39687 GN=mpdC PE=1 SV=1

MTRTLSADADTRTATPPLMYVNGEWLPARSGATFPTIEPSTGRPITEIPRGDSSDVDAAVK
AADVAVEWQFTDAITRAALLRRLAELVAENAEELARIESLDSGHYLA KARELVTAIPLW
LEYWAGAADKVGGRTIAPGNKLSFTLLEPLGVTAHIIPWNYPLLILARSIAPALALGNTC
VVKPAEDTSLSALKFAELVHAAGFPAGVFNVVTGYGSEAGAA LAHPEVRGITFTGSTET
GREIARLGGQHIAQVNLELGGKSPLVVFDPAPLEDAVEVAVQGFCSRAGQVCVAGSRLFL
HEDIADRFL EMLVSRLETVTVGDPFDGATQMGPLASKKH YDRVREYIEVGKQEATLLYG
GGRPTDTPDDGFFVEPTVFVDVATDARIAREEIFGPVTAVMRWSSVDDLIATINDSEFGLF
AVLWCRDITSALDTAKRLQVGSVMINDWFGELPMTPHGGHKQSGTGREEGLEAVHGYT
QVKHIGINLEPSPAKSADWAGAPL

>sp|Q7VL95|MUKE_HAEDU Chromosome partition protein MukE OS=Haemophilus ducreyi (strain 35000HP / ATCC 700724) OX=233412 GN=mukE PE=1 SV=1
MTEYIQDAIPAKLAIAIANPIFPQLDSQLRAGRHSIEMLDDEHAFLMDFQTELESFYRRYHV
DLIRAPGFFYLRLPKASTLIARSAMSEMMLVGKVLCLYLSPERLAQQGIFSQDDVYEEL
LNLADENKLLKAVNPRSTGSDLDRAKLAEKVGGALRRRLARIGIITRVGEQNSKKFIIEAV
FRFGADVRAAGDDPREVQLRLIRDGEATTPPTLLTTEAIEFAEDGARDELEESEAE

>sp|P54300|LUXP_VIBHA Autoinducer 2-binding periplasmic protein LuxP OS=Vibrio harveyi OX=669 GN=luxP PE=1 SV=2
MKKALLFSLISMVGFSPASQATQVLNGYWGYYQEFLEDEFPEQRNLTNALSEAVRAQPVPPLS
KPTQRPIKISVVYPGQQVSDYWVRNIASF EKRLYKLNINYQLNQVFTRPNADIKQQSLSLM
EALKSKSDYLIFTLDTTTRHRKFVEHVLDSTNTKLILQNITTPVREWDKHQPFLYVGFDAE
GSRELATEFGKFFPKHTYYSVLYFSEGYISDVRGDTFIHQVNRDNNFELQSAYYTKATKQS
GYDAAKASLAKHPDVFYIACSTDVALGAVDALAELGREDIMINGWGGGSAELDAIQKG
DLDITVMRMNDDTGIAMAEAIKWLEDKPVPTVYSGDFEIVTKADSPERIEALKKRAFRY
SDN

>sp|P23146|LUXA2_PHOLU Alkanal monooxygenase alpha chain OS=Photobacterium luminescens OX=29488 GN=luxA PE=1 SV=1
MKFGNFLTLYQPPQFSQTEVMKWLVKLGRISEECGFDTVWLLLEHHFTEFGLLGNPYVAA
AYLLGATKKLVNGTAAIVLPTAHPVRQLEEVNLLDQMSKGRFRFGICRGLYNKDFRVFGT
DMNNSRALMECWYKLIRNGMTEGYMEADNEHIKFHKVKVLPTAYSQGGAPIYVVAESA
STTEWAAQHGLPMILSWIINTNDKKAQIELYNEVAQEYGHDIHNIDHCLSYITSVDHDSMK
AKEICRNFLGHWYDSYVNATTIFDDSDKTKGYDFNKGQWRDFVLKGHKNTNRRVDYSY
EINPVGTPQECIDIITDIDATGISNICCGFEANGTVDEIISMKLFQSDVMPFLKEKQQFSYY
IS

>sp|P96379|MAZG_MYCTU Nucleoside triphosphate pyrophosphohydrolase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=mazG PE=1 SV=1
MIVVLVDPRRPTLVPEAIEFLRGEVQYTEEMPVAVPWSLPAARSAHAGNDAPVLLSSDP
NHPAVITRLAAGARLISAPDSQRGERLVDVAMMDKLRTAGPWESEQTHDSLRRYLLEE
TYELLDVAVRSGSVDQLREELGDLLQVLFHARIAEDASQSPFTIDDVADTLMRKLGNRAP
GVLAGESISLEDQLAQWEAAKASEKARKSVADDVHTGQPALALAQKVIQRAQKAGLPAH
LIPDEITSVSVSADVDAENTLRTAVLDFIDRLRCAERAIAVARRGSNVAEQLDVTPLGVITE
QEWLAHWPTAVNDSRGGGSKKRKGMR

>sp|Q819E8|MTNW_BACCR 2,3-diketo-5-methylthiopentyl-1-phosphate enolase OS=Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711) OX=226900 GN=mtnW PE=1 SV=1
MSGIATYLIHDDSHNLEKKAQEQIALGLTIGSWTHLPHLLQEQLKQHKGNVIHVEELAEHE
HTNSYLRKKVKRGIKIEYPLLNFSPLPAILTTTFGKLSLDGEVKLIDLTFSDELKKHFGP
KFGIDGIRNLLQVHDRPLLSIFKGMIGRNIGYLKTQLRDQAIGGVDIVKDDEILFENALTP
LTKRIVSGKEVLQSVYETYGHKTLYAVNLTGRTFDLKENAKRAVQAGADILLFNVFAYG
LDVLQSLAEDDEIPVPIMAHPAVSGAYSASKLYGVSSPLLGLKLLRYAGADFSLFSPYGS
VALEKEEALAIKYLTEDDASFKKSFVSPSAGIHPGFVPFIVRDFGKDVVINAGGGIHHGPN
GAQGGGKAFTATAIDATLQNKPLHEVDDINLHLSALQIWGNPSYEVKL

>sp|O67928|MOAE_AQUAE Molybdopterin synthase catalytic subunit OS=Aquifex aeolicus (strain VF5) OX=224324 GN=moaE PE=1 SV=1
MEVGMIPRVYLGHEWFGAERILSEYQVPEDCGAQVFLGIPRNAPEDGGNIEALEYEAYP
EMAIKEMEKIRQETIEKFGVKEVFIHHLGLVKIGEPSFLVLA VGGHREETFKACRYAVDE
TKKRVPIWKKEIFKEGKGEWVLGEKKNASGQTK

>sp|Q97ML3|MURK_CLOAB N-acetylmuramic acid/N-acetylglucosamine kinase OS=Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787) OX=272562 GN=murK PE=1 SV=1

