

> sp|P95010|LPPA\_MYCTU Putative lipoprotein LppA OS=Mycobacterium tuberculosis GN=lppA PE=1 SV=2  
MIAPQPISRTLPRWQRIVALTMIGISTALIGGCTMDHNPDTSRRLTGEQKIQLIDS  
MRNKGSYEAAERLTATARIADRVSAAPGQTKFDDDPNIQQSDRNGALCD  
KLTADIARRPIANSVMFGATFSAEDFKIAANIVREEAAKYGATTESSLFNESAK  
RDYDVQGNNGYEFRLQIKFATLNITGDCFLQKVLDLPAQQLPPEPPIWPTTST  
PH

> sp|P71995|NARK2\_MYCTU Probable nitrate/nitrite transporter NarK2  
OS=Mycobacterium tuberculosis GN=narK2 PE=1 SV=1  
MRGQAANLVLATWISVNVFWAWNLIGPLSTS YARDMSLSSAEASLLVATPILV  
GALGRIVTGPLTDRFGGRAMLIAVTLASILPVLAVGVAATMGSYALLVFFGLFL  
GVAGTIFAVGIPFANNWYQPARRGFSTGVFGMGMVGTALS AFFTTPRFVRFWGL  
FTTHAIVAAALASTAVVAMVVLRDAPYFRPNADPVLRLKAAARLPVTWEMS  
FLYAIVFGGFVAFSNYLPTYITTIYGFSTVDAGARTAGFALAAVLARPVGGWLS  
DRIAPRHVVLASLAGTALLAFAAALQPPPEVWSAATFITLAVCLGVGTGGVFA  
WVARRAPAASVGSVTGIVAAAGGLGGYFPPLVMGATYDPVDNDYTVGLLLLV  
ATALVACTYTALHAREPVSEEASR

> sp|Q7D5X9|MOEZ\_MYCTU Probable adenyltransferase/sulfurtransferase MoeZ  
OS=Mycobacterium tuberculosis GN=moeZ PE=1 SV=1  
MSTSLPPLVEPASALSREEVARYSRHLIIPDLGVDGQKRLKNARVLVIGAGGLG  
APTLLYLAAAGVGTIGIVDFDVDES NLQRQVIHGVADVGRSKAQSARDSIVA  
INPLIRVRLHELRLAPSNVDFKQYDLILDGTDNFATRYLVNDAAVLAGKPYV  
WGSYIRFEGQASVFWEDAPDGLGVNYRDLYPEPPPPGMVPSCAEGGVLGIC  
ASVASVMGTEAIKLITGIGETLLGRLLVYDALEMSYRTITIRKDPSTPKITELVD  
YEQFCGVVADDAQAQAKGSTITPRELRDWLDSGRKLALIDVRDPVEWDIVHI  
DGAQLIPKSLINSGEGLAKLPQDR TAVLYCKTGVRSAEALAAVKKAGFSDAVH  
LQGGIVAWAKQM QPDMVMY

> sp|A5U127|MSCL\_MYCTA Large-conductance mechanosensitive channel  
OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=mscL PE=1  
SV=1  
MLKGFKEFLARGNIVDLAVAVVIGTAFTALVTKFTDSIITPLINRIGVNAQSDVG  
ILRIGIGGGQTIDLNVLLSAAINFFLIAFAVYFLVLPYNTLRKKGEVEQPGDTQ  
VLLTEIRDLLAQTN GDSRGRHGGRTPSPTDGPRASTESQ

> sp|P64781|Y970\_MYCTU Uncharacterized protein Rv0970/MT0998  
OS=Mycobacterium tuberculosis GN=Rv0970 PE=2 SV=1  
MIHDLMLRWVVTGLFVLTAECGLAIIAKRRPWTLIVNHGLHFAMAVAMAV  
MAWPWGARVPTTGPVFFLLAAVWFGATAVVAVRGTATRGLYGYHGLMMLA  
TAWMYAAMNPRLLPVRSCTEYATEPDGSM PAMDMTAMNMPPNSGSPWFSA  
VNWIGTVGFVA AVFWACRFVMERRQEATQSRLPGSIGQAMMAAGMAMLFF  
AMLFPV

> sp|O33288|PGSA2\_MYCTU Putative CDP-diacylglycerol--glycerol-3-phosphate  
3-phosphatidyl-transferase 2 OS=Mycobacterium tuberculosis GN=pgsA2 PE=1  
SV=1  
MSRSTRYSVAVSAQPETGQIAGRARIANLANILTLLRLVMVPVFLALFYGGG

HHS AARVVAW AIFATA CITDRFDGL LARNYGMATEFGAFVDPIADKTLIGSALI  
GLSMLGDL PWWVTVLILTRELGVTVLRLAVIRRGVIPASWGGK LKTFVQAVAI  
GLFVLP LSGPLHVA AVVVM AAILLTVITGV D YVARALRDIGGIRQTAS

> sp|O53583|DPPRS\_MYCTU Decaprenyl-phosphate phosphoribosyltransferase  
OS=Mycobacterium tuberculosis GN=Rv3806c PE=1 SV=1

MSEDVVTQPPANLVAGVVKAIRPRQWVKNVLVLAAPLAALGGGVRYDYVEV  
LSKVSM AFVVFSLAASAVYLVNDVRDVEADREHPTKRFRPIAAGVVPEWLAY  
TVAVVLGVTSLAGAWMLTPNLALVMVYVYLAMQLAYCFGLKHQAVVEICVVS  
SAYLIRAIAGGVATKIPLSKWFLIMAFGSLFMVAGKRYAELHLAERTGAAIRK  
SLESYTSTYLRFVWTL SATAVVLCYGLWAFERDGYSGSWFAVSMIPFTIAILRY  
AVDVDGGLAGEPEDIALRDRVLQLLALAWIATVGA AVAFG

> sp|P15712|PSTS1\_MYCTU Phosphate-binding protein PstS 1 OS=Mycobacterium  
tuberculosis GN=pstS1 PE=1 SV=1

MKIRLHTLLAVLTAAPLLLAAGCGSKPPSGSPETGAGAGTVATTPASSPVTLA  
ETGSTLLYPLFNLWGPAFHERYPNVTITAQGTGSGAGIAQAAAGTVNIGASDA  
YLSEGDMAAHKGLMNIALAIS AQQVNYNLPGVSEHLKLNKVLAA MYQGTI  
KTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQDPEGWGKS  
PGFGTTVD FPAVPGALGENGNMGMTGCAETPGCVAYIGISFLDQASQRGLGE  
AQLGNSSGNFLLPDAQSIQAAAAGFASKTPANQAISMIDGPAPDGYPIINYEYA  
IVNNRQKDAATAQTLQAFHWAITDGNKASFLDQVHFQPLPPAVVKLS DALIA  
TISS

> sp|O05916|MINTH\_MYCTU Divalent metal cation transporter MntH  
OS=Mycobacterium tuberculosis GN=mntH PE=1 SV=1

MAGEFRLLSHLCSRGSKVGELAQDTRTSLKTSWYLLGPAFVA AIAYVDPGNV  
AANVSSGAQFGYLLLWVIVAANVMAALVQYLSAKLGLVTGRSLPEAIGKRM  
GRPARLAYWAQAEIVAMATDVAE VIGGAI ALRIMFNLPLPIGGIITGVVSLLLT  
IQDRRGQRLFERVITALLLVIAIGFTASFFVVT PPPNAV LGGLAPRFQGTESVLL  
AAAIMGATVM PHAVYLHSG LARDRHGHPDPGPQRRRLLRVTRWDVGLAMLI  
AGGVNAAMLLVAALNMRGRGDTASIEGAYHAVHDTLGATI AVLFAVGLLASG  
LASSV GAYAGAMIMQGLLHWSVPMLVRR LITLGPALAILTLGFDPTRTLVLVLSQ  
VVLSFGIPFAVLPLVKLTGSPAVMGGDTNHRATTWVGWVVAVMVSLLNVM LI  
YLTVTG

> sp|C1AFY9|MP83\_MYCBT Cell surface lipoprotein MPB83 OS=Mycobacterium  
bovis (strain BCG / Tokyo 172 / ATCC 35737 / TMC 1019) GN=mpb83 PE=1 SV=1  
MINVQAKPAAAASLAAIAIAFLAGCSSTKPVSQDTSPKPATSPAAPVTTAAMA  
DPAADLIGRGCAQYAAQNPTGPGSVAGMAQDPVATAASNNPMLSTLTSALSG  
KLNPDVNLVDTLNGGEYTVFAPTNA AFDKLP AATIDQLKTD AKLLSSILTYHVI  
AGQASPSRIDGTHQTLQGADLT VIGARDDL MVNNA GLVCGGVHTANATVYM  
IDTVLMPPAQ

> sp|A5U493|BLAC\_MYCTA Beta-lactamase OS=Mycobacterium tuberculosis  
(strain ATCC 25177 / H37Ra) GN=blaA PE=1 SV=1

MRNRGFGRRRELLVAMAMLVSVTG CARHASGARPASTTLPAGADLADRFAELE  
RRYDARLG VYVPATGT TAAIEYRADERFAFCSTFKAPLVA AVLHQ NPLTHL DK  
LITYTSDDIRSISPAQQHVQTGMTIGQLCDAAIRYSDGTAAANLLADLGGPGG

GTAAFTGYLRSLGDTVSRDLAEEPELNRPDPPGDERDTTTPHAIALVLQQLVLG  
NALPPDKRALLTDWMARNTTGAKRIRAGFPADWKVIDKTGTGDYGRANDIA  
VWVSPTGVPYVVAVMSDRAGGGYDAEPREALLAEAATCVAGVLA

> sp|A0R1Z9|ATPE\_MYCS2 ATP synthase epsilon chain OS=Mycobacterium  
smegmatis (strain ATCC 700084 / mc(2)155) GN=atpC PE=1 SV=1

MADLNVEIVAVERELWSGPATFVFTRTTAGEIGILPRHIPLVAQLVDDAMVRVE  
REGEDDLRIAVDGGFLSVTEETVRILVENAQFESEIDADA AKEDAASDDERTA  
AWGRARLRALGQID

> sp|A1KIJ9|MFS55\_MYCBP MFS-type drug efflux transporter P55

OS=Mycobacterium bovis (strain BCG / Pasteur 1173P2) GN=BCG\_1471c PE=1  
SV=1

MRAGRRAISAGSLAVLLGALDITYVVVTIMRDIMNSVGIPINQLHRITWIVTM  
YLLGYIAAMPLGRASDRFGRKMLQVSLAGFIIGSVVTALAGHFHGFHMLIA  
GRTIQGVASGALLPITLALGADLWSQRNRAAGVLGGIGAAQELGSVLGPLYGIFI  
VWLLHDWRDVFWINVPLTAIAMVMIHFSLSHDRSTEPERVDLVGGLLLALA  
LGLAVIGLYNPNPDGKHVLPDYGAPLLV GALVA AVAFFGWERFARTRLIDPAG  
VHFRPFLSALGASVAAGAALMVTLVDVELFGQGV LQMDQAQAAGMLLWFLI  
ALPIGAVTGGWIATRAGDRAVAFAGLLIAAYGYWLISHWPVDLLADRHNILGL  
FTVPAMHTDLVVAGLGLGLVIGPLSSATLRVVPSAQHGIAAAVVVARMTGML  
IGVAALS AWGLYRFNQILAGLSAAIPPNASLLERAAAIGARYQQAFALMYGEIF  
TITAIVCVFGAVLGLLISGRKEHADEPEVQEQT LAPQVEPL

> sp|P63673|ATPA\_MYCTU ATP synthase subunit alpha OS=Mycobacterium  
tuberculosis GN=atpA PE=1 SV=1

MAELTIPADDIQAIEEYVSSFTADTSREEVGTVVDAGDGIAHVEGLPSVMTQE  
LLEFPGGILGVALNLDEHSVGAVILGDFENIEEGQQVKRTGEVLSVPVGDGFL  
GRVVNPLGQPIDGRGDVSDTRALELQAPSVVHRQGVKEPLQTGK AIDAM  
TPIGRGQRQLIIGDRKTGKTAVCVDITLNQRQNWESGDPKKQVRCVYVAIGQK  
GTTIAAVRRTLEEGGAMDYTTIVAAAASESAGFKWLAPYTGSAIAQHWMYEG  
KHVLIIFDDLTKQAEAYRAISLLRRPPGREAYPGDV FYLHSRLLERCAKLSDD  
LGGGSLTGLPIETKANDISAYIPTNVISITDGQCFL ETDLFNQGV RPAINVGVSV  
SRVGGAAQIKAMKEVAGSLRLDLSQYRELEAFAAFASDLDAASKAQLERGAR  
LVELLKQPQSQPMPVEEQVVSIFLGTGGHLDSVPVEDVRRFETELLDHMRASE  
EILTEIRDSQKLTEEAADKLTEVIKNFKKGFAATGGGSVVPDEHVEALDEDKL  
AKEAVKVKK PAKKKK

> sp|P63687|CTPF\_MYCTU Probable cation-transporting ATPase F

OS=Mycobacterium tuberculosis GN=ctpF PE=1 SV=1

MSASVSATTAHGLPAHEVVLLLESDPYHGLSDGEAAQRLERFGPNTLAVVT  
RASLLARILRQFHPLIYVLLVAGTITAGLKEFVDA AVIFGVV VINAIVGFIQES  
KAEAA LQGLRSMVHTHAKVVREGHEHTMPSEELVPGDLVLLAAGDKVPADL  
RLVRQTGLSVNESALTGESTPVHKDEVALPEGTPVADRRNIAYSGLTVTAGHG  
AGIVVATGAETELGEIHRLVGAAEVVATPLTAKLAWFSKFLTIAILGLAALTFGV  
GLLRRQDAVETFTAIALAVGAIPEGLPTAVTITLAIGMARMMAKRRAVIRRLPA  
VETLGSTTVICADKTGTLTENQMTVQSIWTPHGEIRATGTGYAPDVLLCDD  
APVPVNANAALRWSLLAGACSNDAALVRDGRWQIVGDPTEGAMLVVAAK

AGFNPERLATTLPQVAAIPFSSERQYMATLHRDGTDHVVLAKGAVERMLDLG  
GTEMGADGALRPLDRATVLRATEMLTSRGLRVLATGMGAGAGTPDDFDENVI  
PGSLALTGLQAMSDPPRAAAAASAVAACHSAGIAVKMITGDHAGTATAIATEVG  
LLDNTEPAAGSVLTGAELAALSADQYPEAVDTASVFARVSPEQKRLRVQALQA  
RGHVVAMTGDGVNDAPALRQANIGVAMGRGGTEVAKDAADMVLTDDDFATI  
EAAVEEGRGVFDNLTKFITWTLPTNLGEGLVILAAIAVGVALPILPTQILWINMT  
TAIALGLMLAFEPKEAGIMTRPPRDPDQPLLTGWLVRRTLLVSTLLVASAWWL  
FAWELDNAGLHEARTAALNLFVVVEAFYLFSCRSLTRSAWRLGMFANRWII  
LGVSAQAIAQFAITYLPAMNMVFDTAPIDIGVWVRIFAVATAITIVVATDTLLPRI  
RAQPP

> sp|Q11049|LPRA\_MYCTU Putative lipoprotein LprA OS=Mycobacterium  
tuberculosis GN=lprA PE=1 SV=2

MKHPPCSVVAATAILAVVLAIGGCSTEGDAGKASDTAATASNGDAAMLLKQ  
ATDAMRKVTGMHVRLAVTGDVFNLRVTKLEGDISNTPQTVATGSATLLVGNK  
SEDAKFVYVDGHLVSDLGQPGTYTDFGNGASIYNVSVLLDPNKGLANLLANL  
KDASVAGSQQADGVATTKITGNSSADDIATLAGSRLTSEDVKTVPPTVWIASD  
GSSHLVQIQIAPT KDTSVTLTMSDWGKQVTATKPV

> sp|P71588|PSTP\_MYCTU PP2C-family Ser/Thr phosphatase OS=Mycobacterium  
tuberculosis GN=pstP PE=1 SV=2

MARVTLVLRYAARSDRGLVRANNEDSVYAGARLLALADGMGHAAGEVAS  
QLVIAALAHLDDEPGDLLAKLDAVRAGNSAIAAQVEMEPDLEGMGTTTLT  
AILFAGNRLGLVHIGDSRGYLLRDGELTQITKDDTFVQTLVDEGRITPEEAHSH  
PQRSLIMRALTGHEVEPTLTMREARAGDRYLLCSDGLSDPVSDETILEALQIPE  
VAESAHRLELALRGGGPDNVTVVVADVVDYDYGGTQPILAGAVSGDDDQLT  
LPNTAAGRASAISQRKEIVKRVPQADTFSRPRWSGRRLAFVVALVTVLMTAG  
LLIGRAIIRSNIYYVADYAGSVSIMRGIQGSLLGMSLHQPYLMGCLSPRNELSQI  
SYGQSGGPLDCHLMKLEDLRPPERAQVRAGLPAGTLDDAIGQLRELAANSL  
PPCPAPRATSPPGRPAPPTTSETTEPNVTSSPASPSPTTSAPAPTGTTPAIPTSASP  
AAPASPTTPWPVTSSPTMAALPPPPPQPGIDCRAAA

> sp|A0R200|ATPB\_MYCS2 ATP synthase subunit beta OS=Mycobacterium  
smegmatis (strain ATCC 700084 / mc(2)155) GN=atpD PE=1 SV=1

MTATAEKTAGRVVRITGPVVDVEFPRGSVPELNFALHAEITFGALAKTLTLEVA  
QHLGDSLVRCSMQPTDGLVRGVEVTDTGASISVPVGDGVKGVFNALGDCL  
DDPGYGKDFEHWSIHRKPPAFSDLEPRTEMLTGLKVVDLLTPYVRGGKIALF  
GGAGVGKTVLIQEMINRIARNFGGTSVFAGVGERTREGNDLWVELADANVL  
KDTALVFGQMDEPPGTRMRVALSALTMAEFFRDEQQQDVLLFIDNIFRFTQAG  
SEVSTLLGRMPSAVGYQPTLADEMSELQERITSTRGRSITSMQAVYVPADDYT  
DPAPATTEFAHLDATELSRAVFSKGIFFAVDPLASSSTILDPAIVGDEHYRVAQEV  
IRILQRYKDLQDIIAILGIDELSEEDKQLVNRARRIERFLSQNMMAAEQFTGQP  
GSTVPLKETIEAFDKLTKGEFDHLPEQAFFLIGGLDDLAKKAESLGAKL

> sp|A0R201|ATPG\_MYCS2 ATP synthase gamma chain OS=Mycobacterium  
smegmatis (strain ATCC 700084 / mc(2)155) GN=atpG PE=1 SV=1

MAATLRELGRIRSAGSIKKITKAQELIATSRIAKAQARVEAARPYAAEITNML  
TELAGASALDHPLLVERKQPKRAGVLVSSDRGLCGAYNANVLRRAEELFSL

LRDEGKDPVLYVVGRKALGYFSFRQRTVVESWTGFSEPTYENAREIADTLV  
NAFMAGADDEGDDAGADGILGVDELHIVFTEFRSMLSQTAVARRAAPMEVE  
YVGEVETGPRTLYSFEPDPETLFDALLPRYIATRVYAALLEAAASESASRRRAM  
KSATDNADDLIKALTLAANRERQAQITQEISEIVGGANALAGSK

> sp|P0A5P4|ERP\_MYCTU Exported repetitive protein OS=Mycobacterium  
tuberculosis GN=erp PE=1 SV=1

MPNRRRRKLS TAMS AVAALAVASPCAYFLVYESTETTERPEHHEFKQAAVLTD  
LPGELMSALSQGLSQFGINIPPVPSLTGSGDASTGLTGPGLTSPGLTSPGLTSPGL  
TDPALTSPLTPTLPGSLAAPGTTLAPTPGVGANPALTNPALTSPTGATPGLTSPT  
GLDPALGGANEIPITTPVGLDPGADGTYPILGDPTLGTIPSSPATTSTGGGGGLVN  
DVMQVANELGASQAIDLLKGVLMPSIMQAVQNGGAAAPAASPPVPIPIAAAA  
VPPTDPITVPVA

> sp|Q50496|MTRB\_MYCTU Sensor histidine kinase MtrB OS=Mycobacterium  
tuberculosis GN=mtrB PE=1 SV=2

MIFGSRRRIRGRRGRSGPMTRGLSALSRAVAVAWRRSLQLRVVALTLGLSLAVI  
LALGFVLTSQVTNRVLDIKVRAAIDQIERARTTVSGIVNGEETRS LDSSLQLAR  
NTLTSKTD PASGAGLAGAFDAVLMVPGDGPRAASTAGPVDQVPNALRGFVK  
AGQAAYQYATVQTEGFSGPALIIIGTPTLSRVANLELYLIFPLASEQATITLVRGT  
MATGGLVLLVLLAGIALLSRQVVVPVRSASRIAERFAEGHLSERMPVRGEDD  
MARLAVSFNDMAESLSRQIAQLEEFGNLQRRFTSDVSHELRTPLTTVRMAAD  
LIYDHSADLDPTLRRSTELMVSELDRFETLLNDLLEISRHDAGVAELSVEAVDL  
RTTVNNALGNVGH LAEEAGIELLVDLP AEQVIAEVDARRVERILRNLIANAID  
HAEHKPV RIRMAADEDTVAVTVRDYGVGLRPGEEKLVFSRFWRSDPSRVRRS  
GGTGLGLAISVEDARLHQGRLEAWGEPGEGACFRLLTLP MVRGHKVTTSPLPM  
KPIQPVLQPVAQPNPQMPPEYKERQRPREHAEW SG

> sp|O05586|PMT\_MYCTU Probable dolichyl-phosphate-mannose--protein  
mannosyltransferase OS=Mycobacterium tuberculosis GN=pmt PE=1 SV=2

MVPV VSPGPLVPVADFGPLDRLRGWIVTGLITLLATVTRFLNLGSLTDAGTPIF  
DEKHYAPQAWQVLNNHGVEDNPGYGLVVHPPVGKQLIAIGE AIFGYNGFGW  
RFTGALLGVVLVALVVRIVRRISRSTLVGAIAGVLLICDGVSFVTARTALLDGFL  
TFFVVA AFGALIVDRDQVRERMHIALLAGRSAATVWGPRVGVRRWWRFGAGV  
LLGLACATKWSGVYFVFFGAMALAFDVAARRQYQVQRPWLGTVRRDVLPS  
GYALGLIPFAVYLATYAPWFASETAIDRHAVGQAVGRNSV VPLPDAVRSLWHY  
TAKAFHFHAGLTNSAGNYHPWESKPWTWPM SLRPVLYAIDQQDVAGCGAQS  
CVKAEMLVGTPAMWWLAVPV LAYAGWRMFVRRDWRYAVVLVGYCAGWLP  
WFADIDRQMYFFYAATMAPFLVMGISLV LGDILYHPGQGSERRTLGLIVVCCY  
VALVVTNFAWLYPVLTGLPISQQTWNLEIWLPSWR

> sp|P71997|Y1739\_MYCTU Probable sulfate transporter Rv1739c/MT1781  
OS=Mycobacterium tuberculosis GN=Rv1739c PE=1 SV=1

MIPTMTSAGWAPGVVQFREYQRRWLRGDVLAGLTVAAAYLIPQAMAYATVAG  
LPPAAGLWASIAPLAIYALLGSSRQLSIGPESATALMTAAVLAPMAAGDLRRYA  
VLAATLGLLVGLICLLAGTARLGFLASLRSPVLVGYMAGIALVMISSQLGTIT  
GTSVEGNEFFSEVHSFATSVTRVHWPTFVLAMS VLALLTMLTRWAPRAPGPIIA  
VLAATMLVAVMSLDAKGIAIVGRIPSGLPTPGVPPVSVEDLRALII PAAGIAIVT

FTDGVLARAFARRGQEVNANAELRAVGACNIAAGLTHGFPVSSSSSRTALA  
DVVGGRTQLYSLIALGLVVIVMVFASGLLAMFPIAALGALVVYAALRLIDLSEF  
RRLARFRSELMLALATTA AVLGLGVFYGVLA AVALSILELLRRVAHPHDSVL  
GFVPGIAGMHDIDDYPQAKRVPGLVVYRYDAPLCFANAEDFRRRALTVDQD  
PGQVEWVFLNAESNVEVDLTALDALDQLRTELLRRGIVFAMARVKQDLRESL  
RAASLLDKIGEDHIFMTLPTAVQAFRRR

> sp|Q7D8J9|LPQY\_MYCTU Trehalose-binding lipoprotein LpqY

OS=Mycobacterium tuberculosis GN=lpqY PE=1 SV=1

MVMSRGRIPRLGAAVLVALTTAAAACGADSQGLVVSFYTPATDGATFTAIAQR  
CNQQFGGRFTIAQVSLPRSPNEQRLQLARRLTGNDRTLDMALDVVWTAEFA  
EAGWALPLSDDPAGLAENDAVADTLPGPLATAGWNHKLYAAPVTTNTQLLW  
YRPDLVNSPPTDWNAMIAEAARLHAAGEPSWIAVQANQGEGLVWVFNLLV  
SAGGSVLSEDGRHVTLTDTPAHRAATVSALQILKSVATTPGADPSITRTEEGSA  
RLAFEQGKAALVNWPVVFASMLENAVKGGVPFLPLNRIPQLAGSINDIGTFT  
PSDEQFRIAYDASQQVFGFAPYPAVAPGQPAKVTIGGLNLAVAKTTRHRAEAFE  
AVRCLRDQHNQRYVSLEGLPAVRASLYSDPQFQAKYPMHAIIRQQLTDAAV  
RPATPVYQALSIRLA AVLSPITEIDPESTADELAAQAQKAIDGMGLLP

> sp|O50453|SUGB\_MYCTU Trehalose transport system permease protein SugB

OS=Mycobacterium tuberculosis GN=sugB PE=1 SV=1

MGARRATYWAVLDTLVVGYALLPVLWIFSLSLKPTSTVKDGKLIPSTVTFDNY  
RGIFRGDLFSSALINSIGLITTVIAVVLGAMAAYAVARLEFP GKRL LIGAALLI  
TMFPSISLV TPLFNIERAIGLFDTPGLILPYITFALPLAIYTL SAFFREIPWDLEK  
AAKMDGATPGQAFR KVI VPLAAPGLVTAAILVFIFAWNDLLLALS LTATKAAIT  
APVAIANFTGSSQFEEPTGSIAAG AIVITIPHVFVLIFQRRIVAGLTSGAVKG

> sp|P94974|LYSX\_MYCTU Lysylphosphatidylglycerol biosynthesis bifunctional

protein LysX OS=Mycobacterium tuberculosis GN=lysX PE=1 SV=2

MGLHLTPGLRRDGRGVQSNSHDTSSKTTADISRCPQHTDAGLQRAATPGISR  
LLGISSRSVTLTKPRSATRGNSRYHWVPAAGWTVGV IATLSLLASVSPLIRWII  
KVPREFINDYLFNFPDTNFAWSFVLALLAAALTARKRIAWLVLLANMVLA AV  
VNAAEIAAGGNTAAESFGENLGFVHVVAIVVLVLGYREFWAKVRRGALFRA  
AAVWLAGAVVGIVASWGLVELFPGSLAPDERLGYAANRVVGFALADPDLFTG  
RPHVFLNAIFGLFGAFALIGAAIVLFLSQRADNALTGEDESAIRGLLDLYGKDD  
SLGYFATRRDKSVVFASSGRACITYRVEVGVCLASGDPVGDHRAWPQAVDAW  
LRLCQTYGWAPGVMGASSQGAQTYREAGLTALELGDEAILRPADFKLSGPEM  
RGVRQAVTRARRAGLTVRIRHRDIAEDEMAQTITRADS WRDTETERGFSMA  
LGRLGDPADSDCLLVEAIDPHNQVLAMLSLVPWGTTGVSLDLMRRSPQSPNG  
TIELMVSELALHAESLGITRISLNFVAFRAAFEQGAQLGAGPVARLWRGLLVFF  
SRWWQLETLYRSNMKYQPEWVPRYACYEDARVIPRVGVASVIAEGFLVLPFSR  
RNRVHTGHHPAVPERLAATGLLHHDGSAPDVSGLRQVGLTNGDGVERRLPEQ  
VRVRFDKLEKLRSSGIDAFPVGRPPSHTVAQALAADHQASVSVSGRIMRIRNY  
GGVLF AQLRDWSGEMQVLLDNSRLDQGCAADFNAATDLGDLVEMTGHMGA  
SKTGTPLIVSGWRLIGKCLRPLPNKWKGLLDPEARVRTRYLDLAVNAESRAL  
ITARSSVLRAVRETLFAKGFVEVETPIQLQLHGGATARPFVTHINTYSMDLFLRI  
APELYLKRLCVGGVERVFELGRAFRNEGVDVFSHNPEFTLLEAYQAHADYLEW

IDGCRELIQNAAQAANGAPIAMRPRTDKGS DGTRHHLEPVDISGIWPVRTVHD  
AISEALGERIDADTGLTTLRKLCDAAAGVPYRTQWDAGAVVLELYEHLVECRTE  
QPTFYIDFPTSVSPLTRPHRSKRGVAERWDLVAWGIELGTAYSELTPVEQRRR  
LQEQSLLAAGGDPEAMELDEDFLQAMEYAMPPTGGLGMGIDRVVMLITGRSI  
RETLPFPLAKPH

> sp|P0A4Y0|CYA1\_MYCTU Adenylate cyclase OS=Mycobacterium tuberculosis  
GN=cya PE=1 SV=1

MAARKCGAPPIAADGSTRRPDCVTAVRTQARAPTQHYESVARRQRVLTITAW  
LAVVVTGSFALMQLATGAGGWYIALINVFTAIVPLLHRFGGLVAPLTFIG  
TAYVAIFAIGWDVGT DAGA QFFFLVAAALVLLVGIEHTALAVGLAAVAAGLVI  
ALEFLVPPDTGLQPPWAMSVSFLTTVSACGVAVATVWFALRDTARAEAVME  
AEHDRSEALLANMLPASIAERLKEPERNIIADKYDEASVLFADIVGFTERASST  
APADLVRFLDRLYSADFELVDQHGLEKIKVSGDSYMMVVS GVP RPRPDHTQAL  
ADFALDMTNVAAQLKDP RGNP VPLRVGLATGPVVAGVVGSRRFFYDVWGDA  
VNVASRMESTDSVGQIQVPDEVYERLKDDFVLRERGHINVKGKGMRTWYL  
IGRKVAADPGEVRGAEPRTAGV

> sp|P71707|PBP1A\_MYCTU Penicillin-binding protein 1A OS=Mycobacterium  
tuberculosis GN=ponA1 PE=1 SV=3

MNSDGRHHQSSSGAPRGPANPGQRGQVPPDDRLLTAILPPVTDDRSAPHADSIE  
AVKAAALDGAPMPPPRDPLEEVTAALAAPP GKPPRGDQLGRRRPPGPPGPPG  
SSGQPAGRLPQPRVDLPRVGQINWKWIRRSYLTA AVVILLPMVTFTMAYLIVD  
VPKPGDIRTNQVSTILASDGSEIAKIVPEGNRVDVNLSQVPMHVRQAVIAED  
RNFYSNPGFSFTGFARAVKNNLFGGDLQGGSTITQQYVKNALVGS AQHGWSG  
LMRKAKELVIATKMSGEWSKDDVLQAYLNIIYFGRGAYGISAASKAYFDKPV  
EQLTVAEGALLAALIRRPSTLDPAVDPEG AHARWNWVLDGMVETKALSPNDR  
AAQVFPETVPPDLARAENQTKGPNGLIERQVTRELLELFNIDEQTLNTQGLVV  
TTTIDPQAQRAAEKAVAKYLDGQDPDMRAAVVSIDPHNGAVRAYYGGDNAN  
GFDFQAQAGLQTGSSFKVFALVAALEQGIGLGYQVDSSPLTVDGIKITNVEGEGC  
GTCNIAEALKMSLNTSYRMLKLNGGPQAVADAAHQAGIASSFP GVAHTLS  
EDGKGGPPNNGIVLGQYQTRVIDMASAYATLAASGIYHPPHFVQKVVSANGQ  
VLFDASTADNTGDQRIPKAVADNVTAAMEPIAGYSRGHNLAGGRDSA AKTGT  
TQFGDTTANKDAWMVGYTPSLSTAVWVGT VKGDEPLVTASGAAIYG SGLPSD  
IWKATMDGALKGTSNETFPKPTEVGGYAGVPPPPPPPEVPPSETVIQPTVEIAP  
GITIPIGPPTTITLAPPPPAPPAATPTPPP

> sp|P71970|AFTC\_MYCTU Alpha-(1-3)-arabinofuranosyltransferase  
OS=Mycobacterium tuberculosis GN=aftC PE=1 SV=2

MYGALVTAADSIRTGLGASLLAGFRPRTGAPSTATILRSALWPAAVLSVLHRSI  
VLTNNGNITDDFKPVYRAVLNFRRGWDIYNEHFDYVDPHYLYPPGGTLLMAP  
FGYLPFAPSRYL FISINTAAILVAAYLLLRMFNFTLTSVAAPALILAMFATETVTN  
TLVFTNINGCILLLEVLFLRWLLDGRASRQWCGGLAIGLTLVLKPLLGLLLLLP  
LLNRQWRALVA AVVVPVVVNVAALPLVSDPMSFFTRTLPLYILGTRDYFNSSIL  
GNGVYFGLPTWLILFLRILFTAITFGALWLLYRYRTGDPLFWFTTSSGVLLLW  
SWLVMSLAQGYYSMMLFPFLMTVVL PNSVIRNWP AWLG VYGFMTLDRWLL  
FNWMRWGRALEYLKITYGWSLLLIVTFTVLYFRYLDKADNRLDGGIDPAWL

TPEREGQR

> sp|P65823|CAEA\_MYCTU Carboxylesterase A OS=Mycobacterium tuberculosis  
GN=caeA PE=1 SV=1

MGMRLSRRDKIARMLLIWAALAAVALVLVGCIRVVGGRARMAEPKLGQPVE  
WTPCRSSNPQVKIPGGALCGKLAVPVDYDRPDGDVAALALIRFPATGDKIGSL  
VINPGGPGESGIEAALGVFQTLPKRVHERFDLVGFDPRGVASSRPAIWCNSDA  
DNDRLRAEPQVDYSREGVAHIENETKQFVGRVCVDMGKNFLAHVGTVNVAK  
DLDAIRAALGDDKLTLYLGYSYGTRIGSAYAEFPQVRAMILDGAVDPNADPI  
EAELRQAKGFQDAFNNYAADCAKNAGCPLGADPAKAVEVYHSLVDPLVDPD  
NPRISRPARTKDPRGLSYSDAIVGTIMALYSPNLWQHLLTDGLSELVDNRGDTLL  
ALADMYMRRDSHGRYNNSGDARVAINCVDQPPVTDRDKVIDEDRRAREIAPF  
MSYGKFTGDAPLGTCAFWVPPTSQPHAVSAPGLVPTVVVSTTHDPATPYKA  
GVDLANQLRGSLLTFDGTQHTVVFQGDSCIDEYVTAYLIGGTTPPSGAKC

> sp|A0QTT7|Y1959\_MYCS2 UPF0182 protein MSMEG\_1959/MSMEI\_1915

OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155)

GN=MSMEG\_1959 PE=1 SV=1

MGMRPRTARMPKLTRRSRVLIAFALVAVLLLLLPRLIDTYVDWLWFGELGYRS  
VFTTVLATRLIVFVVVALAIGAIVFAGLALAYRTRPVFVPTAGPNDPVARYRTT  
VMARLRLFGIGVPVFIGLLAGIVAQSYWVKIQLFLHGGDFGITDPEFGKDLGFY  
AFDLPFYRLVLTYL FVATFLAFVANLLGHYLFGGIRLTGRVGALSRAARIQLISL  
AGTLIVLKAFAFWLDRYELLSNDRSAKPFTGAGYTDINAVLPAKLIMLAIavic  
AVAVFSALVLRDLRIPAIGVALLLSSLVVGAGWPLIVEQFSVKPNAAQKEAEY  
ISRSIEATRHAYGLTDETVTYRNYENTGQTAAQVAADRATTSNIRLLDPTIVSP  
AFTQFQQGKNFYYPDQLSIDRYIGPDGNLRDYVVAARELNPDRIDLINQRDWI  
NRHTVYTHGNGFIASPANTVRGVANDPNQNGGYPEFLASVVGANGSVISPGP  
APLDQPRIYFGPVISNTPADYAIVGKTGDTDREYDYETNTETKNYTYGGKGGV  
PIGNWLNRSVFAAKFAERNFLFSNVIGENSKILFNRDPAERVEAVAPWLTTDTS  
VYPAIVNKR MVWIVDGYTTLDNYPYSELTTLSSATADSNEVAVNRLAPDKKVS  
YIRNSVKATV DAYDGTVTLYAQDENDPVLKAWMDVFP GTVKPKADITPELQA  
HLRYPEDLFK VQRALLAKYHVDNPVTFSSAQDFWDVPLDPNPTASSFQPPYYI  
VAKDLVKNDNSASFQLTSALNRFQRDFLAAYVSASSDPETYGKLT VLTIPGQV  
NGPKLAFNAISTDTAVSQDLGVIGRDNQN RIRWGNLLTLPVADGGLLYVAPVY  
ASPGSSDAASSYPRLIRVAMLYNDRVGYGPTVSDALTELFPGGAGATATDVAP  
AEGRPAQSTPNGQQPAASPPPAANADGRPAQAPPPPSAATPTGPVQISQAKAE  
ALQDLESALTAQAQESGDFAEY GQALQRLNDAMKKYDSAK