MKYVIGIDGGGSKTHMKISTLDYKVLLEVFKGPSNINSSTKEEVKRVLQELIMEGLGKLGQ
 SLEEC SAICIGTAGADRTEDKSIIEDMIRSLGYMGKIIVVND AEIALAGGIEKREGIIVISGTG
 SICYGRNKEGRSARS GGWGHII GDEGSGYDIGIKA IKAALKSFDKRGEKTILEGDILDFLKL
 KSHEDLINIYIRSGVTKKEIASLTRVVNSAYIKGDLVSKRILKEAARELFLSVKAVVEVLS
 MQNKKVVLTTAGGVINNINYL YDEF RKFLNLNYPKVKIISMKNDSAFGAVIARSECD
 >sp|A8ZTR0|ILVC_DESOH Ketol-acid reductoisomerase (NAD(+)) OS=Desulfococcus
 oleovorans (strain DSM 6200 / Hxd3) OX=96561 GN=Dole_2039 PE=1 SV=1
 MPTINFGGVEENVVTSEEFTLKKAREVLKNEVITVLGYGVQGP AQALNLKDNGFEVIIGQL
 EGDAYWEKAIADGFVPGKTLFPIEEAAKKGTIIKMLLSDAGQVAVWPVKVKKCLKKGDAL
 YFSHGFGIVYKDQTGIVPPKNVDVILVAPKSGSTNVRRNFKDGS GINSSYAVFQDATGRA
 EERTIALGIAIGSGYLFPTTFEKEVFSDLTGERGVLMGCLAGTMEAQYNVLRKHGHSPSEA
 FNETVEELTQSLIRLVAENGMDWMFANCSTTAQRGALDWAPKFRDAVAPVFDSL YRRVK
 NGAETRRVLKVNSAPNYLEKLRKELDTIKNSEMWQAGAAVRALRPENRKKKK
 >sp|P27294|INAA_ECOLI Protein InaA OS=Escherichia coli (strain K12) OX=83333 GN=inaA
 PE=1 SV=3
 MAVSAKYDEFNHWWATEGDWVEEPNYRRNGMSGVQCVERNGKKLYVKRMTHHLFHS
 VRYPFGRPTIVREVAVIKELERAGVIVPKIVFGEAVKIEGEWRALLVTE DMAGFISIADWY
 AQHAVSPYSDEV RQAMLKAVALAFKKMHSINRQHGCCYVRHIYVKTEGNAEAGFLDLE
 KSRRLRRDKAINHDFRQLEKYLEPIPKADWEQVKAYYYAM
 >sp|P69343|INV F_SALTY Invasion protein InvF OS=Salmonella typhimurium (strain LT2 /
 SGSC1412 / ATCC 700720) OX=99287 GN=invF PE=1 SV=1
 MSFSERHNENCLIQEGALLFCEQAVVAPVSGDLVFRPLKIEVLSKLLAFIDGAGLVDTTY
 AESDKWVLLSPEFRAIWQDRKRCEYWFLQQIITPSAFNKVLALLRKSESYWLVG YLLAQ
 STSGNTMRMLGEDYGVSYTHFRRLCSRALGGKAKSELNRNWRMAQSL LNSVEGHENITQL
 AVNHGYSSPSHFSSEIKELIGVSPRKL SNIIQLADK
 >sp|P9WKG1|ISP H2_MYCTU 4-hydroxy-3-methylbut-2-enyl diphosphate reductase 2
 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=ispH2 PE=1
 SV=1
 MVPTVDMGIPGASVSSRSVADRPNRKRVL LAEPRGYCAGVDRAVETVERALQKHGPPVY
 VRHEIVHNRHVVDTLAKAGAVFVEETE QVPEGAIVVFS AHGVAPT VHVSASERNLQVIDA
 TCPLVTKVHNEARRFARDDYDILLIGHEGHEEVVGTAGEAPDHVQLVDGVD AVDQVTVR
 DEDKVWLSQTTL SVDETMEIVGRLRRRFPKLQDPPSDDICYATQNRQVAVKAMAPECE
 LVIVVGSRNSSNSVRLVEVALGAGARAAHLVDWADDIDSAWLDGVT TVGVTS GASVPEV
 LVRGVLERLAECGYDIVQPVT TANETLVFALPRELRSPR
 >sp|P39375|IRAD_ECOLI Anti-adaptor protein IraD OS=Escherichia coli (strain K12) OX=83333
 GN=iraD PE=1 SV=2
 MMRQSLQAVLPEISGNKTSSLRKSVCSDLLTLFNSPHSALPSLLVSGMPEWQVHNPSDKH
 LQSWYCRQLRSALLFHEPRIAALQVNLKEAYCHTLAISLEIMLYHDDEPLTFDLVWDNGG
 WRSATLENVS
 >sp|P03023|LACI_ECOLI Lactose operon repressor OS=Escherichia coli (strain K12) OX=83333
 GN=lacI PE=1 SV=3
 MKPVTLYDVAEYAGVSYQTVSRVVNQASHVSAKTREKVEAAMAELNYIPNRVAQQLAG
 KQSLIGVATSSLALHAPSQIVAAIKSRADQLGASVVVSMVERSGVEACKAAVHNLLAQR
 VSGLIINYPLDDQDAIAVEAACTNVPALFLDVSDQTPINSIIFSHEDGTRLGVEHLVALGHQ
 QIALLAGPLSSVSARLRLAGWHKYLTRNQIQPIAERE GDWSAMSGFQQT MQMLNEGIVPT
 AMLVANDQMALGAMRAITESGLRVGADISVVG YDDTEDSSCYIPPLTTIKQDFRLLGQTS
 VDRLLQLSQGQAVKGNQLLPVSLVKRKTT LAPNTQTASPRALADSLMQLARQVSRLESG
 Q
 >sp|E1XUJ2|LDI_CASDE Linalool dehydratase/isomerase OS=Castellaniella defragrans
 OX=75697 GN=ldi PE=1 SV=1

MRFTLKTТАIVSAAALLAGFGPPPRAAELPPGRLATTEDYFAQQAKQAVTPDVMAQLAY
MNYIDFISPFYSRGCSFEAWELKHTPQRVIKYSIAFYAYGLASVALIDPKLRALAGHDLDIA
VSKMKCKRVWGDWEEDGFGTDPIEKENIMYKGHLNLMYGLYQLVTGSRRYEAHAHLT
RIIHDEIAANPFAGIVCEPDNYFVQCNSVAYLSLWVYDRLHGTDYRAATRAWLDFIQKDLI
DPERGAFYLSYHPESGAVKPWISAYTTAWTLAMVHGMDPAFSERYYPFRKQTFVEVYDE
GRKARVRETAGTDDADGGVGLASAFTLLLAREMGDQQLFDQLLNHLEPPAKPSIVSASLR
YEHPGSLLFDELLFLAKVHAGFGALLRMPPPAAKLAGK
>sp|Q9IIW5|KU_PSEAE Non-homologous end joining protein Ku OS=Pseudomonas aeruginosa
(strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 /
PAO1) OX=208964 GN=ku PE=1 SV=1
MARAIWKGAISFGLVHIPVSLSAATSSQGIDFDWLDQRSMEPVGYKRVNKNVTGKEIERENI
VKGVEYEKGRYVVLSEEEIRAHPKSTQTIEIFAFVDSQEIPLQHFDTPYYLVPDRRGKGV
YALLRETLERTGKVALANVVLHTRQHLALLRPLQDALVLITLRWPSQVRSLDGLELDES
TEAKLDKRELEMAKRLVEDMASHWEPDEYKDSFSKIMKLVEEKAAGQLHAVEEEEE
VAGKGADIIDLTLKRSLSRAGGGKDKGSEKAGADAKGRAKSGASRSRKA
>sp|P0A3M7|LCIA_LACLL Lactococcin-A immunity protein OS=Lactococcus lactis subsp. lactis
OX=1360 GN=lcia PE=1 SV=1
MKKKQIEFENELRSMMLATALEKDISQEERNALNIAEKALDNSEYLPKIILNLRKALTPLAIN
RTLNHDLSELYKFITSSKASNKNLGGGLIMSWGRLF
>sp|O26009|KTHY_HELPY Thymidylate kinase OS=Helicobacter pylori (strain ATCC 700392 /
26695) OX=85962 GN=tmk PE=1 SV=1
MYVVLEGVDGAGKSTQVELLKDRFKNALFTKEPGGTRMGESLRRIALNENISELARAFLF
LSDRAHTESVIKPALKEKKLIISDRSLISGMAYSQFSSLELNLLATQSVLPAKIILLIDKEG
LKQRLSLKSLDKIENQGIEKLLHIQQLKTHAYALQEKFGCEVLELDAKESVKNLHEKIAA
FIKCAV
>sp|P52062|HEMW_ECOLI Heme chaperone HemW OS=Escherichia coli (strain K12)
OX=83333 GN=hewW PE=1 SV=1
MVKLPPLSLYIHIPWCVCQKCPYCDFNSHALKGEVPHDDYVQHLLNDLDNDVAYAQQGREV
KTIFIGGGTPSLLSGPAMQTLLDGVRARLPLAADAETMEANPGTVEADRFVDYQRAGVN
RISIGVQSFSEEKLRKRLGRIHGPQEAKRAAKLASGLGLRSFNLDLMHGLPDQSLEEALGDL
RQAIELNPPHLSWYQLTIEPNTLFGSRPPVLPDDDALWDIFEQGHQLLTAAGYQQYETSAY
AKPGYQCQHNLNYWRFGDYIGIGCGAHGKVTFPDGRILRTTKTRHPRGFMQGRYLESQR
DVEATDKPFEFFMNRFRLLAAPRVEFIAYTGLCEDVIRPQLDEAIAQGYLTECADYWQIT
EHGKFLFLNSLLEFLAE
>sp|Q8EIX3|HIPA_SHEON Serine/threonine-protein kinase toxin HipA OS=Shewanella
oneidensis (strain MR-1) OX=211586 GN=hipA PE=1 SV=1
MSTAKTLTLEMHLGDLMIGELSFDATADTFVHYTKDWQQSGFPLSPTIPLDGTGTSNQIS
MFLVNLLPENKGLDYLIESLGVSNGNTFALIRAIGLDTAGAIAFVPKGALLPETQLRPIKAE
EVIQRIEDPTMWPMEIWDGKPRLSVAGVQPKLNLFYNGKEFAFAEGTSSSTHIVKFEKYH
HLVINEFITMRLAKVLGMNVANVDIVHFGRYKALCVERFDRRNIPGEQVRRLRHIVDSCQ
ALGFSVSKKYERNFGTGRDVKDIREGVSNRFLSLAAKCRNPVAAKQDMLQWALFNLLT
GNADAHGKNYSFFMTPSGMEPTPWYDLVSVDMEYEDFEQQLAMAIDDEFDPNSIYAYQLA
AFMDGLGLPRNLLISNLTRIARRIPQAIAEVILMLPPLDEDEASFVAHYKTQLLARCERYLG
FVDEV RDVEV
>sp|A0A0H2URJ6|GLYE_STRPN Glycosyltransferase GlyE OS=Streptococcus pneumoniae
serotype 4 (strain ATCC BAA-334 / TIGR4) OX=170187 GN=glyE PE=1 SV=1
MRNTKRAVVFAFDYAYIRQIETAMKSLCRHNSHLKIYLLNQDIPQEWFSQIRIYLQEMGG
DLIDCKLIGSQFQMNWSNKLPHINHMTFARYFIPDFVTEDEKVLVYLDSDLI VTGDLTDLFEL
DLGENYLAAARSCFGAGVGFNAGVLLINNKKWGSETIRQKLIDLTEKEHENVEEGDQSIL
NMLFKDQYSSLEDQYNFQIGYDYGAATFKHQFIFDIPLPLILHYISQDKPWNQFSVGRL