> sp|P67438|Y1816\_MYCTU Uncharacterized HTH-type transcriptional regulator

Rv1816/MT1864 OS=Mycobacterium tuberculosis GN=Rv1816 PE=2 SV=1

MCQTCRVGKRRDAREQIEAKIVELGRRQLLDHGAAGLSLRAIARNLGMVSSA  
VYRYVSSRDELLTLLLDAYSIDLADTVDRARDDTVADSWSDDVIAIARAVRG  
WAVTNPARWALLYGSPVPGYHAPPDRTAGVATR VVGAFDDAIAAGIATGDIRLT  
DDVAPQPMSSDFEKIRQEF GFGDDR VVTKCFLWAGVVG AISLEVFGQYGA  
DMLTDPGVVFD AQTRLLVAVLAEH

> sp|P65081|RSDA\_MYCTU Anti-sigma-D factor RsdA OS=Mycobacterium

tuberculosis GN=rsdA PE=1 SV=1

MREFGNPLGDRPPLDELARTDLLLDALAEREEVDFADPRDDALAALLGQWR  
DDLRWPPASALVSQDEAVAALRAGVAQRRRARRSLAAVGSVAAALLVLSGFG  
AVVADARPGDLLYGLHAMMFNRSRVSDQIVLSAKANLAKVEQMIAQQQWA  
EAQDELAEVSSTVQAVTDGSRQDLNEVNLLNTKVETRDPNATLRPGSPSNP  
AAPGSVGNSTWPLAPVVEPPTPPTPASAAEPSMSAGVSESPMPNSTSTVAASPS  
TPSSKPEPGSIDPSLEPADEATNPAGQPAPETPVSPH

> sp|P71586|PBPA\_MYCTU Penicillin-binding protein A OS=Mycobacterium  
tuberculosis GN=pbpA PE=1 SV=1

MNASLRRISVTVMALIVLLLLNATMTQVFTADGLRADPRNQRVLLDEYSRQR  
GQITAGGQLLAYSVAATDGRFRFLRVYYPNPEVYAPVTGFYSLRYSSTALERAEDP  
ILNGSDRRLFGRRLLADFFTGRDPRGGNVDTTINPRIQQAGWDAMQQGCYGPC  
KGAVVALEPSTGKILALVSSPSYDPNLLASHNPEVQAQAWQRLGDNPASPLTN  
RAISETYPPGSTFKVITTAALAAGATETEQLTAAPTIPLPGSTAQLENYGGAPC  
GDEPTVSLREAFVKSCNTAFVQLGIRTGADALRSMARAFGLDSPRPTPLQVA  
ESTVGIPIPSAALGMTSIGQKDVALTPLANAEIAATIANGGITMRPYLVGSLKG  
PDLANISTTVGYQQRRRAVSPQVAAKLTEL MVGAEKVAQQKGAIPGVQIASKT  
GTAEHGTDPRHTPPHAWYIAFAPAQAPKVAVAVLVENGADRLSATGGALAAPI  
GRAVIEAALQGEP

> sp|O07189|FLQE3\_MYCTU Fluoroquinolones export permease protein  
Rv2687c/MT2761 OS=Mycobacterium tuberculosis GN=Rv2687c PE=1 SV=1

MTRLVPALRLELTLQVRQKFLHAAVFSGLIWLAVLLPMPVSLRPVAEPYVLVG  
DIAIIGFFVGGTVFFFEKQERTIGAIVSTPLRFWEYLA AKLTVLLAISLFVAVVVA  
TIVHGLGYHLLPLVAGIVLGTLLMLLVGFSSSLPFASVTDWFLAAVIPLAIMLAP  
PVVHYSGLWPNPVLYLIPTQGPLLLLGA AFDQVSLAPWQVGYAVVYPIVCAA  
GLCRAAKALFGRYVVQRSGVL

> sp|H8EXN2|RSLA\_MYCTE Anti-sigma-L factor RslA OS=Mycobacterium  
tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) GN=rsIA PE=1 SV=1

MTMPLRGLGPPDDTG VREVSTGDDHHYAMWDAAYVLGALSADRREFEAH  
LAGCPECRGAVTELCGVPALLSQLDRDEVAAISESAPTVVASGLSPELLPSLLA  
AVHRRRRRTRLITWASSAAA AVLAIGVLVGVQGHSAAPQRAAVSALPMAQV  
GTQLLASTVSI SGEPWGTFINLRCVCLAPPYASHDTLAMVVVGRDGSQTRLAT  
WLAEPGHTATPAGSISTPVDQIAAVQVVAADTGQVLLQRS

> sp|O06203|ACYLT\_MYCTU Phosphatidylinositol mannoside acyltransferase  
OS=Mycobacterium tuberculosis GN=Rv2611c PE=1 SV=1

MIAGLKGLKPKDPRSSVTRTATDWAYAAGWMAVRALPEFAVRNAFDTGARY  
FARHGGPEQLRKNLARVLGVPPAAVPDPLMCASLESYGRYWREVFRLPTINH  
RKLARQLDRVIGGLDHLDAALAAGLGAVLALPHSGNWD MAGMWLVQRHGT  
FTTVAERLK PESLYQR FIDYRESLGFEVLPLSGGERPPFEVLSERLRNRRVCL  
MAERDLTRTGVEVDFGEPTRMPVGP AKLAVETGAALLPTHCFEGRGWGF  
QVYPALDCTSGDVAAITQALADRFAQNI AHPADWHMLQPQWLADLSESRR  
AQLRSR

> sp|Q7D5W1|DESA3\_MYCTU Stearoyl-CoA 9-desaturase OS=Mycobacterium  
tuberculosis GN=desA3 PE=1 SV=1

MAITDVDVFAHLTDADIENLAAELDAIRRDVEESRGERDARYIRRTIAAQRAL

EVSGRLLLAGSSRRLAWWTGALTGVAKIIENMEIGHNVMHGQWDWMNDPE  
IHSSTWEWDMMSGSSKHWRYTHNFVHHKYTNILGMDDDVGYGMLRVTRDQR  
WKRYNIFNVVWNTILAIGFEWGVALQHLEIGKIFKGRADREAAKTRLREFSAK  
AGRQVFKDYVAFPALTSLSPGATYRSTLTANVVANVIRNVWSNAVIFCGHFDP  
GAEKFTKTDMIGEPKGQWYLRQMLGSANFNAGPALRFMSGNLCHQIEHHL  
PDLPSNRLHEISVRVREVCDDRYDLPYTTGSFLVQYGKTWRTLAKLSLPDKYLR  
DNADDAPETRSEMFAGLPGFAGADPVTGRRRGLKTAIAAVRGRRRSKRM  
AKSVTEPDDLAA

> sp|P72058|AFTA\_MYCTU Arabinofuranosyltransferase AftA OS=Mycobacterium tuberculosis GN=aftA PE=1 SV=1

MPSRRKSPQFGHEMGAFTSARAREVLVALGQLAAAVVVAVGVAVVSLAIAR  
VEWPAFPSSNQLHALTTVGQVGLAGLVGIGWLWRHGRFRRLARLGGLVLS  
AFTVVTLGMPLGATKLYLFGISVDQQFRTEYLRLTDTAALRDMTYIGLPPFYP  
PGWFWIGGRAAALTGTPAWEMFKPWAITSMAIAVAVALVLWWRMIRFEYALL  
VTVATAAVMLAYSSPEPYAAMITVLLPMLVLTWSGLGARDRQGWAAVVGAG  
VFLGFAATWYTLVAYGAFTVVLMAALLAGSRLQSGIKAAMDPLCRLAVVGAI  
AAAIGSTTWLPYLLRAARDPVSDTGSAQHYPADGAALTFPMLQFSLGAI  
LGLTLWLVMRARSSAPAGALAVYLWVLSLMLATLARTLLSFRLQPTLS  
VLLVAAGAFGFVEAVQALGKRGRGVIPMAAAIGLAGAIAFSQDIPDVL  
RPDLTIAYTDTDGYGQRGDRPPGSEKYYPADAIRRVTKRRDRTVVL  
TADYSFLSYYPYWGFGQLTPHYANPLAQFDKRATQIDSWGLSTADEFIA  
ALDKLPWQPPTVFLMRHGAHNSYTLRLAQDVYPNQPNVRRYTVDLRTAL  
FADPRFVVEDIGPFVLAIRKPQESA

> sp|A0QQ71|PHND\_MYCS2 Phosphate-import protein PhnD OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=phnD PE=1 SV=1

MKIRAHHKIATAAACVALLASACSGSDKQSTTAEGFPETITLAAIPAENSSDL  
KASYDPLIKMLEKQTGSKVEFVQASDYAGVVEGMIAGNVDLAFFGPFAYVVA  
GVNGAKMTPLGAVIKDEGGAPGYQSYGLARADEDNINGLKDFAGKKVCFVD  
PGSTSGFLYPTAGLIEEGVVKSGSEADISAAMSPIFAGGHDSALAIANGDCDA  
GFAFDTMVDKTMIDKGDLPKQGLKTVWKSDMIAGSVFAANDALGPEVIDKL  
KTMFAQDANVKSFEFEEGFCEGDACRITDERAWGVVPVTDADYDGV  
RHVCDVTGSEKCKG

> sp|O53176|Y2449\_MYCTU Putative trans-acting enoyl reductase Rv2449c OS=Mycobacterium tuberculosis GN=Rv2449c PE=1 SV=3

MTATPREFDIVLYGATGFVGLKTAEYLARAGGDARIALAGRSTQRVLAVREAL  
GESAQTPILTADASLPSTLQAMAARAQVVVTTVGPYTRYGLPLVAACAAAG  
TDYADLTGEPFMFRNSIDLYHKQAADTGARIVHACGFDSVPSDLSVYALYHA  
AREDGAGELTDTNCVRSFKGGFSGGTIASMLEVLSTASNDPDARRQLSDPY  
MLSPDRGAPELGPQPDLPSSRRGRRLAPELAGVWTAGFIMAPTNTTRIVRRSNA  
LLDWAYGRRFRYSETMSVGSSTVLPVVSVVGGGVGNAMFGLASRYIRLLPRG  
LVKRVPKPGTGPSAAARERGYRIETYTTTTTGARYLARMAQDGDPGYKAT  
SVLLGECGLALALDRDKLSDMRGVLTAAAMGDALLERLPAAGVSLQTRRL  
AS

> sp|Q10801|DIPZ\_MYCTU Protein DipZ OS=Mycobacterium tuberculosis

GN=dipZ PE=1 SV=1

MVESRRAAAAASAYASRCGIAPATSQRSLATPPTISVPSGEGRCRCHVARGAG  
RDPRRLRRRRWCGRCGYHSHLTGGEFDVNRLCQQRSRERSCQLVAVPADPR  
PKRQRITDVLTLALVGFLGGLITGISPCILPVLPIFFSGAQSVDAAQVAKPEGA  
VAVRRKRALSATLRPYRVIGGLVLSFGMVTLGGSALLSVLHLPQDAIRWAALV  
ALVAIGAGLIFPRFEQLLEKPFSTRIPQKQIVTRSNGFGLGLALGVLYVPCAGPIL  
AAIVVAGATATIGLGTVVLTAATFALGAALPLFFALAGQRIAERVGAFRRRQREI  
RIATGSVTILLAVALVFDLPAALQRAIPDYTASLQQQISTGTEIREQLNLGGIVN  
AQNAQLSNCSDGAAQLESCGTAPDLKGITGWLNTPGNKPIDLKSLRGKVLI  
DFWAYSCINCQRAIPHVVGWYQAYKDSGLAVIGVHTPEYAFEKVPGNVAKGA  
ANLGISYPIALDNNYATWTNYRNRYPAEYLIDATGTVRHIKFGEGDYNVTET  
LVRQLLNDKPGVKLPQPSSTTTPDLTPRAALTPETYFGVGKVVNYGGGGAY  
DEGSAVFDYPPSLAANSFALRGRWALDYQGATSDGNDAIKLNYHAKDVYIV  
VGGTGTLTVVRDGPATLPISGPPTTHQVVAGYRLASETLEVRPSKGLQVFSFT  
YG

> sp|O06293|INIA\_MYCTU Isoniazid-induced protein IniA OS=Mycobacterium  
tuberculosis GN=iniA PE=1 SV=1

MVPAGLCAYRDLRRKRARKWGDTVTQPDDPRRVGVIVELIDHTIAIAKLNER  
GDLVQRLTRARQRITDPQVRVVIAGLLKQGKSQLLNSLLNLPAAARVGDDEATV  
VITVVSYSQAQPSARLVLAAGPDGTTAAVDIPVDDISTDVRAPHAGGREVLRV  
EVGAPSPLLRGGLAFIDTPGVGGLGQPHLSATLGLLPEADAVLVSDTSQEFTE  
PEMWFVRQAHQICPVGAVVATKTDLYPRWREIVNANAHLQRARVPMPIIAVS  
SLLRSHAVTLNDKELNEESNFP AIVKFLSEQVLSRATERVRAGVLGEIRSATEQ  
LAVSLGSELSVNDPNLRDRLASDLERRKREAAQAVQQTALWQQVLGDGFN  
DLTADVDHDLRTRFRVTEDAERQIDSCDPTAHWAEIGNDVENAIATAVGDNF  
VWAYQRSEALADDVARSFADAGLDSVLSAELSPHVMGTDFGRLKALGRMES  
KPLRRGHKMIIGMRGSYGGVVMIGMLSSVVGGLFNPLSVGAGLILGRMAYK  
EDKQNRLLRVRSEAKANVRRFVDDISFVVSQSRDRLKMIQRLLRDHYREIA  
EETRSLTESLQATIAAAQVAETERDNRIRELQRQLGILSQVNDNLAGLEPTLTP  
RASLGRA

> sp|O53471|Y2025\_MYCTU Probable cation efflux system protein

Rv2025c/MT2084 OS=Mycobacterium tuberculosis GN=Rv2025c PE=2 SV=1

MTHDHAHSRGPAMIKEIFAPSHDAADSVDTTLESTAAGIRTVKISLLVLGLT  
ALIQIVIVVMSGVALAADTIHNFADALTAVPLWIAFALGAKPATRRYTYGFGR  
VEDLAGSFVVAMITMSAIIAGYEAIARLIHPQQIEHVGWVALAGLVGFIGNEW  
VALYRIRVGHRISSAALIADGLHARTDGFTSLAVLCSAGGVALGFPLADPIVGL  
LITAAAILAVLRTAARDVFRLLDGVDPAMVDAAEQALAAARPGVQAVRSVRMR  
WIGHRLHADAELDVPALDLAQAHRIAHD AEHELTHTVPKLTTALIHAYPAEH  
GSSIPDRGRTVE

> sp|O69734|ECCB1\_MYCTU ESX-1 secretion system protein eccB1

OS=Mycobacterium tuberculosis GN=eccB1 PE=1 SV=1

MGLRLTTKVQVSGWRFLRRLEHAIVRRDTRMFDDPLQFYSRSIALGIVVAVL  
ILAGAALLAYFKPQKLGGSFTDRATNQLYVLLSGQLHPVYNLTSARLVLG  
NPANPATVKSSSELSKLPMGQTVGIPGAPYATPVSAGSTSIWTLCDTVARADSTS

PVVQTAVIAMPLEIDASIDPLQSHEAVLVSYQGETWIVTTKGRHAIDLTDRALT  
SSMGIPVTARPTPISEGMFNALPDMGPWQLPPIPAAGAPNSLGLPDDLVIQSVF  
QIHTDKGPQYYVVLDPGIAQVNATTAALRATQAHGLVAPPAMVPSLVVRIAE  
RVYPSPLPDEPLKIVSRPQDPALCWSWQRSAGDQSPQSTVLSGRHLPISPSAM  
NMGIKQIHGTATVYLDGGKFVALQSPDPRYTESMYIYDPQGVRYGVPNAETA  
KSLGLSSPQNAPWEIVRLLVDGPVLSKDAALLEHDTLPADPSPRKVPAGASGA  
P

> sp|A0QPD4|AFTD\_MYCS2 Alpha-(1-3)-arabinofuranosyltransferase  
OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=aftD PE=1  
SV=1

MVAAATLVLTFAQSPGQISPDTKLDLTANPLRFLARAFNLWNSDLPGQAQNNQ  
AYGYLFPHGTFLLGDVVGVPGWVTQRLWWALLTVGFWGVLRVAEALGIG  
STPSRLIGAAAFALSPRVLTTLGAISSETLPMMLAPWVLLPVILALRGQHSVRL  
MAARSAGAVALMGAVNAVATLTGCLA AVIWWACHRPNRLWWRFTAWWLLC  
GALAVTWWVVALLMLGRISPPFLDFIESSGVTTQWMSLTEMRLGTMSWTPFV  
APSATAGASLVTSTAVLATTVVAAGLAGLALRTMPARGRLITMLLIGVVLL  
GLGYSGLGSPVALQVQAFLDGSGTPLRNLA KLEPVIRLPLALGLVHLLGRIPL  
PGSAPRAVWVSAFAHPERDKRVAVAIVVLSALAAGTSLAWTARLTPPGSFTAIP  
QHWHDAAAWLDEHNTDRGRVLVAPGAPFATQVWGNSHDEPLQVLGDNPWG  
VRDSIPLTPPETIRALDSVQRLFASGRPSPGLADTLARQGISYVVVRNDLDPDT  
SRSARPILVHRAVEGSPGLTKVAEFGDPVGPVTLEGFVADSGLRPRYPAVEIFRV  
EPADAGSSQQRSPMHPYLVDSAMTRVAGAPEALLRLDERRRLNGEPPLGPM  
LLAADARRAGLPVDGVIVTDTPTAREIDYGRVDDHASAIRTPDDARHTYNRVP  
DYPSDGADLVYGKWTGGRLSVSSAADSTALPYVAPATGPAA AIDS DSSTAWV  
SNALQAAVGQWLQVDFDHPVTNATLTITPSATAVGAQVRRIEIATATGTSSLRF  
DTAGKPLTIPLPVGETPWVVRVTAVATDDGSPGVQFGVTDLAITQYDASGFAHP  
VTLRHTVEVPGPPAGSVVQQWDLGTELLGRPGCADSPVGVRC AAAMALASE  
EPVNL SRTLTPQDTEVQPTVWIRGRQGNLADLVAQPDTTRA FGSDSDPIDVL  
GSAYAATDGDPRTSWTAPQRVVQFQTPPTLTLKLPRPTEVSGMRIVPGDTEPPA  
HPTLVAIDLGDGPQMHLR PADGEPRTVTLKPRVTDVTV SLLAWNDIIDRTSLG  
FDQLKPPGLAELTVLDGRGAPVGAADA AKNRSRAVALPCGQGPII AVAGQFIQ  
TSVHTTVGALLDGEPIPARPCRSEPVKLPAGQQELVVSPGAA FIVDGVELPTPA  
ADEIRSAPT TSAETGTWTADRREVRV SAAAQQRVLVVPESVNRGWSAHPAG  
AELQSVTVNGWQQGWVVPAGTEGTVTLTFASNMPYRVGLIGGLALLPLLALL  
ALIPVRRPVRAAAPARPWNPGPVL TGAAALVAGTAISGVAGLLVVGAA MGVRI  
LLNRRGAAGEKVWDNVTVVVAAGGLILAGSVLSQYPWRSVDG YVGHTPGV  
QFLALLSVAFLAASAVRLVNRPEPSEDGRSAKPEHTGASAHAG

> sp|P64783|Y1258\_MYCTU Probable multidrug-efflux transporter  
Rv1258c/MT1297 OS=Mycobacterium tuberculosis GN=Rv1258c PE=1 SV=1  
MRNSNRGPAFLILFATLMAAAGDGV SIVAFPWLVLQREGSAGQASIVASATML  
PLL FATLVAGTAVDYFGRRRVSMVADALSGAAVAGVPLVAVG YGGDAVNVLV  
LAVLAALAAAFGPAGMTARDSMLPEAAARAGWSLDRINGAYEAILNLA FIVG  
PAIGGLMIATVGGITTMWITATAFGLSILAI AALQLEGAGKPHHTSRPQGLVSGI  
AEGLR FVWNLRVLR TLGMIDLTVTALYLPMESVLFPKYFTDHQQPVQLG WAL

MAIAGGGLVGALGYAVLAIRVPRRVTMSTAVLTLGLASMVIAFLPPLPVIMVLC  
AVVGLVYGPIQPIYNYVIQTRAAQHRLRGRVVGVMSTLAYAAGPLGLLLAGPLT  
DAAGLHATFLALALPIVCTGLVAIRLPALRELDLAPQADIDRPVGSQAQ

> sp|A1KH33|ARFC\_MYCBP Uncharacterized membrane protein ArfC

OS=Mycobacterium bovis (strain BCG / Pasteur 1173P2) GN=arfC PE=2 SV=1

MEHVHWWLAGLAFTLGMVLTSTLMVRPVEHQVLVKKSVRGSSAKSKPPTAR  
KPAVKSGTKREESPTAKTKVATESAAEQIPVAGEPAAEPIPVAGEPAARIPVVPY  
APYGPGSARAGADGSGPQGWLVKGRSDTRLYYTPEDPTYDPTVAQVWFQDE  
ESAARAFFTPWRKSTRRT

> sp|P0A608|SODC\_MYCTU Superoxide dismutase [Cu-Zn] OS=Mycobacterium  
tuberculosis GN=sodC PE=1 SV=1

MPKPADHRNHA AVSTSVLSALFLGAGAALLSACSSPQHASTVPGTTPSIWTGS  
PAPSGLSGHDEESPGAQSLTSTLTAPDGTKVATAKFEFANGYATVTIATTGVGKL  
TPGFHGLHIHQVGKCEPNSVAPTGGAPGNFLSAGGHYHVPGHGTGPASGDLA  
SLQVRGDGSAMLVTTTDAFTMDDLSSAKTAAIIHAGADNFANIPPERYVQVN  
GTPGPDETTLTGDAGKRVACGVIGSG

> sp|A1KH31|ARFA\_MYCBP Peptidoglycan-binding protein ArfA

OS=Mycobacterium bovis (strain BCG / Pasteur 1173P2) GN=arfA PE=1 SV=1

MASKAGLGQTPATTDARRTQKFYRGSPGRPWLIGAVVIPLLIAAIGYGAFERP  
QSVTGPTGVLPTLTPTSTRGASALSLSLLSISRSGNTVTLIGDFPDEAAKAALM  
TALNGLLAPGVNVIDQIHVDPVVRSLDFSSAEPVFTASVPIPDFGLKVERDVT  
LTGTAPSSEHKDAVKRAATSTWPDMMKIVNNEVTGQAPPGPPASGPCADLQSA  
INAVTGGPIAFGNDGASLIPADYEILNRVADKCLKACPDARVTINGYTDNTGSEG  
INIPLSAQRAKIVADYLVARGVAGDHIATVGLGSVNPIASNATPEGRAKNRRVEI  
VVN

> sp|P0A5K2|MMPS4\_MYCTU Putative membrane protein mmpS4

OS=Mycobacterium tuberculosis GN=mmpS4 PE=1 SV=1

MLMRTWIPLVILVVVIVGGFTVHRIRGFFGSENRPYSYSDTNLENSKPFNPKHLT  
YEIFGPPGTVADISYFDVNSEPQRVDGAVLPWSLHITTNDAAVMGNIVAQGNS  
DSIGCRITVDGKVRRAERVSNEVNAYTYCLVKSA

> sp|O05871|PKND\_MYCTU Serine/threonine-protein kinase PknD

OS=Mycobacterium tuberculosis GN=pknD PE=1 SV=1

MSDAVPQVGSQFGPYQLLRLGRGGMGEVYEAEDTRKHRVVALKLISPQYSD  
NAVFRARMQREADTAGRLTEPHIVPIHDYGEINGQFFVEMRMIDGTSRLALLK  
QYGPLTPARAVAIVRQIAAALDAAHANGVTHRDVKPENILVTASDFAYLVDFGI  
ARAASDPGLTQTGTAVGTYNMAPERFTGDEVTYRADIYALACVLGECLTGA  
PPYRADSVERLIAAHLMDPAPQPSQLRPGRVPPALDQVIAKGMMAKNPAERFMS  
AGDLAIAAHDALTSEQHQAATTILRRGDNATLLATPADTGLSQSESGIAGAGTG  
PPTPGAARWSPGDSATVAGPLAADSRGGNWPSQTGHSPAVPNALQASLGHAV  
PPAGNKRKVWAVVGAAAIVLVAIVAAAGYLVLRPSWSPTQASGQTVLPFTGID  
FRLSPSGVAVDSAGNVYVTSEGMYGRVVKLATGSTGTTVLPFNGLYQPQGLA  
VDGAGTVYVTDNFNRVVTLAAGSNNQTVLPFDGLNYPEGLAVDTQGAVYVA  
DRGNRNVVKLAAGSKTQTVLPFTGLNDPDGVAVDNSGNVYVTDTDNRRVVK  
LEAESNNQVLPFTDITAPWGIAVDEAGTVYVTEHNTNQVVKLLAGSTSTV

LPFTGLNTPLAVAVDSVRTVYVADRGNDRVVKLTS

> sp|P64168|FTSQ\_MYCTU Cell division protein FtsQ OS=Mycobacterium tuberculosis GN=ftsQ PE=1 SV=1

MTEHNEDPQIERVADDAADEEAVTEPLATESKDEPAEHPEFEGPRRRARRERA  
ERRAAQARATAIEQARRAAKRRARGQIVSEQNPAKPAARGVVRGLKALLATV  
VLAVVGIGLGLALYFTPAMSAREIVIIGIGAVSREEVLDAARVRPATPLLQIDTQ  
QVADRVATIRRVASARVQRQYPSALRITIVERVPVVVKDFSDGPHLFDRDGVDF  
ATDPPPPALPYFDVDNPGPSDPTTKAALQVLTALHPEVASQVGRIAAPSVASITL  
TLADGRVVIWGTDRCEEKAEKLAALLTQPGRTYDVSSPDLPTVK

> sp|O07188|FLQE2\_MYCTU Fluoroquinolones export permease protein

Rv2686c/MT2760 OS=Mycobacterium tuberculosis GN=Rv2686c PE=1 SV=1

MRAISSLAGPRALAAFGRNDIRGTYRDPLLMLVIAPVIWTTGVALLTPLFTEM  
LARRYGFDLVGYYPILITAFLLLSIIVAGALAAFLVLDDVDAGTMTALRVTPV  
PLSVFFGYRAATVMVVTIYVATMSCSGILEPGLVSSLIPGLVAGLSAVVTLL  
LILAVANNKIQGLAMVRALGMLIAGLPCLPWFISSNWNLAFGVLPPYWAAKA  
FWVASDHGTWWPYLVGGAVYNLAIVWVLFRRFRKHA

> sp|A1KML4|RIP1\_MYCBP Zinc metalloprotease Rip1 OS=Mycobacterium bovis (strain BCG / Pasteur 1173P2) GN=rip1 PE=1 SV=1

MMFVTGIVLFAILISVALHECGHMWVARRTGMKVRRYFVGFPTLWSTRR  
GETEYGVKAVPLGGFCDIAGMTPVEELDPDERDRAMYKQATWKRVAFLFAG  
PGMNLAICLVLIYAIALVWGLPNLHPPTRAVIGETGCVAQEVSQGKLEQCTGP  
GPAALAGIRSGDVVVKVGDTPVSSFDEMAAAVRKSHGSVPIVVERDGTAVT  
YVDIESTQRWIPNGQGGELQPATVGAIGVGAARVGPVRYGVFSAMPATFAFTG  
DLTVEVGKALAALPTKVGALVRAIGGGQRPQTPISVVGASIIIGGDTVDHGL  
WVAFWFFLAQLNLILATINLLPLLPFDGGHIAVAVFERIRNMVRSARGKVAAAP  
VNYLKLLPATYVVLVLVGYMLLTVTADLVNPIRLFQ

> sp|A5U7B6|FTSX\_MYCTA Cell division protein FtsX OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ftsX PE=1 SV=1

MRFGFLLNEVLTGFRRNVTMTIAMILTTAISVGLFGGMLVVRLADSSRAIYL  
DRVESQVFLTEDVSANDSSCDTTACKALREKIETRSQVAVRFLNRQQAYDD  
AIRKFPQFKDVAGKDSFPASFIVKLENPEQHKDFDTAMKGPQGVLDVNLQKEL  
IDRLFVLDGLSNAFAVALVQAIGAILLIANMVQVAAYTRRTEIGIMRLVGAS  
RWYTQLPFLVEAMLAATMGVGIAGVGLMVVRAFLFLENALNQFYQANLIAKV  
DYADILFITPWLLLLGVAMSGLTAYLTLRLYVRR

> sp|P95241|Y2345\_MYCTU UPF0603 protein Rv2345/MT2410

OS=Mycobacterium tuberculosis GN=Rv2345 PE=2 SV=1

MRLVRLGMLVTLAAGLLGPPAGAQPFRSLSNYVTDNAGVLTSSGRTAVTA  
AVDRLYADRRIRLWVYVENFSGQSALNWAQRTTRTSELGNYDALLAVATTG  
REYAFLVPSAMPGVSEGQVDNVRRYQIEPALHDGDYSGAAVAANGLNRS  
SSSRVLLVTVGIIIVVAVLLVVMRHRNRRADELAARRVDPTNVMALAA  
VPLQALDDLRSRMVVDVNAVRTSTNELALAEIEFGERRTAPFTQAVNNAKA  
ALSQAFTVRQQLDDNTPETPAQRRELLTRVIVSAAHADRELASQTEAFEKLRD  
LVINAPARLDLLTQQYVELTTRIGPTQQRLAELHTEFDAAAMTSIAGNVTTATE  
RLAFADRNISAARDLADQAVSGRQAGLVDAVRAAESALGQARALLDAVDSAA

TDIRHAVASLPAVVADIQTGIKCRANQHLQQAQQPQTGRTGDLIAARDAARAL  
DRARGAADPLTAFDQLTKVDADLDRLLATLAEEQATADRLNRSLEQALFTAES  
RVRAVSEYIDTRRGSIGPEARTRLAEAKRQLEAAHDRKSSNPTEAIAYANAAS  
LAAHAQSLANADVQSAQRAYTRRGGNAGAILGGIIIIGDLLSGGTRGGLGGW  
IPTSGGSSNAPGSSPDGGFLGGGGRF

> sp|P60479|DPDS\_MYCTU Decaprenyl diphosphate synthase OS=Mycobacterium  
tuberculosis GN=uppS PE=1 SV=1

MARDARKRTSSNFPQLPPAPDDYPTFPDTSTWPVVFPELPAAPYGGPCRPPQH  
TSKAAAPRIPADRLPNHVAIVMDGNRWATQRGLARTEGHKMGEAVVIDIAC  
GAIELGIKWLSLYAFSTENWKRSPEEVRFMLMGFNRDVVRRRRDTLKCLGVIR  
WVGSRPRLWRSVINELAVAEEMTKSNDVITINYCVNYGGRTTEITREIAREV  
AAGRLNPERITESTIARHLQRPDIPVDLFLRTSGEQRSSNFMLWQAAYAEIF  
QDKLWPDYDRRDLWAACEEYASRTRRFGSA

> sp|P72030|EMBB\_MYCTU Probable arabinosyltransferase B OS=Mycobacterium  
tuberculosis GN=embB PE=2 SV=2

MTQCASRRKSTPNRAILGAFASARGTRWVATIAGLIGFVLSVATPLLPVVQTTA  
MLDWPQRGQLGSVTAPLISLTPVDFTATVPCDVVRAMPAGGVVLGTAPKQG  
KDANLQALFVVSAQRVDVTDNRNVILSVPREQVTSPQCQRIEVTSTHAGTF  
ANFVGLKDPGAPLRSGFPDNLRPQIVGVFTDLTGPAPPGLAVSATIDTRFSTR  
PTTLKLLAIIGAIIVATVVALIALWRLDQLDGRGSIAQLLRPFRPASSPGMRRL  
IPASWRTFTLTDVAVIFGFLWHVIGANSSDDGYILGMARVADHAGYMSNYFR  
WFGSPEDPFGWYYNLLALMTHVSDASLWMRLPDLAAGLVCWLLSREVLPR  
LGPAVEASKPAYWAAAMVLLTAWMPFNGLRPEGIILGSLVTYVLIERSMRY  
SRLTPAALAVVTAFTLGVQPTGLIAVAALVAGGRPMLRILVRRHRLVGTLPV  
SPMLAAGTVILTVVFADQTLSTVLEATRVRKIGPSQAWYTENLRYYYLILPT  
VDGSLSRFGFLITALCLFTAVFIMLRKRIPS VARGPAWRLMGVIFGTMFFLM  
FTPTKWVHHFGLFAAVGAAMAALTTVLVSPSVLRWSRNRMAFLAALFFLLAL  
CWATTNGWWYVSSYGVFNSAMPKIDGITVSTIFFALFAIAAGYAAWLHFAPR  
GAGEGRLIRALTAPVPIVAGFMAAVFVASMVAGIVRQYPTY SNGWSNVRAFV  
GGCGLADDVLVEPDTNAGFMKPLDGDGSGSWGPLGPLGGVNPVGFPTNGVPE  
HTVAEAIVMKPNQPGTDYDWDAPTCLTSPGINGSTVPLPYGLDPAVPLAGTY  
TTGAQQQSTLVS AWYLLPKPDDGHPLVVVTAAGKIAGNSVLHGYPGQTVVL  
EYAMPGPALVPAGRMVPDDLYGEQPKAWRNLR FARAKMPADAVAVRVVAE  
DLSLTPEDWIAVTPPRVPDLRSLQEYVGSTQPVLDDWAVGLAFPCQPMLHAN  
GIAEIPKFRITPDYS AKKLDTD TWEDGTNGLLGITDLLLRAHV MATYLSRDW  
ARDWGSRLRKFDTLVDAPPAQLELGTATRSGLWSPGKIRIGP

> sp|P96206|DRRB\_MYCTU Doxorubicin resistance ABC transporter permease  
protein DrrB OS=Mycobacterium tuberculosis GN=drrB PE=1 SV=1

MSGPAIDASPALTFNQSSASIQRRRLSTGRQMWWLYRRFAAPSLNNGEVLTTV  
GAPIIFMVGFYIPFAIPWNQFVGGASSGVASNLGQYITPLVTLQAVSFAAIGSGF  
RAATDSLLGVNRRFQSMAPLTPLLARVWVAVDRCFTGLVISLVCGYVIGFR  
FHRGALYIVGFCLLVIAIGAVLSFAADLVGTVTRNPDAMLPLLSLPILIFGLLSIG  
LMPLKLFPHWIHPFVRNQPI SQFVAALRALAGDTTKTASQVSWPVMAPTLTW  
LFAFVVILALSSTIVLARRP

> sp|P63762|FTSW\_MYCTU Lipid II flippase FtsW OS=Mycobacterium tuberculosis  
GN=ftsW PE=1 SV=1

MLTRLLRRGTSDDTGDGQTRGAEPVEGQRTGPEEASNPGSARPRTRFGAWLGR  
PMTSFHLIIAVALLLTTLGLIMVLSASAVRSYDDDGSAAVIFGKQVLWTLVGLI  
GGYVCLRMSVRFMRRIAFSGFAITIVMLVLVLPVPGIGKEANGSRGWVAVAGFS  
MQPSELAKMAFAIWGAHLLAARRMERASLREMLIPLVPAAVVALALIVAQPD  
LGQTVSMGIILLGLLWYAGLPLRVFLSSLAAVVVSAAILAVSAGYRSRDRVRSW  
LNPENDPQDSGYQARQAKFALAQQGGIFGDGLGQGVAKWNYLPNAHNDIFIFAI  
IGEELGLVGALGLLGLFGLFAYTGMRIASRSADPFLRLLTATTTLWVLGQAFINI  
GYVIGLLPVTGLQLPLISAGGTSTAATLSLIGIIANAARHEPEAVAALRAGRDDK  
VNRLRLPLPEPYLPPRLEAFRDRKRANPQPAQTQPARKTPRTAPGQPARQMG  
LPPRPGSPRTADPPVRRSVHHGAGQRYAGQRTRRVRALEGQRYG

> sp|H8EZH5|RPFB\_MYCTE Resuscitation-promoting factor RpfB  
OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) GN=rpfb  
PE=2 SV=1

MLRLVVGALLVLAFAAGGYAVAACKTVTLTVDGTAMRVTTMKSVIDIVEEN  
GFSVDDRDDLPAAGVQVHDADTIVLRRSRPLQISLDGHDQVWTTASTVD  
EALAQLAMTDTAPAAASRASRVPLSGMALPVVSAKTVQLNDGGLVRTVHLPA  
PNVAGLLSAAGVPLLQSDHVPAATAPIVEGMQIQVTRNRIKKVTERLPLPPN  
ARRVEDPEMNMSREVVDPGVPVGTQDVTFAVAEVNGVETGRLPVANVVVTP  
AHEAVVRVGTGKPGTEVPPVIDGSIWDAIAGCEAGGNWAINTGNGYYGGVQFD  
QGTWEANGGLRYAPRADLATREEQIAVAEVTRLRQGWGAWPVCAARAGAR

> sp|O69710|CTPJ\_MYCTU Probable cation-transporting P-type ATPase J  
OS=Mycobacterium tuberculosis GN=ctpJ PE=2 SV=1

MAVRELSPARCTSASPLVLARRTKLFALSEMRWAALALGLFSAGLLTQLCGAP  
QWVRWALFLACYATGGWEPGLAGLQALQRRTLVDLLMVVAAIGAAAIGQI  
AEGALLVIFATSGALEALVTARTADSVRGLMGLAPGTATRVGAGGGEETVNA  
ADLRIGDIVLVRPGERISADATVLAGGSEVDQATVTGEPLPVDKSIDQVFAGT  
VNGTGALRIRVDRLARDSVARIATLVEQASQTKARTQLFIEKVEQRYSIGMVA  
VTLAVFAVPPLWGETLQRALLRAMTFMIVASPCAVLATMPPLAAIANAGRH  
GVLAKSAIVMEQLGTTTRIAFDKTGTLTRGTPELAGIWVYERRFTDDELLRLA  
AAAEYPSEHPLGAAIVKAAQSRRLPTVGEFTAHPGCRVTARVDGHVIAVGS  
ATALLGTAGAAALEASMITAVDFLQGEYTVVVVVCDSPVGLLAITDQLRPE  
AAAISAATKLTGAKPVLLTGDNRATADRLGVQVGIDDVRAGLLPDDKVA  
RQLQAGGARLTVVGDGINDAPALAAAHVGIAMGSARSELTLQTADAVVVRD  
DLTTIPTVIAMSRARRIVVANLIVAVTFIAGLVVWDLAFTLPLPLGVARHEGST  
IIVGLNGLRLLRHTAWRRAAGTAHR

> sp|P71577|CWSA\_MYCTU Cell wall synthesis protein CwsA OS=Mycobacterium  
tuberculosis GN=cwsA PE=1 SV=1

MSEQVETRLTPRERLTRGLAYSAVGPVDVTRGLLELGVGLGLQSARSTAAGLR  
RRYREGRLAREVAAAQETLAQELTAAQDVVANLPQALQDARTQRRSKHHLWI  
FAGIAAAILAGGAVAFSIVRRSSRPEPSRPPSVEVQPRS

> sp|P95246|PHLB\_MYCTU Phospholipase C 2 OS=Mycobacterium tuberculosis  
GN=plcB PE=1 SV=2

MGSEHPVDGMTRRQFFAKAAAATTAGAFMSLAGPIIEKAYGAGPCPGHLTDIE  
HIVLLMQENRSFDHYFGTSLDTRGFDDTTPPVVFAQSGWNPMTQAVDPAGVT  
LPYRFDTTRGPLVAGECVNDPDHSWIGMHNSWNGGANDNWLPAQVPFSPLQ  
GNVPVTMGFYTRRDLPIHYLLADTFTVCDGYFCSLLGGTTPNRLYWMSAWID  
PDGTDGGPVLIENIQPLQHYSWRIMPENLEDAGVSWKVYQNKLLGALNNTV  
VGYNGLVNDFKQAADPRS NLARFGISPTYPLDFAADVRNNRLPKVSWVLPGF  
LLSEHPAFPVNVGAVAIVDALRILLSNPAVWEKTALIVNYDENGFFDHVVPPT  
PPPGTGPEFVTVPDIDSVPGSGGIRGPIGLGFRVPCLVISPYSRGPLMVHDTFDH  
TSTLKLIRARFGVVPVNLTAWRDATVGDMTSTFNFAAPPNPSKPNLDHPRNA  
LPKLPQCVPNAVLTGTVTKTAIPYRVFPQSMPTQETAPTRGIPSGLC

> sp|O69735|ECC1A\_MYCTU ESX-1 secretion system protein EccCa1

OS=Mycobacterium tuberculosis GN=eccCa1 PE=1 SV=1

MTTKKFTPTITRGPRLTPGEISLTPDDLIDIPPSGVQKILPYVMGGAMLGMIA  
IMVAGGTRQLSPYMLMMPLMMIVMMVGGLAGSTGGGGKKVPEINADRKEY  
LRYLAGLRTRVTSSATSQVAFFSYHAPHPEDLLSIVGTQRQWSR PANADFYAAT  
RIGIGDQPAVDRLKPAVGGELAAASAAPQPFLEPVSHMWVVKFLRTHGLIHD  
CPKLLQLRTFPTIAIGGDLAGAAGLMTAMICHLAVFHPPDLLQIRVLTEEPDDP  
DWSWLKWLPHVQHQTETDAAGSTR LIFTRQEGLSDLAARGPHAPDSLPGGP  
YVVVVDLTGGKAGFPDGRAGVTVITLGNHRGSAYRIRVHEDGTADDRLPNQ  
SFRQVTSVTDRMSPQQASRIARKLAGWSITGTILDKTSRVQKKVATDWHQLV  
GAQSVEEITPSRWRMYTDTDRDLKIPFGHELKTGNVMYLDIKEGA EFGAGP  
HGMLIGTTGSGKSEFLRTLILSLVAMTHPDQVNLLTDFKGGSTFLGMEKLPHT  
AAVVTNMAEEAELVSRMGEVLTGELDRRQSILRQAGMKVGAAGALSGVAEY  
EKYRER GADLPPLPTLFVVVDEFAELLQSHPDFIGLFDRICRVGRSLRVHLLLA  
TQSLQTGGVRIDKLEPNLTYRIALRTTSSHESKAVIGTPEAQYITNKESGVGFLR  
VGMEDPVKFSTFYISGPYMPAAAGVETNGEAGGPGQQTTRQAARIHRFTAAP  
VLEEATP

> sp|P71991|Y1733\_MYCTU Probable membrane protein Rv1733c/MT1774

OS=Mycobacterium tuberculosis GN=Rv1733c PE=1 SV=1

MIATTRDREGATMITFRLRLPCRTILRVFSRNPLVRGTDRL EAVVMLLAVTVSL  
LTIPFAAAAGTAVQDSRSHVYAHQAQTRHPATATVIDHEGVIDSNTTATSAPPR  
KITV PARWV VNGIERSGEVNAKPGTKSGDRVGIWVDSAGQLVDEPAPPARAIA  
DAALAALGLWLSVA AVAGALLALTRAILIRVNASWQH DIDS LFACTQR

> sp|A0R036|PIMG\_MYCS2 Polyprenol-phosphate-mannose-dependent

alpha-(1-2)-phosphatidylinositol mannoside mannosyltransferase OS=Mycobacterium  
smegmatis (strain ATCC 700084 / mc(2)155) GN=MSMEG\_4247 PE=1 SV=1

MLEMSKRQSPRGAGLAPTIAWRVFQLLTLAGVLWVGWRLGRVPYRIDIDVY  
RMGGRAWLDGRPLYADGAIFHTQGGLDL PFTY PPLAAIAFAPFAWLSLPLASS  
AITATTLVLLIVATTIVLTRL DVWPHTT VTSEPAWMRRAWLAAAMVAPAVIYLE  
PIRSNF EFGQIN VLM TLVIADCVPRRTPWPRG LLLGLAIALKLT PAVFLLYFLL  
RRDIHTLLRTAATAVVASLAGFALAWSDSVEYWTETVRNTDRIGTATLNTNQ  
IAGALARLGLGESPRFILWV LACFAVLALT VWAARRALRGDTADQTTEAPVLA  
LVCVALFGLVSPVSWSHHWVWMLPVLV TAVLAYRRRSVWFTALTAAGLA  
LTVWTPITLLPEHRETTASLWRQLAGGSYVWWAFAVIVVIGLVSSSRHTHTGDA

HETDEPLVPLARGEAG

> sp|O53895|MPRB\_MYCTU Signal transduction histidine-protein kinase/phosphatase MprB OS=Mycobacterium tuberculosis GN=mprB PE=1 SV=1  
MWWFRRRDRAPLRATSSLSLRWRVMLLAMSMVAMVVVLMSFAVYAVISAAL  
YSDIDNQLQSRAQLLIASGSLAADPGKAIEGTAYSDVNAMLVNPQSIYTAQQ  
PGQTLVPVGAEEKAVIRGELFMSRRTTADQRVLAIRLTNGSSLLISKSLKPTEAV  
MNKLRWVLLIVGGIGVAVAAVAGGMVTRAGLRPVGRLTEAAERVARTDDLRP  
IPVFGSDELARLTEAFNLMLRALAESRERQARLVTDAGHELRTPLTSLRTNVEL  
LMASMAPGAPRLPKQEMVDLRADVLAQIEELSTLVGDLVDLSRGDAGEVVH  
EPVDMADVDRSLERVRRRRNDILFDVEVIGWQVYGD TAGLSRMALNLMDN  
AAKWSPPGGHVGVRLSQLDASHAELVSDRGPGIPVQERRLVFERFYRSASA  
RALPGSGLGLAIVKQVVLNHGGLLRIEDTDPGGQPPGTSIYVLLPGRRMPIPQL  
PGATAGARSTDIENSRRGSANVISVESQSTRAT

> sp|O53585|GLFT2\_MYCTU Galactofuranosyl transferase Glt2  
OS=Mycobacterium tuberculosis GN=glt2 PE=1 SV=1  
MSELAASLLSRVILPRPGEPLDVRKLYLEESTTNARRAHAPTRTSLQIGAESEV  
SFATYFNAPASYWRRWTTCKSVVLRVQVTGAGRVDVYRTKATGARIFVEGH  
DFTGTEDQPAAVETE VVLQPFEDGGWVWFDITTD TAVTLHSGGWYATSPAGT  
ANIAVGIPTFNRPADCVNALRELTADPLVDQVIGAVIVPDQGERKVRDHPDFPA  
AAARLGSRLSIHDQPNLGGSGGYSRVMYEALKN TDCQQILFMDDDIRLEPDSI  
LRVLAMHRFAKAPMLVGGQMLNLQEP SHLHIMGEVVDRSIFMWTAAPHA EY  
DHDFAEYPLNDNNSRSKLLHRRIDVDYNGWWT CMIPRQVAEELGQPLPLFIK  
WDDADYGLRAAEHGYPTVTLPGA AIWHMAWSKD DAIDWQAYFHLRNRLV  
VAAMHWDGPKAQVIGLVRSHLKATL KHLACLEYSTVAIQNK AIDDFLAGPEHI  
FSILESALPQVHRIRKSYPD AVVLPAA SELPPPLHKNKAMKPPVNPLVIGYRLA  
RGIMHNLTAANPQHRRRPEFNVPTQDARWFL LCTVDGATVTTADGCGVYR  
QRDRAKMFALLWQSLRRQRQLLKRFEEMRRIYRDALPTLSSKQKWETALLPA  
ANQEPEHG

> sp|P67376|CRGA\_MYCTU Cell division protein CrgA OS=Mycobacterium tuberculosis GN=crgA PE=1 SV=1  
MPKSKVRKKNDFTVSAVSRTPMKVKVG PSSVWFVSLFIGLMLIGLIWLMVFQ  
LAAIGSQAPTALNWMAQLGPWNYAIAFAFMITG LLLLTMRWH

> sp|P69926|MMR\_MYCTU Multidrug resistance protein Mmr OS=Mycobacterium tuberculosis GN=mmr PE=1 SV=1  
MIYLYLLCAIFAEVVATSLLKSTEGFTRLWPTV GCLVGYGIAFALLALSISHGM  
QTDVAYALWSAIGTAAIVLVAVLFLGSPISVMKVVGVGLIVGVVTLNLAGAH

> sp|O05435|MVIN\_MYCTU Probable peptidoglycan biosynthesis protein MviN  
OS=Mycobacterium tuberculosis GN=mviN PE=1 SV=2  
MRPSPGEVPTASQRQPELSDAALVSHSWAMA FATLISRITGFARIVLLAILGA  
ALASSFSVANQLPNLVAALVLEATFTAIFVPVLARAEQDDPDGGA AFVRLVT  
LATTLLL GATTLSVLAAPLLVRLMLGTNPQVNEPLTTAFAYLLLPQVLVYGLSS  
VFMAILNTRNVFGPPAWAPVVNNVVAIATLAVYLAVPGELS VDPVRMGNAKL  
LVLGIGTTAGVFAQTAVLLVAIRREHISLRPLW GIDQRLKRFGAMAAAMVLYV  
LISQLGLVVG NRIASTAAASGPAIYNYTWLV LMLPFGMIGVTVLTVM PRLSR

NAAADDTPAVLADLSLATRLTMITLIPTVAFMTVGGPAIGSALFAYGNFGDVD  
AGYLGAAIALSAFTLIPYALVLLQLRVFYAREQPWTPITIIVVITGVKILGSELLAP  
HITGDPQLVAAYLGLANGLGFLAGTIVGYIILRRALRPDGGQLIGVGEARTVL  
VTVAASLLAGLLAHVADRLGLSELTAHAGSVGSLLRLSVLALIMLPILAAVTL  
CARVPEARAALDAVRARIRSRRLKTGPQTQNVLDQSSRPGPVTYPERRRLAPP  
RGKSVVHEPIRRRPPEQVARAGRAKGPEVIDRPSENASFGAASGAELPRPVAD  
ELQLDAPAGRDPGPVSRPHPSDLQNGDLPADAARGPIAFDALREPDRESSAPP  
DDVQLVPGARIANGRYRLLIFHGGVPPLQFWQALDALTALDRQVALTFVDPQGV  
LPDDVLQETLSRTLRLSRIDKPGVARVLDVVHTRAGGLVVAEWIRGGSLQEVA  
DTSPSPVGAIRAMQSLAAAADAAHRAGVALSIDHPSRVRVSDGDVVLAYPAT  
MPDANPQDDIRGIGASLYALLVNRWPLPEAGVRSGLAPAERDTAGQPIEPADID  
RDIPFQISAVAARSVQGDGGIRSASTLLNLMQQATAVADRTEVLGPIDEAPVSA  
APRTSAPNSETYTRRRRNLLIGIGAGAAVLMVALLVLA SVLSRIFGDVSGGLNK  
DELGLNAPTASTSAASSAPPGSVVKPTKVTVFSPDGGADNPGEADLAIDGNPA  
TSWKTDIYTDPVPFSPFKNGVGLMLQLPQATVVGTVAIDVASTGTKVEIRSAS  
TPTPATLEDTAVLTSATALRPGHNTISVEAAAPTSNLLVWISTLGTDTGKSQADI  
SEITIYAAS

> sp|O50452|SUGA\_MYCTU Trehalose transport system permease protein SugA  
OS=Mycobacterium tuberculosis GN=sugA PE=1 SV=1

MTSVEQRTATAVFSRTGSRMAERRLAFMLVAPAAMLMVAVTAYPIGYALWLSL  
QRNNLATPNDTAFI GLGNYHTILIDRYWWTALAVTLAITAVSVTIEFVLGLALA  
LVMHRTLIGKGLVRTAVLIPYGIVTVVASYSWYYAWTPGTGYLANLLPYDSAP  
LTQQIPSLGIVVIAEVWKTTPFMSLLL LAGLALVPEDLLRAAQVDGASAWRRL  
TKVILPMIKPAIVVALLFRTLDAFRIFDNIYVLTGGSNNTGVS SILGYDNLFKGF  
NVGLGSAISVLIFGCVAVIAFIFIKLFGAAAPGGEPSGR

> sp|P65815|HTPX\_MYCTU Protease HtpX homolog OS=Mycobacterium  
tuberculosis GN=htpX PE=1 SV=1

MTWHPHANRLKTFLLVGMSALIVAVGALFGRTALMLAALFAVGMNVYVYF  
NSDKLALRAMHAQPVSELQAPAMYRIVRELATSAHQMPRLYISDTAAPNAFA  
TGRNPRNAAVCCTTGILRILNERELRAVLGHELISHVYNRDILISCVAGALAAVI  
TALANMAMWAGMFGGNRDNANPFALLVALLGPIAATVIRMAVSRSREYQA  
DESGAVLTGDPLALASALRKISGGVQAAPLPPEPQLASQAHLMIANPFRAGERI  
GSLFSTHPPIEDRIRLRLEAMARG

> sp|A0QWG6|PIMA\_MYCS2 GDP-mannose-dependent  
alpha-(1-2)-phosphatidylinositol mannosyltransferase OS=Mycobacterium smegmatis  
(strain ATCC 700084 / mc(2)155) GN=pimA PE=1 SV=1

MRIGMVC PYSFDVPGGVQSHVLQLAEVLRDAGHEVSVLAPASPHVKLPDYV  
VSGGKAVPIPYNGSVARLRFGPATHRKVKK WIAEGDFDVLHIHEPNAPLSML  
ALQAAEGPIVATFHTSTTKSLTSLVFQGILRPYHEKIIIGRIAVSDLARRWQMEAL  
GSDAVEIPNGVDVASFADAPLLDGYPREGRTVFLFLGRYDEPRKGMVLLAALP  
KLVARFPDVEILIVGRGDEDELREQAGDLAGHLRFLGQVDDATKASAMRSAD  
VYCAPHLGGESFGIVLVEAMAAGTAVVASDLDAFRRVLADGDAGRLVPVDD  
ADGMAAALIGILEDQLRAGYVARASERVHRYDWSVSAQIMRVYETVSGA  
GIKVQVSGAANRDETAGESV

> sp|P71781|GLYTR\_MYCTU Putative glycosyltransferases OS=Mycobacterium tuberculosis GN=pimF PE=1 SV=1  
MRLSIVTTMYMSEPYVLEFYRRARAAADKITPDVEIIFVDDGSPDAALQQAVS  
LLDSDPCVRVIQLSRNFGHHKAMMTGLAHATGDLVFLIDSDLEEDPALLEPFY  
EKLISTGADVVFVGCHARRPGGWLRNFGPKIHYRASALLCDPPLHENTLTVRL  
MTADYVRSVLVQHQRERELSIAGLWQITGFYQVPM SVNKAWKGTTTYTFRRKVA  
TLVDNVT SFSNKPLVFIFYLGA AIFISSSAAGYLIIDRIFFRALQAGWASVIVSIW  
MLGGVTIFCIGLVGIYVSKVFIETKQRPTYTIIRRIYGSDLTTREPSSLKTAFPAAH  
LSNGKRV TSEPEGLATGNR

> sp|P95315|PPE36\_MYCTU Uncharacterized PPE family protein PPE36  
OS=Mycobacterium tuberculosis GN=ppe36 PE=1 SV=1  
MPNFWALPPEINSTRIYLGPGSGPILAAAQGWNALASELEKTKVGLQSALDTL  
LESYRGQSSQALIQQTLPYVQWLTTTAEHAHKTAIQLTAAANAYEQARAAMV  
PPAMVRANRVQTTVLKAINWFGQFSTRIADKEADYEQMWFQDALVMENYW  
EAVQEAIQSTSHFEDPPEMADDYDEAWMLNTVFDYHNENAKEEVIHLVPDVN  
KERGPIELVTKVDKEGTIRLVYDGEPTFSYKEHPKF

> sp|Q9F7Y9|PISA\_MYCSM CDP-diacylglycerol--inositol 3-phosphatidyltransferase  
OS=Mycobacterium smegmatis GN=pgsA PE=1 SV=1  
MSNVYLMTRAAYVKLSRPVAKAALRAGLTPDIVTLAGTAAVIGALTLFPIGQ  
LWWGAVVVSFFVLADMLDGAMAREQGGGTRFGAVLDATCDRLGDGAVFAG  
LTWWAAFGLDPSLVVATLICLVTSQVISYIKARAEASGLRGDGGIIRPERLVI  
VLIGAGLSDLPPFPLPWTLHVAMWVLA VASVV TLLQRVHAVRTSPGAMEPLHP  
ANGEKPETSEP

> sp|H8EVS9|RSKA\_MYCTE Anti-sigma-K factor RskA OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) GN=rskA PE=1 SV=1  
MTEHTDFELLELATPYALNAVSDDERADIDRRVAAAPSPVAAAFNDEVRAVRE  
TMAVVSAATTAEPHAHLRTAILDATKPEVRRQSRWR TAAFASAAAIAVGLGAF  
GLGLVLRPSPPPTVAEQVLTAPDVRTVSRPLGAGTATV VFSRDRNTGLLMN  
VAPPSRGT VYQMWLLGGAKGPRSAGTMGTA AVTPSTTATLTDLGASTAL AFT  
VEPGTGSPQPTGTILAEPLG

> sp|H8F2P5|RSMAF\_MYCTE Anti-sigma-M factor RsmA OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) GN=rsmA PE=1 SV=1  
MSAADKDPDKHSADADPPLTVELLADLQAGLLDDATAARIRSRVRS DPQAQQ  
ILRALNRVRRDVAAMGADPAWGPAARPAVVDSISAALRSARPNS SPGAAHAA  
RPHVHPVRMIAGAAGLCAVATAIGVGAVVDAPPPAPSAPTTAQHITVSKPAPVI  
PLSRPQVLDLLHHTPDYGP PGPLGDPSRRTSCLSGLGYPASTPVLGAQPIDID  
ARPAVLLVIPADTPDKLAVFAVAPHCSAADTGLLASTVVPRA

> sp|O69639|Y3671\_MYCTU Serine protease Rv3671c OS=Mycobacterium tuberculosis GN=Rv3671c PE=1 SV=1  
MTPSQWLDIAVLAVAFIAAISGWRAGALGSMLSFGGVLLGATAGVLLAPHIVS  
QISAPRAKLFAALFLILALVVVGEVAGVVLGRAVRG AIRNRPIRLIDSVIGVGV  
QLVVVLTAAWLLAMPLTQSKEQPELAAAVKGSRVLARVNEAAPT WLKTVPKR  
LSALLNTSGLPAVLEPFSRTPVIPVASPD PALVNNPVVAATEPSVVKIRSLAPRC  
QKVLEGTGFVISPDRVMTNAHV VAGSNNVT VYAGDKPF EATVVS YDPSVDVA

ILAVPHLPPPPLVFAAEPAKTGADVVLGYPGGGNFTATPARIREAIRLSGPDY  
GDPEPVTRDVYTIRADVEQDSSGGLIDLNGQVLGVVFGAAIDDAETGFVLTA  
GEVAGQLAKIGATQPVG TGACVS

> sp|H8EUF2|RIP3\_MYCTE Putative zinc metalloprotease Rip3 OS=Mycobacterium  
tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) GN=rip3 PE=2 SV=1

MRDAIPLGRIAGFVNVHWSVLVILWLFTWSLATMLPGTVGGYPVVYWLL  
GAGGAVMLLASLLAHELAAHVARRAGVSVESVTLWLFGGVTALGGEAKTP  
KAAFRIAFAGPATSLALSATFGALAITLAGVTRPAIVISVAWWLATVNLGLFN  
LLPGAPLDGGRLVRAYLWRRHGDSVRAGIGAARAGRVALVLIAGLAEFVA  
GGLVGGVWLAFIGWFIFAAAREEETRISTQQLFAGVRVADAMTAQPHTAPGWI  
NVEDFIQRYVLGERHSAYPVADRDRGSITGLVALRQLRDVAPSRSTTSVGDIAL  
PLHSVPTARPQEPLTALLERMAPLGPSSRALVTEGSAVVGIVTPSDVARLIDVY  
RLAQPEPTFTTSPQDADRFS DAG

> sp|L0T911|PBPB\_MYCTU Penicillin-binding protein PbpB OS=Mycobacterium  
tuberculosis GN=pbpB PE=1 SV=1

MSRAAPRRASQSQSTRPARGLRPPGAQEVGQRKRPGKTQKARQAQEATKSR  
PATRSDVAPAGRSTRARRTRQVVDVGTGRGASVFRHRTGNVILVLMVAATQ  
LFFLQVSHAAGLRAQAAGQLKVTDVQPAARGSI VDRNNDRLAFTIEARALTF  
QPKRIRRLQEEARKKTS AAPDPQQLRDIAQEVAGKLNKPDAAVLKKLQS  
DETFVYLARAVDPAVASAICAKYPEVGAERQDLRQYPGGS LAANVVGIDWD  
GHGLLGLSDSLDAVLGTDG SVTYDRGSDGVVIPGSYRNRHKAVHGSTVVLT  
LDNDIQFYVQQQVQQAKNLSGAHNVS AVVLD AKTGEVLAMANDNTFDPSQ  
DIGRQGDKQLGNPAVSSPFEPGSVNKIVAASAVIEHGLSSPDEVLQVPGSIQMG  
GVTVHDAWEHGVMPYTTTG VFGKSSNVGTLMLSQRVGPERY YDMLRKFG  
GQRTGVGLPGESAGLVPPIDQWSGSTFANLPIGQGLSMTLLQMTGMYQAIAN  
DGV RVPPRIKATVAPDGS RTEPRPDDIRVSAQTAQT V RQMLRAVVQRDPM  
GYQQGTGPTAGVPGYQMAGKTGTAQQINPGCGCYFDDVY WITFAGIATADNP  
RYVIGIMLDNPARNSDGAPGHSAAPLFHNIAGWLMQRENVPLSPDPGPPLVLQ  
AT

> sp|A1KH32|ARFB\_MYCBP Uncharacterized membrane protein ArfB

OS=Mycobacterium bovis (strain BCG / Pasteur 1173P2) GN=arfB PE=2 SV=1

MDFVIQWSCYLLAFLGGS AVAVVVVTL SIKRASRDEGAAEAPSAAETGAQ

> sp|Q02251|MCAS\_MYCBO Mycocerosic acid synthase OS=Mycobacterium bovis  
(strain ATCC BAA-935 / AF2122/97) GN=mas PE=1 SV=2

MESRVTPVAVIGMGCRLPGGINS PKLWESLLRGDDL VTEIPPDRWDADDYY  
DPEPGVPGRSVSRWGGFLDDVAGFDAEFFGISEREATSIDPQQRLLETSWEAI  
EHAGLDPASLAGSSTAVFTGLTHEDYLVLT TTAGGLASPYVVTGLNNSVASGRI  
AHTLGLHGPA MTFDTACSSGLMAVHLACRSLHDGEADLALAGGCAVLLEPH  
ACVAASAQGMLSSTGRCHSFDADADGFVRSEGCAMVLLKRLPDALRDGNRIF  
AVVRGTATNQDGR TETLTMPSEDAQVAVYRAALAAAGVQPETVGVVEAHGT  
GTPIGDPIEYRSLARVYGAGTPCALGSAKSNMGHSTASAGTVGLIKAILSLRH  
GVVPPLLHFNRLPDELSDVETGLFVPQAVTPWPNGNDHTPKRVAVSSFGMSGT  
NVHAIVEEAPAEASAPESSPGDAE VGPRLFMLSSTSSDALRQTARQLATWVEE  
HQDCVAASDLAYTLARGRAHRPVRTAVVAANLPELVEGLREVADGDALYDAA

VGHGDRGPVWVFSGQGSQWAAMGTQLLASEPVFAATIAKLEPVIAAESGFSV  
TEAITAQQTVTGIDKVQPAVFAVQVALAATMEQTYGVRPGAVVGHSMGESAA  
AVVAGALSLEDAARVICRRSKLMTRIAGAGAMGSVELPAKQVNSELMARGID  
DVVVSVVASPQSTVIGGTSDTVRLIARWEQRDVMAREVAVDVASHSPQVDPI  
LDDLAALADIAPMTPKVPYYSATLFDPREQPVCDGAYWVDNLRNTVQFAA  
AVQAAMEDGYRVFAELSPHPLLTHAVEQTGRSLDMSVAALAGMRREQPLPHG  
LRGLLTELHRAGAALDYSALYPAGRLVDAPLPAWTHARLFIDDDGQEQRAGG  
ACTITVHPLLGSVRLTEEPERHVWQGDVGTSLVSWLSDHQVHNVAALPGAA  
YCEMALAAAAEVFGEEAEVRDITFEQMLLLDEQTPIDAVASIDAPGVVNFTVE  
TNRDGETTRHATAALRAAEDDCPPPGYDITALLQAHPHAVNGTAMRESFAER  
GVTLGAAFGGLTTAHTAEAGAATVLAEVALPASIRFQQGAYRIHPALLDACFQ  
SVGAGVQAGTATGGLLLPLGVRSLRAYGPTRNARYCYTRLTKAFNDGTRGGE  
ADLDVLDHEGTVLLAVRGLRMGTGTSENDERDRLVSERLLTLGWQQRALPE  
VGDGEAGSWLLIDTSNAVDTPDMLASTLTDALKSHGPQGTECASLSWSVQDT  
PPNDQAGLEKLGSQLRGRDGVVIVYGPRVGPDEHSLLAGREQVRHLVRITR  
ELAEFEGELPRLFVVTRQAQIVKPHDSGERANLEQAGLRGLLRVISSEHPMLR  
TTLIDVDEHTDVERVAQQLSGSEEDETAWRNGDWYVARLTPSPLGHEERRTA  
VLDPDHDGMRVQVRRPGDLQTLFVASDRVPPGPGQIEVAVSMSSINFADVLI  
AFGRFPIIDDREPLGMDFVGVVTAVGEGVTGHQVGDRVGGFSEGWCWRTFL  
TC DANLAVTLPPGLTDEQAITAATAHATAWYGLNDLAQIKAGDKVLIHSATGG  
VGQAAISIARAKGAEIFATAGNPAKRAMLRDMGVEHVYDSRSVEFAEQIRRD  
DGYGVDIVLNSLTGAAQRAGLELLAFGGRFVEIGKADVGNTRLGLFPFRRG  
LTFYYLDLALMSVTQPDRVRELLATVFKLTAADGVLTAPOCTHYPLAEAADAIR  
AMSNAEHTGKLVLDVPRSGRRSVAVTPEQAPLYRRDGSYIITGGLGGLGLFFA  
SKLAAAGCGRIVLTARSQPNPKARQTIEGLRAAGADIVVECGNIAEPDTADRL  
VSAATATGLPLRGVLHSAAVVEDATLTNITDELIDRDWSPKVFGSWNLHRATL  
GQPLDWFCFLFSSGAALLGSPGQGAYAAANSWVDVFAHWRRRAQGLPVSAIAW  
GAWGEVGRATFLAEGGEIMITPEEGAYAFETLVRHLDRAYSYIPILGAPWLAD  
LVRRSPWGEMFASTGQRSRGP SKFRMELLSLPQDEWAGRLRLLVEQASVILR  
RTIDADRSFIEYGLDSLGMLEMRTHVETETGIRLTPKVIATNNTARALAQYLAD  
TLAEEQAAAPAAS

> sp|O05462|ECCE1\_MYCTU ESX-1 secretion system protein EccE1

OS=Mycobacterium tuberculosis GN=eccE1 PE=1 SV=2

MRNPLGLRFSTGHALLASALAPPCIIAFLETRYWWAGIALASLGVIVATVTFYG  
RRITGWVAAYAWLRRRRRPPDSSSEPVGATVKPGDHVAVRWQGEFLVAVIE  
LIPRPFTPTVIVDGAHTDDMLDTGLVEELLSVHCPDLEADIVSAGYRVGNTA  
APDVVSLYQQVIGTDPAPANRRTWIVLRADPERTRKSAQRRDEGVAGLARYLV  
ASATRIADRLASHGVDAVCGRSFDDYDHATDIGFVREKWSMIKGRDAYTAAY  
AAPGGPDVWWSARADHTITRVRVAPGMAPQSTVLLTTADKPKTPRGFARLFG  
GQRPALQGQHLVANRHCQLPIGSAGVLVGETVNRCVPYMPFDDVDIALNLGD  
AQTFTQFVVRAAAAGAMVTVGPQFEEFARLIGAHIGQEVKVAWPNATTYLG  
HPGIDRVILRHNVIGTTPRHRQLPIRRVSPPEESRYQMALPK

> sp|P71993|Y1735\_MYCTU Uncharacterized membrane protein Rv1735c/MT1776

OS=Mycobacterium tuberculosis GN=Rv1735c PE=1 SV=4

MFLYVAVGSLVVARLLLYPLRPADLTPPYWVAMGATAITVLAGAHIVEMADAP  
MAIVTSGLVAGASVVFVAFGPWLIPPLVAASIWKHVHRVPLRYEATLWSVVF  
PLGMYGVGAYRLGLAAHLPIVESIGEFEGWVALAVWTITFVAMLHHLAATIGR  
SGRSSHAIGAADDTHAIICRPPRSFDHQVRAFRRNQPM

> sp|Q10789|LEP\_MYCTU Signal peptidase I OS=Mycobacterium tuberculosis  
GN=lepB PE=1 SV=1

MTETTDSPSERQGPAPPELSSRDPDIAGQVFDAAPFDAAPDADSEGDSKAAK  
TDEPRPAKRSTLREFAVLAVIAVVLYVMLTFVARPYLIPSESMEPTLHGCSTCV  
GDRIMVDKLSYRFGSPQPGDVIVFRGPPSWNVGYKSIRSHNVAVRWVQNALS  
FIGFVPPDENLKVAVGGQTVQCRSDTGLTVNGRPLKEPYLDPATMMADP  
SIYPCLGSEFGPVTVPPGRVWVMGDNRTHSADSRAHCPLLCTDDPLPGTVPVA  
NVIGKARLIVWPPSRWGVVRSVNPQQGR

> sp|P64883|MCTB\_MYCTU Copper transporter MctB OS=Mycobacterium  
tuberculosis GN=mctB PE=1 SV=1

MISLRQHAVSLAAVFLALAMGVVLGSGFFSDTLSSLRSEKRDLYTQIDRLTD  
QRDALREKLSAADNFDIQVGSRIVHDALVGKSVVIFRTPDAHDDIAAVSKIV  
GQAGGAVTATVSLTQEFVEANSAEKLSVNVSSILPAGSQLSTKLVDQGSQAG  
DLLGIALLSNADPAAPTVEQAQRDTVLAALRETGFITYQPRDRIGTANATVVV  
TGGALSTDAGNQGVSVARFAAALAPRGSGLLAGRDGSANRPAAVAVTRADA  
DMAAEISTVDDIDAEPGRITVILALHDLINGGHVGHYGTGHGAMSVTVSQ

> sp|A0QQ68|PHNE\_MYCS2 Phosphate-import permease protein PhnE  
OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=phnE PE=1  
SV=1

MTTEITRPPAPPSRPSESRRKPSLPGLLHLVAIAAVLATIVSAWAIDFVPTALIDGS  
DNIVALLQRMIPRLDDPARIGMLAVETLLMAVLGTTLAAIASVPLAFLAARNT  
TPHPAVQAVARAVITFCRAMPDLLFAVLFVRALGIGVLPGLALALHSIGMLGK  
VFADAIEQTDAGPREAVRSTGVGYFRELLNAVVPQVPSWIAMFVYRIDINLR  
MSVVLGFVGAGGIGFALQDALRGLIYPRALGIVCVILVIIAGMELLAIAIRRILL  
DPSRSNPLRDRIARFGLSGVLVGSVAFAFVLLKINPLALFTWVFPSVGIFTRMV  
PPNFDALGVDLFTAQAQTVAIGVVATAIGIALSIPAGILAARNVSPHPALYWP  
AWILVVRAPPELILAVVFVAALGLGPIAGTCALAIGSIGFLAKLVADAVEEIDPG  
PMEAVRSVGGGWWKTLFAAVLPQSMALVGSLLYFDVNVRTSTILGIVGAG  
GVGYLLFESIRTLNFDVAGAIIVIVFVIVYAIERLSGWIRSRLV