REVWWEYSLMDWSVILNEWFSKSVKYPSSQIFKLQCVNLTNSWCVEKIDYLAEQLP
 HFHIVAYTNMANELLALTRFPNVTVPNSLPMLLEQIVIASDLYLDLNHDRKLEDAYEFV
 LKYKKPMIAFDNTCSENLSSEISYEGIYPSSIPKKMVAAIRSYMR
 >sp|Q2YK18|HDEA_BRUA2 Probable acid stress chaperone HdeA OS=Brucella abortus (strain 2308) OX=359391 GN=hdeA PE=1 SV=1
 MIKALFNKNTALAAVAILALSSGAMAESAETHKTDMAKKKVSELTCEDFNGLEESFKPT
 VVGWVVGFNKKGKEEDAVIDVDGIETVTPAIEACKQEPKASFWKKAEAEELKKVF
 >sp|Q5FPE5|GMDH_GLUOX Glucose 1-dehydrogenase OS=Gluconobacter oxydans (strain 621H) OX=290633 GN=GOX2015 PE=1 SV=1
 MPAPYKDRFAGKKVLVTGASQGIGETALRFAEEGAQVALNGRKKEDKLIAREKLPKVS
 GGEHPATGDISKEDDVKRLVAESIKAMGGDLVLCNAGYQIPSPSEDIKLEDFEGVMAV
 NVTGVMLPCREVIRYWLENGIGTIIVNSSVHQIIPKPHYLGYSASKGAVGNIVRTLAEY
 ATRGIRVNAVAPGAIVTPINMSWIDDPEQYKAVSSHIPMKRPGESREIADAITFLAAEDSTY
 ITGQTLTYVDGGLTLYGDFENNWSS
 >sp|P18079|HEM1_RHOCB 5-aminolevulinate synthase OS=Rhodobacter capsulatus (strain ATCC BAA-309 / NBRC 16581 / SB1003) OX=272942 GN=hemA PE=1 SV=2
 MDYNLALDKAIQKLHDEGRYRTFIDIEREKGAFFKAQWNRPDGGKQDITVWCGNDYLG
 MGQHPVLAAMHEALEAVGAGSGGTRNISGTTAYHRRLEAEIADLHGKEAALVFSSAYI
 ANDATLSTLRVLFPGLIYSDSLNHASMIIEGKRNAGPKRIFRHNDVAHLRELIAADDPAP
 KLIAFESVYSMDGDFGPIKEICDIADEFGALTYIDEVHAVGMYGPRGAGVAERDGLMHRI
 DIFNGTLAKAYGVFGGYIAASAKMVDAVRSYAPGFIFSTSLPPAIAAGAQAIAFLKTAEG
 QKLRDAQQMHAQVLMRLKALGMPIDHGHSHIVPVVIGDPVHTKAVSDMLLSYGVYV
 QPINFPTVPRGTERLRFTPSPVHDLKQIDGLVHAMDLLWARCALNRAEASA
 >sp|P0ACL5|GLCC_ECOLI Glc operon transcriptional activator OS=Escherichia coli (strain K12) OX=83333 GN=glcC PE=1 SV=1
 MKDERRPICEVVAESIERLIIDGVLVKGQPLPSERRLCEKLGFSRSALREGLTVLRGRGIIET
 AQGRDSRVARLNRVQDTSPLIHLFSTQPRTLYDILLVRLLEGESARLAATLTGTQADFFVI
 TRCYEKMLAASENNKEISLIEHAQLDHAFHLAICQASHNQVLVFTLQSLTDLMFNSVFASV
 NNLYHRPQQKKQIDRQHARIYNAVLRQLPHVAQRAARDHVRTVKKNLHDIELEGHHLIR
 SAVPLEMNLS
 >sp|O67359|GPH_AQUAE Phosphoglycolate phosphatase OS=Aquifex aeolicus (strain VF5) OX=224324 GN=gph PE=1 SV=1
 MRVILFDLDGTLIDSAKDIALALEKTLKELGLEEYYPDNVTKYIGGGVRALLEKVLKDKFR
 EEYVEVFRKHYLENPVYTKPYPEIPYTLALSKSGFKLAVVSNKLEELSKKILDILNLSG
 YFDLIVGGDTFGEKKPSPTPVLTLEILGEEPEKALIVGDTDADIEAGKRAGTKTALALWG
 YVKLNSQIPDFTLSRPSDLVKLMDNHIVEF
 >sp|P16618|HEM1_BACSU Glutamyl-tRNA reductase OS=Bacillus subtilis (strain 168) OX=224308 GN=hemA PE=1 SV=1
 MHILVVGVDYKSAPIEIREKVSFQPNELAEAMVQLKEEKSILENIIVSTCNRTIYAVVDQL
 HTGRYYIKKFLADWFQLSKEELSPFLTIFYESDAAVEHLFRVACGLDSMVIGETQILGQVRD
 SFKTAQQEKTIGTIFNELFKQAVTVGKRTHAETDIGSNAVSVSYAAVELAKKIFGNLSSKHI
 LILGAGKMGELAAENLHGQGIGKVTVINRTYLKAKELADRFSGEARSLNQLESALAEADI
 LISSTGASEFVVSKEMMENANKLRKGRPLFMVDIAVPRDLDPALNDLEGVFLYDIDDLEGI
 VEANMKERRETAEKVELLIEETIVEFKQWMNTLGVPVISALREKALAIQSETMDSIERKL
 PHLSTREKKLLNKHTKSIINQMLRDPILVKELAADADSEEKLALFMQIFDIEEAAGRQMM
 KTVESSQKVHSFKKAESKAGFSPLVSE
 >sp|O06925|MDCC_MALRU Malonate decarboxylase acyl carrier protein OS=Malonomonas rubra OX=57040 GN=mdcC PE=1 SV=1
 MEGMLNELNFKFKSENPDVVLPHHHYGVVSGDLEVLLKKHELEGAVEIRVVSPVRGF
 DHVWEKVLEKVISDAEVGNVAIEINDNNATPVVVALRLAQALSEAKSAEQSVN