> sp|P71879|STP\_MYCTU Multidrug resistance protein stp OS=Mycobacterium  
tuberculosis GN=stp PE=1 SV=1

MNRTQLLTLIATGLGLFMIFLDALIVNVALPDIQRSFAVGEDGLQWVVASYSLG  
MAVFIMSAAATLADLDGRRRWYLIGVSLFTLGSACGLAPSIAVLTTARGAQGL  
GAAAVSVTSLALVSAAPPEAKEKARAIGIWTAIASIGTTTGPTLGGLLVDQWG  
WRSIFYVNLPMGALVFLTLCYVEESCNERARRFDLSGQLLFIVAVGALVYAVI  
EGPQIGWTSVQTIVMLWTAAVGCALFVWLERRSSNPMDLTLFRDTSYALAI  
ATICTVFFAVYGMILLTTQFLQNVRGYTPSVTGLMILPFSAAVAIVSPLVGHV  
GRIGARVPILAGLCMLMLGMLIFSEHRSSALVLVGLGLCGSGVALCLTPITT  
VAMTAVPAERAGMASGIMSQAQRAIGSTIGFAVLGSVLAAWLSATLEPHLERAV  
PDPVQRHVLAEIIDSANPRAHVGGIVPRRHIEHRDPVAIAEEDFIEGIRVALLVA

TATLAVVFLAGWRWFPRDVHTAGSDLSERLPTAMTVECAVSHMPGATWCRL  
WPA

> sp|P64895|Y1825\_MYCTU UPF0749 protein Rv1825/MT1873

OS=Mycobacterium tuberculosis GN=Rv1825 PE=1 SV=1

MSENRPEPVAE TSAATTARHSQADAGAHDAVRRGRHELHPADHPRSKVGPLR  
RTRLTEILRGGRSRLVFGTLAILLCLVLGVAVITQVRQTDSGDSLETARPADLLV  
LLDSLRQREATLNAEVIDLQNTLNALQASGNTDQAALESAQARLAALSILVGA  
VGATGPGVMITIDDPGPGVAPEVMIDVINELRAAGAEAIQINDAHRSVRVGVD  
TWVVGVPGLTVDTKVLSPPYSILAIGDPPTLAAAMNIPGGAQDGVKRVGGR  
MVVQQADRVDVTALRQPKQHQAQPVK

> sp|O07797|FAC23\_MYCTU Probable long-chain-fatty-acid--CoA ligase FadD23

OS=Mycobacterium tuberculosis GN=fadD23 PE=1 SV=1

MVSLSIPSMRQC VNLHPDGTAFYIDYERDSEGISESLTWSQVYRRTLNVAA  
EVRRHAAIGDRAVILAPQGLDYIVAFALGALQAGLIAVPLSAPLGGASDERVDA  
VVRDAKPNVLTTS AIMGDVVPRVTPPPGIASPTVAVDQLDLDSPIRSNIVDD  
SLQTTAYLQYTS GSTRTPAGVMITYKNILANFQQMISAYFADTGAVPPLDLFIM  
SWLFPYHDMGLVLGVC APIIVGCGAVLTSPVAFLQRPARWLQLMAREGQAFS  
AAPNF AFELTAAKAIDDDL AGLDLGRIKTILCGSERVHPATLKRFDVDRFSRNL  
REFAIRPAYGLAEATVYVATSQAGQPPEIRYFEPHEL SAGQAKPCATGAGTALV  
SYPLPQSPIVRIVDPNTNTECPPGTIGEIVVHGDNVAGGYWEKPDERTFGG  
ALVAPSAGTPVGPWLRTGDSGFVSEDKFFIIGRIKDLLIVYGRNHSPDDIEATIQ  
EITRGRCAAIAVPSNGVEKLVAIVELNNRGNLDTERLSFVTREVTSAISTSHGLS  
VSDLVLVAPGSIPITTS GKVRRAECKLYRHNEFTRLDAKPLQASDL

> sp|O69741|ECCD1\_MYCTU ESX-1 secretion system protein eccD1

OS=Mycobacterium tuberculosis GN=eccD1 PE=1 SV=1

MSAPAVAAGPTAAGATAARPATTRVTILTGRRMTDLVLPAAVPMETYIDDTVAV  
LSEVLEDTPADV LGGDFTAQGVWAFARPGSPPLKLDQSLDDAGVVDGSLTL  
VSVSRTERYRPLVEDVIDAIAVLDESPEFDRTALNRFVGA AIPLLTAPVIGMAM  
RAWWETGRSLWWPLAIGILGIAVLVGSFVANRFYQSGHLAECLLVTTYLLIAT  
AAALAVPLPRGVNSLGAPQVAGAATAVFLFTLMTRGGPRKRHELASFVITAIA  
VIAAAAFGYGYQDWVPAGGIAFGLFIVTNAAKLTVAVARIALPPIVVPGETVD  
NEELDPVATPEATSEETPTWQAIASVPASAVRLTERS KLAQQLLIGYVTSGL  
ILAAGAIAVVVRGHFFVHSLVVAGLITTVCGFRSRLYAERWCAWALLAATVAIP  
TGLTAKLIIWPHYAWLLLSVYLTVALVALVVVGSM AHVRRVSPVVKRTLELI  
DGAMIAAIIPMLLWITGVYD TVRNIRF

> sp|P0A595|TRHBO\_MYCTU Group 2 truncated hemoglobin G1bO

OS=Mycobacterium tuberculosis GN=g1bO PE=1 SV=1

MPKSFYDAVGGAKTFDAIVSRFYAQA EDEVLRVYPEDDLAGAEERLRMFL  
EQYWGGPRTYSEQRGHPRLRMRHAPFRISLIERDAWLRCMHTAVASIDSETLD  
DEHRRELLDYLEMAAHSLVNSPF

> sp|Q7D4V6|GLFT1\_MYCTU Galactofuranosyl transferase G1fT1

OS=Mycobacterium tuberculosis GN=g1fT1 PE=1 SV=1

MTESVFAVVVTHRRPDELAKSLDVLTAQTRLPDHLIVVDNDGCGDSPVRELVA  
GQPIATTYLGSRRNLGGAGGFALGMLHALAQQADWVWLADDDGHAQDARV

LATLLACAKEYSLAEVSPMVCNIDDPTRLAFPLRRGLVWRRRASELRTEAGQE  
LLPGIASLFNGALFRAS TLAAIGVPDLRLFIRGDEVEMHRRLIRSGLPFGTCLD  
AAYLHPCGSDEFKPILCGRMHAQYPDDPGKRFFTYRNRGYVLSQPGLRKL  
LAEWLRFGWFFLVTRRDPKGLWEWIRLRLGRREKFGKPGGSA

> sp|O07800|MMPL8\_MYCTU Membrane transport protein mmpL8

OS=Mycobacterium tuberculosis GN=mmpL8 PE=1 SV=2

MCDVLMQPVRTPRPSTNLRSKPLRPTGDGGVFPRLGRLIVRRPWVIAFWVA  
LAGLLAPTVP SLDAISRHPVAILPSDAPVLVSTRQMTAAFREAGLQSVAVVVL  
SDAKGLGAADERSYKELVDALRRDTRDVVMLQDFVTTPLRELMTSKDNQA  
WILPVG LPGDLGSTQSKQAYARVADIVEHQVAGSTLTANLTGPAATVADLNLTG  
QRDRSRIEFAITILLVILLIYGNPITMVLPLITIGMSVVVAQRLVAIAGLAGLGI  
ANQSIIFMSGMMVGAGTDYAVFLISRYHDYLRQGADSDQAVKKALTSIGKVIA  
ASAATVAITFLGMVFTQLGILKTVGPMLGISVAVVFFAAVTL PALMVLTGRRG  
WIAPRRDLTRRFWRSSGVHIVRRPKTHLLASALVLVILAGCAGLARYNYDDR  
KTLPASVESSIGYAALDKHFPSNLIPEYLFIQSSTDLRTPKALADLEQMVQRVS  
QVPGVAMVRGITRPAGRSLEQARTSWQAGEVGSKLDEGSKQIAVHTGDIDKL  
AGGANLMASKLGDVRAQVNRAISTVGG LIDALAYLQDLLGGNRVLGELEGA  
EKLIGSMRALGDTIDADASFVANTEWASVVLGALDSSPMCTADPACASARTE  
LQRLVTARDDGTLAKISELARQLQATRAVQTLAATVSGLRGALATVIRAMGSL  
GMSSPGGVRSKINLVNKGVNDLADGSRQLAEGVQLLVDQVKKMGFGLGEAS  
AFLAMKDTATTPAMAGFYIPPELLSYATGESVKAETMPSEYRDLLGGLNVDQ  
LKKVAAAFISPDGHSIRYLIQTDLNPFTAAMDQIDAITAAARGAQPN TALADA  
KVSVVGLPVVLKDTRDYS DHDLRLIIMTV CIVLLILIVLLRAIVAPLYLIGSVI  
VSYLAALGIGVIVFQFLLGQEMHWSIPGLTFVILVAVGADYNMLLISRLREEAV  
LGVRSGVIRTVA STGGVITAAGLIMAASMYGLVFASLGSVVQGA FVLGTGLLL  
DTFLVRTVTVPAIAVLVGQANWWLPSSWRPATWWPLGRRRGRAQRTRK KPLL  
PKEEEEQSPDDDDLIGLWLHDGLRL

> sp|O06559|NARG\_MYCTU Nitrate reductase alpha subunit OS=Mycobacterium  
tuberculosis GN=narG PE=2 SV=1

MTVTPHVGGPLEELLERSGRFFTPGEFSADLRTVTRRGGREGDVFYRDRWSH  
DKVVRSTHGVNCTGSCSWKIYVKDGIITWETQQTDYPSVGPDRPEYEPGCP  
RGASFSWYSYSPTRVRYPYARGVLVEMYREAKTRLGDPVLAWADIQADPERR  
RRYQQARGKGLVRVSWAEASEMVA AAHVHTIKTYGPDRVAGFSPIPAMSMV  
SHAAGSRFVELIGGVM TSFYDWYADLPV ASPQVFGDQTDVPESGDWWDASY  
LVMWGSNPITRTPDAHWM AEARYRGAKVVVVSPDYADNTKFADEWVRCA  
AGTDTALAMAMGHVILSECYVRNQV PPFVDYVRRYTDL PFLIKLEKRGDLLV  
PGKFLTAADIGEESENA AFKPALDELNTV VVPQGS LGFRFGEDGVGKWNL  
DLGSVVPALSVEMDKAVNGDRSAELVTLPSFD TIDGHGETVSRGVPVRRAGK  
HLVCTVFDLMLAHYGVARAGLPGEWPTGYHDRTQQNTPAWQESITGV PAAQ  
AIRFAKEFARNATESGGRSMIIMGGGICHWFHSDVMYRSVLALLMLTGMGR  
NGGGWAHYVGQEKVRPLTGWQTMAMATDWSRPPRQVPGASYWYAHTDQW  
RYDGYGADKLASPVGRGRFAGKHTMDLLTSATAMGWSPFYPQFDRSSLDVA  
DEARAAGRVDYVAEQLAQHKLKLSITDPDNPVNWPRVLTVWRANLIGSS  
GKGGEYFLRHLLGTDSNVQSDPPTDGVHPRDVVWDSDIPEGKLDLIMSIDFR

MTSTTLVSDVVLPAATWYEKSDLSSSTMHPYVHSFSPAIDPPWETRSDFDAFA  
AIARAFSALAKRHLGTRTDVVLTAHQDTPDEMAYPDGTERDWLATGEVPVP  
GRMSKLTVVERDYTAIYDKWLTGLPLIDQFGMTTKGYTVHPPREVSELAAN  
FGVMNSGVAVGRPAITAKRMADVILALSGTCNGRLAVEGFLELEKRTGQRLA  
HLAEGSEERRITYADTQARPVPVITSPEWSGSESGRRYAPFTINIEHLKPFHTL  
TGRMHFYLAHDWVEELGEQLPVYRPLDMARLFNQPELGPTDDGLGLTVRY  
LTPHSKWSFHSTYQDNLYMLSLSRGGPTMWMSPGDAAKINVRDNDWVEAV  
NANGIYVCRAIVSHRMPEGVVFVYHVQERTVDTPTRETNGKRGGNHNALTRV  
RIKPSHLAGGYGQHAFAFNYLGPTGNQRDEVTVVRRRSQEVRY

> sp|P0C5C0|FTSH\_MYCTU ATP-dependent zinc metalloprotease FtsH

OS=Mycobacterium tuberculosis GN=ftsH PE=1 SV=1

MNRKNVTRTITAIAVVLLGWSFFYFSDDTRGYKPVDTSSVAITQINGDNVKS  
A QIDDREQQLRLILKKGNNETDGSEKVTKYPTGYAVDLFNALSAKNAKVSTVV  
NQGSILGELLVYVPLLLLVLGFMFSRMQGGARMGFGFGKSRAKQLSKDMP  
KTTFADVAGVDEAVEELYEIKDFLQNSRYQALGAKIPKGVLLYGPPGTGKTL  
LARAVAGEAGVPPFTISGSDVFVMFVGVGASRVRDLFEQAKQNSPCIIFVDEID  
AVGRQRGAGLGGGHDEREQTLNQLLVEMDGFDRAGVILIAATNRPDILDPA  
LLRPGRFDRQIPVSNPDLAGRRAVLRVHSHKGPMAADADLDGLAKRTVGMT  
GADLANVINEAALLTARENGTVITGPALVEAVDRVIGGPRRKGRRISEQEKKITA  
YHEGGHTLAAWAMPDIEPIYKVITLARGRTGGHAAVAVPEEDKGLRTRSEMIAQ  
LVFAMGGRAAEELVFREPTTGAVSDIEQATKIARSMVTEFGMSSKLGAVKYGS  
EHGDPFLGRTMGTQPDYSHEVAREIDEEVRKLIIEAAHTEAWEILTEYRDVLDT  
LAGELLEKETLHRPELESIFADVEKRPRMTFDDFGGRIPSDKPKPTPGELAIE  
RGEPWPQPPEPAFKAAIAQATQAAEAARS DAGQTGHGANGSPAGTHRSGDR  
QYGSTQPDYGAAGWHAPGWPPRSSHRPSYSGEPAPTYPGQPYPTGQADPGS  
DESSAEQDDEVSRTPAHG

> sp|A0R211|WECA\_MYCS2 Decaprenyl-phosphate

N-acetylglucosaminophosphotransferase OS=Mycobacterium smegmatis (strain

ATCC 700084 / mc(2)155) GN=wecA PE=1 SV=1

MLQYGAPVITATRETGMDSQVVLALS DTGAGVPLRELALVGLTAAIITYFATG  
WVRVLAIRFGAVAYPRERDVHVQPTPRMGGLAMYIGVASAVLLASQLPALTR  
GFVYSTGMPAVVAVAGGLIMAIGLIDDRWGLDALTKFAGQITAASVLVTMGVA  
WSVLYPIGGVGTIVLDQVSSILLTLALTVSIINAMNFVDGLDGLAAGLGLITAL  
AICVFSVGLLRDHGGDVLFFYPAVISVVLGACLGFLPHNFHRAKIFMGDSGS  
MLIGLMLGAASTTAAGPISQNAYGARDV FALLSPFLLVAVMLVPALDTLLAI  
VRRTRAGRSPLSPDKMHLHHRLQLIGHSHRRAVLLIYLWVGIIAFGAASTIFFD  
PGQTAMVMGVAIVVAIVVTLIPLLRGPDGAQEP

> sp|P0A5P2|CFP6\_MYCTU Low molecular weight protein antigen 6

OS=Mycobacterium tuberculosis GN=cfp6 PE=1 SV=1

MAHFAVGFLTGLLVPVLTWPVSAPLLVIPVALSASIIRLRTLADERGVTVRTL  
V GSRAVRWDDIDGLRFHRGSWARATLKDGTRELRLPAVTFATLPHLTEASSGRVP  
NPYR

> sp|P0A5F9|Y2004\_MYCTU Uncharacterized protein Rv2004c/MT2060

OS=Mycobacterium tuberculosis GN=Rv2004c PE=1 SV=1

MDSPTNDGTCDAHPVTDEPFIDVREHTAVVVLAGDRAFKAKKPVVTFDCDF  
RTAEQRERACIREFELNSRLAAQSYLGHIAHLSDPSSGGHAEPVVVMRRYRDKQ  
RLASMVTAGLPVEGALDAIAEVLARFHQRAQRNRCIDTQGEVGAVARRWHE  
NLAELRHHADKVVSGDVIRRIEHMVDEFVSGREVLVAFAGRIKEGCIVDGHADL  
LADDIFLVDGEPALLDCLEFEDELRYLDRIDDA AFLAMDLEFLGRKDLGDYFL  
AGYAVRSGDTAPASLRDFYIAYRAVVRKVECVRFSSQKPEAAADAVRHIIA  
TQHLQHATVRLALVGGNPGTGKSTLARGVAELVGAQVISTDDVRRRLRDCGV  
ITGEPGVLDSGLYSRANVVAVYQEALRKARLLLGSVILDTGTDGDPQMR  
CARRLAADTHSAIVEFRCSATVDVMADRIVARAGGNSDATAEIAAALAAARQA  
DWDTGHRIDTAGPRERSVGQAYHIWRS

> sp|P0A564|ESXA\_MYCTU 6 kDa early secretory antigenic target

OS=Mycobacterium tuberculosis GN=esxA PE=1 SV=2

MTEQQWNFAGIEAAASAIQGNVTSIHSLLDEGKQSLTKLAAAWGGSGSEAYQ  
GVQQKWDATATELNALQNLARTISEAGQAMASTEAGNVVTGMFA

> sp|P0A4V4|A85C\_MYCTU Diacylglycerol acyltransferase/mycolyltransferase

Ag85C OS=Mycobacterium tuberculosis GN=fbpC PE=1 SV=1

MTFFEQVRRRLRSAATTLPRRLAIAAMGAVLVYGLVGTFFGGPATAGAFSRPGLP  
VEYLQVPSASMGRDIKVQFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEE  
YYQSGLSVIMPVGGQSSFYTDWYQPSQSNQNYTYKWETFLTREMPAWLQA  
NKGVSPTGNAAVGLSMSGGSALILAAAYPQQFPYAASLSGFLNPSEGWWPTLI  
GLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTRIWVYCGNG  
TPSDLGGDNIPAKFLEGLTLRTNQTFRDTYAADGGRNGVFNFPNGTHSWPY  
WNEQLVAMKADIQHVLNGATPPAAPAAPAA

> sp|P0A618|MPT53\_MYCTU Soluble secreted antigen MPT53 OS=Mycobacterium  
tuberculosis GN=mpt53 PE=1 SV=1

MSLRLVSPKAFADGIVAVAIAVVLMFGLANTPRAVAADERLQFTATTLSGAPF  
DGASLQKPAVLWFWTPWCPCNAEAPSLSQVAAANPAVTFVGIATRADVGA  
MQSFVSKYNLNFNLNDADGVIWARYNVPWQPAFVFYRADGTSTFVNNPTA  
AMSQDELSGRVAALTS

> sp|P0A5Q4|MP64\_MYCTU Immunogenic protein MPT64 OS=Mycobacterium  
tuberculosis GN=mpt64 PE=1 SV=1

MRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINI  
SLPSYYPDQKSLENYIAQTRDKFLSAATSSTPREAPYELNITSATYQSAIPPRGT  
QAVVLKVYQNAGGTHPTTTYKAFDWDQAYRKPITYDTLWQADTDPLPVVFP  
VQGELSKQTGQQVSIAPNAGLDPVNYQNFVAVTNDGVIFFFNPGELLPEAAGPT  
QVLVPRSAIDSM

> sp|P0A566|ESXB\_MYCTU ESAT-6-like protein EsxB OS=Mycobacterium  
tuberculosis GN=esxB PE=1 SV=2

MAEMKTDAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAA  
QAAVVRVFQEAANKKQKQELDEISTNIRQAGVQYSRADEEQQALSSQMGF

> sp|A0QX22|RIPA\_MYCS2 Peptidoglycan endopeptidase RipA OS=Mycobacterium  
smegmatis (strain ATCC 700084 / mc(2)155) GN=ripA PE=1 SV=1

MRRTVRALATRVHGRVCAVPLVVGMLLATALYGGGPAADPAAPDNLATLVA  
KVASADQKLQELGAAIQTQQETVNKAIVDVQAARDAAAAAQRELEAGQRGV

ADANAAIEAAQKRFDSSFAAATYMNGPSRSYLTATDPADIVNTTATGQALIASS  
QQVMAKLQRARTEQVNRESAARLAKEKADQAARDAESSQDNAVAALKQAQ  
QTFNAQQGELERLAAERAAAQAELDSVRKVSATGNAAPAAAPAAAPAAAP  
APVPNSAPAPVPGAQPNPQAAAGNWDRAPSGPASSGQNWAVWDPTLPAIPSA  
FVSGDPIAIIAVLGIASSTAQVTADMGRSFLQKLGILPTPTGFTNGAIPRVYGR  
EAVEYVIRRGMSQIGVPYSWGGGNAAGPSRGIDSGAGTVGFDCSGLMLYMFA  
GVGIKLDHYSGSQYNAGRKIPSSQMRRGDMIFYGPNASQHVAMYLGNQML  
EAPYTGSHVKVSPVRTSGMTPYVTRLIEY

> sp|O06186|HRP1\_MYCTU Hypoxic response protein 1 OS=Mycobacterium  
tuberculosis GN=hrp1 PE=1 SV=1

MTTARDIMNAGVTCVGEHETLAAAQYMRHDIGALPICGDDDRLHGMLTD  
RDIVIKGLAAGLDPNTATAGELARDSIYYVDANASIQEMLNVMEEHQVRRVP  
VISEHRLVGIVTEADIARHLPEHAIVQFVKAICSPMALAS

> sp|O53526|DAGK\_MYCTU Diacylglycerol kinase OS=Mycobacterium  
tuberculosis GN=dagK PE=1 SV=1

MSAGQLRRHEIGKVTALTNPLSGHGAAVKAAHGAIARLKHRGVDDVVEIVGG  
DAHDARHLLAAAVAKGTDAMVMTGGDGVVSNALQVLAGTDIPLGIIPAGTGN  
DHAREFGLPTKNPKAAADIVVDGWTETIDLGRIQDDNGIEKWFGTVAATGFD  
SLVNDRANRMRWPHGRMRYIAMLAEALSRLRPLPFRLVLDGTEEIVADTLA  
DFGNTRS YGGGLLICPNADHSDGLLDITMAQSDSRTKLLRFLPTIFKGAHVEL  
DEVSTTRAKTVHVECPGINVYADGDFACPLPAEISAVPAALQVLRPRHG

> sp|P65087|ESPC\_MYCTU ESX-1 secretion-associated protein EspC  
OS=Mycobacterium tuberculosis GN=espC PE=1 SV=1

MTENLTVQPERLGV LASHHDNAAVDASSGVEAAAGLGESVAITHGPYCSQFN  
DTLNVYLTAHNALGSSLHTAGVDLAKSLRIA AKIYSEADEAWRKAIDGLFT

> sp|P0A5P8|MTB12\_MYCTU Low molecular weight antigen MTB12  
OS=Mycobacterium tuberculosis GN=mtb12 PE=1 SV=1

MKMVKSIAAGLTA AAAAIGAAAAGVTSIMAGGPV VYQM QP VVFGAPLPLDPA  
SAPDVPTAAQLTSLNLSLADPNVSFANKGSLVEGGIGGTEARIADHKLKKAEE  
HGDLPLSFSVTNIQPA AAGSATADVS VSGPKLSSPVTQNVTFVNQGGWMLSR  
ASAMELLQAAGN

> sp|Q933K8|ESPB\_MYCTU ESX-1 secretion-associated protein EspB  
OS=Mycobacterium tuberculosis GN=espB PE=1 SV=1

MTQSQTVTVDQQEILNRANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLS  
ADNMREYLAAGAKERQRLATSLRNAAKAYGEVDEEAATALDNDGEGTVQA  
ESAGAVGGDSSAELTDTPRVATAGEPNFMDLKEAARKLETGDQGASLAHFAD  
GWNTFNLT LQGDVKRFRGFDN WEGDAATA CEASLDQQRQWILHMAKLSAA  
MAKQAQYVAQLHVWARREHPTYEDIVGLERLYAENPSARDQILPVYAEYQQR  
SEKVLTEYNNKAALEPVNPPKPPPAIKIDPPPPPEQGLIPGFLMPPSDGSGVTP  
GTGMPAAPMVPPTGSPGGGLPADTAAQLTSAGREAAALSGDVAVKAASLGGG  
GGGGVPSAPLGS AIGGAESVRPAGAGDIAGLGQGRAGGGAALGGGGMGMP  
MGA AHQGGGAKSKGSQQE DEALYTEDRAWTEAVIGNRRRQDSKESK

> sp|P0A5Q2|MP63\_MYCTU Immunogenic protein MPT63 OS=Mycobacterium  
tuberculosis GN=mpt63 PE=1 SV=1

MKLTTMIKTAVAVVAMAAIATFAAPVALAAYPITGKLGSELTMTDTVGGQVVLG  
WKVSDLKSSTAVIPGYPVAGQVWEATATVNAIRGSVTPAVSQFNARTADGINY  
RVLWQAAGPDTISGATIPQGEQSTGKIYFDVTGPSPTIVAMNNGMEDLLIWEF  
> sp|P17670|SODF\_MYCTU Superoxide dismutase [Fe] OS=Mycobacterium  
tuberculosis GN=sodB PE=1 SV=1  
MAEYTLPDLDWDYGALEPHISGQINELHHSKHHATYVKGANDAVAKLEEAR  
AKEDHSAILLNEKNLAFNLGHVNHTIWWKNLSPNGGDKPTGELAAAIAADAF  
GSFDKFRQFHAAATTVQSGSWAALGWDTLGNKLLIFQVYDHQTNFPLGIVP  
LLLLDMWEHAFYLQYKNVKVDFAKAFWNVNWADVQSRVAAATSQTKGLI  
FG

> sp|O07746|SCMU\_MYCTU Secreted chorismate mutase OS=Mycobacterium  
tuberculosis GN=Rv1885c PE=1 SV=1  
MLTRPREIYLATAVSIIGILLSLIAPLGPPLARADGTSQLAELVDAAAERLEVADP  
VAAFKWRAQLPIEDSGRVEQQLAKLGEDARSQHIDPDYVTRVFDQIRATEAI  
EYSRFSDWKLNPAAPPEPPDLSASRSAIDSLNNRMLSQIWSHWSLLSAPSCA  
AQLDRAKRDIRSRHLDSLYQRALTTATQSYCQALPPA

> sp|O06267|ESPA\_MYCTU ESX-1 secretion-associated protein EspA  
OS=Mycobacterium tuberculosis GN=espA PE=1 SV=1  
MSRAFIIDPTISAIDGLYDLLGIGIPNQQGILYSSLEYFEKALEELAAAFPGDGW  
LGSAADKYAGKNRNHVNFQELADLDRQLISLIHDQANAVQTTTRDILEGAKK  
GLEFVRPVAVDLTYIPVVGHALSAAFQAPFCAGAMAVVGGALAYLVVKTLIN  
ATQLLKLLAKLAELVAAAIAADIISDVADIKGTLGVEVWEFITNALNGLKELWDK  
LTGWVTGLFSRGSWNLESFFAGVPGLTGATSGLSQVTGLFGAAGLSASSGLAH  
ADSLASSASLPALAGIGGGSGFGGLPSLAQVHAASRQALRPRADGPVGGAAA  
EQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKYSEGAAAGT  
EDAERAPVEADAGGGQKVLVRNVV

> sp|P80069|APA\_MYCBP Alanine and proline-rich secreted protein Apa  
OS=Mycobacterium bovis (strain BCG / Pasteur 1173P2) GN=apa PE=1 SV=2  
MHQVDPNLTRRKGRLAALAIAMASASLVTVAVPATANADPEPAPPVPTTAAS  
PPSTAAAPPAPATPVAPPPAAANTPNAQPGDPNAAPPPADPNAPPPVIANP  
QPVRIDNPVGGFSFALPAGWVESDAAHLDYGSALLSKTTGDPPFPQPVPVAN  
DTRIVLGRDLQKLYASAEATDSKAAARLGSMDGFEFYMPYPGTRINQETVSLD  
ANGVSGSASYEYVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVWVWG  
TANNPVDKGAAKALAESIRPLVAPPPAPAPAPAPAPAPAGEVAPTPTPTPQ  
RTLPA

> sp|P0A4Z2|AROK\_MYCTU Shikimate kinase OS=Mycobacterium tuberculosis  
GN=aroK PE=1 SV=1  
MAPKAVLVGLPGSGKSTIGRRLAKALGVLLDVAIEQRTGRSIADIFATDGE  
QEFRRIEEDVVRAALADHDGVLSLGGGAVTSPGVRAALAGHTVVYLEISAAE  
GVRTTGGNTVRPLLAPDRAEKYRALMAKRAPLYRRVATMRVDTNRRNPGA  
VVRHILSRLQVPSPEAAT

> sp|O53454|3BHS\_MYCTU 3 beta-hydroxysteroid dehydrogenase/Delta  
5--4-isomerase OS=Mycobacterium tuberculosis GN=Rv1106c PE=1 SV=1  
MLRRMGDASLTTELGRVLVTGGAGFVGANLVTLLDRGHVRSFDRAPSLLP

AHPQLEVLQGDITDADVCAA AVDGDITIFHTAAI IELMGGASVTDEYRQRSFA  
VNVGGTENLLHAGQRAGVQRFVYTSSNSVVMGGQNIAGGDETLPYTDRFND  
LYTETKVVAERFVLAQNGVDGMLTCAIRPSGIWGNQDQTMFRKLFESVLKGH  
VKVLVGRKSARLDNSYVHNLIHGFILAA AHLVPDGTAPGQAYFINDAEPINMF  
EFARPVLEACGQRWPKMRISGPAVRWVMTGWQRLHFRFGFPAPLLEPLAVER  
LYLDNYFSIAKARRDLGYEPLFTTQQALTECLPYYVSLFEQMKNEARAEKTA  
TVKP

> sp|A0QVM0|SYP\_MYCS2 Proline--tRNA ligase OS=Mycobacterium smegmatis  
(strain ATCC 700084 / mc(2)155) GN=proS PE=1 SV=1

MITRMSSELFLRTL RDDPADAEVPSHKL LIRAGYVRAVGP GIYSWLPLGLRVL R  
KIENVVRSEMNAIGAQEILLPALLPRGPYETTNRWTEYGD TLFRLQDRRNDY  
LLGPTHEELFTLTVKGEYSSYKDFPVILYQIQTKYRDEARPRAGILRGREFVMK  
DSYSFDVDDDGLKNAYYQHREAYQRIFARLGVRYVIVSAVSGAMGGSASEEF  
LAESEVGEDTFVRCVESGYAANVEAVITRAPEAQPT EGLPEAKVYDTPDTPTIA  
TLVEWANSASLPQFEGRTVTAADTLKNVLLKTREPGGEWELLAVGVPGDREV  
DEKRLGAALPEAFALLDDADFAANPFLVKGYVGP KALQDNGVRYLVDP RVV  
HGSSWITGADAPNRHV VGLVAGRDFTPDGTIEAAEVRDGDPSPDGAGVLTSA  
RGIEIGHIFQLGRKYTDAFSADVLGEDGKPLRLTMGSYGIGVSRLVAVIAEQQH  
DQLGLRWPSVAPFDVHV VVANKDAGARAGAAELVADLDR LGHEVLFDDRQ  
ASPGVKFKDAELLGMPWIVVVGRGWADGVVELRN RFTGETREIAADGAAAE  
ISSVLAG

> sp|P0A676|URE3\_MYCTU Urease subunit gamma OS=Mycobacterium  
tuberculosis GN=ureA PE=1 SV=1

MRLTPHEQERLLLSYAAELARRRRARGRLRNHPEAIAVIADHILEGARDGRTV  
AELMASGREVLGRDDVMEGVPEMLAEVQVEATFPDGT KLVTVHQPIA

> sp|O33294|Y2752\_MYCTU Putative ribonuclease J Rv2752c OS=Mycobacterium  
tuberculosis GN=Rv2752c PE=1 SV=1

MDVDLPPPGLTSGGLRV TALGGINEIGRNMTVFEHLGRLLIIDCGVLFPGHDE  
PGVDLILPDMRHVEDRLDDIEALVLTHGHEDHIGAIPFL LKLRPDIPVVGSKFT  
LALVAEKCREYRITPVFVEVREGQSTRHG VFECEYFAVNHSTPDALAI AVYTG  
AGTILHTGDIKFDQLPPDGRPTDLP GMSRLGDTGVDLLLCDSTNAEIPGVGPS  
ESEVGPTLHRLIRGADGRVIVACFASNVD RVQQIIDA AVALGRRVSFVGRSMVR  
NMRVARQLGFLRVADSDLIDIAAAETMAPDQVVLIT TGTQGEPMSALSRMSR  
GEHRSITLTAGDLIVLSSSLIPGNEEAVFGVIDAL SKIGARVVTNAQARVHVS GH  
AYAGELLFLYNGVRPRNVMPVHGTWRMLRANAKLA ASTGVPQESILLAENG  
VSVDLVAGKASISGAVPVGKMFVDGLIAGDVG DITLGERLILSSGFVAVTVVV  
RRGTGQPLAAPHLHSRGSFSEDPKALEPAVRKVEAE LESLVAANVTDPPIAQQ  
VRRTVGKWVGETYRRQPMIVPTVIEV

> sp|A0R199|TIG\_MYCS2 Trigger factor OS=Mycobacterium smegmatis (strain  
ATCC 700084 / mc(2)155) GN=tig PE=1 SV=1

MKSTVEQLSPTRVRINVEVPFTELEPDFDRAFKE LAKQVRLPGFRPGKAPRKL  
LEARIGRGAVLEQVVNDALPSRYSEAVSTSDLKPLGQPEIEITKLEDNEELVFTA  
EVDIRPEITLPELESKITVDPIEVTDEEVD AELQSLRARFGTLKGV ERGVQEG  
DFV SIDLSATVDGNEVPEAATEGLSHEVSGQLIDGLDEA IIGLKADESKTFTT

KLVAGEYAGQDAEVTVTVKSVKERELPEPDDEFAQLASEYDTIEELRNSLVDQ  
VRRLLKSVQQAQEQIRDKAIEALLEQTEVPLPEKIVQAQIDEVVHNAIHGLDHDE  
EKFAEQLAEQGSREEFDAETRTEAEKAVKTQLLMDAVADKLEIQVSQNDLTE  
RLVLMRQYGLEPQQLIQILQQNNQLPAMFADVRRGLTIAAVVHAATVTDTD  
GNVIDTMEFFGPSGEQAAEDSAEESTDAAEGEAAEDADDDTK

> sp|A5U4I2|MURD\_MYCTA UDP-N-acetylmuramoylalanine--D-glutamate ligase  
OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=murD PE=1  
SV=1

MLDPLGPGAPVLVAGGRVTGQAVAAVLTFRGATPTVCDDDPVMLRPHAERGL  
PTVSSSDAVQQITGYALVVASPGFSPATPLLAAGVPIWGDVELAWRLDA  
AGCYGPPRSWLVTGTNGKTTTTTSMHLAMLIAGGRRVLCGNIGSAVLVDVLD  
EPAELLEVELSSFQLHWAPSLRPEAGAVLNIAEDHLDWHATMAEYTAARV  
LTGGVAVAGLDDSRAAALLDGSPAQVRVGFRLGEPAAARELGVRDAHLVDRAF  
SDDLTLPLVASIPVPGPVGVLDALAAALARSVGVPAIAADAVTSFRVGRHR  
AEVVAVADGITYVDDSKATNPHAARASVLAYPRVWIAGGLLKGASLHAEVA  
AMASRLVGAVLIGRDRAVAEALS RHAPDVPVQV VAGEDTGM PATVEVPVA  
CVLDVAKDDKAGETVGAAVMTAAVAAARRMAQPGDTVLLAPAGASFDQFTG  
YADRGEAFATAVRAVIR

> sp|P0A5S6|PPNK\_MYCTU Inorganic polyphosphate/ATP-NAD kinase  
OS=Mycobacterium tuberculosis GN=ppnK PE=1 SV=1

MTAHRSVLLVHTGRDEATETARRVEKVLGDNKIALRVLSAEAVDRGSLHLA  
PDDMRAMGVEIEVVDADQHAADGCELVLVLGGDGTFLRAAELARNASIPVL  
GVNLGRIGFLAEAEAEIDA VLEHVVAQDYRVEDRLTLDVVVRQGGRIVNRG  
WALNEVSLEKGPRLGVLGVVVEIDGRPVS AFGCDGVLVSTPTGSTAYAFSAGG  
PVLWPDLEAILVVPNNAHALFGRPMVTSPEATIAIEIEADGHDALVFCDGRE  
MLIPAGSRLEVTRCVTSVKWARLDSAPFTDRLVRFRLPVTGWRGK

> sp|O50399|DNAE2\_MYCTU Error-prone DNA polymerase OS=Mycobacterium  
tuberculosis GN=dnaE2 PE=2 SV=4

MFDILWNVGWSNGPPSWAEMERVLNGKPRHAGVPAFDADGDVPRSRKRGA  
YQPPGRERVGSSVAYAE LHAHSAYSFLDGASTPEELVEEAARLGLCALALTDH  
DGLYGAVRFAEAAAELDVRTVFGAELSLGATARTERPDPPGPHLLVLARGPEG  
YRRLSRQLAAAHLAGGEK GKPRYDFDALTEAAGGHWHILTGCRKGHVRQAL  
SQGGPAAQRALADLVDRFTPSRVSIELTHHGHPLDDERNAALAGLAPRFGV  
GIVATTGAHFADPSRGR LAMAMA AIRARRSLDSAAGWLAPLGG AHLRS GEE  
MARLFAWCPEAVTAAAELGERCA FGLQLIAPRLPPFDVDPDGHTEDSWLRS LV  
MAGARERYGPPKSAPRAYSQIEHELKVIAQLRFPGYFLVVHDITRFCRDNDILC  
QGRGSAANSV CYALGVTA VDPVANELLFERFLSPARDGPPDIDIDIESDQREK  
VIQYVYHKYGRDYAAQVANVITYRGRSAVRDMARALGFSPGQQDAWSKQVS  
HWTGQADDVDGIPEQVIDLATQIRNLPRHLGIHSGMVICDRPIADVCPVEWA  
RMANRSVLQWDKDDCAAIGLVKFDLLGLGMLSALHYAKDLVAEHK GIEVDL  
ARLDLSEPAVYEMLARADSVGVFQVESRAQMATL PRLKPRVFDLVVEVALIR  
PGPIQGGSVHPYIRRRNGVDPVIYEHPSMAPALRKT LGVPLFQEQLMQLAVDC  
AGFSAEADQLRRAMGSKRSTERMRRLRGRFYDGMRALH GAPDEVIDRIYE  
KLEAFANFGFPESHALS FASLVFYSAWFKLHHPAAFC AALLRAQPMGFYSPQS

LVADARRHGVAVHGPCVNASLAHATCENAGTEVRLGLGAVRYLGAELAELKLV  
AERTANGPFTSLPDLTSRVQLSVPQVEALATAGALGCFGMSRREALWAAGAA  
ATGRPDRLPGVGGSSSHIPALPGMSELELAAADVWATGVSPDSYPTQFLRADLD  
AMGVLPAERLGSVSDGDRVLIAGAVTHRQRPATAQGVTFINLEDETGMVNVL  
CTPGVWARHRKLAHTAPALLIRGQVQNASGAI TVVAERMGRLLTAVGARSRD  
FR

> sp|P65929|PYRH\_MYCTU Uridylate kinase OS=Mycobacterium tuberculosis  
GN=pyrH PE=1 SV=1

MTEPDVAGAPASKPEPASTGAASAAQLSGYSRVLLKLGEMFGGGQVGLDPD  
VVAQVARQIADVVRGGVQIAVVIGGGNFFRGAQLQQLGMERTRSDYMGMLG  
TVMNSLALQDFLEKEGIVTRVQTAITMGQVAEPYLPLRAVRHLEKGRVVIFGA  
GMGLPYFSTDTTAAQRALEIGADVVLMAKAVDGVFAEDPRVNPEAELLTAVS  
HREVLDRGLRVADATAFSLCMDNGMPILVFNLLTDGNIARAVRGEKIGTLVTT

> sp|P0A662|URE2\_MYCTU Urease subunit beta OS=Mycobacterium tuberculosis  
GN=ureB PE=1 SV=1

MIPGEIFYGSGDIEMNAAALSRLQMRIINAGDRPVQVGSHVHLPQANRALSFD  
RATAHGYRLDIPAATAVRFEPGIPQIVGLVPLGGRREV PGLTLNPPGRLDR

> sp|P0A660|URE1\_MYCTU Urease subunit alpha OS=Mycobacterium tuberculosis  
GN=ureC PE=1 SV=3

MARLSRERYAQLYGPTTGDRIRLADTNLLVEVTEDRCGGPGLAGDEAVFGGG  
KVLRESMGQGRASRADGAPDTVITGAVIIDYWGIIKADIGIRDGRIVGIGKAGN  
PDIMTGVHRDLVVGPESTEIISGNRRIVTAGTV DCHVHLICPQIIVEALAAGTTTII  
GGGTGPAEGTKATTVTPGEWHLARMLES LDGWPNFALLGKGNTVNPDALW  
EQLRGGASGFKLHEDWGSTPAAIDTCLAVADVAGVQVALHSDTLNETGFVED  
TIGAIAGRSIHAYHTEGAGGGHAPDIITVAAQPNVLPSSNTPTRPHTVNTLDEH  
LDMLMVCHHLNPRIPEDLAFAESRIRPSTIAAEDVLHDMGAISMIGSDSQAMG  
RVGEVVLRTWQTAHV MKARRGALEGDPSGSQAADNNRVRRYIAKY TICPAIA  
HGM DHLIGSVEVGKLADLVLWEPAFFGVRPHVVLKGGAIWAAMGDANASI  
PTPQPVLPRPMFGAAAATAAATSVHFVAPQSIDARLADRLAVNRGLAPVADVR  
AVGKTDLPLNDALPSIEVDPDTFTVRIDGQVWQPQPAELPMTQRYFLF

> sp|P0A5L8|NAT\_MYCTU Arylamine N-acetyltransferase OS=Mycobacterium  
tuberculosis GN=nat PE=1 SV=1

MALDLTAYFDRIN YRGATDPTLDVLQDLVTVHSRTIPFENLDPLLGVVDDLSP  
QALADKLV LRRRGGYCFEHNGLMGYVLAELGYRVR RFAARVVWKLAPDAP  
LPPQTH TLLGVTFPGSGGCYLVDVGF GGQTPTSPLRLETGAVQPTTHEPYRLE  
DRVDGFVLQAMVRDTWQTLYEFTTQTRPQIDLKVASWYASTHPASKFVTGLT  
AAVITDDARWNLSGRDLAVHRAGGTEKIRLADAAAVVDTLSERFGINVADIGE  
RGALETRIDELLARQPGADAP

> sp|P63803|KCY\_MYCTU Cytidylate kinase OS=Mycobacterium tuberculosis  
GN=cmk PE=1 SV=1

MSRLSAAVVAIDGPAGTGKSSVSRRLARELGARFLDTGAMYRIVTLAVLRAG  
ADPSDIAAVETIASTVQMSLGYDPDG DSCYLAGEDVSVEIRGDAVTRAVSAVS  
SVP AVRTRLVELQRTMAEGPGSIVVEGRDIGTVVFPDAPVKIFLTASAETRARR  
RNAQNVAAGLADDYDGV LADVRRRDHLDSTRAVSPLQAAGDAVIVDTS DMT

EAEVVAHLELVTRRSEAVR

> sp|P64192|G6PI\_MYCTU Glucose-6-phosphate isomerase OS=Mycobacterium tuberculosis GN=pgi PE=1 SV=1

MTSAPIPDITATPAWDALRRHHDQIGNTHLRQFFADDPGRGRELTVSVGDLYID  
YSKHRVTRETLALLIDLARTAHLEERRDQMFAGVHINTSEDRAVLHTALRLPR  
DAELVVDGQDVVTDVHAVLDAMGAFTDRLRSGEWGATGKRISTVVNIGIG  
GSDLGPVMVYQALRHYADAGISARFVSNVDPADLIATLADLDPATTLFIVASK  
TFSTLETLTNATAARRWLTDALGDAAVSRHFVAVSTNKRLVDDDFGINTDNMFG  
FWDWVGGRYSVDSAIGLSLMTVIGRDAFADFLAGFHIIDRFATAPLESNAPV  
LLGLIGLWYSNFFGAQSRTVLPYSNDLSRFPAYLQQLTMESNGKSTRADGSPV  
SADTGEIFWGEPTNGQHAFYQLLHQGTRLVPADFIGFAQPLDDLPTAEGTGS  
MHDLLMSNFFAQTQVLAFGKTAEEIAADGTPAHVVAHKVMPGNRPSTSILAS  
RLTPSVLGQLIALYEHQVFTEGVVWGIDSFDQWGVELGKTQAKALLPVITGA  
GSPPPQSDSSTDGLVRRYRTERGRAG

> sp|P65648|LSR2\_MYCTU Nucleoid-associated protein Lsr2 OS=Mycobacterium tuberculosis GN=lsr2 PE=1 SV=1

MAKKVTVTLVDDFDGSGAADETVEFGLDGVTYEIDLSTKNATKLRGDLKQW  
VAAGRRVGGRRRGRSGRGRGAIDREQSAAIREWARRNGHNVSTRGRIPAD  
VIDAYHAAT

> sp|A0QWR4|EFP\_MYCS2 Elongation factor P OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=efp PE=1 SV=1

MASTADFKNGLVLQIDGQLWQIVEFQHVKPGKGPVVRTKLKNVVSQKVV  
KTYNAGVKVETATVDRRDATYLYRDGSDVFVMDSEDFEQHPLPESLVGRLAD  
FLLESMPVQIAFHGDGTPLYLELPVSVELEVTHTEPGLQGDRSSAGTKPATVETG  
AEIQVPLFINTGDRLKVDTRDGSYLGRVNA

> sp|P95114|DDL\_MYCTU D-alanine--D-alanine ligase OS=Mycobacterium tuberculosis GN=ddl PE=1 SV=2

MSANDRRRRRVAVVFGGRSNEHAISCVSAGSILRNLDSSRRFDVIAVGITPAG  
SWVLTDANPDALTITNRELQVKSQSGTELALPADPRRGQVLVSLPPGAGEVL  
ESVDVVPVVLHGYPYGEDGTIQGLLELAGVPYVGAGVLASAVGMDKEFTKKLL  
AADGLPVGAYAVLRPPRSTLHRQECERLGLPVFVKPARGGSSIGVSRVSSWDQ  
LPAAVARARRHDPKVIVEAAISGRELECGVLEMPDGTLEASTLGEIRVAGVRG  
REDSFYDFATKYLDDAAELDVPAKVDDQVAEAIKQLAIRAFAAIDCRGLARVD  
FFLTDDGPVINEINTMPGFTTISMYPRMWAASGVDPYPTLLATMIETTLARGVG  
LH

> sp|O05302|DAPD\_MYCTU 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase OS=Mycobacterium tuberculosis GN=dapD PE=1 SV=1

MSTVTGAAGIGLATLAADGSVLDTWFPAPELTESGTSATSRLAVSDVPVELAA  
LIGRDDDRRTETIAVRTVIGSLDDVAADPYDAYLRLHLLSHRLVAPHGLNAGG  
LFGVLTNVVWTNHGPCAIDGFEAVRARLRRRGPVTVYGVDFKFRMVDYVVP  
TGVRIADADRVLGAHLAPGTTVMHEGFVNYNAGTLGASMVEGRISAGVVV  
GDGSDVGGGASIMGTLSSGGGTHVISIGKRCLLGANSGLGISLGDDCVVEAGL  
YVTAGTRVTPDSNSVKARELSGSSNLLFRRNSVSGAVEVLARDGQGIALNE  
DLHAN

> sp|P0A512|CP51\_MYCTU Lanosterol 14-alpha demethylase OS=Mycobacterium tuberculosis GN=cyp51 PE=1 SV=1

MSAVALPRVSGGHDEHGHLEEFRTDPIGLMQRVRDECGDVGTFQLAGKQVVL  
LSGSHANEFFFRAGDDDLQAKAYPFMTPIFGEGVVFDA SPERRKEMLNAA  
LRGEQMKGHAATIEDQVRRMIADWGEAGEIDLLDFFAELTIYTSSACLIGKKF  
RDQLDGRFAKLYHELERTDPLAYVDPYLPPIESFRRRDEARNGLVALVADIMN  
GRIANPPTDKSDRDMLDVLIKAVKAETGTPRFSADEITGMFISMMFAGHHTSSG  
TASWTLIELMRHRDAYAAVIDELDELYGDGRSVSFHALRQIPQLENVLKETLR  
LHPPLIILMRVAKGEFEVQGHRIHEGDLVAASPAISNRIPEDFPDPHDFVPARYE  
QPRQEDLLNRWTWIPFGAGRHRVCVGAFAIMQIKAFS VLLREYEFEMAQPPE  
SYRNDHSMVQVLAQPACVRYRRRTGV

> sp|P64326|MFD\_MYCTU Transcription-repair-coupling factor OS=Mycobacterium tuberculosis GN=mfd PE=1 SV=1

MTAPGPACSDTPIAGLVELALSAPTFFQQLMQRAGGRPDELTLIAPASARLLVAS  
ALARQGPLLVTATGREADDLAEELRGVFGDAVALLPSWETLPHERLSPGVD  
TVGTRLMALRRLAHPDDAQLGPPLGVVVTSVRSLLQPMTPQLGMMEPLTLTV  
GDESPFDGVVARLVELAYTRVDMVGRGGEFAVRGGILDIFAPTAEHVVRVEFW  
GDEITEMRMFSVADQRSIPEIDIHTLVAFACRELLLEDVRRARAQAARHPAA  
ESTVTGSASDMLAKLAEGIAVDGMEAVLPVLWSDGHALLTDQLPDGTPVLC  
DPEKVRTRAADLIRTGREFLEASWSVAALGTAENQAPVDVEQLGGSGFVELD  
QVRAAAARTGHPWWTSLQSDSAIELDVRAAPSARGHQRDIDEIFAMLRRAH  
IATGGYAALVAPGTGTAHRVVERLSESDTPAGMLDPGQAPKPGVGVVLQGPL  
RDGVIIPGANLVVITETDLTGSRSVAAEGKRLAAKRRNIVDPLALTAGDLVVH  
DQHIGIRFVEMVERTVGGARREYLVEYASAKRGGGAKNTDKLYVPMDSL  
QLSRYVGGQAPALSRLGGSDWANTKTKARRAVREIAGELVSLYAKRQASPGH  
AFSPDTPWQAELEDAFGFTETVDQLTAIEEVKADMEKPIPMDRVICGDVGYG  
KTEIAVRAAFKAVQDGKQVAVLVPTLLADQHLQTFGERMSGFPVTIKGLSRF  
TDAAESRAVIDGLADGSVDIVIGTHRLLQTGVRWKDLGLVVVDEEQRFGVEH  
KEHIKSLRTHVDVLTMSATPIPRTEMLSLAGIREMSTILTPPEERYPVLTYYVGP  
DDKQIAAALRRELLRDGQAFYVHNRVSSIDAAAARVRELVPEARVVVAHQ  
MPEDLLETTVQRFWNREHDILVCTTIVETGLDISNANTLIVERADTFGLSQLHQ  
LRGRVGRSRERGYAYFLYPPQVPLTETAYDRLATIAQNNELGAGMAVALKDLE  
IRGAGNVLGIEQSGHVAGVGFVLYVRLVGEALETYRDAYRAAADGQTVRTAE  
EPKDVRIDLVPDAHLPPDYIASDRLRLEGYRRLAAASSDREVAAVDELTDY  
GALPEPARRLAAVARLRLCRGSGITDVTAASAATVRLSPLTLPDSAQVRLKR  
MYPGAHYRATTATVQVPIPRAGGLGAPRIRDVELVQMVADLITALAGKPRQHI  
GITNPSPPGEDGRGRNTTIKERQP

> sp|P84284|NDK\_MYCTU Nucleoside diphosphate kinase OS=Mycobacterium tuberculosis GN=ndkA PE=1 SV=1

MTERTLVLIKPDGIERQLIGEIISRIERKGLTIAALQLRTVSAELASQHYAEHEGK  
PFFGSLLEFITS GPVVAIVEGTRAIAAVRQLAGGTDPVQAAAPGTIRGDFALE  
TQFNLVHGSDSAESAQREIALWFPGA

> sp|P64368|HIS7\_MYCTU Imidazoleglycerol-phosphate dehydratase  
OS=Mycobacterium tuberculosis GN=hisB PE=1 SV=1

MTTQTAKASRRARIERTRESDIVIELDLDTGTGQVAVDTGVPFYDHMLTALG  
SHASFDLTVRATGDVEIEAHHTIEDTAIALGTALGQALGDKRGIRRFGDAPFIPM  
DETLAHA AVDL SGRPYCVHTGEPDHLQHTTIAGSSVPYHTVINRHVFESLAAN  
ARIALHVRVLYGRDPHHITEAQYKAVARALRQAVEPDPRVSGVPSTKGAL

> sp|A0QV39|RIMM\_MYCS2 Ribosome maturation factor RimM

OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=rinM PE=1  
SV=1

MDLVVGRVVKAHGISGEVVVEIRTDDPEARFAPGAVLRGRPRSGAEREYTIES  
VRAHGGRLVRLAGVADRNGADELRGTVFLVDTAELPAIDDPDEFYDHELEG  
MRVVTVD DAPV GKV A E V L H T A G G E I L A V K A D E G G R E I L V P F V G A I V T S V S R Q  
NATIVIDPPEGLDLA

> sp|A0QRN6|HUTI\_MYCS2 Imidazolonepropionase OS=Mycobacterium  
smegmatis (strain ATCC 700084 / mc(2)155) GN=hutI PE=1 SV=1

MTLLIDNIGSLVTNDPTLDAGPLGVLRDA AVVVEDGRIAWYGATSAAPAADT  
RLDAAGRAVIPGFVDSHAHLVFAGDRSEEFAARMSGTPYQAGGIRTTVTATRD  
ATDATLKSTVTRLAAEALRSGTTTLECKSGYGLTVEQELRSLQVAAEITDEVTF  
MGAHVVPPEYAETPDDYVELVCTAMLDACAPAAKWVDVFCERGAFDLDQSR  
AILQAGIARGLQPRVHANQLGPGPGVQLAVECNAASADHVTHVSDADIAALA  
GSNTVATLLPAAEFSTRAAYPDGRRLIDAGVTVALSPDCNPGSSFTTNMPFCIA  
VAVREMHLPDEAVWAATAGGARALRRDDVGH LAVGARADLALLDAPSHIH  
LAYRPGVPLVA AVLRNGEIVWQTKEVTS

> sp|O33244|PSA\_MYCTU Proteasome subunit alpha OS=Mycobacterium  
tuberculosis GN=prcA PE=1 SV=1

MSFPYFISPEQAMRERSELARKGIARAKSVVALAYAGGVLFVAENPSRSLQKIS  
ELYDRVGFAAAGKFNEFDNLRRGGIQFADTRGYAYDRRDVTGRQLANVYAQT  
LGTIFTEQAKPYEVELCVAEVAHYGETKRPELYRITYDGSIADPHFVVMGGT  
TEPIANALKESYAENASLTDALRIAVAALRAGSADTSGGDQPTLGVASLEVAVL  
DANRPRRAFRRITGSALQALLVDQESPQSDGESSG

> sp|O69540|IPYR\_MYCLE Inorganic pyrophosphatase OS=Mycobacterium leprae  
(strain TN) GN=ppa PE=1 SV=1

MQFDVTIEIPKGQRNKYEVDHKTGRVRLDRYLYTPMAYPTDYGFIEDTLGED  
GDPLDALVLLPEPLFPGVLVEARPVGMFRMVDEHGGDDKVLCPVNDHRWD  
HIHGIIDVPTFELDAIKHFFVHYKDLEPGKFVKAADWVGRDEAEAEVQRSVE  
RFKAGGH

> sp|A0QLL2|DEOC\_MYCA1 Deoxyribose-phosphate aldolase OS=Mycobacterium  
avium (strain 104) GN=deoC PE=1 SV=1

MTPTRAQLAAFVDHTLLKPEATAADVAALVTEAAELGVYAVCVSPPMVPAAV  
QAGAGVRVASVAGFPSGKHVS AVKAHEAALAVASGAAEIDMVIDVGAALAG  
DLDGVRADIAAVRGAVGGAVLKVIVESSALLALADEHTLVRCRAAEDAGAD  
FVKTSTGFHPSGGASVRAVALMAEAVGGRLGVKASGGIRTAADALAMLDAG  
ATRLGLSGTRAVLDGLG

> sp|A5TY69|DNAA\_MYCTA Chromosomal replication initiator protein DnaA  
OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=dnaA PE=1  
SV=1

MTDDPGSGFTTVWNAVVSELNGDPKVDDGPSSDANLSAPLTPQQRAWLNLV  
QPLTIVEGFALLSVPSSFVQNEIERHLRAPITDALSRRLLGHQIQLGVRIAPPATDE  
ADDTTVPPSENPAATSPDTTTTDNDEIDDSAAARGDNQHSWPSYFTERPHNTDS  
ATAGVTSLNRRYTFDTFVIGASNRFAHAAALAI AEAPARAYNPLFIWGESGLG  
KTHLLHAAGNYAQR LFPGM RVKYVSTEEFTNDFINSLRDDRK VAFKRSYRDV  
DVLLVDDIQFIEGKEGIEQEEFFHTFN TLHNANKQIVISSDRPPKQLATLEDRLRT  
RFEWGLITDVQPPELETRIAILR KKAQMERLAVPDDVLELIASSIERNIRELEGA  
LIRVTAFASLNKTPIDKALAEIVLRDLIADANTMQISAATIMAATAEYFDTTVEE  
LRGPGKTRALAQSRQIAMYLCRELTDLSLPKIGQAFGRDHTTVMYAQRKILSE  
MAERREVFHDHVKELTTRIRQRSKR

> sp|P0A5H3|ACEA\_MYCTU Isocitrate lyase OS=Mycobacterium tuberculosis  
GN=icl PE=1 SV=1

MSVVGTPKSAEQIQEWD TNPRWKDVTRTYSAEDVVALQGSVVEEHTLARR  
GAEVLWEQLHDLEWVNALGALTGNMAVQQVRAGLKAIYLSGWQVAGDANL  
SGHTYPDQSLYPANSVPQV VRRINNALQRADQIAKIEGDTSVENWLAPIVADG  
EAGFGGALNVYELQKALIAAGVAGSHWEDQLASEKKCGHLGGKVLIP TQQHI  
RTLTSARLAADVADVPTVVIARTDAEAATLITSDVDERDQPFITGERTREGFYR  
TKNGIEPCIAKAYAPFADLIWMETGTPDLEAARQFSEAVKAEYPDQMLAY  
NCSPSFNWKKHLDDATIAKFQKELAA MGFKFQFITLAGFHALNYSMFDLAYG  
YAQNQMSAYVELQEREF AAEERGYTATKHQREVGAGYFDRIATTVPNSST  
ALTGSTEEGQFH

> sp|P0A640|RSMI\_MYCTU Ribosomal RNA small subunit methyltransferase I  
OS=Mycobacterium tuberculosis GN=rsmI PE=2 SV=1

MSSGRLLL GATPLGQPSDASPRLAAALATADVVA AEDTRRVRKLAKALDIRIG  
GRVVS LFD RVEALRV TALLDA INNGATV LVVSDAGTPVISDPGYRLVAACIDA  
GVSVTCLPGPSAVTTALVMSGLPAEKFCFEGFAPRKGAARRAWLAELAEERT  
CVFFESPRRLAACLNDAVEQLGGARPA AICRELTKVHEEVVRGSLDELAIWAA  
GGVLGEITVVVAGAAPHAELSSLIAQVEEFVAAGIRVKDACSEVAAAHPGVRT  
RQLYDAVLQSRRETGGPAQP

> sp|P0A5U4|RECA\_MYCTU Protein RecA OS=Mycobacterium tuberculosis  
GN=recA PE=1 SV=1

MTQTPDREKALELAVAQIEKSYGKGSVMRLGDEARQPISVIPTGSIALDVALGI  
GGLPRGRVIEIYGPESSGKTTVALHAVANAQAAGGVAA FIDAEHALDPDYAKK  
LGVD TDSL LVSQPDTGEQALEIADMLIRSGALDIVVIDSVAALVPRAELEGEM  
GDSHVGLQARLMSQALRKMTGALNNSGTTAIFINQLRDKIGVMFGSPETTTG  
GKALKFYASVRMDVRRVETLKDGTNAVGNRTRVKVVK NKCLAEGTRIFDPV  
TGTHRIEDVVDGRKPIHVVA AAKDGT LHARPVVS WFDQGT RDVIGLRIAGG  
AIVWATPDHKVLTEYGWRAAGELRKGDRVAQPRRFDGFGDSAPIPADHARLL  
GYLIGDGRDGWVGKTPINFINVQRALIDDVTRIAATLGCAAHPQGRISLAIA  
HRPGERNGVADLCQQAGIYGKLAW EK TIPNWFEPDIAADIVGNLLFGLFESD  
GWVSREQTGALRVGYTTTSEQLAHQIHWLLLRFGV GSTVRDYDPTQKRPSIV  
NGRRIQSKRQVFEVRISGMDNVTAF AESVPMWGPRGAALIQAIPEATQGRRRG  
SQATYLAAEMTDAVLNYLDERGVTAQEAAAMIGVASGDPRGGMKQVLGASR  
LRRDRVQALADALDDKFLHDM LAEELRYSVIREVLPTRRARTFDLEVEELHTL

VAEGVVVHNCSPFFKQAEFDILYGKGISREGSLIDMGVDQGLIRKSGAWFTYE  
GEQLGQGKENARNFLVENADVADIEKKIKEKLGIGAVVTDDPSNDGVLPAPV  
DF

> sp|A0QI26|METK\_MYCA1 S-adenosylmethionine synthase OS=Mycobacterium  
avium (strain 104) GN=metK PE=1 SV=1

MSEKGRFTSESVTEGHPDKICDAISDSVLDALLAQDPRSRVAVETLVTTGQV  
HVVGEVTTTAKEAFADITNTVRERILDIGYDSSDKGFDGASCGVNIIGIGAQSPD  
IAQGVDTAHETRVEGAADPLDAQGAGDQGLMFGYAINDTPERMPLPIALHR  
LSRRLTEVRKNGVLPYLRPDGKTQVTIEFEDDVPVRLDTVVISTQHAADIDLE  
NTLTPDIREKVLNTVNLNDLAHDTLDTSSSTRLLVNPTGKFVVGGMGDAGLTG  
RKIIVDTYGGWARHGGGAFSGKDPKVDKSAAYAMRWVAKNIVAAGLAERV  
EVQVAYAIGKAAPVGLFIETFGTATVDPVKIEKIVPEVFDLRPGAIIRDLLRPI  
YAQTAAYGHFGRTDVELPWEQLNKVDDLKRAI

> sp|A0QWQ4|SYA\_MYCS2 Alanine--tRNA ligase OS=Mycobacterium smegmatis  
(strain ATCC 700084 / mc(2)155) GN=alaS PE=1 SV=1

MQTHEIRKRFLDHFVKAGHTEVPSASVILDDPNLLFVNAGMVQFVPYFLGQR  
TPPWNRATSIQKCIPTDIDEVGITTRHNTFFQMAGNFSFGDYFKRGAIELAWT  
LLTNPVEEGGYGFDPERLWATVYLDDDEAIGLWQEVAGLPAERIQRGMADN  
YWSMGIPGPCGPSSEIYYDRGPEYGVVEGGPEANEDRYIEIWNLVFMQNERGE  
GTSKEDFEILGPLPRKNIDTGMGIERVACLLQGVDNVYETDLLRPVIDKVAVA  
PRGYGAGNHDDDVRYRIIADHTRTAAIIADGVSPGNEGRGYVLRLLRRIIRA  
AKLLGVEQPVMGDLIATVRDAMGPSYPELVTDFERINRIAVAEETA FNRTLAS  
GSKLFEDAAARATKKSATVLSGSDAFTLHDTYGFPIDLTLEMAAEAGLSVDQE  
GFRTLMAEQRQRAKADAAARKQAHTDLSAYRELVDAGPTEFTGFDELTEAT  
ILGIFVDGKRVPVSHDGLEADRVELILDRTPFYAEAGGQIADDEGTISGTGASG  
TARAAVTDVQKIARTLWAHRVNVESGEFVEGDTVTAAVDPKWRRGATQGH  
GTHMVHAALREVLGPNVAVQAGSLNRPGYLRFDNFVWQGPLSDDQRTQIEEVT  
NQAVEADYE VHTFVTELEKAKAMGAMAMFGERYPDQVRVVEIGGPFSELELC  
GGTHVHNSAQIGPVTILGESSVSGSVRRVEAYVGLDSFRHLAKERALMAGLA  
SSLKVPSEEVPARVANLVERLKA AEKELDRMLANARAAAVNAVAGAETVVK  
VRLVAQRMSGGMSANDLRSVGDVIRGKLGSEPAVVALIAEGENDAVPFVAVN  
PAAQDLGLRANDLVKQFAAPVNGRGGGKADLAQSGKGAAGIDAALAALR  
AEIGRS

> sp|A0R5E1|CSPA\_MYCS2 Probable cold shock protein A OS=Mycobacterium  
smegmatis (strain ATCC 700084 / mc(2)155) GN=cspA PE=1 SV=1

MPQGTVKWFNAEKGFIFAPEDGSADV FVHYTEIQSGFRTLEENQKVEFEV  
GQSPKGPQATGVRTI

> sp|P0A5U8|RECX\_MYCTU Regulatory protein RecX OS=Mycobacterium  
tuberculosis GN=recX PE=1 SV=1

MTVSCPPPSTSEREEQARALCLRLTARSRTAELAGQLAKRGYPEDIGNRVL  
DRLAAVGLVDDTDFAEQWVQSRRANA AKSKRALAAELHAKGVDDDDVITTVL  
GGIDAGAERGRAEKLVRARLRREVLIDDGTDEARVSRRLVAMLARRGYGQTL  
ACEVVIAELAAERERRRV

> sp|B8ZQU1|DAPF\_MYCLB Diaminopimelate epimerase OS=Mycobacterium

leprae (strain Br4923) GN=dapF PE=1 SV=1

MIFAKGHGTQNDVFVLPDVEADVTFATAQVAALCNRRQGLGADGVLRVTTA  
GAAVTAGVLEHLDPDGVSCSDWYMDYRNADGSVAQMCGNGVRVFAHYLRAS  
GLESCDEFVVGSLAGPRLVNVHHVDELNADVTVDMGKANLLGSGGPAFAVT  
VGGRRFSGVAVDVGNPHLACMDPQLSLEELAALDLGAPVHLDRVQFPDGVNI  
EVLTA PVDGMVQMRVHERGVGETRSCGTGTVA AAVAALASAGADTGTLTVR  
VPGGDVVITITDVTSYLRGPSVLVAHGELADAWWYSLARSC

> sp|A0R638|SYS\_MYCS2 Serine--tRNA ligase OS=Mycobacterium smegmatis  
(strain ATCC 700084 / mc(2)155) GN=serS PE=1 SV=1

MIDLRLLENPDIVRASQRARGEDPALVDALLAADTARRSAVSAADNLRAEQ  
KAASKLVGKASPDERPALLQRAKDLAEQVKAEEAAQAEAEQAFTA AHMAIS  
NVIFEGVPAGGEDDFVVLDTVGEPRAIENPKDHLELGESLGLIDMERGAKVSG  
SRFYFLTGAGALLQLGLLQLATQVAVQNGFTLMIPPVLRPEVMRGTGFLGAH  
ADEVYRLEADDMYLVGTSEVPLAGYHADEILDLSAGPRRYAGWSSCFRREAG  
SYGKDTRGIIRVHQFDKVEGFIYCKPEDAEAEHQRLLGWQREMLAAIEVPYR  
VIDVAAGDLGSSAARKYDCEAWVPTQQTYRELTSTSNCTTFQARRLSTRYRD  
DNGKPQIAATLNGTLATTRWLVAILENHQQPDGSRVPAALVPYVRTEVLEP

> sp|P60759|HIS1\_MYCTU ATP phosphoribosyltransferase OS=Mycobacterium  
tuberculosis GN=hisG PE=1 SV=1

MLRVAVPNKGALSEPATEILAEAGYRRRTDSKDLTVIDPVNNVEFFFLRPKDIAI  
YVGS GELDFGITGRDLVCDSGAQVRERLALGFGSSSFRYAAPAGRNWTTADL  
AGMRIATAYPNLVRKDLATKGIEATVIRLDGAVEISVQLGVADAIADVVGSGRT  
LSQHDLVAFGEPLCDSEAVLIERAGTDGQDQTEARDQLVARVQGVVFGQQYL  
MLDYDCPRSALKKATAITPGLESPTIAPLADPDWVAIRALVPRRDVNGIMDEL  
AAIGAKAILASDIRFCRF

> sp|A0QWW2|G3P\_MYCS2 Glyceraldehyde-3-phosphate dehydrogenase  
OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=gapA PE=1  
SV=1

MTIRVGVNGFGRIGRNFYRALATQKAEGKNTDIEIVAVNDLTDNATLAHLLKF  
DSILGRLPQDVSLEGDDTIVIGDTKIKALEVKEGPAALPWGDLGVDVVVESTG  
IFTNAAKAKGHLDAGAKKVIISAPATDEDITIVLGVNDDKYDGSQNIISNASCT  
TNCLGPLAKVLNDEFGIVKGLMTTIHAYTQDQNLQDGPBKDLRRARAAALNI  
VPTSTGAAKAIGLVLPKLGKLDGYALRVPIPTGSVTDLTAELAKSASVEDINA  
AMKAAAEGPLKILKYDAPIVSSDIVTDPHSSLYDAGLTKVIDNQAKVVS  
WYDNEWGYSNRLADLVALVGKSL

> sp|P65720|PHOU2\_MYCTU Phosphate-specific transport system accessory protein  
PhoU homolog 2 OS=Mycobacterium tuberculosis GN=phoU2 PE=1 SV=1

MRTAYHEQLSELSERLGEMCGLAGIAMERATQALLQADLVLAEQVSDHEKIA  
TLSARAEESAFVLLALQAPVAGDLRAIVSAIQMVADIDRMGALALHVAKIARR  
RHPQHALPEEVNGYFAEMGRVAVELGNSAQEVVLSHDPEKAAQIREEDDAM  
DDLHRHLFTVLM DREW KHGVA AAVDVTLLSRFYERFADHAVEVARRVIFQAT  
GAFP

> sp|P67071|UNG\_MYCTU Uracil-DNA glycosylase OS=Mycobacterium  
tuberculosis GN=ung PE=1 SV=1

MTARPLSELVERGWAAALEPVADQVAHMGQFLRAEIAAGRRLPAGSNVLR  
FTFPFDNVRVLIVGQDPYPTPGHAVGLSFSVAPDVRPWPRSLANIFDEYTADLG  
YPLPSNGDLTPWAQRGVLLLNRLVLRPSNPASHRGKWEAVTECAIRALAA  
RAAPLVAILWGRDASTLKPMLAAGNCVAIESPHPSPLSASRGFFGSRPFSRANE  
LLVGMGAEPIDWRLP

> sp|Q07702|GYRA\_MYCTU DNA gyrase subunit A OS=Mycobacterium  
tuberculosis GN=gyrA PE=1 SV=3