>sp|A8YER2|MTNW_MICAE 2,3-diketo-5-methylthiopentyl-1-phosphate enolase
OS=Microcystis aeruginosa OX=1126 GN=mtnW PE=1 SV=1
MTIIVDYRFPPAINAEKQAKTIAIGQTAGTWSERHSHRQKQLQQHLAEVVGIREEADGYK
VARVRFPQINVENTIASLLTMIFGKYSMAGAGKVVGVPYLPESYGTAKLGITGIRQLGV
YDRPLVMAIFKPALGLSAQDHADILREVAFAGLDVIKDDDEIMADLPVAPHTHERLDCCRRV
LEEVRQQTGRNVLYAVNVTGKADELQRKARLLVKHGANALLNVLTYGFSVLEALASDP
AIDVPIFAHPAFAGAMCAGSDTGLAYSVVLGTMMMAHAGADAVLYPAAYGSLPFDPEEG
KIRDILDRNVFPVPSAGIRPGIVPQVLGDYGRNVILNAGTGIMDHPSGPASGVRAFFEALA
RIEAGESFDPANLPEGALKQAILEWG

>sp|Q3M5Q6|METXA_ANAVT Homoserine O-acetyltransferase OS=Anabaena variabilis (strain
ATCC 29413 / PCC 7937) OX=240292 GN=metXA PE=1 SV=1
MNYQDFISEQTEYYHLPVPFELEGGGVLTGVQVAYRTWGKLSAGDNGVLICHALTGSA
DADEWWEGLLGANKALDSDRDFIICSNILGSCYGTGATSINPQTGIPYGASFPAITIRDMV
RLQAALIQHLGIKSLQLVIGGSLGGMQVLEWALLYPEIVQAIPIATSGRHSWCIGLSEA
QRQAIYADPNWKGGNYTKEQPPSQGLAVARMMAMSAYRSWQSFTARFGRQYDAVADQ
FAIASYLQHHGQKLVRFDANTYITLTQAMDSHDVAQGRDYKSVLQSIKQPALVVAIDSD
ILYPPTEQQELADFIPDAQLGWLQSSYGHDAFLIDIATLSQLVINFRQSLSLKTFSDVTT

>sp|P76114|MCBR_ECOLI HTH-type transcriptional regulator McbR OS=Escherichia coli (strain
K12) OX=83333 GN=mcbR PE=1 SV=2
MPGTGKMKHVSLLTQVENDLKHQLSIGALKPGARLITKNLAEQLGMSITPVREALRLVS
VNALSVAPAQAFTVPEVGKRQLDEINRIRYELELMAVALAVENLTPQDLAELQELLEKLQ
QAQEKGDMEQIINVNRLFRLAIYHRSNMPILCEMIEQLWVRMGPGHLHYLYEAINPAELRE
HIENYHLLLAALKAKDKEGCRHCLAEMQQNIAILYQQYNR

>sp|Q9X0V7|MGGS_THEMA Mannosylglucosylglycerate synthase OS=Thermotoga maritima
(strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) OX=243274 GN=mggS PE=1 SV=1
MKIALIHYRGGLMDGVSLEMEKWKKVLTCKMGHEVHIVAENKKEGVDTLKEIGFENPDF
ERVNRNFFGGIKDFLSEKEFLDFLKEKEEELFHILNEALKDYDLIVPNNIWSLGLFPSLGLA
LSRLEKNFVAHHHDFWVERKHLIPENRRFREILDKHFPPDLPNVKHVINTIAQRELKRRR
NIDSVVVPNVMDFSSPITSEEMYHRVREELQIAPGTIVALQATRDRRKTIELSIDVVSLLKE
TLTSKKEADLYNGERYSGEVILLFSGICEDEEYLKELKEYASSKGVSLLVLSSEVRKNTSLF
WKLYNAADFVTYPSILEGWGNQLLEAIAAKKPVVLFEYEVFKSDIKPAGLKYYVSLGDRCF
REGLVKVDERILKKAVEEISRLFLDPSLYRETVEHNFEVGKRHFSLERLEDILSREVL

>sp|O82881|LSOA_ECO57 mRNA endoribonuclease LsoA OS=Escherichia coli O157:H7
OX=83334 GN=lsOA PE=1 SV=1
MAQNPFKALNINIDKIESALTQNGVTNYSSNVKNERETHISGTYKGIDFLIKLMPSGGNTTI
GRASGQNNTYFDEIALIKENCLYSDTKNFYTIKFSDDDRANLFEFLSEEGITITEDNNND
PNCKHQYIMTTSNGDRVRAKIYKRGSIQFQGYLQIASLINDFMCSILNMKEIVEQKNKEF
NVDIKKETIESELHSLPKSIDKIHEDIKKQLSCSLIMKKIDVEMEDYSTYCFSALRAIEGFIY
QILNDVCNPSSSKNLGEYFTENPKKYIIREIHQETINGEIAEVLCECYTYWHENRHGLFHMK
PGIADTKTINKLESIAIIDTVCQLIDGGVARLKL

>sp|Q2RXI0|MTNA_RHORT Methylthioribose-1-phosphate isomerase OS=Rhodospirillum
rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIB 8255 / S1) OX=269796
GN=mtnA PE=1 SV=1
MNVKGTPTRTIWPAREGGAVWIIDQTRLPHFVVTQRLNDLGAVAHAIRAMLVRGAPLIGA
TAAYGVALGMAEDPSDEGLTRACQTLLATRPTAVNLRWAIEAMAESLAAVPPDQRAQA
AWAKAGAICDEDVALNEAIGDHGLGIIKDLARTKGVEKGGEGPINILTHCNAGWLATVD
WGTALAPLYKAHDAGLPIHVWVDETRPRNQGASLTAWELNSHGVPHTVIADNTGGHLM
QHGLVDMVIVGTDRTTATGDVCNKIGTYLKALAAFDNAVPFYVALPGPTIDWTVNDGLR
EIPIEQRDAAEVTRVWGRTAAGALEWVTITPTGSPAANYAFDVTPTARLITGLITERGVCAA
SAAGLAGLYPERAPAPVPAGSAAGKGAAATADGAL

>sp|P9WQF9|MBTN_MYCTU Acyl-[acyl-carrier-protein] dehydrogenase MbtN
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=mbtN PE=1
SV=1
MTAGSDLDDFRGLLAKAFDERVVAWTAEEAQERFPRQLIEHLGVCVFDKAWATDAR
PDVGKLVELAFALGQLASAGIGVGVSLHDSAIAILRRFGKSDYLRDQCAIRGA AVL CIG
ASEESGGSDLQIVETEIRSRDGGFEVRGVKKFVSLSPIADHIMVVARSVHDPTSRHGNVA
VVAVPAAQVSVQTPYRKVGAGPLDTAAVCIDTWVPADALVARAGTGLAAISWGLAHER
MSIAGQIAASCQRAIGITLARMMSRRQFGQTLFEHQALRLRMADLQARVDLLRYALHGIA
EQGRLELRATAAAVKVTAARLGEEVISECMHIFGGAGYLVDETTLGKWWRDMKLARVGG
GTDEVLWELVAAGMTPDHDGYAAVVGASKA

>sp|P71650|MAZF9_MYCTU Endoribonuclease MazF9 OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) OX=83332 GN=mazF9 PE=1 SV=2
MMRRGEIWQVDLDPARGSEANNQRPVVVSNDRANATATRLGRGVITVVPVTSNIAKVY
PFQVLLSATTTGLQVDCKAQAEQIRSIATERLLRPIGRVSAELAQLDEALKLHLDLWS