MTDTTLPDDSLDRIEVDIEQEMQRSYIDYAMSVIVGRALPEVRDGLKPVHR  
RVLYAMFDSGFRPDRSHAKSARSVAETMGNYHPHGDASIYDSLVRMAQPWSL  
RYPLVDGQGNFGSPGNDPPAAMRYTEARLTPLAMEMLREIDEETVDFIPNYDG  
RVQEPTVLPSPFPNLLANGSGGIAVGMATNIPPHNLRELADAVFWALENHDAD  
EETLAAVMGRVKGPDPFPTAGLIVGSQGTADAYKTGRGSIRMRGVVEVEEDS  
RGRTSLVITELPYQVNHDFITSIAEQVRDQGLAGISNIEDQSSDRVGLRIVIEIK  
RDAVAKVVINLYKHTQLQTSFGANMLAIVDGVPRTLRLDQLIRYYVDHQLD  
VIVRRTTYRLRKANERAHILRGLVKALDALDEVIALIRASETVDIARAGLIELL  
DIDEIQAQAILDMQLRRLAALERQRIIDDLAKIEAEIADLEDILAKPERQRGIVR  
DELAEIVDRHGDDRRTRIIAADGDVSDEDIAREDDVVVTITETGYAKRTKTDL  
YRSQKRGKGVQAGLQDDIVAHFFVCSTHDLILFFTTQGRVYRAKAYDLP  
EASRTARGQHVANLLAFQPEERIAQVIQIRGYTDAPYLVLATRNLVKKSKLT  
DFDSNRSGGIVAVNLRDNDELVGAVLCSAGDDLLVSANGQSIRFSATDEALR  
PMGRATSGVQGMRFNIDRLLSLNVVREGTYLLVATSGGYAKRTAIEEYPVQG  
RGGKGVLTVMYDRRRGRLV GALIVDDSELYAVTSGGGVIRTAARQVRKAGR  
QTKGVRLMNLGEGDTLLAIARNAEESGDDNAVDANGADQTGN

> sp|P0A5M2|NUSA\_MYCTU Transcription termination/antitermination protein  
NusA OS=Mycobacterium tuberculosis GN=nusA PE=1 SV=1

MNIDMAALHAIEVDRGISVNELLETIKSALLTAYRHTQGHQTDARIEIDRKTG  
VVRVIARETDEAGNLISEWDDTPEGFGRIAATTARQVMLQRFRDAENERTYGE  
FSTREGEIVAGVIQRDSRANARGLVVVRIGTETKASEGVIPAAEQVPGESYEHG  
NRLRCYVVGVTARGAREPLITLSRTHPNLVRKLFSLVPEIADGSVEIVAVAREA  
GHRSKIAVRSNVAGLNAKGACIGPMGQVRVNVMSSELSGEKIDIIDYDDDPARF  
VANALSPAKVVSVIDQTARAARVVVPDFQLSLAIGKEGQNARLAARLTGW  
RIDIRGDAPPPPGQPEPGVSRGMAHDR

> sp|P71590|FHAA\_MYCTU FHA domain-containing protein FhaA  
OS=Mycobacterium tuberculosis GN=fhaA PE=1 SV=1

MGSQKRLVQRVERKLEQTVGDAFARIFGGSIVPQEVEALLRREAADGIQSLQG  
NRL LAPNEYIITLGVHDFEKLADPELKSTGFARDLADYIQEQGWQTYGDVV  
VRFEQSSNLHTGQFRARGTVNPDVETHPPVIDCARPQSNHAFGAEPGVAPMS  
DNSSYRGGQGGQGRPDEYYDDRYARPQEDPRGGPDPQGGSDPRGGYPPETGG  
YPPQPGYPRRHPDQGDYPEQIGYPDQGGYPEQRGYPEQRGYPDQRGYQDQ  
GRGYPDQGGQGGYPPPYEQRPPVSPGPAAGYGAPGYDQGYRQSGGYGPPSPGG  
GQPGYGGYGEYGRGPARHEEGSYVPSGPPGPPEQRPAYPDQGGYDQGYQQG  
ATTYGRQDYGGADYTRYTESPRVPGYAPQGGGYAEPAGRDYDYGQSGAPD  
YGPAPGGYSGYGQGGYGSAGTSVTLQLDDGSGRTYQLREGSNIIGRGQDAQ  
FRLPDTGVSRRHLEIRWDGQVALLADLNSTNGTTVNNAPVQEWQLADGDVIR

LGHSEIIVRMH

> sp|A5U4H7|FTSZ\_MYCTA Cell division protein FtsZ OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ftsZ PE=1 SV=1

MTPPHNYLAVIKVVGIGGGGVNAVNRMI EQGLKGV FIAINTDAQALLMSDA  
DVKLDVGRDSTRGLGAGADPEVGRKAAEDAKDEIEELLRGADMVFTAGEG  
GGTGTGGAPVVASIARKLGALT VGVVTRPFSFEGKRRSNQAENGIAALRESCD  
TLIVIPNDRLLQMGDAAVSLMDAFRSADEVLLNGVQGITDLITTPGLINVDFA  
DVKGIMSGAGTALMGIGSARGEGRSLKAAEIAINSPLLEASMEGAQGVLMMSIA  
GGSDLGLFEINEAASLVQDAAHPDANIIFGTVIDDSLGDVVRVTVIAAGFDVSG  
PGRKPVMGETGGAHRIESAKAGKLTSTLFEPVDAVSVPLHTNGATLSIGGDDD  
DVDVPPFMRR

> sp|P0A5B1|HIS2\_MYCTU Phosphoribosyl-ATP pyrophosphatase  
OS=Mycobacterium tuberculosis GN=hisE PE=1 SV=1

MQQSLAVKTFEDLFAELGDRARTRPADSTTVAALDGGVHALGKKLLEEAGEV  
WLAAEHESNDALAE EISQLLYWTQVLMISRGLSLDDVYRKL

> sp|P67611|SYY\_MYCTU Tyrosine--tRNA ligase OS=Mycobacterium tuberculosis  
GN=tyrS PE=1 SV=1

MSGMILDELSWRGLIAQSTDLDTLAAEAQRGPMTVYAGFDPTAPSLHAGHLV  
PLLTLRRFQRAGHRPIVLAGGATGMIGDPRDVGERSLNEADTVAEWTERIRGQ  
LERFVDFDDSPMGAIVENNLEWTGSLSAIEFLRDIGKHFSVNVMLARDTIRRR  
LAGEGISYTEFSYLLQANDYVELHRRHGCTLQIGGADQWGNIIAGVRLVRQ  
KLGATVHALTVPLVTAADGTKFKGKSTGGGSLWLDPQMTSPYAWYQYFVNTA  
DADVIRYLRWFTFLSADELAELEQATAQRPPQRAAQRRLASELTVLVHGEAAT  
AAVEHASRALFGRGELARLDEATLAAALRETTVAELKPGSPDGIVDLLVASGL  
SASKGAARRTIHEGGVSVNNIRVDNEEWVPQSSDFLHGRWLVLRRGKRSIAG  
VERIG

> sp|P95313|LEU3\_MYCTU 3-isopropylmalate dehydrogenase OS=Mycobacterium  
tuberculosis GN=leuB PE=1 SV=1

MKLAIAGDGIGPEVTAEAVKVLDAVVPGVQKTSYDLGARRFHATGEVLPDSV  
VAELRNHDAILLGAIGDPSVPSGVLERGLLLRLRFELDHHINLRPARLYPGVAS  
PLSGNPGIDFVVREGTEGPYTGNGGAI RVTGTPNEVATEVSVNTAFGVRRVVA  
DAFERARRRRKHLTLVHKTNVLTFAAGLWLRTVDEVGECYPDVEVAYQHVD  
AATIHMITDPGRFDVIVTDNLF GDIITDLAAAVCGGIGLAASGNIDATRANPSM  
FEPVHGSAPDIAGQGIADPTAAIMSVALLLSHLGEHDAAARVDRAVEAHLATR  
GSERLATS DVGERIAAAL

> sp|A0QWW3|PGK\_MYCS2 Phosphoglycerate kinase OS=Mycobacterium  
smegmatis (strain ATCC 700084 / mc(2)155) GN=pgk PE=1 SV=1

MSVKTLDDLLAEGVQGRGVLRSDLNPLDDDDGNITDPGRVIASVPTLQALA  
EAGAKVIVTAHLGRPKEPDPKLSLAPVAAALGEKLGRHVQLAGDVVGTDA  
LARAEGLTGDVLLLENIRFDARETSKDDSERLSLAKALAALVEGPDGSPGVF  
VSDGFGVVHRKQASVYDVATLLPHYAGTLVAAEVKVLQQLTSSTDRPYAVVL  
GGSKVSDKLAVIENLATAKADSLIIGGMCFTFLAAQGFSVGSSLLQEEMVDTC  
RRLLEDEYADVHLPVDIVVADKFAADAEAEETVAADRIPDGKMGLDIGPGSVER  
FTALLSNAKT VFWNGPMGVFEFPAFAAGTKGVAEAIIGATGKGAFSVVGGGD

SAAAVRRLGLPEDGFSHISTGGGASLEYLEGKELPGIQVLES

> sp|P67044|TYSY\_MYCTU Thymidylate synthase OS=Mycobacterium tuberculosis  
GN=thyA PE=1 SV=1

MTPYEDLLRFVLETGTPKSDRTGTGTRSLFGQQMRYDLSAGFPLLTTKKVHF  
KSVAYELLWFLRGDSNIGWLHEHGVTIWDEWASDTGELGPIYGVQWRSWPAP  
SGEHIDQISAALDLLRTDPDSRRIIVSAWNVGEIERMALPPCHAFFQFYVADGR  
LSCQLYQRSADLFLGVFNIASYALLTHMMAAQAGLSVGEFIWTGGDCHIYD  
NHVEQVRLQLSREPRPYPKLLLADRDSIFEYTYEDIVVKNYDPHPAIKAPVAV

> sp|P64803|PDUO\_MYCTU Cob(I)yrinic acid a,c-diamide adenosyltransferase  
OS=Mycobacterium tuberculosis GN=Rv1314c PE=1 SV=1

MAVHLTRITYTRTGDDGTTGLSDMSRVAKTDARLVAYADCDEANAAIGAALAL  
GHPDTQITDVLRLQIQNDLFDAGADLSTPIVENPKHPPLRIAQSYIDRLEGWCDA  
YNAGLPALKSFVLPGGSPSALLHVARTVVRRAERSAWAAVDAHPEGVSVLP  
AKYLNRLSDLLFILSRVANPDGDVLWRPGGDRTAS

> sp|O53447|GLPX\_MYCTU Fructose-1,6-bisphosphatase class 2  
OS=Mycobacterium tuberculosis GN=glpX PE=1 SV=2

MTAEGSGSSTA AVASHDPSHTRPSRREAPDRNLAMELVRVTEAGAMAAGRW  
VGRGDKEGGDGA AVDAMRELVNSVSMRGVVVIGEGEKDHAPMLYNGEEVG  
NGDGPECDFAVDPIDGTTLMSKGMTNAISVLAVADRGTMFDP SAVFYMNKIA  
VGPDAAHVLDITAPISENIRAVAKVKDLSVRDMTVCILDRPRHAQLIHDVRAT  
GARIRLITDGDVAGAISACRPHSGTDLLAGIGGTPEGIIAAAIRCMGGAIQAQ  
LAPRDDAERRKALEAGYDLNQLVLTEDLVSGENVFFCATGVTGDLLKGVRY  
YPGGCTTHSIVMRSKSGTVRMIEAYHRLSKLNEYS AIDFTGDSSAVYPLP

> sp|Q50790|DPO3B\_MYCTU DNA polymerase III subunit beta OS=Mycobacterium  
tuberculosis GN=dnaN PE=1 SV=2

MDAATTRVGLTDLTFRLLRESFADAVSWVAKNLPARPAVPVLSGVLLTGSDNG  
LTISGFDYEVS AEAQVGA EIVSPGSVLVSGRLLSDITRALPNKPV DVHVEGNRV  
ALTTCGNARFSLPTMPVEDYPTLPTLPEETGLLPAELFAE AISQVAIAAGRDDTL  
PMLTGIRVEILGETV VLAATDRFRLAVRELKWSASSPDIEAAVLVPAKTLA EAA  
KAGIGGSDVRLSLGTGPGV GKDGLLGISNGKRSTTRLLDAEF PKFRQLLPTE  
HTAVATMDVAELIEAIKLVALVADRG AQVRMEFADGSVRLSAGADDV GRAEE  
DLVV DYAGEPLTIAFNPTYLTDGLSSLRSERVSFGFTTAGKPALLRPVSGDDR P  
VAGLNGNGPFP AVSTDYVYLLMPVRLPG

> sp|A0QVQ8|DHA\_MYCS2 Alanine dehydrogenase OS=Mycobacterium smegmatis  
(strain ATCC 700084 / mc(2)155) GN=ald PE=1 SV=1

MLVGIPTEIKNNEYRVAITPAGVAELTRRGHEVIIQAGAGEGSAISDRDFKAAG  
AEIVNTADQVWSEAE LLLKVKEPIEPEYSRMRKGQTLFTYLHLAASKPCTDAL  
LASGTTSIAYETVQTAEGALPLLAPMSEVAGRLSAQVGAYHLMRSYGGRGVL  
MGGVPGVAPAEVVVIGAGTAGYNAARVAAGMGAHVTVFDLNINTLRRVDGE  
FGGRIETRYSSSLELEEAVKKADLVIGAVLVP GAKAPKLVNTSTVAHMKPGAVL  
VDIAIDQGGCFEDSRPTTHDEPTFKVHDTIFYCVANMPGAVPRTSTFALTNSTM  
PYVLKLADKGWQAACASDSALAKGLSTHDGKLLSEAVAKDL DLPFTDAAQF  
LA

> sp|A0R006|WAG31\_MYCS2 Cell wall synthesis protein Wag31

OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=wag31 PE=1 SV=1

MPLTPADVHNVAFSKPPIGKRGYNEDEVD AFLDLVENELTRLIEENADLRQRV  
AELDQELAAARSGAGASSQATSSIPLYEPEPEPAPAPPQPVYEAPAQPAAPQSE  
DTAVRAARVLSLAQDTADRLTSTAKAEADKLLSDARAQAEAMVSDARQTAET  
TVSEARQRADAMLADAQTRSEAQLRQAQEKADALQADAERKHSEIMGTINQ  
QRTVLEGRLEQLRTFEREYRTRLKTYLESQLEELGQRGSAAPVDSSANSDASG  
FGQFNRGNN

> sp|P22487|AROA\_MYCTU 3-phosphoshikimate 1-carboxyvinyltransferase

OS=Mycobacterium tuberculosis GN=aroA PE=1 SV=1

MKTWPAPTAPTVPV RATVTVPGSKSQTNRALVLAALAAAQGRGASTISGALRS  
RDT ELM DALQTLGLRVDGVGSELT VSGRIEPGPGARVDCGLAGTVLRFV PPL  
AALGSVPVTFDGDQQARGRPIAPLLDALRELGVAVDGTGLPFRVRGNGSLAG  
GTVAIDASASSQFVSGLLLSAASFTDGLTVQHTGSSLPSAPHIAMTAAMLRQA  
GVDIDDSTPNRWQVRPGPVAARRWDIEPDLTNAVAFLSAAVVSGGTVRITGWP  
RVS VQPADHILAILRQLNAVVIHADSSLEVRGPTGYDGFVDLRAVGELTPSVA  
ALAALASPGSVSRLSGIAHLRGHETDRLAALSTEINRLGGTCRETPDGLVITAT  
PLRPGIWRAYADHRMAMAGAIIGLRVAGVEVDDIAATTKTLPEFPRLWAEMV  
GPGQGWGYPQPRSGQRARRATGQGSGG

> sp|A0QVE0|RRF\_MYCS2 Ribosome-recycling factor OS=Mycobacterium

smegmatis (strain ATCC 700084 / mc(2)155) GN=frr PE=1 SV=1

MIDETLFD AEEKMEKAVS VARDELGSIRTGRANPGMFNRINIDYYGSMT PITQ  
LASINVPEARLVVIKPYEASQLRAIEDAIRNSDLGVNPSNDGNIIRVAIPQLTEER  
RRELVKQAKSKGEDAKVSVRNIRRKAMEELSRIKKDGEAGEDEV SRAEKDLD  
KSTHTYTAQIDELVKHKESELLE V

> sp|A0QQ72|PHNF\_MYCS2 HTH-type transcriptional repressor PhnF

OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=phnF PE=1

SV=2

MTAGAAPRILKHQVVRAELDRMLDGM RIGDPFPAEREIAEQFEVARETVRQA  
LRELLIDGRVERRGRTTVVARPKIRQPLGMGSYTEAAKAQGLSAGRILVAWSD  
LTADEVLAGVLGVDVGAPVLQLERVLT TDGVRVGL ETTKLPAQRY PGLRETF  
DHEASLYAEIRSRGIAFTRTVDTIDTALPDAREAA LLGADARTPMFLLNRVSYD  
QDDVAIEQRRSLYRGDRMTFTAVMHAKNSAIVS

> sp|P0A4Y6|ARGB\_MYCTU Acetylglutamate kinase OS=Mycobacterium

tuberculosis GN=argB PE=1 SV=1

MSRIEALP THIKAQVLA EALPWLKQLHGKVVVVKYGGNAMTDDTLRRAFAA  
DMAFLRNCGIHPVVVHGGGPQITAMLRRLGIEGDFKGGFRVTTPEVLDVARM  
VLFQV GRELVNLINAHGPYAVGITGEDAQLFTAVRRSVTV DGVATDIGLVGD  
VDQVNTAAML DLVAAGRIPVVSTLAPDADGVVHNINADTAAA AVAEALGAE  
KLLMLTDIDGLYTRWPDRDSLSEIDTGTLAQLLPTLES GMV PKVEACLRAVI  
GGVPSAHIIDGRVTHCVLVELFTDAGTGTKVVRG

> sp|P96228|ESPR\_MYCTU Nucleoid-associated protein EspR OS=Mycobacterium

tuberculosis GN=espR PE=1 SV=1

MSTTFAARLNRLFDTVYPPGRGPHTSAEVIAALKAEGITMSAPYLSQLRSGNR

TNPSGATMAALANFFRIKAAYFTDDEYYEKLDKELQWLCTMRDDGVRRIAQ  
RAHGLPSAAQQKVLDRIDELRRAEGIDA

> sp|A0R692|DPS\_MYCS2 DNA protection during starvation protein

OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=dps PE=1  
SV=1

MTSFTIPGLSDKKASDVADLLQKQLSTYNDLHLTLKHVHWNVVGPNFIGVHE  
MIDPQVELVRGYADEVAERIATLGKSPKGTGAIKDRTWDDYSVERDTVQAH  
LAALDLVYNGVIEDTRKSIEKLEDLDLVSQDLLIAHAGELEKFQWFVRAHLES  
AGGQLTHEGQSTEKGAADKARRKSA

> sp|P0A514|KGUA\_MYCTU Guanylate kinase OS=Mycobacterium tuberculosis  
GN=gmk PE=1 SV=1

MSVGEGPDTKPTARGQPAAVGRVVVLSGPSAVGKSTVVRCLRERIPNLHFSVS  
ATTRAPRPGVDGVDYHFIDPTRFQQLIDQGELLEWAEIHGGLHRSGTLAQPV  
RAAAATGVPVLIEVDLAGARAIKKTMP EAVTVFLAPPSWQDLQARLIGRG TET  
ADV IQRRLDTARIELAAQGD FDKVVVNRRL ESACAELV SLLVGTAPGSP

> sp|A0QZ47|PSB\_MYCS2 Proteasome subunit beta OS=Mycobacterium smegmatis  
(strain ATCC 700084 / mc(2)155) GN=prcB PE=1 SV=2

MTWRDNQSFPQPTLNTTGIPSVVDLSSFSELLSRQAPPELLPVNRVAYGTTTPVG  
PTDAVPHGTTIVALKYPPGGVLIAGDRRSTQGNMIAGR DVQKVYITDDYTATGI  
AGTAAIAVEFARLYAVELEHYEKLEGVPLTFRGKVNRLAIMVRGNLGAALQGF  
VALPLLVG YDLDDPHPEGAGRIVSFD AAGGWNIEEGYQSVGSGSIFAKSSMK  
KLYSQVSDADSALKVAVEALYDAADDDSATGGPDLVRGIYPTAVTIGAEGAE  
VPETRIAE LAREVIESRSRTDTFGPDARRGIDARGDS

> sp|P71691|GNGF\_MYCTU Putative gluconeogenesis factor OS=Mycobacterium  
tuberculosis GN=Rv1422 PE=1 SV=1

MTDGIVALGGGHGLYATLSAARRLTPYVTAVVTVADDGGSSGRLRSEL DVVPP  
GDLRMAL AALASDSPHGR LWATILQHRFGGSGALAGHPIGNLMLAGLSEVLA  
DPVAALDELGRILGVKGRVLP MCPVALQIEADVSGLEADPRMFRLIRGQVAIA  
TTPGK VRRVRL LPTDPPATRQAVDAIMAADLVVLGPGSWFTSVIPHVLVPGLA  
AALRATSARRALVNLVAEPGETAGFSVERHLHVLAQHAPGFTVHDIIDAERV  
PSE REREQLRRTATMLQAEVHFADVARPGTPLHDPGKLA AVLDGVCARDVGA  
SEPPVAATQEIPIDGGRPRGDDAWR

> sp|A0QU63|SSRP\_MYCS2 SsrA-binding protein OS=Mycobacterium smegmatis  
(strain ATCC 700084 / mc(2)155) GN=smpB PE=1 SV=1

MTKKSASSNKKVVATNRKARHNYTILD TYEAGIVLMGTEVKSLREGQASLAD  
AFATVDDGEIWL RNVHIAEYHHGTW TNHAPRRNRKLLLHRKQIDNLIGKIRD  
GNLTLVPLSIYFTDGKVKVELALARGKQA HDKRQDLARRDAQREVIRELGRR  
AKGKI

> sp|A0R580|PANC\_MYCS2 Pantothenate synthetase OS=Mycobacterium  
smegmatis (strain ATCC 700084 / mc(2)155) GN=panC PE=1 SV=1

MTISRTPKFSAGELNVYSAPADVA AVTRALRTAGRRIVLVPTMGALHEGH LTL  
VRAAKRTPGAVVVVSIFVNPLQFGPNEDLNAYPRTLEDDLTALRAEGVEIVFTP  
TGSDMYPDGTRTSVHPGPLGDDLEGSSRPGHFAGVLTVV LKLSIVRPDRAYF  
GEKDYQQLTL LRQMVADLNVDVQIVGVPTVRES DGLALSSRNRYLDK DQRE

QAGALSAALLAGKYAAAGGAEAAALDAARAVLDEVPALVDYLQVRDPMGLP  
APAEGQARLLVAARLGRTRLIDNIAIDVGASAGIDGHPRVGNQNHHELPWRN  
> sp|P95163|BLAI\_MYCTU Transcriptional regulator BlaI OS=Mycobacterium  
tuberculosis GN=blaI PE=1 SV=1

MAKLTRLGDLERAVMDHLWSRTEPQTVRQVHEALSARRDLAYTTVMTVLQR  
LAKKNLVLQIRDDRAHRYAPVHGRDELVAGLMVDALAQAEDSGSRQAALVH  
FVERVGADEADALRRALAELEAGHGNNRPPAGAATET

> sp|P0A4Y8|ARGR\_MYCTU Arginine repressor OS=Mycobacterium tuberculosis  
GN=argR PE=1 SV=1

MSRAKAAPVAGPEVAANRAGRQARIVAILSSAQVRSQNELAALLAAEGIEVT  
QATLSRDLEELGAVKLRGADGGTGIYVVPEDGSPVRGVSGGTDRMARLLGEL  
LVSTDDSGNLAVLRTPPGAAHYLASAIDRAALPQVVGTIAGDDTILVVAREPTT  
GAQLAGMFENLR

> sp|A0R2N3|NDP\_MYCS2 NAD-dependent protein deacylase Sir2  
OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=sir2 PE=1  
SV=1

MQVTVLSGAGISAESGVPTFRDAETGLWAQVDPYEISSTDGWQRNPEKVWA  
WYLWRHYMMARVAPNEAHRVAAWEDHLDVDVVTQNIDDLHERAGSTNVY  
HLHGSLFEFRCDACGSAFEGNLPEMPEPVETIDPPVCPCSGLIRPSVWWFGEPL  
PDAAWNRSVLAVSSADVIVVGTSSIVYPAAGLPEAALAAGKPVIEVNPERTP  
LSDSATVSLRETASEALPTLLQRLPELLNRSA

> sp|A5U161|GLMU\_MYCTA Bifunctional protein GlnU OS=Mycobacterium  
tuberculosis (strain ATCC 25177 / H37Ra) GN=glnU PE=1 SV=1

MTFFPGDTAVLVLAAGPGTRMRSPTPKVLHTLAGRSMLSHVLHAIKLAQRL  
IVVLGHDHQRIAPLVGELADTLGRTIDVALQDRPLGTGHAVLCGLSALPDDYA  
GNVVVTSGDTPLLDADTLADLIATHRAVSAAVTVLTTTLDDPFYGRILRTQD  
HEVMAIVEQTDATPSQREIREVNAGVYAFDIAALRSALSRLSSNNAQQELYLT  
DVIAILRSDGQTVHASHVDDSSALVAGVNNRVQLAELASELNRRVVAHQLAG  
VTVVDPATTWIDVDVTIGRDTVIHPGTQLLGRTOIGGRCVVGPDTTLTDVAVG  
DGASVVRTHGSSSSIGDGAAVGPFTYLRPGTALGADGKLGAFVEVKNSTIGTG  
TKVPHLTYVGDADIGEYSNIGASSVFVNYDGTSKRRTTVGSHVRTGSDFMFV  
APVTIGDGAYTGAGTVVREDVPPGALAVSAGPQRNIENWVQRKRPGSPAAQA  
SKRASEMACQOPTQPPDADQTP

> sp|A0QQU5|CH601\_MYCS2 60 kDa chaperonin 1 OS=Mycobacterium smegmatis  
(strain ATCC 700084 / mc(2)155) GN=groL1 PE=1 SV=1

MAKTIAYDEEARRGLERGLNSLADAVKVTLGPKGRNVVLEKKWGAPTITND  
GVSIKEIELEDPYEKIGAELVKEVAKKTDDVAGDGTATVLAQALVREGLR  
NVAAGANPLGLKRGIEKAVEKVTTLLKSAKEVETKEQIAATAGISAGDQSIG  
DLIAEAMDKVGNVITVEESNTFGLQLELTEGMRFDKGYISGYFVTDARQ  
EAVLEDPYILLVSSKVSTVKDLLPPEKVIQSGKPLLIAEDVEGEALSTLVVVK  
IRGTFKSVAVKAPGFGDRRKAMLQDMAILTGGQVISEEVGLSLETADVSLGK  
ARKVVVTKDETTIVEGAGDAEAIQGRVAQIRAEIENSDDSDYDREKLQERLAKL  
AGGVAVIKAGAATEVELKERKHRIEDAVRNAKAAVEEGIVAGGGVALLQSAPS  
LEELSLTGDEATGANIVRVALSAPLKQIALNGGLEPGVVAEKVSNLPAGHGLN

AATGEYEDLLAAGVADPVKVTRSALQNAASIAALFLTTEAVVADKPEKAAAP  
AGDPTGGMGGMDF

> sp|P66875|METB\_MYCTU Cystathionine gamma-synthase OS=Mycobacterium  
tuberculosis GN=metB PE=1 SV=1

MSEDRTGHQGISGPATRAIHAGYRPDPATGAVNVPIYASSTFAQDGVGGGLRGG  
FEYARTGNPTRAALASLAAVEEGAFARAFSSGMAATDCALRAMLRPGDHVV  
IPDDAYGGTFRLIDKVFTRWDVQYTPVRLADLDAVGAAITPRTRLIWWVETPTN  
PLLSIADITAIAELGTDRSAKVLVDNTFASPALQQPLRLGADVVLHSTTKYIGG  
HSDVVGGALVTNDEELDEEFAFLQNGAGAVPGPFDAYLTMRGLKTLVLRMQR  
HSENACAVAEFLADHPSVSSVLYPGLPSHPGHEIAARQMRGFGGMVSVRMRA  
GRRAAQDLCAKTRVFILAESLGGVESLIEHPSAMTHASTAGSQLEVPDDLVR  
LVRL  
SVGIEDIADLLGDLEQALG

> sp|P71543|CSOR\_MYCTU Copper-sensing transcriptional repressor CsoR  
OS=Mycobacterium tuberculosis GN=csoR PE=1 SV=2

MSKELTAKKRAALNRLKTVRGHLDGIVRMLES DAYCVDVMKQISAVQSSLER  
ANRVMLHNLHLETCFSTAVLDGHGQAAIEELIDAVKFTPALTGPHARLGGAAVG  
ESATEEPMPDASNM

> sp|A0R148|PROB\_MYCS2 Glutamate 5-kinase OS=Mycobacterium smegmatis  
(strain ATCC 700084 / mc(2)155) GN=proB PE=1 SV=1

MSEHREAVRTARSVVVKIGTTALTTPSGVFDANRLASLVEAIEGRMKAGSDVV  
IVSSGAIAAGIEPLGLSKRPTDLATKQAAASVGQVALVNAWSAAFVYNRTVG  
QVLLTAHDISM RVQHNN AQRTLDRLRALHAVAIVNENDTVATNEIRFGDNDRL  
SALVAHLVGADALILLSIDIDGLYDGDPRKATPDKPARFIPEVAAQGDLDGVVA  
GRGSSLGTGGMASKLSSALLAADAGVPVLLAAAADAGRALDDASVGTVFAP  
RPERMSARKFWMRYAAESAGALTLDDGAVRAVIKQRRSLLPAGITSVTGRFH  
GGDVVDLRALDGHTVARGVVAYDQAE LASIIGRSTHELPVEMRRPAVHADDL  
VRT

> sp|P0A556|EFG\_MYCTU Elongation factor G OS=Mycobacterium tuberculosis  
GN=fusA PE=1 SV=1

MAQKDVLTDL SRVRNFGIMAHIDAGKTTTTERILY YTGINYKIGEVHDGAAT  
MDWMEQE QERGITITSAATTTFWKDNQLNIIDTPGHVDFTVEVERNLRVLDG  
AVAVFDGKEGVEPQSEQVWRQADKYDVPRICFVNKMDKIGADFYFSVRTMG  
ERLGANAVPIQLPVGAEADFE GVVDLVEMNAKVWRGETKLGETYDTVEIPAD  
LAEQAEEYRTKLLLEVVAESDEHLLKYLGG EELTVDEIKGAIRKLTIASEIYPV  
LCGSAFKNKG VQPMLDAVVDYLP SPLDVPPAIGHAPAKED EEVVRKATTDEPF  
AALAFKIATHPFFGKLT YIRVYSGTVESGSQVINATKGKKERLGKLFQMHSNK  
ENPVDRASAGHIYAVIGLKD TTTGDTLSDPNQQIVLESMTFPDPVIEVAIEPKTK  
SDQEKL SLSIQKLA EEDPTFKVHLDSETGQTVIGGMGELHLDILVDRMRREFK  
VEANVGK PQVAYKETIKRLVQNVEYTHKKQTGGSGQFAKVIINLEPFTGEEGA  
TYEFESKVTGGRIPREYIP SVDAGA QDAMQYGVLAGYPLVNLKV TLLDGAYH  
EVDSS EMAFKIAGS QVLKKA AALAQPVILEPIMAVEV TTPEDYMGD VIGDLNS  
RRGQIQAMEERAGARVVRAHVPLSEMFGYVGD LRSKTQGRANYSMVFDSYS  
EVPANVSKEIIAKATGE

> sp|A0QSS3|CH10\_MYCS2 10 kDa chaperonin OS=Mycobacterium smegmatis

(strain ATCC 700084 / mc(2)155) GN=groS PE=1 SV=1

MASVNIKPLEDKILVQANEATTTASGLVIPDTAKEKPQEGTVVAVGPGRWDE  
DGEKRIPLDVAEGDTVIYSKYGGTEIKYNGEYLLSARDVLAVVSK

> sp|P0A582|FURA\_MYCTU Transcriptional regulator FurA OS=Mycobacterium  
tuberculosis GN=furA PE=1 SV=1

MSSIPDYAEQLRTADLRVTRPRVAVLEAVNAHPHADTETIFGAVRFALPDVSRQ  
AVYDVLHALTAAGLVRKIQPSGSVARYESRVGDNHHHIVCRSCGVIADVDCAV  
GEAPCLTASDHNGFLLDEAEVIYWGLCPDCSISDTSRSH

> sp|P63810|COAA\_MYCTU Pantothenate kinase OS=Mycobacterium tuberculosis  
GN=coaA PE=1 SV=1

MSRLSESPYVEFDRRQWRALRMSTPLALTEELVGLRGLGEQIDLLEVEEVY  
LPLARLIHLQVAARQRLFAATAEFLGEPQQNPDRPVVFIIGVAGSVAVGKSTTAR  
VLQALLARWDHHPRVLDLVTDDGFLYPNAELQRRNLMHRKGFPESSYNRRALM  
RFVTSVKSGSDYACAPVYSHLHYDIIPGAEQVVRHPDILILEGLNVLQTGPTL  
MVSDLDFDFSLYVDARIEDIEQWYVSRFLAMRTTAFADPESHFHYYA AFSDSQA  
VVAAREIWRITINRPNLVENILPTRPRATLVLRKADADHSINRLRLRKL

> sp|P65880|PURA\_MYCTU Adenylosuccinate synthetase OS=Mycobacterium  
tuberculosis GN=purA PE=1 SV=1

MPAIVLIGAQWGDEGKKGKATDLLGGRVQWVVRYQGGNNAGHTVVLPTGEN  
FALHLIPSGVLTPGVTNVINGVVIDPGVLLNELRGLQDRGVDTAKLLISADA  
HLLMPYHIAIDKVTERYMGSKKIGTTGRGIGPCYQDKIARIGIRVADVLDPEQL  
THKVEAAACEFKNQVLVKIYNRKALDPAQVVDALLEQAEGFKHRIADTRLLL  
AALEAGETVLLEGSQGTLLDVDHGTYPYVTSNPTAGGA AVGSGIGPTRIGTV  
LGILKAYTTRVGSFPTELDFEHGEYLSKTGREFGVTTGRRRRCGWFD AVIA  
RYAARVNGITDYFLTKLDVLSLESVPVCVGYEIDGRRTRDMPMTQRDLCRA  
KPVYEELPGWWEDISGAREFDDLPAKARDYVLRLEQLAGAPVSCIGVGP GRE  
QTIVRRDVLQDRP

> sp|A0QWX9|TAL\_MYCS2 Transaldolase OS=Mycobacterium smegmatis (strain  
ATCC 700084 / mc(2)155) GN=tal PE=1 SV=1

MAQNPNLAALSAAGVSVWLDDLSRDRLQTGNLTELINTRSVVGVTNPSIFQ  
AALSKGTAYDAQVNELAARGADV DATIRTVTDDVRNACDLLAKEYEASDG  
VDGRVSIEVDPRLAHD TDKILQAIELWKIVDRPNLLIKIPATMAGLPAISAVIA  
EGISVNVTLIFSVERHRLVMDAYLEGLEKAKEAGHDLSKIHSVASFFVSRVDTE  
IDARLEKIGSDEALALRGKAGVANARLAYAAYEEVFGSDRFAKLKADGARVQ  
RPLWASTGVKNPEYSDTLYVTEL VAPNTVNTMPEKTLEAVADHGEITGNTIAG  
TAASSQETFDKLA AIGIDL PDVFRVLEDEGVEKFEKSWQELLDATQGQLDAAK  
K

> sp|P0A5L2|MURA\_MYCTU UDP-N-acetylglucosamine 1-carboxyvinyltransferase  
OS=Mycobacterium tuberculosis GN=murA PE=1 SV=1

MAERFVVTGGNRLSGEVAVGGAKNSVLKLMAATLLAEGTSTITNCPDILDVP  
LMAEVLRLGLGATVELDGDVARITAPDEPKYDADFAAVRQFRASVCVLGPLVG  
RCKRARVALPGGDAIGSRPLDMHQAGLRQLGAHCNIEHGCVVARAETLRGAE  
IQLEFPSVGATENILMAAVVAEGVTTIHNAAREPDVVDLCTMLNQMGAQVEG  
AGSPTMTITGVPRLHPTEHRVIGDRIVAATWGIAAAMTRGDISVAGVDP AHLQ

LVLHKLHDAGATVTQTDASFRVTQYERPKAVNVATLPPFGFPTDLQPMAIALA  
SIADGTSMITENVFEARFRFVEEMIRLGADARTDGHHAVVRGLPQLSSAPVWC  
SDIRAGAGLVLAGLVADGDTEVHDVHFHIDRGYPLFVENLVSLGAEIERVCC

> sp|P0A654|Y3716\_MYCTU Nucleoid-associated protein Rv3716c/MT3819

OS=Mycobacterium tuberculosis GN=Rv3716c PE=1 SV=1

MQPGGDMSALLAQAQQMQQKLEAQQQLANSEVHGQAGGGLVKVVVKGS  
GEVIGVTIDPKVVDPPDIETLQDLIVGAMRDASQQVTKMAQERLGALAGAM  
RPPAPPAAPPGAPGMPGMPGMPGAPGAPPVPGI

> sp|A0QNE0|GYRB\_MYCS2 DNA gyrase subunit B OS=Mycobacterium

smegmatis (strain ATCC 700084 / mc(2)155) GN=gyrB PE=1 SV=1

MAAQKNNAPKEYGADSITILEGLEAVRKRPGMYIGSTGERGLHHLIWEVVDN  
AVDEAMAGFATRV DVKIHADGSVEVRDDGRGIPVEMHATGMPTIDVVM TQL  
HAGGKFDGETYAVSGLHGVGVSVVNALSTRLEATVLRDGYEWFQYYDRSV  
PGKLGQGETKETGTTIRFWADPEIFETTDYNFETVARRLQEMAFLNKGLTIEL  
TDERVTAEEVDDVVKDTAEAPKTADEKAAEATGPSKV KHRVFHYPGGLVD  
YVKHINRTKTPIQQSIIDFDGKGPGEVEIAMQWNAGYSESVHTFANTIN THE  
GGTHEEGFRAALTSV VNR YAKDKKLLKDKDPNLTGDDIREGLAAVISVKVAEP  
QFEGQTKTKLGNTEVKSFVQKICNEQLQHWFEANPAEAKTVVNKAVSSAQA  
RIAARKARELVRRKSATDIGGLPGKLADCRSTDPSKSELYVVEGDSAGGSAKS  
GRDSMFQAILPLRGKIINVEKARIDRVLKNTEVQSIITALGTGIHDEFDISKLRY  
HKIVLMADADV DQG HISTLLL TLLFRFMKPLVENGHIFLAQPPLYKWKQRSE  
PEFAYS DRERDGLLEAGRAAGKKINVDDGIQRYKGLGEMDAKELWETTMDP  
SVRVLRQVTLDDAAADELFSILMGEDVEARRSFITRNAKDVRFLDV

> sp|L0T905|RSEA\_MYCTU Anti-sigma-E factor RseA OS=Mycobacterium

tuberculosis GN=rseA PE=1 SV=1

MADPGSVGHVFRRAFSWLP AQFASQSDAPV G APRQFRSTEHL SIEAIAAFVDG  
ELRMNAHLRAAHLSLCAQCAA EVDDQSRARAALRDSHP IRIPSTLLGLLSEI  
PRCPPEGPSK GSSGGSSQGPPDGAAAGFGDRFADGDGGNRGRQSRVRR

> sp|Q7D547|Y3659\_MYCTU Putative conjugal transfer protein Rv3659c/MT3759

OS=Mycobacterium tuberculosis GN=Rv3659c PE=2 SV=1

MLGDTEVLANLRVLQTELTGAGILEPLLSADGTTDVLVTAPDSVWVDDGNGL  
RRSQIRFADES AVRRLAQRLALAAGRRLDDAQPWVDGQLTGIGVGGFAVRLH  
AVLPPVATQGTCLSLRVLRPATQDLAALAAAG AIDPAAAALVADIVTARLAFLV  
CGGTGAGKTTLLAAMLGAVSPDERIVCVEDAAELAPRHPHLVKLVARRANVE  
GIGEVTVRQLVRQALRMRPDRIVVGEVRGAEVVDLLAALNTGHEGGAGTVH  
ANNPGEV PARMEALGALGGLDRAALHSQLAAAVQVLLHVARDRAGRRRLAE  
IAVLRQAEGRVQAVTVWHADRGM SDDAAALHDLLRSRASA

> sp|P0A4X6|BIOA\_MYCTU Adenosylmethionine-8-amino-7-oxononoate

aminotransferase OS=Mycobacterium tuberculosis GN=bioA PE=1 SV=1

MAAATGGLTPEQIIAVDGAHLWHPYSSIGREAVSPVVAVAAHGAWLTLIRDGQ  
PIEVL DAMSSWWT AIHGHPALDQALTTQLRVMNHVMFGGLTHEPAARLA  
KLLVDITPAGLDTVFFSDSGSVSVEVA AKMALQYWRGRGLPGKRRLMTWRG  
GYHGD TFLAMSICDPHGGMHS LWTDLAAQVFAPQVPRDYDPAYSAAFEAQ  
LAQHAGELAAVVVEPVVQGAGGMRFHDP RYLHDLRDICRRYEVLLIFDEIAT

GFGRTGALFAADHAGVSPDIMCVGKALTGGYLSLAATLCTADVAHTISAGAA  
GALMHGPTFMANPLACAVSVASVELLLGQDWRTRITELAAGLTAGLDTARAL  
PAVTDVRVCGAIGVIECDRPPVDLAVATPAALDRGVWLRPFRNLVYAMPPYICTP  
AEITQITSAMVEVARLVGSLP

> sp|P0A696|OGT\_MYCTU Methylated-DNA--protein-cysteine methyltransferase  
OS=Mycobacterium tuberculosis GN=ogt PE=1 SV=1

MIHYRTIDSPIGPLTLAGHGSVLTNLRMLEQTYEPSRTHWTPDPGAFSGAVDQL  
NAYFAGELTEFDVELDLRGTDFFQQRVWKALLTIPYGETRSYGEIADQIGAPGA  
ARAVGLANGHNPIAIIVPCHRVIASGKLTGYGGGINRKRALLELEKSRAPADL  
TLFD

> sp|P63288|CLPB\_MYCTU Chaperone protein ClpB OS=Mycobacterium  
tuberculosis GN=clpB PE=2 SV=1

MDSFNPTTKTQAALTAALQAASTAGNPEIRPAHLLMALLTQNDGIAAPLLEAV  
GVEPATVRAETQRLLDRLPQATGASTQPQLSRESLAAITTAQQLATELDDEYVS  
TEHVMVGLATGDSVAKLLTGHGASPQALREAFVKVRGSARVTSPEPEATYQ  
ALQKYSTDLTARAREGKLDPVIGRDNEIRRVVQVLSRRTKNNPVLIGEPGVGK  
TAIVEGLAQRIVAGDVPESLRDKTIVALDLGSMVAGSKYRGEFEERLKAVLDDI  
KNSAGQIITFIDELHTIVGAGATGEGAMDAGNMIKPMMLARGELRLVGATTLDE  
YRKHIEKDAALERRFQQVYVGEPSVEDTIGILRGLKDRYEVHHGVRITDSALV  
AAATLSDRYITARFLPKAIDLVDAAASRLRMEIDSRPVEIDEVERLVRRLIEIEE  
MALSKEEDEASAERLAKLRSELADQKEKLAELTTRWQNEKNAIEIVRDLKEQ  
LEALRGESERAERDGD LAKAAELRYGRIPEVEKKLDAALPQAQAREQVMLK  
EEVGPDDIADVSAWTGIPAGRLLEGETAKLLRMEDELGKRVIQKAAVAVS  
DAVRRSRAGVSDPNRPTGAFMFLGPTGVGKTELAKALADFLDDERAMVRID  
MSEYGEKHTVARLIGAPPGYVGYEAGGQLTEAVRRRPYTVVLFDEIEKAHPD  
VFDVLLQVLDEGRITDGHGRTVDFRNTILILTSNLGSGGSAEQVLA AVRATFK  
PEFINRLDDVLIFEGLNPEELVRIVDIQLAQLGKRLAQRRQLQVSLPAKRWLA  
QRGFDPVYGARPLRRLVQQAIGDQLAKMLLAGQVHDGDTVPVNVSPDADSL  
ILG

> sp|A0R0T0|YBEY\_MYCS2 Endoribonuclease YbeY OS=Mycobacterium  
smegmatis (strain ATCC 700084 / mc(2)155) GN=ybeY PE=1 SV=1

MSIEVSNESGYDVSEPELISVARFVIEKMDVHPAAELSMVLLDSAAMADLHM  
RWMDLPGPTDVMSFPMDELEPGGRPDPEPGPAMLGDIVLCPEFAEQQA  
GHS LGHELALLTVHGV LHL LGYDHAEPDEEKEMFALQRQLLEEWVADQVEA  
YHAD RQSEKDRRLLDKSRYFDEP

> sp|P63562|ARGC\_MYCTU N-acetyl-gamma-glutamyl-phosphate reductase  
OS=Mycobacterium tuberculosis GN=argC PE=1 SV=1

MQNRQVANATKVAVAGASGYAGGEILRLLLGHYPAYADGRLRIGALTAATSAGS  
TLGEHHPHLTPLAHRVVEPTAAVLGGHDAVFLALPHGHSVLAQQLSPETLII  
DCGADFRLTDAAVWERFYGSSHAGSWPYGLPELPGARDQLRGTRRIAVPGCY  
PTAALLALFPALAADLIEPAVTVVAVSGTSGAGRAATTDLLGAEVIGSARAYNI  
AGVHRHTPEIAQGLRAVTDRDVSVSFTPVLPASRGILATCTARTRSPLSQLRAA  
YEKAYHAEPFIYLMPEGQLPRTGAVIGSNAAHIAVAVDEDAQTFVAIAAIDNLV  
KGTAGAAVQSMNLALGWPETDGLSVVGVAP

> sp|P0A5J4|MASZ\_MYCTU Malate synthase G OS=Mycobacterium tuberculosis  
GN=glcB PE=1 SV=2

MTDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDKVVADLTPQNQA  
LLNARDELQAQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSQVD  
AEITTTAGPQLVVPVLNARFALNAANARWGSLYDALYGTDVIPETDGAKEGPT  
YNKVRGDKVIAYARKFLDDSVPLSSGSGFDATGFTVQDQGLVVALPDKSTGL  
ANPGQFAGYTGAAESPTSVLLINHGLHIEILIDPESQVGTTRDRAGVKDVILESAI  
TTIMDFEDSVAAVDAADKVLGYRNWLGLNKGDLAAAVDKDGTAFRLVLRD  
RNYTAPGGGQFTLPGRSLMFVRNVGHLMTNDAIVDTDGSEVFEGIMDALFTG  
LIAIHGLKASDVNGPLINSRTGSIYIVKPKMHGPAEVAFTCELSRVEDVGLPQ  
NTMKIGIMDEERRTTVNLKACIKAAADRVPFINTGFLDRTGDEIHTSMEAGPM  
VRKGTMKSQPWILAYEDHNVDAGLAAGFSGRAQVKGGMWTMTELMADMV  
ETKIAQPRAGASTAWVPSPTAATLHALHYHQVDVAAVQQGLAGKRRATIEQLL  
TIPLAKELAWAPDEIREEVDNQCQSILGYVVRWVDQGVGCSKVPDIHDVALM  
EDRATLRISQLLANWLRHGVITSADVRSASLERMAPLVDRQNAGDVAYRPM  
PNFDDSI AFLAAQELILSGAQQPNGYTEPILHRRRREFKARAAEKPA PSDRAGD  
DAAR

> sp|P0A5P0|CMAS2\_MYCTU Cyclopropane mycolic acid synthase 2  
OS=Mycobacterium tuberculosis GN=cmaA2 PE=1 SV=1

MTSQGDTTSGTQLKPPVEAVRSHYDKSNEFFKLWLDPSMTYSCAYFERPDMT  
LEEAQYAKRKLALDKLNLEPGMTLLDIGCGWGSTMRAVAEYDVNVIGLTL  
ENQYAHDKAMFDEVDSRRRKEVRIQGWEEFDEPVDIVSLGAFEFADGAGD  
AGFERYDTFFKKFYNLTPDDGRMLLHTITIPDKEEAQELGLTSPMSLLRFIKFIL  
TEIFPGRLPRISQVDYYSSNAGWKVERYHRIGANYVPTLNAWADALQAHKD  
EAIKLGQETYDIYMHYLRGCSDLFRDKYTDVCQFTLVK

> sp|P63945|DAPA\_MYCTU 4-hydroxy-tetrahydrodipicolinate synthase  
OS=Mycobacterium tuberculosis GN=dapA PE=1 SV=1

MTTVGFDVAARLGTLLTAMVTPFSGDGLDTATAARLANHLVDQGCGLVVS  
GTTGESPTTTDGEKIELLRVLEAVGDRARVIAGAGTYDTAHSIRLAKACAAE  
GAHGLLVVTPYYSKPPQRGLQAHFTAVADATELPMMLYDIPGRSAVPIEPTIR  
ALASHPNIVGVKDAKADLHSGAQIMADTGLAYYSGDDALNLPWLAMGATGF  
ISVIAHLAAGQLRELLSAFGSGDIATARKINIAVAPLCNAMSRLGGVTLSKAGL  
RLQGIDVGDPRLPQVAATPEQIDALAADMRAASVLR

> sp|A0QVB9|EFTS\_MYCS2 Elongation factor Ts OS=Mycobacterium smegmatis  
(strain ATCC 700084 / mc(2)155) GN=tsf PE=1 SV=1

MANYTAADV KRLRELTGAGMLDSKNALVEADGDFDKAVELLRIKGAKDVG  
KRAERATAEGLVAAKDGALIELNSETDFVAKNAEFQALADQIVAAVAAKAN  
DIETLKA AKTGDTTVEQAIADLSAKIGEKLELRRAYFDGTVEAYLHKRAAD  
LPPAVGVLVEYQAGDADKGKEAAHAVALQIAALKAKYLTREDVPEDIVANER  
RIAEETARNEGKPEQALPKIVEGRVTGFYKDVVLLDQPSVSDNKKTVKALLD  
EAGVTVTRFVRFEVGQA

> sp|O07776|TCRA1\_MYCTU Transcriptional regulatory protein TcrA  
OS=Mycobacterium tuberculosis GN=tcrA PE=1 SV=1

MADETTMRAGRGPGRACGRVSGVRILVVEDEPKMTALLARALTEEGHTVDT

VADGRHAVA AVDGGDYDAV VLDVMLPGIDGFEVCARLRRQRVWTPVLM LTA  
RGA VTDRIAGLDGGADDYLT KPFNLDEL FARLRALSRRGPIPRPPTLEAGDLRL  
DPSEHRVWRADTEIRLSHKEFTLLEALIRRP GIVHTRAQLLERCWDAAYEARS  
NIVDVYIRYL RDKIDRPFVTSLETIRGAGYRLRKDGGRHALPR

> sp|P59957|HIS5\_MYCBO Imidazole glycerol phosphate synthase subunit HisH  
OS=Mycobacterium bovis (strain ATCC BAA-935 / AF2122/97) GN=hisH PE=1  
SV=1

MTAKSVV VLDYGS GNLRSAQRALQRVGA EVEVTADTDAAMTADGLV VPGV  
GAFAACMAGLRKISGERIIAERVAAGR PVLGVCVGMQILFACGVEFGVQTPGC  
GHWP GAVIRLEAPVIPHMGNV VDS AAGSALFKGLD V DARFYFVHSYAAQR  
WEGSPD ALLTWATYRAPFLAAVEDGALAA TQFHPEKSGDAGAAVLSNWVDG  
L

> sp|P65477|MURE\_MYCTU  
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase  
OS=Mycobacterium tuberculosis GN=murE PE=1 SV=1

MSSLARGISRRRTEVATQVEAAPTGLRPN AVVGVRLAALADQVGAALAE GPA  
QRAVTE DRTVTGVTLRAQDVSPGDLFAALTGSTTHGARHVGD AIARGAVAVL  
TDPAGVAEIAGRAAVPVLVHPAPRGV LGGLAATVYGHPSERLTVIGITGTS GKT  
TTTTYLVEAGLRAAGR VAGLIGTIGIRVGGADLPSALTTPEAPTLQAMLAAMVE  
RGVDTV VMEVSSHALALGRVDGTRFAVGAFTNLSRDHLD FHP SMADYFEAK  
ASLFD PDSALRARTAVVCIDDDAGRAMAARAADAITVSAADRPAHW RATDV  
APTDAGGQQFTAIDPAGVGH HIGIRLPGRY NVANCLVALAILDTVGV SPEQAVP  
GLREIRVPGRLEQIDRGQGF LALVDYAHKPEALRSVLTTLAHPDRRLAVVFGA  
GGDRDPGKRAPMGRIAAQLADLVVVTDDNPRDEDPTAIRREILAGAAEVGGD  
AQVVEIADRRDAIRHAVA WARPGDVVLIAGKGHETGQRGGGRVRPFDDRVEL  
AAALEALERRA

> sp|A0QW23|DCUP\_MYCS2 Uroporphyrinogen decarboxylase OS=Mycobacterium  
smegmatis (strain ATCC 700084 / mc(2)155) GN=hemE PE=1 SV=1

MNTRRELPE SPYLAAASGRSPHRVPVWFMRQAGRSLPEYRELRAQHRMLQA  
CFDAELVCEITMQPVRRHKVDAAILFSDIVVPLKAAGIGLDIVPDVGPVIDNPI  
RTLGDVQAMPAL ESPQVAPVAEAVRLLTAELGDVPLIGFAGAPFTLAS YLVEG  
GPSRHHERTKAMMLGESSTW HALMTALD TLIAFLQAQVDAGVDALQV FDS  
WAGTLSLTDYREYVLP HSSRVFATMAAAGVPMTHFGVGTAE LLGAMSEALAP  
GAARVVGVDWRTSLADAAARVLP GAALQGNLDPV VLLAGWPVVEKAVRRV  
VEDGRAAVAAGAAGHIFNLGHGVLPATDPGIITDAVELVHSL

> sp|P0A576|HEMH\_MYCTU Ferrochelatase OS=Mycobacterium tuberculosis  
GN=hemH PE=1 SV=1

MQFDAV LLLSFGGPEGPEQVRPFLENVTRGRGVPAERLDAVAEHYLFHGGVSP  
INGINRTLIAELEAQ QELPVYFGNRNWE PYVEDAVTAMRDNGVRRAAVFATSA  
WSGYSSCTQYVEDIARARRAAGRDAPELVKLRPYFDHPLFVEMFADAITAAA  
ATVRGDARLVFTAHSIPTAADRRCGNLYSRQVAYATRLVAAAAGYCDFDLAW  
QSRSGPPQVPWLEPDVTDQLTGLAGAGINAVIVCPIGFVADHIEVVWDLDEL  
RLQAEAAAGIAYARASTPNADPRFARLARGLIDELRYGRIPARVSGPDPVPGCLS  
SINGQPCRPPHCVASVSPARPSAGSP

> sp|P0A514|CP121\_MYCTU Mycocyclosin synthase OS=Mycobacterium tuberculosis GN=cyp121 PE=1 SV=1  
MTATVLLVPPFSARGDRIPDAVAELRTREPIRKVRTITGAEAWLVSSYALCTQV  
LEDRRFSMKETAAAGAPRLNALTVPPEVVNNMGNIADAGLRKAVMKAITPK  
APGLEQFLRDTANSLLDNLITEGAPADLRNDFADPLATALHCKVLGIPQEDGP  
KLFRSLSIAFMSSADPIPAAKINWDRDIEYMAGILENPNITTGLMGELSRLRKD  
PAYSHVSDDEL FATIGVTFFGAGVISTGSFLTALISLIQRPQLRNLLHEKPELIPAG  
VEELLRINLSFADGLPRLATADIQVGDVLRK GELVVLVLEGANFDPEHFNPNG  
SIELDRPNPTSHLAFGRGQHFCPGSALGRRHAQIGIEALLKKMPGVDLAVPIDQ  
LVWRTRFQRRIPERLPVLW

> sp|P0A4W6|ACPM\_MYCTU Meromycolate extension acyl carrier protein  
OS=Mycobacterium tuberculosis GN=acpM PE=1 SV=1  
MPVTQEEIIAGIAEIIIEVTGIEPSEITPEKSFVDDLDIDSLSMVEIAVQTEDKYG  
VKIPDEDLA GLRTVGDVVAYIQKLEENPEAAQALRAKIESENPD AVANVQAR  
LEAESK

> sp|Q10878|FAD10\_MYCTU Putative fatty-acid--CoA ligase FadD10  
OS=Mycobacterium tuberculosis GN=fadD10 PE=2 SV=1  
MGGKKFQAMPQLPSTVLDREVFEQARQQPEAIALRRC DGTSALRYRELVAE VG  
GLAADLRAQSVSRGSRVLVISDNGPETYLSVLACAKLGAI VMADGNLPIAAI  
ERFCQITDPAAALVAPGSKMASSAVPEALHSIPVIAVDIAAVTRESEHSLDAASL  
AGNADQGS EDPLAMIFTS GTTGE PKAVLLANRTFFAVPDILQKEGLNWVTWV  
VGETTYSPLPATHIGGLWWILTCLMHGGLCVTGGENTTSLEILTNAVATTCL  
VPTLLSKLVSELKSANATVPSLRLVGYGGSRAIAADVRFIEATGVRTAQVYGLS  
ETGCTALCLPTDDGSIVKIEAGAVGRPYPGVDVYLAATDGIGPTAPGAGPSASF  
GTLWIKSPANMLGYWNNPERTAEVLIDGWVNTGDLLERREDGFFYIKGRSSE  
MIICGGVNIAPDEV DRIAEGVSGVREAA CYEIPDEEFGALVGLAVVASAELDES  
AARALKHTIAARFRRESEPMARPSTIVIVTDIPRTQSGKVMRASLAAAATADK  
ARVVVRG

> sp|A0QVR3|DAPB\_MYCS2 4-hydroxy-tetrahydrodipicolinate reductase  
OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=dapB PE=1  
SV=1  
MRVGVLGARGKVGATMVA AVEAAEDLTFSAGVDAGDDL SLLTESKTEVVIDF  
THPDVVM DNLFVIDNGIHAVVGTGFTWERIEQVEAWVKAKPGASVLIAPN  
FAIGAVLSMHFAKQAAKYFESVEIIE LHHPHKADAPSGTAARTAKLIAEARKGL  
PPNPDATSTGLDGARGADVDGIPVHSVRLAGLVAHQEV LFGTQGETLTIRHDS  
LDRTSFVPGVLLAVRKISGLQGLTVGIEPLLDLS

> sp|A0QWH1|Y2940\_MYCS2 Probable transcriptional regulatory protein  
MSMEG\_2940/MSMEI\_2866 OS=Mycobacterium smegmatis (strain ATCC 700084 /  
mc(2)155) GN=MSMEG\_2940 PE=1 SV=1  
MSGHSKWATTKHKKAVIDAKRGKMF AKLIKNIEVAARVGGGDPGGNPTLYDA  
IQKAKKSSVPNDNIERARKRGAGEEAGGADWQNITYEGYGPNGVAVLVECLT  
DNRNRAAGEVRVAMTRNGGNMADPGSVAYLFSRKG VVTLEKNGLTEDDVLL  
AVLEAGAEVNDLGD SF EI SEPSDLVAVRTALQEAGIDYDSADASFQPSVTVP  
VDLEGARKVLKLVDALEDSDDVQDVYTNMDIPDDVAAQLDEE

> sp|O69743|ESPK\_MYCTU ESX-1 secretion-associated protein EspK  
OS=Mycobacterium tuberculosis GN=espK PE=1 SV=1  
MSITRPTGSYARQMLDPGGWVEADEDTFYDRAQEYSQVLQRVTDVLDTCRQ  
QKGHVFEGLWSGGAANAANGALGANINQLMTLQDYLATVITWHRHIAGLI  
EQAKSDIGNNVDGAQREIDILENDPSLDADERHTAINSLVTATHGANVSLVAET  
AERVLESKNWKPPKNALEDLLQQKSPPPDVPTLVVPSPGTPGTPGTPITPGTPI  
TPGTPITPIPGAPVTPITPTPGTPVTPVTPGKPVTPVTPVKPGTPEGTPITVTPP  
VAPATPATPATPVTPAPAPHPQPAPAPAPSPGPQPVTPATPGSPATPGTPGGEPA  
PHVKPAALAEQPGVPGQHAGGGTQSGPAHADESAASVTPAAASGVPGARAA  
AAAPSGTAVGAGARSSVGTAAASGAGSHAATGRAPVATSDKAAAPSTRAASA  
RTAPPARPPSTDHIDKPDRSESADDGTPVSMIPVSAARAARDAATAAASARQR  
GRGDALRLARRIAAALNASDNNAGDYGFFWITAVTTDGSIVVANSYGLAYIPD  
GMELPNKVYLASADHAIPVDEIARCATYPVLAVQAWAAFHDMTLRAVIGTAE  
QLASSDPGVAKIVLEPDDIPESGKMTGRSRLEVVDPSAAAQLADTTDQRLDL  
LPPAPVDVNPPGDERHMLWFELMKPMTSTATGREAAHLRAFRAYAHSQEIA  
LHQAHTATDAAVQRVAVADWLYWQYVTGLLDRALAAAC

> sp|P65232|KPRS\_MYCTU Ribose-phosphate pyrophosphokinase  
OS=Mycobacterium tuberculosis GN=prs PE=1 SV=1  
MSHDWTDNRKNLMLFAGRAHPELAEQVAKELDVHVTSQDAREFANGEIFVR  
FHESVRGCDAFVLQSCPAPVNRWLMEQLIMIDALKRGS AKRITAVMPFYYPAR  
QDKKHRGREPISARLIADLLKTAGADRIVTVDLHTDQIQGFFDGPVDHMRGQ  
NLLTGYIRDNYPDGNM VVVSPDSGRVRIA EKWADALGGVPLAFIHKTRDPRV  
PNQVVSNRVVG DVAGRTC VLIDDMIDTGGTIAGAVALLHNDGAGDVIIAATHG  
VLSDPAAQRLASC GAREVIVTNTLP IGEDKRFPQLTVLSIAPLLASTIRAVFENG  
SVTGLFDGDA

> sp|P0A672|IDER\_MYCTU Iron-dependent repressor IdeR OS=Mycobacterium  
tuberculosis GN=ideR PE=1 SV=1  
MNELVDTTMYLRTIYDLEEEGVTPLRARIAERLDQSGPTVSQTVSRMERDGL  
LRVAGDRHLELTEKGRALAIAMRKHRLAERLLVDVIGLPWEEVHAEACRWE  
HVMSERVEDRLVKVLNNTTSPFGNPIPLVELGVGPEPGADDANLVRLTELP  
AGSPVAVVVRQLTEHVQGDIDLITRLKDAGVVPNARVTVETTPGGGVTVIVIPG  
HENVTLPHEMAHAVKVEKV

> sp|A0QP32|PCKG\_MYCS2 Phosphoenolpyruvate carboxykinase [GTP]  
OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=pckG PE=1  
SV=1  
MTSATIPGLDTAPT KHQGLLAWVQEVAELTQPDRVVFADGSDEEYERLCAHLV  
EAGTFQKLNPEKQPNSYLALSDPSDVARVESRTFICTEREIDAGPTNNWMDPA  
EMRGIMTDLYRGS MRGRTLYVVPFCMGLDAEDPKLGVEITDSEYVVVSMRT  
MTRMGRAALDKLGDDGFFVKALHSIGAPLEPGQKDVPWPCNDTKYITHFPET  
REIWSFGSGYGGNALLGKKCYSLRIASAMAHDEGWLAEHMLILKLISPENKA  
YFIAAAFPSACGKTNLAMLQPTIEGWRAETVGDIAWMRFGKDGRLYATNPE  
FGFFGVAPGTNWSSNP NAMKTIAAGNTVFTNVAKTDDGDVWWEGLGDPQ  
HLIDWKGN DWTPESGEKA AHPNSRYCTPISQCPTLAP EWDDPQGVPI SAILFG  
GRRKTTVPLITEARDWQHGVFIGATLGSEQTAAAEKGKVGTVRRDPMAMPLPFL

GYNVGDYFAHWINVGKNADESKLPKVFFVNWFRRGDDGRFLWPFGENSRV  
LKWAVERIEHKADGKSTPIGIVPTAADLDLEGLDVPADVDEALAVKPEEWR  
AELPLIEEWFVGEKLPGLKDEFDALKHRLSEEG

> sp|A0R079|GLNA1\_MYCS2 Glutamine synthetase 1 OS=Mycobacterium  
smegmatis (strain ATCC 700084 / mc(2)155) GN=glnA PE=1 SV=1

MAEKTSDDIFKLIKDENVEYVDIRFCDLPGVVQHFSIPASAFDES VFEDGLAFD  
GSSVRGFQSIHESDMMLLPDPNTARIDPFRAAKTLNMNFFVHDPFTREAYSRD  
PRNVARKAENYLASTGIADTAFFGAEAEFYIFDSVSFDSKINGTFYEVDSESGW  
WNTGEPFESDGSANRGYKVRPKGGYFPVAPYDHYVDLRDQMATNLQNAGFT  
LERGHHEVGTAGQAEINYKFNTLLAAADDVLLFKYIKNATAWQAGKTVTFMP  
KPLFGDNGSGMHAHQSLWKDGQPLFHDESGYAGLSDIARHYGGILHHAPSL  
LAFTNPTVNSYKRLVPGYEAPINLVYSQRNRSACVRIPITGNNPKAKRLEFRCP  
DSSGNPYLAFAMLMAGIDGIKKKIEPLQPVDKDYELPPDEAAAIPQAPTSLS  
AVIDKLEEDHEYLTEGGVFTEDLIETWISYKRENEIMPIQIRPHPYEFSLYYDV

> sp|P66844|SRP54\_MYCTU Signal recognition particle protein OS=Mycobacterium  
tuberculosis GN=ffh PE=1 SV=1

MFESLSDRDLTAALQGLRGKGRITDADIDATTREIRLALLEADVSLPVVRAFIHR  
IKERARGAEVSSALNPAQQVVKIVNEELISILGGETRELAFAKTPPTVVMLAGL  
QSGSKTTLAGKLAARLRGQGHTPLLACDLQRPAAVNQLQVVGERAGVPVF  
APHPGASPESGPGDPVAVAAAGLAEARAKHFDVVIVDTAGRLGIDEELMAQA  
AAIRDAINPDEVLFVLDAMIGQDAVTTAAAFGEGVGFTGVALTKLDGDARGG  
AALSVREVTGVPILFASTGEKLEDFDVFHPDRMASRILGMGDVLSLIEQAEQV  
FDAQQAEAAAIAKIGAGELTLEDFLEQMLAVRKMGPIGNLLGMLPGAQAQMKD  
ALAEVDDKQLDRVQAIIRGMTPQERADPKIINASRRLRIANGSGVTVSEVNQL  
VERFFEARMMSSMLGGMGIPGIGRKSATRKSAGKAGKSGKSKKGTGRGPTP  
PKVKSPFGVPGMPGLAGLPGLDLSQMPKGLDELPPGLADFDLSKLFPGK  
K

> sp|P0A664|UREG\_MYCTU Urease accessory protein UreG OS=Mycobacterium  
tuberculosis GN=ureG PE=1 SV=1

MATHSHPHSHTVPRRVRKPGELRIGVGGPVGSGKTALVAALCRQLRGEL  
SLAVLTNDIYTTEDADFLRTHAVLPDDRIAAVQTGGCPHTAIRDDITANLDAID  
ELMAAHDALDLILVESGGDNLTATFSSGLVDAQIFVIDVAGGDKVPRKGGPGV  
TYSDLLVVNKTDLAALVGADLAVMARDADAVRDGRPTVLQSLTEDPAASDV  
VAWVRSQLAADGV

> sp|A0R2V7|GLYA\_MYCS2 Serine hydroxymethyltransferase OS=Mycobacterium  
smegmatis (strain ATCC 700084 / mc(2)155) GN=glyA PE=1 SV=1

MAADPSSNSSSVPAANGADYADTASAAAYQAALQVIESVEPRVAAATRKEAD  
QRDSLKLIASENYASPAVLLTMGTWFSKYAEGTIGHRFYAGCQNVDTVESVA  
AEHARELFGAPYAYVQPHSGIDANLVAFWAILATRVEAPELANFGAKHINDLS  
EADWETLRNKLGNQRLGMSLDAGGHLTHGFRPNISGKMFHQRSYGTNPET  
GFLDYDAVAAAAREFKPLVLVAGYSAYPRRVNFAKMREIADEVGATLMVDM  
AHFAGLVAGKVFTGDEDPVPHAHVTTTTTHKSLRGPRGGMVLATEEYAPAVD  
KGCPMVLGGPLSHVMAAKAVALAEARQPAFQQYAQQVADNAQALADGFVK  
RDAGLVTGGTDNHIVLLDVTSFGLTGRQAESALLDAGIVTNRNSIPADPNGAW

YTSQVRLGTPALTSRQFGADDFDRVAELIVEVLANTQPEGTSKAKYKLADGTA  
ERVHAASSELLSANPLYPGLTL

> sp|A0QSH8|KAD\_MYCS2 Adenylate kinase OS=Mycobacterium smegmatis  
(strain ATCC 700084 / mc(2)155) GN=adk PE=1 SV=1

MRVVLLGPPGAGKGTQAEKLSEKLGIPQISTGDLFRKNIGDGTPLGLEAKRYL  
DAGDLVPAELTNRLVEDRIDQPDAAEGFILDGYPRSVQAGALKDMLAARNT  
KLDVLEFQVSEDELLTRLKGRGRADDTDEVIRNRMKVYREETEPLLEYRD  
DLKTVNAV GALDEVFARALSALGQ

> sp|A0R1H6|ACPS\_MYCS2 Holo-[acyl-carrier-protein] synthase  
OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=acpS PE=1  
SV=1

MAIVGVGIDLVSIPDFAEQVDRPGTVFAETFTPGERRDAADKSSSAARHLAAR  
WAAKEAVIKAWSSSRFSKRPALPEGIHRDIEVVTDMMWGRPKVRLSGEIAKHLE  
DVTIHVSLTHEDQTAAAVAIIEEP

> sp|P64767|CHMU\_MYCTU Intracellular chorismate mutase OS=Mycobacterium  
tuberculosis GN=Rv0948c PE=1 SV=1

MRPEPPHHENAELAAMNLEMLSQPVPEIDTLREEIDRLDAEILALVKRRAEV  
SKAIGKARMASGGTRLVHSREMKVIERYSSELGPDGKDLAILLLRLGRGRLGH

> sp|A0QSL3|IF1\_MYCS2 Translation initiation factor IF-1 OS=Mycobacterium  
smegmatis (strain ATCC 700084 / mc(2)155) GN=infA PE=1 SV=1

MAKKDGAIEVEGRVIEPLPNAMFRIELENHGKVLAHISGKMRQHYIRILPEDR  
VVVELSPYDLSRGRIVYRYK

> sp|A5U654|PPGK\_MYCTA Polyphosphate glucokinase OS=Mycobacterium  
tuberculosis (strain ATCC 25177 / H37Ra) GN=ppgK PE=1 SV=1

MTSTGPETSETPGATTQRHGFIDVGGSGIKGGIVDLDTGQLIGDRIKLLTPQPA  
TPLAVAKTIAEVVNGFGWRGPLGVVTHGVVVRTAANVDKSWIGTNAR  
DTIGAEELGGQQVTILNDADAAGLAETRYGAGKNNPGLVLLTFGTGIGSAVIH  
NGTLIPNTEFGHLEVGGKEAEERAASSVKEKNDWTYPKWAKQVIRVLAIENA  
IWPDLFIAGGGISRKADKVVPLENRTVPAALQNTAGIVGAAMASVADTT  
H

> sp|A1KG37|Y605\_MYCBP Uncharacterized protein BCG\_0605c  
OS=Mycobacterium bovis (strain BCG / Pasteur 1173P2) GN=BCG\_0605c PE=1  
SV=1

MSTVLTYYIRAVDIYEHMTESLDLEFESAYRGESVAFGEGVRPPWSIGEPQPELA  
ALIVQKGKFRGDVLDVGCGEAAISLALAERGHTTVGLDLSPA AVELARHEAAK  
RGLANASFEVADASSFTGYDGRFDTIVDSTL FHSMPVESREGYLQSIVRAAAP  
GASYFVLVFDRAAIEGPINAVTEDELRAAVSKYWIIDEIKPARLYARFPAGFAG  
MPALLDIREEPNGLQSIGGWLLSAHLG

> sp|A0QVQ5|PNP\_MYCS2 Polyribonucleotide nucleotidyltransferase  
OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=ppn PE=1  
SV=1

MSVVELEDGVYESTAVIDNGSFGTRTIRFETGRLAQQAAAGSAVAYLDDETMLL  
SATTASKNPKDHFDFPLTV DVEERMYAAGRIPGSFFRREGRPSTDAILTCLRID  
RPLRPSFVDGLRNEIQVVVTVMSLDPKDLYDVLAINAASMSTQLAGLPFSGPV