>sp|Q8CQL3|MIAA_STAES tRNA dimethylallyltransferase OS=Staphylococcus epidermidis
(strain ATCC 12228) OX=176280 GN=miaA PE=1 SV=1
MTEMTPFLIVIVGPTASGKTELSIEVAKKFNGEISGDSMQVYQGMDIGTAKVTTEEMEG
IPHYMIDILPPDASFSAIEFKKRAEKYIKDITRRGKVPPIAGGTGLYIQSLLYNYAFEDESIS
DKMKQVKLKLKELEHLNNKLHEYLASFDKESAKDIHPNNRKRVLRAIEYYLTKKLLS
SRKKVQQFTENYDTLLIGIEMSRETLYLIRNKRVDIMLGHGLFNEVQHLVEQGFEASQSM
QAIGYKELVPVIKGNISMENAVEKQKQHSRQYAKRQLTWFKNKMNVHVLNKERMSLQM
MLDEITTQINKRSSNHDCKRKHPRPSTREL

>sp|Q8GQC5|GLGB_DICCH 1,4-alpha-glucan branching enzyme GlgB OS=Dickeya
chrysanthemi OX=556 GN=glgB PE=1 SV=1
MFVAAMTESDQNIINLLFSGHYADPFAVLGMHDTASGLEVRALLPDAIDVWVVDAAHSGR
KVANLQCRDPRGFFASAIIPRRKKPFSYRLAVTWPQDTQVIDDPYRFGTLLQELDIWLLAE
GRHLRPFETLGAHPSTLDGVVGTCFAVWAPNAQRVS VVGDFNFDGRRHPMRRRRENG
VWELFVPGVGPGLYKFEIIDCYGNVLVKS DPYAFESQMRPDTASVVSRLPPALPVDEAR
QHANELQSPISIEVHLGSWRRHTHNNFWLSYRELADQLVPYVKEMGFTHVELMPVHKH
PFDGSWGYQPLGLYAPTRRFGSPDDFRYLVSAFHEAGINVLLDWVSGHFPADSYGLARFD
GPALY EYADPKEGYHQDWNTLIYNFDRHEVRNYLAGNALYWTERFGVDGLRVDAS
MIYRDYSRRDGEWVPNYFGGKENLEAIGFLRYTNQMLGQHHA GAVTIAEESTDYAGVTL
PPEHGGGLGFHYKWNMGWMHDSLAYMQLDPVHRKYHHDLLTFGMLYAYS ENFVLPLSH
DEVVH GKRSLLDRMPGDVWQKFANL RAYYGFMWAYPGKKLLFMGGEFAQGREWNHD
TSLDWHL LDEPEGWHAGVQQLVRDLNHCYRQHPPLYQCDYLHQGF EWVVVDDRENSV
FAFIRRDADGNEMLIISNFTPVRDSYRVGINQPGAWREVLNTDSWHYHGGNLGNQGLVY
SETVGSHSRPQSLVLALPPLATLYLVKEA

>sp|P50727|FER_BACSU Ferredoxin OS=Bacillus subtilis (strain 168) OX=224308 GN=fer PE=1
SV=2
MAKYTIVDKDTCIACGACGAAAPDIYDYDDEGIAFVTLDENKGVVEVPEVLEEDMIDAFE
GCPTDSIKVADEPFEGDPLKFE

>sp|O82833|GELLY_BACSP Gellan lyase OS=Bacillus sp. OX=1409 PE=1 SV=1
MRFSWKKLVSAALVMALLVGIVYPAASGRGAVASAA SGTVELVPTDDAFTSAVAKDA
NANGTWMQLKGSIGGQRYIYMKFDLTALAGVEADRIENAKVWLKKMG TNGTAMTVGL
RAVDDTSWSESTLTWNNAPVYGSQVLSQQSVLSTPDVYYPFDLDEY LKTQLAAGKSKLA
IAFVPISTLNENMEFYARESTANTPKLVVELKDEPPAPTGLMQLVQSFGGH NKGHLRVVEF
DATPASTTGNGTVGITADGAAPAAAADFPIALRFGTDGTIKAANAAGFESKTPVNYTAGQ
KYHVKAMINLSLGTYDLWLTPPNAGQPVLLAADY AFAASAPALNDIGGVHATADAQSTD
VPAVANARLIADHFVSKAPFKDEQGQSLAIRLESDNSLANRSYAIKFDMNLTGNPLETDAL
ISYADRSVTLNGFPDLAYIVRSNFGNFDVRNDNVYASSHPSTAQSNRTYQVEVRINPASGT

GQPTRTYDVWIAPEGEQPVQLADQFKARNYANTGYALNNIGQAFVYSQADGLLSIDNHV
VQDGQRLDEALARVNAASGEAAMTALESNALGLPMERYRLMDAAKRAQVAQDVLG
RPAEGYAHALSVQAVFVSAVANRLDTENPTAPANVQVAISNTMQAHVSWTASSDDTGIL
YYKVFRD GALVGTVTNATSFVDNGLAPATEYTYVVKAYDLVLKEAVSQPATATSPGEQA
QVRIPFSAEAIATAFGQPLLDYNLETHSGTLKWMMEWREEYEKSANALKLLTLLSASAPD
YIGPDGVT TASAKALQHLSVTAGGNEPGFAGNGLSGQGYMPLLSAIVMAKKKAPAIWN
ALTAAEKEKLDLMILAGLYGAKFAYDDENDNKTGIDATGNFDKEWNPNNHRSGIAGAIMA
MYFEDAQWLNDQMRSFNYDDWLARLTAAGLTNVRTIYQNSGKTLTEREIRKDAAGDG
FVYKGHPLSQPGKIMAEFVNYTFSHPVSPVGGFDSGIGKYRGYIVDGQDDLPLNLGADSMG
FEFDTLDANGKRSSLVYVFMGWKPNVDAITPVLLLDNIDSGLTSAETRDVVSRLSIGTTD
MLYKNEHGYMTYAKGVNEGKSLNGPILTINEEIWNRLNPAAPMEAVNQASSAGQMR
TALEASALGMILYGYGALSETGKNAVAQHVLDPARPAAGYANKAAAQNELYEGVRLQAL
LALSQAQTAEQMRSALESRALGLYKPKYETASQDKKQFVAQYLLDNKPADGFLTKEVR
EQVESALEPQGNQLRNLPPLASGEKRINLADYDHWPQQHGDAEVALWADDKTGAFSLTI
DDNFENEHDTWRSLAQQYGFKFSWFVITSLIKDPNKWRTLAAEGHEIGSHTVTHEDKGST
LDPAHLHSEYADSQALLNTIEGVRATTLAYPFGSGREDIAAEYYIAARGTVGLPNPADSIN
YMNTQSLSVRPGSLELTNQAANGNSVEAMVKTLDVDPNHKVWSASYRGWSNMLVHSL
NESGKTPSDGVTRTSRDLTQYLLTLLDTYRDQIWWGRYGDIVRYSQQRDTAHIVVTRKDD
RKITFNLTD RMDDTLFDYPLTVKVRVDDAWS DIGATQAGEPIPFVETIRDGKRYLLVKAV
PDKGSVSIVPDAASPLNVVNGAVTSEQMLS AIAAPGLGLDLGEFNALGAGKKRMVGSRL
EVRPADGYADAAALQDALDAAVEEANNAPSLSENASLSDLKVNGVTIAGFAPETYAYDI
MLPEGTTALPVVSFKVADTGKATAVLQNA PALPGTAKVTVT AEDNWT VATYTLRFQVRI
SALQRVNTAPDASAMRTAIENAAALGLVLAAYNGLTSEQKNSVAASVLTHRPATGYADVQ
AVQAE LNAALPKINAPLLAHAIVDQLNPDTVSTANWTNLYGGTSGRKGGVYMKFNIASL
AGLEADAIGDAKVQFFTTREGTVIGYAAPSSWEAPLTWNTQPLADLKNSNMAALAEIGRT
AVQATGANYEMNITQYVKDAAAADKTELSLVLLGSNNTNITMQKIPTAFALSVTLATYG
EPNPEPSPLAAVNEAGDAAAMQGAIAAVELDLNLTA YNGLTAAQRIDVAQALLDNRPAA
GYAHALAVQVALDAAVAAAQPANQAPGGTLAASAEQLQPGQQLTVGVSDASRFTGA
DILVHYDPQALTFATELYEGVRMLKAEAIASLQANYQVAAAMA EQPGTIKILLFTAGAGQ
PLSGTLPLFKLRASVKDDAQTGVSTAVSLSDFELTFEGEDSVWPDTTAAVSLQIAAHPVE
ADKTALIAKIAHAQALLTGATVGANPGQYPQAA YDALADAIGLAE EKRDLTGVSQA AVD
EAVASLGTAEEQQFLNAVIPGV PADLTALNAAIAKAQRLHDNGPYGEKIGQYPQSAKVPLK
SALDAAKAVGGSGASSQESVNAAAASLNGAIQTFERSLVTLVGGGATKVGIRDLSIVAKY
YGV TSSDPNWKVSA A AIDGGNEITIEVLA AVARMILADWAAGQ

>sp|P9WFM1|GCH1L_MYCTU GTP cyclohydrolase 1 type 2 homolog OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=Rv2230c PE=1 SV=1
MSVRLADVIDVLDQAYPPRLAQSWDSVGLVCGDPDDVVD SVTVAVDATPAVVDQVPQA
GLLLVHHPLLLRGVDTVAANTPKGVLVHRLIRTGRSLFTAHTNADSASPGVSDALAHAVG
LTVDAVLDPVPGAADLDKWWIYVPRENSEAVRAAVFEAGAGHIGDYSHCSWSVAGTGQF
LAHDGASPAIGSVGTVERVAEDRVEVVAPARARA EVLAAMRAAHPYEEPAFDIFALVPPP
VGSGLGRIGR LPKPEPLRTFVARLEAALPPTATGVRAAGDPDLLVSRVAVCGGAGDSLLA
TVAAADVQAYVTADLRHHPADEHCRASQVALIDVAHWASEFPWCGQAAEVLRSHFGAS
LPVRVCTICTDPWNLDHETGRDQA

>sp|Q6T1W8|FDTA_ANETH TDP-4-oxo-6-deoxy-alpha-D-glucose-3,4-oxoisomerase
OS=Aneurinibacillus thermoaerophilus OX=143495 GN=fdtA PE=1 SV=1
MENKVINFKKIIDS RGS LVAIEENKNIPFSIKRVYYIFDTKGEEPRGFHAHKKLEQVLVCLN
GSCR VILDDGNIIQEITLDSPAVGLYVGPAVWHEMHDFSSDCVMMVLASDYYDETDIRQ
YDNFKKYIAKINLEKEG

>sp|Q6N2R1|GMHBB_RHOPA D-glycero-beta-D-manno-heptose-1,7-bisphosphate 7-phosphatase OS=Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009) OX=258594 GN=gmhB PE=1 SV=1
MTASAPRRPAAFLDRDGVINYNDHYVGTRERLRWMPGIAAAIRQLNAAGYYVFIITNQSG
VARGMFSEDDVRLHRWMLDELNTQGARIDDVRFCHHVEGTLDAYRVACEHRKPGPG
MILDLAKTWPVDMTRSFVIGDSASDVEAAKAAGIPGFRFEGEDIDVFVKQVLIEMQRAAV
SN

>sp|Q5U924|HADB_CLODI (R)-2-hydroxyisocaproyl-CoA dehydratase alpha subunit OS=Clostridioides difficile OX=1496 GN=hadB PE=1 SV=1
MSEKKEARVVINDLLAEQYANAFKAKEEGRPVGWSTSVFPQELAEVFDLNVLYPENQAA
GVAACKGSLELCEIAESKGYSIDLCAYARTNFGLLENGGCEALDMPAPDFLLCCNNICNQ
VIKWEYENISRELDIPLIMIDTTFNNEDEVTSRIDIYKAQFEEAIKQLEISGKKFDPKKFEEV
MKISAENGRLLWKYSMSLPADSSPSPMNGFDLFTYMAVIVCARGKKETTEAFKLLIEELED
NMKTGKSSFRGEEKYRIMMEGIPCWPYIGYKMKTLAKFGVNMTGSVYPHAWALQYEVN
DLGMAVAYSTMFN NVNLD RMTKYRVD SLVEGKCDGAFYH MNRSCKLMSLIQYEMQR
RAAEETGLPYAGFDGDQADPRAFTNAQFETRIQGLVEVMEERKKLNRGEI

>sp|Q9ZND9|HACB_THET2 Homoaconitase small subunit OS=Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039) OX=262724 GN=hacB PE=1 SV=1
MPRVWKFGDQINTDDILPGKYAPFMVGEDRFHLYAFAHLRPEFAKEVRPGDILVFGRNAG
LGSSREYAPEALKRLGVRAIIAKSYARIFFRNLVNLGIVPFESEEVVDALEDGDEVELDLES
GVLTRGEERFALRPPPPFLLEALKEGSLDYKHKHGRFPGE

>sp|P07103|GUNZ_DICD3 Endoglucanase Z OS=Dickeya dadantii (strain 3937) OX=198628 GN=celZ PE=1 SV=2
MPLSYLDKNPVIDSKKHALRKKLFLSCAYFGLSLACLSSNAWASVEPLSVNGNKIYAGEK
AKSFAGNSLFWSNNGWGGEKFYTADTVASLKKDWKSSIVRAAMGVQESGGYLQDPAGN
KAKVERVVDAAIANDMYAIIGWHSASHAENNRSEAIRFFQEMARKYGNKPNVIYEIYNEPL
QVSWSENTIKPYAEAVISAIRAIDPDNLIIIVGTSPWSQNVDEASRPINAKNIAITLHFYAGT
HGESLRNKARQALNNGIALFVTEWGTVNADGNGGVNQTETDAWVTFMRDNNISANANW
ALNDKNEGASTYYPDSKNLTESGKKVKSIQSWPYKAGSAASATTDPTDTTTTDTTVDEPT
TTDTPATADCANANVYPNWVSKDWAGGQPTHNEAGQSIVYKGNLYTANWYTASVPGS
DSSWTQVGSCN

>sp|Q84DC4|MANHY_PSEPU Mandelamide hydrolase OS=Pseudomonas putida OX=303 GN=mdlY PE=1 SV=1
MRHPVDMPEKVGTDARLFAQPEHLWELTLTEASALVRHRRITSRQLVEAWLSRIADFSE
LNAFISVDAALAAKQADSVDHYLEAGGDPLPLGGVPIAVKDNIQVVGAFANTAGTPALSKF
FPTCNARVIEPLLKAGAI VVGKT NMHELAFGTSGYNTAYHIPGVIGVRNAFDHSCIAGGSS
SGSGTAVGALLIPAALGTDGTGGSVRQPGAVNGCVGFRPTVGRYPVDGITPISPTRDTPGPIA
RSVEDIVLLDSIITGALPAEVPAAESIRLGVVDQLWADLSEPVRKLTEALRKLEQQGVQI
VRVSMSEIFEMSHAVSMPLALHECRSALTEYLSANETGVSFDEL VAGISSPDVRTIFEDYIL
PGRLGELEGQSV DLEQAYATAMKDARPKLIQSFEFLFKEHQLDAIIHPTTPDLAIKSNPAAT
SFEAFARMIRNADPASNAGMPGISLPAGLSQQEGLPVGIEIEGLPGSDARLLSIANFIESILG
RGTPTRSGVESKISM