GGARIALIDGTWVAFPTVEQLERAVFDMVVAGRIVGDGDSADVAIMMVEAEA  
TENVVELVAGGAQAPTEAVVAEGLEAAKPFIKALCAAQQELADRAAKPAGEY  
PVFPDYEADVYDAVASVATEALAEALTIAGKTERNDRTDEIKVEVLERLAEPY  
AGREKEIGAAFRSLTKKLVQRILTDHFRIDGRGITDIRALS AEVAVIPRAHGSA  
L FERGETQILGVTTLDMIKMAQQIDSLGPENTKRYMHHYNFPPYSTGETGRVG  
SPKRREIGHGALAERALVPVLPSIEEFPYAIRQVSEALGSNGSTSMGSCASTL  
ALLNAGVPLKAPVAGIAMGLVSDDVDVDGKVEKRYVALTDILGAEDAFGDM  
DFKVAGTKDFVTALQLDTKLDGIPSQVLGALSQAKDARLTILDVMAEAIDRP  
DEMSPYAPRITTIKVPVDKIGEVIKPKGKMINSITEETGAQISIEDDGTVFVGAA  
DGLSAQAAIDKINAIANPQLPKVGERFLGTVVKTDFGAFVSLLPGRDGLVHI  
SKLGK GKRIAKVEDVVKVGDKLRVEIADIDNRGKISLVLVAEESAESAESAGD  
KGAEKAEGAAADVTPAEA

> sp|P63783|CLPP2\_MYCTU ATP-dependent Clp protease proteolytic subunit 2  
OS=Mycobacterium tuberculosis GN=clpP2 PE=1 SV=1

MNSQNSIQPQARYILPSFIEHSSFGVKESNPYNKLFEEIIFLGVQVDDASAN  
DIMAQLLVLES LDPDRDITMYINSPGGGFTSLMAIYDTMQYVRADIQTVCLGQ  
AASAAAVLLAAGTPGKRMALPNARVLHQPSLSGVIQGGQFS DLEIQAAEIERM  
RTLMETTLARHTGKDAGVIRKDTDRDKILTAEAEAKDYGIIDTVLEYRKL SAQT  
A

> sp|P66004|DLDH\_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium  
tuberculosis GN=lpdC PE=1 SV=1

MTHYDVVVLGAGPGGYVAAIRAAQLGLSTAIVEPKYWGGVCLNVGCIPSKA  
LLRNAELVHIFTKDAKAFGISGEVTFDYGIA YDRSRKVAEGRVAGVHFLMKKN  
KITEIHGYGTFADANTLLVDLNDGGTESVTFDN AIIATGSSTRLVPGTSLSANV  
VTYEEQILSRELPKSIIIAGAGAIGMEFGYVLKNYGVDVTIVEFLPRALPNEDA  
DVSKEIEKQFKKLGVTILTATKVESIADGGSQVTVTVTKDGV AQELKAEKVLQ  
AIGFAPNVEGYGLDKAGVALTDRKAIGVDDY MRTNVGHIYAIGDVNGLLQLA  
HVAEAQGVVAAETIAGAETLTLGDHRMLPRATFCQPNVASFGLTEQQARNEG  
YDVVVAKFPFTANAKAHGVGDPSGFVKLVADAKHGELLGGHLVGH DVAELL  
PELTLAQRWDLTASELARNVHHTPTMSEALQECFHGLVGHMINF

> sp|O05875|DESET\_MYCTU Stearoyl-CoA 9-desaturase electron transfer partner  
OS=Mycobacterium tuberculosis GN=Rv3230c PE=1 SV=1

MSKKHTTLNASIIDTRRPTVAGADRHPGWHALR KIAARITTPLLPDDYLHLAN  
PLWSARELRGRILGVRRETEDSATLFIKPGWGF SFDYQPGQYIGIGLLVDGRW  
RWRSYSLTSSPAASGSARMVTVTKAMPEGFLSTHLVAGVKPGTIVRLAAPQ  
GNFVLPDPAPPLILFLTAGSGITPVM SMLRTLVR RNQITDVVHLHSAPTAADV M  
FGAELAALAADHPGYRLSVRETRAQGRDLTRIGQQVPDWRERQ TWACGPE  
GVLNQADKVWSSAGASDRLHLERFAVSKTAPAGAGGTVTFARSGKSVAADA  
ATSLMDAGEGAGVQLPFGCRMGICQSCVVDLVEGHVRDLRTGQRHEPGTRV  
QTCVSAASGDCVLDI

> sp|P0A530|COAD\_MYCTU Phosphopantetheine adenyltransferase  
OS=Mycobacterium tuberculosis GN=coaD PE=1 SV=1

MTGAVCPGSFDPVTLGHVDIFERAAAQFDEVV VAILVNP AKTGMFDLDERIA  
MVKESTTHLPNLRVQVGHGLVVD FVRSCGMTAIVKGLRTGTD FEYELQMAQ

MNKHIAGVDTFFVATAPRYSFVSSSLAKEVAMLGGDVSELLPEPVNRRLRDRL  
NTERT

> sp|O69736|ECC1B\_MYCTU ESX-1 secretion system protein EccCb1

OS=Mycobacterium tuberculosis GN=eccCb1 PE=1 SV=1

MTAEPEVRTLREVVLDQLGTAESRAYKMWLPPLTNPVPLNELIARRRQPLRF  
ALGIMDEPRRHLQDVWGVDSGAGGNIGGAPQTGKSTLLQTMVMSAAAT  
HSPRNVQFYCIDLGGGGLIYLENLPHVGGVANRSEPKVNRVVAEMQAVMRQ  
RETTFKHRVGSIGMYRQLRDDPSQPVASDPYGDVFLIIDGWPGFVGEFPDLE  
GQVQDLAAQGLAFGVHVIISTPRWTELKSRVDYLGTKIEFRLGDVNETQIDR  
ITREIPANRPGRAVSMEKHHLMIGVPRFDGVHSADNLVEAITAGVTQIASQHTE  
QAPPVRVLPERIHLELDPNPPGPESDYRTRWEIPIGLRETDLTPAHCHMHTNP  
HLLIFGAAKSGKTTIAHAIARAICARNSPQQVRFMLADYRSGLLDVAVPDTHLL  
GAGAINRNSASLDEAVQALAVNLKKRLPPTDLTTAQLRSRSWWSGFDVLLV  
DDWHMIVGAAGGMPPMAPLAPLLPAAADIGLHIVTCQMSQAYKATMDKFV  
GAAFGSGAPTMFLSGEKQEFPSSEFKVKRRPPGQAFVSPDGKEVIQAPYIEPP  
EEVFAAPPSAG

> sp|O53446|FUMC\_MYCTU Fumarate hydratase class II OS=Mycobacterium  
tuberculosis GN=fumC PE=1 SV=1

MAVDADSANYRIEHDTMGEVVRPAKALWRAQTQRAVENFPISGRGLERTQIR  
ALGLLKGACAQVNSDLGLLAPEKADAIIAAAAEIADGQHDDQFPIDVFQTGS  
GTSSNMNTNEVIASIAAKGGVTLHPNDDVNMSQSSNDTFPTATHIAATEAAVA  
HLIPALQQLHDALAAKALDWHTVVKSGRTHLMDAVPVTLGQEFSGYARQIEA  
GIERVRACLPRLGELAIGGTAVGTGLNAPDDFGVRVAVLVAQTGLSELRTAA  
NSFEAQAARDGLVEASGALRTIAVSLTKIANDIRWMGSGPLTGLAEIQLPDLQP  
GSSIMPGKVNPNVLPPEAVTQVAAQVIGNDAAIAWGGANGAFELNVYIPMMARN  
ILESFKLLTNVSRIFAQRCIAGLTANVEHLRRLAESSPSIVTPLNSAIGYEEAAAV  
AKQALKERKTIRQTVIDRGLIGDRLSIEDLDRRLDVLAMAKAEQLDSDRL

> sp|A0QQLO|THIG\_MYCS2 Thiazole synthase OS=Mycobacterium smegmatis  
(strain ATCC 700084 / mc(2)155) GN=thiG PE=1 SV=1

MADSVLRIGGREFGSRLIMGTGGAPNLSVLEEALIASGTELTVMARRVDAET  
GTGVLDLLNRLGIAALPNTAGCRGAAEAVLTAQLAREALGTMVKLEVIAD  
RTLLPDAVELVKAAEQLVDDGFTVLPYTNDDPVLARRLEDIGCAAVMPLGSP  
GTGLGISNPHNIEMIVAAAGVPVVDAGIGTASDAALAMELGCDVLLATAVT  
RASDPPTMAAAMASAVTAGHLARQAGRIPKRFWAQASSPAL

> sp|O06620|BIOD\_MYCTU ATP-dependent dethiobiotin synthetase BioD

OS=Mycobacterium tuberculosis GN=bioD PE=1 SV=1

MTILVVTGTGTGVGKTVVCAALASAARQAGIDVAVCKPVQTGTARGDDDLA  
EVGRLAGVTQLAGLARYPQPMAPAAAAEHAGMALPARDQIVRLIADLDRPG  
RLTLVEGAGLLVELAEPGVTLRDVAVDVAAAALVVVTADLGTNLNHTKLTLE  
ALAAQQVSCAGLVIGSWPDPPLVAASNRSALARIAMVRAALPAGAASLDAG  
DFAAMSAAAFDRNWVAGLVG

> sp|A0QYS8|OTC\_MYCS2 Ornithine carbamoyltransferase OS=Mycobacterium  
smegmatis (strain ATCC 700084 / mc(2)155) GN=argF PE=1 SV=1

MIRHFLRDDDLSPEEQAEVLTAAADLKKTPFSRRPLEGPRGVAVIFEKNSTRTR

FSFEMGIAQLGGHAIIVVDGRSTQLGREETLEDTGAVLSRYVDAIVWRTFAQER  
LTAMASGASVPIVNALSDFEHPCQVLADLQTLAERKGLAGLRMTYFGDGA  
NNMAHSLMLGGVTAGVHVITIAAPDGFEPDPRFVDAARRRAAETGATVALTK  
DAKAGADGADVLTDTWTSMGQENDGLDRVRPFRPFQVNADLLELADPAAV  
VLHCLPAHRGHEITDEVIDGPQSAVFDEAENRLHAQKALLVWLEKR

> sp|P0A636|SYE\_MYCTU Glutamate--tRNA ligase OS=Mycobacterium  
tuberculosis GN=glX PE=1 SV=1

MTATETVVRVFCPSPTGTPHVGLVRTALFNWAYARHTGGTFVFRIEDTDAQRD  
SEESYLALLDALRWLGLDWDEGPEVGGPYGPYRQSQRAEIYRDVLARLLAA  
GEAYHAFSTPEEVEARHVAAGRNPCLGYDNFDRHLTDAQRAAYLAEGRQPV  
VRLRMPDDDLAWNDLVRGPVTFAAGSVPDFALTRASGDPLYTLVNPCDDAL  
MKITHVLRGEDLLPSTPRQLALHQALIRIGVAERIPKFAHLPTVLGEGTKKLSK  
RDPQSNLFAHRDRGFIPEGLLNYLALLGWSIADDHDLFGLDEMVAAFDVADV  
NSSPARFDQKKADALNAEHIRMLDVGDFTVRLRDHLDTGHGHIALDEAAFAA  
AAELVQTRIVVLGDAWELLKFFNDDQYVIDPKAAAKELGPDGAAVLDAALA  
ALTSVTDWTAPLIEAALKDALIEGLALKPRKAFSPIRVAATGTTVSPPLFESLEL  
LGRDRSMQRLRAARQLVGHA

> sp|P66666|RNC\_MYCTU Ribonuclease 3 OS=Mycobacterium tuberculosis  
GN=rnc PE=1 SV=1

MIRSRLPLDALGVLDLPDELLSLALTHRSYAYENGGGLPTNERLEFLGDAVLGL  
TITDALFHRHPDRSEGLAKLRASVNTQALADVARRLCAEGLGVHVLLGRG  
EANTGGADKSSILADGMESLLGAIYLQHGMEKAREVILRLFGPLLDAAPTGL  
AGLDWKTSLQELTAARGLGAPSYLVTSTGPDHDKEFTAVVVVMDSEYGSV  
GRSKKEAEQAAAAAWKALEVLDNAMPGKTS

> sp|O53870|DAPC\_MYCTU Probable N-succinyl-diaminopimelate aminotransferase  
DapC OS=Mycobacterium tuberculosis GN=dapC PE=1 SV=1

MTVSRLRPYATTVFAEMSALATRIGAVNLGQGFPEDEDGPPKMLQAAQDAIAG  
GVNQYPPGPGSAPLRRRAIAAQRRRHFGVDYDPETEVLVTVGATEAIAAAVLGL  
VEPGSEVLLIEPFYDSYSPVAMAGHRVTVPLVPDGRGFALDADALRAVTP  
RTRALIINSPHNPTGAVLSATELAAIAEIAVAANLVVITDEVYEHVFDHARHLP  
LAGFDGMAERTITISSAAKMFNCTGWKIGWACGPAELIAGVRAAKQYLSYVG  
GAPFQPAVALALDTEAWVAALRNSLRARRDRLAAGLTEIGFAVHDSYGTYFL  
CADPRPLGYDDSTEFCAALPEKVGVAIPMSAFCDPAAGQASQQADVWNHL  
VRFTFCKRDDTLDEAIRRLSVLAERPAT

> sp|P0A5Q8|PANB\_MYCTU 3-methyl-2-oxobutanoate hydroxymethyltransferase  
OS=Mycobacterium tuberculosis GN=panB PE=1 SV=1

MSEQTIYGANTPGGSGPRTKIRTHHLQRWKADGHKWAMLTAYDYSTARIFDE  
AGIPVLLVGDSAANVVYGYDTTVPISIDELIPLVRGVVRGAPHALVVADLPGFS  
YEAGPTAALAAATRFLKDGGAHAVKLEGGERVAEQIACLTAAGIPVMAHIGFT  
PQSVNTLGGFRVQGRGDAAEQTIADAIVAEAGAFVVMEMVPAELATQITG  
KLTIPTVGIGAGPNCQDQVVLVWQDMAGFSGAKTARFVKRYADVGGELRRAA  
MQYAQEVAGGVFPADEHSF

> sp|Q10765|SYI\_MYCTU Isoleucine--tRNA ligase OS=Mycobacterium tuberculosis  
GN=ileS PE=1 SV=1

MTDNAYPKLAGGAPDLPAALELEVLDYWSRDDTFRASIARRDGAPEYVFYDGP  
PFANGLPHYGHLLTGYVKDIVPRYRTMRGYKVERRFGWDTHGLPAELEVERQ  
LGITDKSQIEAMGIAAFNDACRASVLRYTDEWQAYVTRQARWVDFDNDYKT  
LDLAYMESVIWAFKQLWDKGLAYEGYRVLPCWRDETPLSNHELMMDDVY  
QSRQDPAVTVGFKVVGQPDNGLDGAYLLVWTTTPWTLPSNLAVAVSPDITY  
VQVQAGDRRFVLAEARLAAYARELGEEPVVLGTYRGAELGTRYLPPFAYFM  
DWPNAFQVLGDFVTTDDGTGIVHMAPAYGEDDMVVAEAVGIAPVTPVDSK  
GRFDVTVADYQGQHVFDANAQIVRDLKTQSGPAVNGPVLIRHETYEHPYPH  
CWRCRNPLIYRSVSSWFVRVTDFRDRMVELNQQITWYPEHVKDGQFGKWLQ  
GARDWSISRNYWGTPIPVWKSDDPAYPRIDVYGSLELERDFGVRPANLHRP  
YIDELTRPNPDDPTGRSTMRRIPVLDVWFDSGSMPIYAQVHYPFENLDWFQG  
HYPGDFIVEYIGQTRGWFYTLHVLATALFDRPAFKTCVAHGIVLGFQKMSK  
SLRNYPDVTEVFDRDGSAMRWFLMASPILRGGNLIVTEQGIRDGVRQVLLP  
LWNTYSFLALYAPKVGTRVDSVHVLDRYILAKLAVLRDDLSESMEVYDIPG  
ACEHLRQFTEALTNWYVRRSRSRFWAEDADAIDTLHTVLEVTTTLAAPLLPI  
TEIWRGLTRERSVHLTDWPAPDLLPSDADLVAAMDQVRDVCSAASSLRKAK  
KLRVRLPLPKLIVAVENPQLLRPFVDLIGDELNVKQVELTDAIDTYGRFELTVN  
ARVAGPRLGKDVQAAIKAVKAGDGVINPDGTLLAGPAVLTPDEYNSRLVAADP  
ESTAALPDGAGLVVLDGTVTAELEAEGWAKDRIRELQELRKSTGLDVSDRIRV  
VMSVPAEREDWARTHRLIAGEILATDFEFADLADGVAIGDGVRSIEKT

> sp|A0R3D3|PTH\_MYCS2 Peptidyl-tRNA hydrolase OS=Mycobacterium  
smegmatis (strain ATCC 700084 / mc(2)155) GN=pth PE=1 SV=1

MAEPLLVVGLGNPGPTYAKTRHNLGFMVADVLAGRIGSAFKVHKKSGAEVV  
TGRLAGTSVVLAKPRCYMNESGRQVGPLAKFYSVPPQQIVVIHDELDDIFGRI  
RLKLGEGEGHNGLSVASALGTKNFHRVRIGVGRPPGRKDPAAFVLENFTA  
AERAEVPTIVEQAADATELLIAQGLEPAQNTVHAW

> sp|P63514|SERC\_MYCTU Phosphoserine aminotransferase OS=Mycobacterium  
tuberculosis GN=serC PE=1 SV=1

MADQLTPHLEIPTAIKPRDGRFGSGPSKVRLEQLQTLTTTAAALFGTSHRQAPV  
KNLVGRVRSGLAELFSLPDGYEVILGNGGATAFWDAAAFGLIDKRSLHLTYGE  
FSAKFASAVSKNPFVGEPIIITSDPGSAPEPQTDPSVDVIAWAHNETSTGVAVAV  
RRPEGSDDALVVIDATSGAGGLPVDIAETDAYYFAPQKNFASDGGLWLAIMSP  
AALSRIEIAIATGRWVPDFLSLPIAVENSLKNQTYNTPAIATLALLAEQIDWL  
GNGGLDWAVKRTADSSQRLYSWAQERPYTTPFVTDPLRSQVVGTTIDFVDDV  
DAGTVAKILRANGIVDTEPYRKLGRNQLRVAMFPAVEPDDVSALTECVDWV  
ERL

> sp|P0A4Z4|AROB\_MYCTU 3-dehydroquinate synthase OS=Mycobacterium  
tuberculosis GN=aroB PE=1 SV=1

MTDIGAPVTVQVAVDPPYPVIGTGLLDELEDLLADRHKVAVVHQPLAETA  
EEIRKRLAGKGVDAHRIEIPDAEAGKDLVVGFIWEVLGRIGRGRKDALVSLG  
GGAATDVAGFAAATWLRGVSIVHLPTLLGMVDAAVGGKTGINTDAGKNLV  
GAFHQPLAVLVDLATLQTLPRDEMICGMAEVVKAGFIADPVILDIEADPQAA  
LDPAGDVLPVPELIRRAITVKAEVVAADEKESELREILNYGHITLGHAIERRERYR  
WRHGAAVSVGLVFAAELARLAGRLDDATAQRHRTILSSLGLPVSYPDALPQ

LLEIMAGDKKTRAGVLRVFLDGLAKPGRMVGPDPGLLVTAAYAGVCAP  
> sp|P0A602|SIGA\_MYCTU RNA polymerase sigma factor SigA  
OS=Mycobacterium tuberculosis GN=sigA PE=1 SV=1  
MAATKASTATDEPVKRTATKSPAASASGAKTGAKRTAAKSASGSPPAKRATKP  
AARSVKPASAPQDTTSTIPKRKTRAAAKSAAKAPSARGHATKPRAPKDAQ  
HEAATDPEDALDSVEELDAEPDLVPEGEDLDLDAADLNLDLEDDVAPDAD  
DDLDSGDDEDHEDLEAEA AVAPGQTADDDEEIAEPTKDKASGDFVWDEDES  
EALRQARKDAELTASADSVRAYLKQIGKVALLNAEEVELAKRIEAGLYATQL  
MTELSERGEKLPAAQRDMMWICRDGDRAKNHLLLEANLRLVVSLAKRYTGR  
GMAFLDLIQEGLIRAVEKFDYTKGYKFSTYATWWIRQAITRAMADQARTI  
RIPVHMVEVINKLGRIQRELLQDLGREPTPEELAKEMDITPEKVLEIQQYAREP  
ISLDQTIGDEGDSQLGDFIEDSEAVVAVDAVSFTLLQDQLQSVLDTLSEREAGV  
VRLRFGLTDGQPRTLDEIGQVYGVTRERIRQIESKTMSKLRHPSRSQVLRDYL  
D

> sp|Q10404|LIPB\_MYCTU Octanoyltransferase OS=Mycobacterium tuberculosis  
GN=lipB PE=1 SV=2  
MTGSIRSKLSAIDVRQLGTVDYRTAWQLQRELADARVAGGADTLLLLLEHPAV  
YTAGRRTETHERPIDGTPVVDTRGGKITWHGPGQLVGYPIIGLAEPLDVVNY  
VRRLEESLIQVCADLGLHAGRVDGRSGVWLPGRPARKVAAIGVRVSRATTLH  
GFALNCDCDLAAFTAIVPCGISDAAVTSLAELGRTVTVDVVRATVAAAVCAA  
LDGVLPVGDRVPSHAVPSPL

> sp|B2HPZ3|ACKA\_MYCMM Acetate kinase OS=Mycobacterium marinum (strain  
ATCC BAA-535 / M) GN=ackA PE=1 SV=1  
MSASRPNRVVLVNSGSSSLKFQLVEPDSGMSRATGNIERIGEESSVDPHDAA  
LRRVFEILAEDDIDLQSCGLVAVGHRVVHGGKDFYEPTLLNDAVIGKLDLSPL  
APLHNPPAVLCIRVARALLPDVPHIAVFDTAFFHQLPPAAATY AIDRELADVWKI  
RRYGFHGTSHEYVSQQA AEF LGKPIGDLNQIVLHLGNGASASAVAGGRP VETS  
MGLTPLEGLVMGTRSGDLDPGVIGYLWRTAKLGVDEIESMLNHRSGMLGLAG  
ERDFRRLRAMIDDGPAAELAYDVFIHRLRKYVGAYLAVLGHTDVVSFTAGI  
GEHDAVRRDTLAGMAELGISLDERRNACPSGGARRISADDSPVTVLVIPTNE  
ELAIARHCCSVLVAV

> sp|A0PV49|PAND\_MYCUA Aspartate 1-decarboxylase OS=Mycobacterium  
ulcerans (strain Agy99) GN=panD PE=1 SV=2  
MLRTMLKSKIHRATVTQADLHYVGSVTIDADLMDAADLLEGEQVTIVDIDNG  
ARLVTYAITGERGSGVIGINGAAHLVHPGDLVILIAYGTMQDAEARAYQPRIV  
FVDADNKQIDVGHDPAFVPAFDIPGA EELLNPRIGAR

> sp|A0QRN3|HUTU\_MYCS2 Urocanate hydratase OS=Mycobacterium smegmatis  
(strain ATCC 700084 / mc(2)155) GN=hutU PE=1 SV=1  
MEGARPVRAPRGTTLTARSWATEAPLRMLMNNLDPENAERPDDL VVYGGTG  
RAARNWASFDAMVRTLTTLREDETMLVQSGKPVGVFQTHEWAPRVLIANSNL  
VGDWATWPEFRLEAMGLTMYGQMTAGSWIYIGTQGIVQGTYETFAAAAEK  
RFGGTLAGTLTLTGCGGMGGAQPLAVTLNGGACLIVDVDEARLRRRVEHRY  
LDEVADNLDDAVTKAVATRKDKRAWSVGVGNAAEVPELLRRGVPIDLVTD  
QTS AHDPLSYLPIGISVEDWEDYATKKPDEFTERAEESMAVQVRAMVEFQDA

GAEVFDYGN SIRDEARKAGYDRAFEFPGFVPAYIRPQFCEGRGPFRWVALSGD  
PKDIHATDEAIMKLFDDRLQKWMRGAREKISFQGLPARICWLG YGERDKA  
GVLFN DLVASGKVSAPIVIGRDHLD SGSVASPYRETEAMLDGSDAIADWPLL  
ALTATSSGATWVSIHHGGGVGIGRSIHAGQVGVADGTELAQAQKLSRLLTNDPG  
MGVIRHVDAGYERAE EIAAERGVRIPMREGE

> sp|Q10769|TREZ\_MYCTU Malto-oligosyltrehalose trehalohydrolase

OS=Mycobacterium tuberculosis GN=treZ PE=1 SV=1

MPEFRVWAPK PALVRLD VNGAVHAMTRSADGW WHTTVAAPADARYGYLLD  
DDPTVLPDR SARQPDGVHARSQRWEPPGQFGAARTDTGW PGRSVEGAVIYE  
LHIGTFTTAGTFDAAIEKLDYLV DLGIDFVELMPVNSFAGTRGWGYDGV LWY  
SVHEPYGGPDGLVRFIDACHARRLGVLIDAVFNHLGPSGNYLPRFGPYLSSAS  
NPWGDGINIAGADSDEV RHYIIDCALRWMRDFHADGLRLDAVHALVDTTAVH  
VLEELANATRWLSGQLGRPLSLIAETDRNDPRLITRPSHGGYGIT AQWNDDIH  
HAIHTAVSGERQGY YADFGSLATLAYTLRNGYF HAGTYSSFRRRRHGRALDTS  
AIPATRL LAYTCTHDQVGNRALGDRPSQYLTGGQLAIKAALTLGSPYTAMLFM  
GEEWGASSPFQFFCSHPEPELAHSTVAGRKEEFAEHGWAADDIPDPQDPQTFQ  
RCKLNWAEAGSGEHARLHRFYRDLIALRHNEADLADPWLDHLMVDYDEQQ  
RWVVMRRGQLMIACNLGA EPTCVPVSGELVLAWESPIIGDNSTELAAYS LAIL  
RAAEPA

> sp|A0QU58|RF2\_MYCS2 Peptide chain release factor 2 OS=Mycobacterium

smegmatis (strain ATCC 700084 / mc(2)155) GN=prfB PE=1 SV=1

MDPDRQADIAALDTTLT TVERVLDVDGLRNRIEQLEKDASDPNLWDDQTRAQ  
KVTSDLSHAQNELRRVEGLRQRLDDLPVLYELAAEAGGPDEVAEADAELAKL  
REDIEAMEVRTLLSGEYDEREAVVTIRSGAGGVDAADWAEMLMRMYIRWAE  
KHDYPVEIFDTSYAE EAGIKSATFAVHAPFAYGTL SVEQGTHRLVRISPFDNQSR  
RQTSFADVEVLPV VETTDHIEIPENDIRVDVYRSSGPGGQSVNTTDSAVRLTHIP  
TGIVVTCQNEKSQLQNKVSAMRVLQAKLLERKRLEERAELDALKGDGSSW  
GNQMRSYVLHPYQMVKDLRTEYEVGNPASVLDGDIDGFLEAGIRWRNRKDD  
D

> sp|P60176|SAHH\_MYCTU Adenosylhomocysteinase OS=Mycobacterium

tuberculosis GN=ahcY PE=1 SV=2

MTGNLVTKNSLTPDVRNGIDFKIADLSLADFGRKELRIAEHEMPGLMSLRREY  
AEVQPLKGARISGSLHMTVQTAVLIETLTALGAEVRWASCNIFSTQDHAAA AV  
VVGPHGTPDEPKGV PVFAWKGETLEEYWWAAEQMLTWPD PKPANMILDD  
GGDATMLVLRGMQY EKAGVPPAEEDDPAEWKVFLNLLRTRFETDKDKWTK  
IAESVKGVTEETTTGVLRLYQFAAAGDLA FPAINVND SVTKSKFDNKYGRHS  
LIDGINRGTDALIGGKKVLICGYGDV GKGCAEAMKGGGARVSVTEIDPINALQ  
AMMEGFDVVTVEEAIGDADIVVTATGNKDIIMLEHIKAMKD HAILGNIGHFD  
NEIDMAGLERSGATRVNVKPQVDLWTFGDTGRSIIVLSEGRLLNLGNATGHPS  
FVMSNSFANQTIAQIELWTKNDEYDNEVYRLPKHLDEK VARIHVEALGGHLT  
KLTKEQAEYLGVDVEGYPYKPDHYRY

> sp|P65762|PPIA\_MYCTU Peptidyl-prolyl cis-trans isomerase A

OS=Mycobacterium tuberculosis GN=ppiA PE=1 SV=1

MADCDSVTNSPLATATATLHTNRGD IKIALFGNHAPKTVANFVGLAQGTKDYS

TQNASGGPSGPFYDGAVFHRVIQGFMIQGGDPTGTGRGGPGYKFADEFHPEL  
QFDKPYLLAMANAGPGTNGSQFFITVGKTPHLNRRHTIFGEVIDAESQRVVEA  
ISKATDGNDRPTDPVVIESTIS

> sp|P0A574|FABH\_MYCTU 3-oxoacyl-[acyl-carrier-protein] synthase 3

OS=Mycobacterium tuberculosis GN=fabH PE=1 SV=1

MTEIATTSGARSVGLLSVGAYRPERVVTNDEICQHIDSSDEWIYTRTGIKTRRF  
AADDESAASMATEACRRALSNAAGLSAADIDGVIVTTNTHFLQTPPAAPMVAA  
SLGAKGILGFDLSAGCAGFGYALGAAADMIRGGGAATMLVVGTEKLSPTIDM  
YDRGNCFIFADGAAAVVVGETPFQIGIPTVAGSDGEQADAIRQDIDWITFAQN  
PSGPRPFVRLGPAVFRWAAFKMGDVGRRAMDAAGVRPDQIDVFPVPHQANS  
RINELLVKNLQLRPDAVVANDIEHTGNTSAASIPLAMAELLTTGAAKPGDLAL  
LIGYGAGLSYAAQVVRMPKG

> sp|P63380|UVRA\_MYCTU UvrABC system protein A OS=Mycobacterium  
tuberculosis GN=uvrA PE=1 SV=1

MADRLIVKGAREHNLRSVDLDLPRDALIVFTGLSGSGKSSLAFDTIFAEGQRR  
YVESLSAYARQFLGQMDKPDVDFIEGLSPAVIDQKSTNRNPRSTVGTITEVYD  
YLRLLYARAGTPHCPTCGERVARQTPQQIVDQVLAMPEGTRFLVLAPVVRTRK  
GEFADLFDKLNAAQYSRVRVDGVVHPLTDPPKLLKQEKHDIEVVDRLTVKA  
AAKRRLTDSVETALNLADGIVVLEFVDHELGAPHREQRFSEKLACPNGHALA  
VDDLEPRSFNSPYGACPECSGLGIRKEVDPELVVPDPDRTLAQGAVAPWSN  
GHTAEYFTRMMAGLGEALGFDVTPWRKLPKARKAILEGADEQVHVRYRN  
RYGRTRSYYADFEGLAFLQKMSQTESEQMKERYEGFMRDVPCPVCAGTR  
LKPEILAVTLAGESKGEHGAKSIAEVCELSIADCADFLNALTLPREQAIAQV  
LKEIRSRLGFLLDVGLYLSLSRAAATLSGGEAQRIRLATQIGSGLVGVLYVLD  
EPSIGLHQRDNRRLIETLRLRDLGNTLIVVEHDEDTIEHADWIVDIGPGAGEH  
GGRIVHSGPYDELLRNKDSITGAYLSGRESIEIPAIRRSVDPQRQLTVVGAREH  
NLRGIDVSFPLGVLTSTVTGVS GSKSTLVNDILAAVLNRLNGARQVPGRHTR  
VTGLDYLDKLVVRVDQSPIGRTPRSNPATYTG VFDKIRTLFAATTEAKVIRGYQPG  
RFSFNVKGGRCRCEACTGDGTIKIEMNPLPDVYVPCEVCQGARYNRETLEVHYK  
GKTVSEVLDMSEIEAAEFFEPIAGVHRYLR TLVDVGLGYVRLGQPAPTLSGGE  
AQRVKLASELQKRSTGRTVYILDEPTTGLHFDDIRKLLNVINGLVDKGNVTIVI  
EHNLDVIKTSDWIIDLGPEGGAGGGTVVAQGTPELVAAVPASYTGKFLAEVV  
GGGASAATSRNRRRNVSA

> sp|P0DKR7|WHB5B\_MYCTU Transcriptional regulator WhiB5

OS=Mycobacterium tuberculosis GN=whiB5 PE=2 SV=1

MAHPCATDPELWFGYPDDDGS DGA AKARAYERSATQARIQCLRRCPLLQQR  
CAQHAVEHRVEYGVWAGIKLP GGQYRKREQLAAAHDLRRIAGGEINSRQLP  
DNAALLARNEGLEVTPVPGVVVHLP IAQVGPQPA

> sp|P63571|ARGJ\_MYCTU Arginine biosynthesis bifunctional protein ArgJ

OS=Mycobacterium tuberculosis GN=argJ PE=1 SV=1

MTDLAGTTRLLRAQGV TAPAGFRAAGVAAGIKASGALDLALVFNEGPDYAAA  
GVFTRNQVKAAPVLWTQQVLT TGRLRAVILNSGGANACTGPAGFADTHATAE  
AVAAALSDWGTETGAIEVAVCSTGLIGDRLPMDKLLAGVAHVHMHGGLV  
GGDEAAHAIMTTDNV PKQVALHHDNWTVGGMAKGAGMLAPSLATMLCV

LTDDAAAEPAAALERALRRAAAATFDRLDIDGSCSTNDTVLLLSSGASEIPPAQA  
DLDEAVLRVCDDLCAQLQADAEGVTKRVTVTVTGAATEDDALVAARQIARDS  
LVKTALFGSDPNWGRVLAAVGMAPITLDPDRISVSFNAAVCVHGVGAPGAR  
EVDLSADADIDITVDLGVGDGQARIRTTDLSHAYVEENSAYSS

> sp|P0A5H8|EFPP\_MYCTU (2E,6E)-farnesyl diphosphate synthase

OS=Mycobacterium tuberculosis GN=Rv3398c PE=1 SV=1

MRGTDEKYGLPPQPSDRMTRRTLPLVGLAHELITPTLRQMADRLDPHMRPV  
VSYHLGWSDERGRPVNNCGKAIRPALVFVAEEAAGADPHSAIPGAVSVELV  
HNFSLVHDDLMDRDEHRRHRPTVWALWGDAMALLAGDAMLSLAHEVLLDC  
DSPHVGAALRAISEATRELIRGQAADTA FESRTDVALDECLKMAEGKTAALM  
AASAEVGALLAGAPRSVREALVAYGRHIGLAFQLVDDLLGIWGRPEITGKPVY  
SDLRSRKKTLPTWTVAHGGSSAGRRLAAWLVDGSGQTASDDELA AVAELIE  
CGGGRRWASAEARRHVTQGIDMVARIGIPDRPAAELQDLAHYIVDRQA

> sp|P66940|TPIS\_MYCTU Triosephosphate isomerase OS=Mycobacterium

tuberculosis GN=tpiA PE=1 SV=1

MSRKPLIAGNWKMNLNHYEAIALVQKIAFSLPKYYDRVDVAVIPPFTDLRSV  
QTLVDGDKLRLTYGAQDLSPHDSGAYTGDVSGAFLAKLGCSYVVVGHSE  
TYHNEDDALVA AKAATALKHGLTPIVCIGEHLDVREAGNHVAHNIEQLRGLA  
GLLAEQIGSVVIAYEPVWAIGTGRVASAADAQEVCAAIRKELASLSPRIADTV  
RVLYGGSVNAKNVGDIVAQDDVDGGLVGGASLDGEHFATLAAIAAGGPLP

> sp|P60578|HIS4\_MYCTU Phosphoribosyl isomerase A OS=Mycobacterium

tuberculosis GN=priA PE=1 SV=1

MPLILLPAVDVVEGRAVRLVQGKAGSQTEYGS AVDAALGWQRDGAEWIHLV  
DLDAAFGRGSNHELLAEVVGKLDVQVELSGGIRDDESLAAALATGCARVNV  
GTAALNPQWCARVIGEHGDQVAVGLDVQIIDGEHRLRGRGWETDGGDLWD  
VLERLDSEGCSR FVVTDITKDGTGGLPNLDLLAGVADRTDAPVIASGGVSSLD  
DLRAIATLTHRGVEGAIVGKALYARRFTLPQALAAVRD