>sp|P45868|MAO2_BACSU Probable NAD-dependent malic enzyme 2 OS=Bacillus subtilis (strain 168) OX=224308 GN=maeA PE=1 SV=1
MGYYLTWLTISRKKEICLNNIKKTKEGHLETTLRGKEVLSIPTLNKGVAFSLEERQELGLE
GLLPPTVLSLDQQAQRAYEQFQAQPDRLRQNVYLSDLANRNEVLFYKLLKNHLREMLPV
VYTPTVGEAIEQYSHEYRRPQGIYLSIDNIDGIEKAFENLHATAGDIDLIVATDSESILGIGD
WGVGGINIAIGKLAVYTAAAGIDPSRVIPVVLVDVGTNNEKLLNDPLYIGNKHervQGERY
EAFIDAYVKAALKFFPKALLHWEDLGKNKNARNIMKKYNHEILTFNDDIQGTGAITLAGVL
AAMKKTGASIKDQRVVIFGAGSAGIGIADQIRDTMVLAGLSEEEANKRFYTLDYRGLLTE

DIEGILDFQKPYLRNADEVKDWKRDEKGQIPFDEVVRQAKPTILIGTSGVSGAFTEEIVKE
MASHVDRPVIMPMSNPHTLAEAVPEDLFKWTGKVLATGSPFDNVEYNGVSYEIGQSN
AFAPGLGLGSIVAEARIITPAMFAATADAIAEMVDLETPGAGLLPSIDKLQEVSIQVAIAV
AEAAIKDGVANRQPEDVKQAVLDAMWTPEYKKVIAK
>sp|P67062|MENG_STAAN Demethylmenaquinone methyltransferase OS=Staphylococcus
aureus (strain N315) OX=158879 GN=menG PE=1 SV=1
MADNKANKEQVHRVFQNISKKYDRLNNISFEQHKVWRKRVMKDMGVRKGTKALDVC
CGTGDWTIALSKAVGPTGEVTGIDFSENMLEVGKEKTASMENVKL VHGDAMELPFEDNS
FDYVTIGFGLRNVPDYLVALKEMNRVLKPGGMVVCLETSQPTLPVFKQMYALYFKFVMP
IFGKLFAKSKEEYEWLQQSTFNFPGKEELKRMFEEAGFINVRVRSFTGGVAAMHLGYKEK
DNTKGD
>sp|Q25QU7|MDH_FLAFR Malate dehydrogenase OS=Flavobacterium frigidimaris OX=262320
GN=mdh PE=1 SV=2
MKVTIVGAGNVGATCADVISYRGIASEVVLLDIKEGFAEGKALDIMQCATNTGFNTKVSG
VTNDYSKTAGSDV VVITSGIPRKPGMTREELIGINAGIVKTV AENVLKHSPNTIIVVSNPM
DTMTYLALKATGV PKNRIIGMGALDSSRFRTYLSLALDKPANDISAMVIGGHGDTTMIP
LTRLASYNGIPVTEFLSEEVLQKVAADTMVGGATLTGLLGTS AWYAPGASVAYLVDSILN
DQKKMIACSVFVEGEYGQNDICIGVPCIIGKNGVEEILDIKLNDQEKALFAKSADAVRGMN
DALKSILV
>sp|P37569|MCSA_BACSU Protein-arginine kinase activator protein OS=Bacillus subtilis (strain
168) OX=224308 GN=mcsA PE=1 SV=1
MICQECHEPATFHF TKVVNGEKIEVHICEQCAKENS DSYGISANQGFSIHNLLSGLLNMD
SSFQNAGTQMFSHSEQISACPKCGMTFQQFRKIGRFGCSECYKTFHSNITPILRKVHSGNTV
HAGKIPKRIGGNLHVRRQIDMLKKELESLIHQEEFENAAHVRDQIRLLEQSLKSTDSEEEQE
>sp|P9WK7|MBTG_MYCTU L-lysine N6-monooxygenase MbtG OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=mbtG PE=1 SV=1
MNPTLAVLGAGAKAVAVAAKASVLRDMGVDVPDVIAVERIGVGANWQASGGWTDGAH
RLGTSPEKDVGF PYRSALVPRRNAELDERMTRYSWQSYLIATASFAEWIDRGRPAPTHRR
WSQYLAWVADHIGLKVIHGEVERLAVTGDRWALCTHETTVQADALMITGPGQAEKSLP
GNPRVLSIAQFWDRAAGHDRINAERVAVIGGGETAASMLNELFRHRVSTITVISPVTLFT
RGEGFFENSLFSDPTDWAALTFDERRDALARTDRGVFSATVQEALLADDRIHHLRGRVAH
AVGRQGQIRLTLSTNRGSENFETVHGFDLVIDGSGADPLWFTSLFSQHTLDLLELGLGGPL
TADRLQEAIGYDLAVTDVTPKFLPTLSGLTQGP GFPNLSCLGLLSDRVLGAGIFTPTKH
DTRRSGEHQSF
>sp|E2JA31|DDAF_ENTAG Dapdiamide A synthase OS=Enterobacter agglomerans OX=549
GN=ddaF PE=1 SV=1
MSILNNKEVIVIIDAWSGGKHLIPAFQALGYFCLHVQSTFLPEVFIADNQLAIARSDRHIVH
DGNIELLLSQLQPYTIKAILAGSEGAVGLADCLNDALELTFSNQFELSAARRNKYLMQEQL
ALKGVASINQQLAGHSDELKQWLAGHAHWPVVLKPIQSAGTDGVFICHDLAQAALQAFE
ILAKKDFFGSPNREVLCQEFLAGEEFVNGIACQGEYFFTELWQSKKQQRNGFPVYETQY
LHYQNDAGFDVLTAYTVQVCQTLGINNGAFHAEVMMTSGGPVLEIGARVAGGADPYIIE
ECLGHSQISKLAQAVLHPAKFLQECRRQHDFSGHRR AAYVYMISPSPGRVQVSPEEKFIKI
DGVISINYHYAPGDIQQETCDLLSSPGVIIAIRDNPALLKQTIAEIRDVEADFYHLGLIDE
>sp|P02966|DESS_MYXXA Development-specific protein S OS=Myxococcus xanthus OX=34
GN=tps PE=1 SV=1
MANITVFYNEDFQGKQVDLPPGNYTRAQLAALGIENNTISSVKVPPGVKAILYQNDGFAG
DQIEVVANAEELGPLNNNVSSIRVISVPVQPRARFFYKEQFDGKEVDLPPGQYTQAELE
RIDNNTISSVKPQGLAVVLFKNDNFSGDTLPVNSDAPTLGAMNNNTSSIRIS

>sp|Q03AZ0|DLTC_LACP3 D-alanyl carrier protein OS=Lactobacillus paracasei (strain ATCC 334 / BCRC 17002 / CIP 107868 / KCTC 3260 / NRRL B-441) OX=321967 GN=dltC PE=1 SV=1
MADEAIKNGVLDILADLTGSDDVKTNLDLNLFTGLLD SMGT VQLLLELQSQFGVEAPVS
EFDRSQWDTPNKIIAKVEQAAQ

>sp|D0ZLR2|DGAF_SALT1 2-dehydro-3-deoxy-phosphogluconate aldolase OS=Salmonella typhimurium (strain 14028s / SGSC 2262) OX=588858 GN=dgaF PE=1 SV=1
MQQINFYRQRVAINVLAKDIANAKAIYEAAEGHAVIGVLSAQFATVEEGVPEVKRWMAE
VPSISVGLGAGDPAQYYKAAMIAAHTHPAHVNQTFTGSGFAAGALAATGGEQTHINALV
SPTGTPGEVVISTGVSSSQGTPARVSCEAAVRMMQDMGAHAAKFFPMGGEKSLPELYAL
ATTAARHGMTLIEPTGGISLDNFGIILQTCLEAGVPRVMPHVYSSIIDPQTGNTRPEDIIRLM
EIVKALV

>sp|P74893|DNAG_SYNE7 DNA primase OS=Synechococcus elongatus (strain PCC 7942)
OX=1140 GN=dnaG PE=1 SV=3
MDTPRLHPETIAAVKERADIVDIVSEQVVLKKRGKDFVGLCPFHDDKSPSFTVSPAKQFYF
CFSCGAGGNPIKFLMELGKQSFSEVVDLAKRYQVPVRTLEVQQHQELQRQLSRRRERLYE
VLAVATQFYEQSLRRPEGAAALDYLRRLSRQLQUESTIQKFQLGYAPAQWASLATHLIEQKR
FPADLVEEAGLVVARRNGQGYDRFRDRLMPIHDLQGRVVGFGRRLTGEEPKYLNLSPE
TTLFEKGKLLFGLDKARAAIAKQDQAVVVEGYFDVIALHAAGIDHAVASLGTALSRRQQV
KLLSRYSESNQIVLNFDADRAGAKAAERAIGEVEDLAYQGQVQLRVNLPGGKDADEYL
QRHSVADYRELLARSPLWLDWQIDQLLRDRNLQADQFQAVVQAIQVLLGKLPNTPLRT
HYVHQVAERLSQGEARTAVQLASDLRAQVRGQRWHGQASRWEKPGDVSIREQAEAEQIL
KVYLHCPRRLRAVRKTLHDREIQGFSLQPHRLLWQAIAEIEEAHLGFAAMYQVERGEGNG
DDLAIDLVPILRDRDLQLTGVSLGGFLELSENDHADLTHPLPLRGAVLVERLRCEKRC
RHLLDSWARQSIHTFEHCIEQLLQAGIGEDVDAEAQITALHEQLNQEALHFQKLYYNERR
YLQQLDQERCLNPQAFGLMTEHDATAIAPTPQPISA

>sp|P9WIY3|MUTT1_MYCTU Probable 8-oxo-dGTP diphosphatase 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) OX=83332 GN=mutT1 PE=1 SV=1
MSIQNSSARRRSAGRIVYAAGAVLWRPGSADSEGPVEIAVIHRPRYDDWSLPKKGKVDPE
TAPVGAVREILEETGHRANLGRRLT VTYPTDSPFRGVKKVHYWAARSTGGEFTPGSEVD
ELIWLVPDAMNKLDYAQDRKVLRCFAKHPADTQTVLVVRHGTAGSKAHFSGDDSKRPL
DKRGRAQAEALVPQLLAFGATDVYAADRVRCHQTMEPLAAELNVTIHNEPTLTEESYAN
NPKRGRHRVLQIVEQVGTPVICTQGKVIPDLITWWCERDGVHPDKSRNRKGSTWVLSLSA
GRLVTADHIGGALAANVRA

>sp|P13702|MVAA_PSEMV 3-hydroxy-3-methylglutaryl-coenzyme A reductase
OS=Pseudomonas mevalonii OX=32044 GN=mvaA PE=1 SV=1
MSLDSRLPAFRNLSPAARLDHIGQLGLSHDDVSLANAGALPMDIANGMIENVIGTFELP
YAVASNFQINGRDVLVPLVVEEPSIVAAASYMAKLARANGGFTTSSSAPLMHAQVQIVGI
QDPLNARLSLLRRKDEIIELANRKDQLLNSLGGGCRDIEVHTFADTPRGPMLVAHLIVDVR
DAMGANTVNTMAEAVAPLMEAITGGQVRLRILSNLADRLRLARAQVRITPQQLETAEFSGE
AVIEGILDAYAFAAVDPYRAATHNKGIMNGIDPLIVATGNDWRAVEAGAHAYACRS GHY
GSLTTWEKDNNGHLVGTLEMPMPVGLVGGATKTHPLAQLSLRILGVKTAQALAEIAVAV
GLAQN LGAMRALATEGIQRGHMALHARNIAVVAGARGDEVDWVARQLVEYHDVADR
AVALLKQKRGQ

>sp|A0QU88|NAGB_MYCS2 Glucosamine-6-phosphate deaminase OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) OX=246196 GN=nagB PE=1 SV=1
MEVIILPDPGRIGSLAADAITLTKPD AVLGLATGSSPLAVYDELVSRYEAGQISFRQAR
GFTLDEYVGLPADHPERYRNVIDTAFARVDFAPGAVQGPDGLADDIPAACAAYEAAIRD
AGGVDLQILGIGTDGHIAFNEPGSSLASRTRIKTLTRQTRVDNARFFGGDLQVPTHCLTQ

GLGTIMEARHLILIAMGRSKAEAVHHLVEGAVSAMW PATVLQMHPHVTVLLDDAAAQR
LQLVDYYRETYRAKPAWQGI
>sp|D5FKJ3|MRSA_PSESY 2-ketoarginine methyltransferase OS=Pseudomonas syringae pv.
syringae OX=321 GN=mrsA PE=1 SV=1
MNLDSIKSENTGFETTLIKGIEPIRQFVLAISYHLFDTKLFSLLIKHEVASPEVACNELGME
KEKLLGLFRYLKNEGILLETIDGFSLSKEGHALAPFEGWYVMLVGGYATTFLQMGERLQE
GAGWATRDATKVGVGSCGISHFDAIPLTRSLMAQAPGTCTKLDDLGCNGRylaEFCKA
LPQIQAWGAEPDRGGFEEAVDLIEKEGLSHRVHISHSGAVEFLDSDFDFEPDFIVLGFVLHE
ILGQAGRPVVNFLKKIVHRFPAINLIIEVDNQFDNAGAMRHGLALAYNPYYLLHCFTN
QLLVQDADWLDIFAEAGLSLV TRETTS DQVDSTGLEIGYLLRRA
>sp|Q9KV40|MURB_VIBCH UDP-N-acetylenolpyruvoylglucosamine reductase OS=Vibrio
cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961) OX=243277 GN=murB PE=1
SV=2
MQIQLGANLKPYHTFGIEQLAAQLVVAESIDDLKALYCSAEWASLPKLIIGKGSNMLFTCH
YTGMIVVNRLNGIEHQDDDYHRLHVAGGEDWPSLVSWCVEQGIGGLENLALIPGCAGS
APIQNIGAYGVEFKDVCDYVEYLCLETGTVKRLTMEECQFGYRDSIFKHQLYQKAVVTA
VGLKFAKAWQPIIQYGPLKDLSSDCAIHDVYQRVCATRMEKLPDPAVMGNAGSFFKNPVI
SQQAFARLQIEHPDVVAYPAEQGVKVAAGWLIDQAGLKGHQIGGAKVHPKQALVIVNTG
DASAQDVLMLAADIQQRVFN CYGIELEHEVRFIGESEETNLKQWMSEQA
>sp|O25338|MUTS2_HELPY Endonuclease MutS2 OS=Helicobacter pylori (strain ATCC 700392
/ 26695) OX=85962 GN=mutS2 PE=1 SV=1
MSDAPKRS LNPTLMMNNNTPPKPLEESLDLKEFIALFKTFFAKERD TIALENDLKQTFTY
LNEVDAIGLPTPKSVKESDLIIKLT KLGLTLHLDEIFEIVKRLHYIVVLQNAFKTFTHLKFHE
RLNAIVLPPFFNDLIALFDDEGKIKQGANATLDALNESLNRLKKESVKIIHHYARSKELAPY
LVDTQSHLKHGYECLLLKSGFSGAIKGVVLERSANGYFYLLPESAQKIAQKIAQIGNEIDC
CIVEMCQTLSHSLQKHLLFLKFLFKEFDFLDSLQARLNFAKAYNLEFVMPSTQKKMILEN
FSHPILKEPKPLNLKFEKSMLAVTGVNAGGKTMLLKSLLSAAFLSKHLIPMKINAHHSIIPY
FKEIHAIINDPQNSANNISTFAGRMKQFSALLSKENMLLGVDEIELGTDADAEASSLYKTLLE
KLLKQNNQIIITTHHKRLSVLMAENKEVELLAALYDEEKERPTYTFLKGVIGKSYAFETAL
RYGVPHFLIEKAKTFYGEDKEKLNVL IENSSALERELKQKNEHLENALKEQEYLKNAWLL
EMEKQKEIFHNKKLELEKSYQQALNILKSEVASKDTSSMHKEIHKASEILSKHKTNQEIPI
ITNFQANEKARYKNESVLIVQILDKGYW IETELGMRLKAHGSLKKIQKPPKNKFKPPKT
TIPKPKEASRLRLDRGQRSEEALDLLDAFLNDALLGGFEEVLICHGKGSGILEK FVKEFLKN
HPKVVSFS DAPINLGSGVKIVKL