

Secretory protein

>sp|P9WQN9|A85C_MYCTU Diacylglycerol acyltransferase/mycolyltransferase Ag85C
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=fbpC PE=1 SV=1

MTFFEQVRRRLRSAATTLPRRLAIAAMGAVLVYGLVGTGGPATAGAFSRPGLPVEYLQVPSASMGRDIKVQFQG
GGPHAVYLLDGLRAQDDYNGWDINTPAFEEYYQSGLSVIMPVGGQSSFYTDWYQPSQSNQNYTYKWETFL
TREMPAWLQANKGVSPGTNAAVGLSMSGGALILAAAYPQQFPYAASLSGFLNPSEGWWPTLIGLAMNDSG
GYNANSMWGPSSDPAWKRNDDPMVQIPRLVANNTRIWVYCGNGTSPDLGGDNIPAKFLEGLTLRTNQTFRDT
YAADGGRNGVFNFPNGTHSWPYWNEQLVAMKADIQHVLNGATPPAAPAAPAA

>sp|P9WKD3|BLAC_MYCTU Beta-lactamase OS=Mycobacterium tuberculosis (strain ATCC 25618
/ H37Rv) GN=blaC PE=1 SV=1

MRNRGFGRRLLVAMAMLVSVTGCARHASGARPASTTLGADLADRFAELERRYDARLGVVYPATGTAAIE
YRADERFAFCSTFKAPLVAALVHQNPLTHLDKLYTSDDIRSIPVAQQHVQGTGMTIGQLCDAAIRYSDGTAANL
LLADLGGPGGGTAAFTGYLRSLGDTVSRLDAEPELNDRPPGDERDTTTPHAIALVLQQLVLGNALPPDKRALLT
DWMARNTTGAKRIRAGFPADWKVIDKTGTGDYGRANDIAVWWSPTGVPYVAVMSDRAGGGYDAEPREAL
LAEAATCVAGVLA

>sp|P9WP65|CPDA_MYCTU 3',5'-cyclic adenosine monophosphate phosphodiesterase CpdA
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=cpdA PE=1 SV=1

MHRLRAAEHPRPDYVLLHISDTHLIGGDRRLYGAVDADDRLGELLEQLNQSGLRPDAIVFTGLADKGEPAAYR
KLRGLVEPFAAQLGAELVWVMGNHDDRAELRKFLLEAPSMAPLDRVCMIDGLRIIVLDTSVPGHHHGEIRAS
QLGWLAEEELATPAPDGTILALHHPPIPSVLDMAVTVELRDQAALGRVLRGTDVRAILAGHLHYSTNATFVGIPVS
VASATCYTQDLTVAAGGTRGRDGAQGCNLVHVYPDVTVHVSIVPLGGGETVGTFFVSPGQARRKIAESGIFIEPSR
RDSLFKHPPMVLTSAPRSPVD

>sp|P9WNK5|ESXB_MYCTU ESAT-6-like protein EsxB OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) GN=esxB PE=1 SV=1

MAEMKTDAAATLAQEAGNFERISGDLKTQIDQVESTAGSLQGQWRGAAGTAAQAAVVRFQEAANKQKQELDE
ISTNIRQAGVQYSRADEEQQALSSQMGF

>sp|P9WIP1|MP63_MYCTU Immunogenic protein MPT63 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=mpt63 PE=1 SV=1

MKLTMTMIKTAVAVVAMAAIATFAAPVALAAYPITGKLGSELTMTDTVGQVVLGWKVSDDLKSSSTAVIPGYVAGQ
VWEATATVNAIRGSVTPAVSQFNARTADGINYRVLWQAAGPDTISGATIPQGEQSTGKIYFDVTGPSPTIVAMN
NGMEDLLIWEP

>sp|P9WGE7|SODF_MYCTU Superoxide dismutase [Fe] OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) GN=sodB PE=1 SV=1

MAEYTLPLDLDWDYGALEPHISGQINELHHSKHATYVKGANDAVAKLEEARAKEDHSAILLNEKNLAFNLAGH
VNHTIWWKNLSPNGDKPTGELAAAIADAFSGFDKFAAQFHAAATTVQGSWALGWDTLGNKLLIFQVYD
HQTNFPLGIVPLLLLDMEHAFYLQYKNVKVDFAKAFWNVNWDVQSRVAAATSQTKLIFG

>sp|P9WIN9|MP64_MYCTU Immunogenic protein MPT64 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=mpt64 PE=1 SV=1

MRIKIFMLVTAVVLLCCSGVATAAPKTYCEELKGTDTGQACQIQMSDPAYNINISLPSYYPDQKSLENYIAQTRDK
FLSAATSSTPREAPYELNITSATYQSAIPRGTQAVVLKVYQNAGGTHPTTTYKAFDWDQAYRKPITYDTLWQA
DTDPLPVVFPVQVQELSKQTGQVSIAPNAGLDPVNYQNFVAVTNDGVVIFFFNPGELLPEAAGPTQVLVPRSAIDS
MLA

>sp|P9WQB1|DHA_MYCTU Alanine dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ald PE=1 SV=1

MRVGIPTETKNEFRVAITPAGVAELTRRGHEVLIQAGAGEGSAITDADFKAAQAQLVGTADQVWADADLLK
VKEPIAAEYGRRLRHGQILFTFLHLAASACTDALLDSGTTISAIYETVQTADGALPLLAPMSEVAGRLAAQVGYH
LMRTQGGRGVLMGGVPGVEPADVVVIGAGTAGYNAARIANGMGATVTVLDINIDKLRQLDAEFCGRIHTRYS
SAYELEGAVKRADLVIGAVLVPAGAKAPKLVSNLSVAHMKPGAVLVDIAIDQGGCFEGSRPTTYDHPFVHDTLF
YCVANMPASVPKTSTYALTNATMPYVLELADHWRAACRSNPALAKGLSTHEGALLSERVATDLGVPFTEPASV
LA

>sp|P9WI65|PKNK_MYCTU Serine/threonine-protein kinase PknK OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pknK PE=1 SV=1

MTDVPDHPATRRDLVNPAPAELEAGFDNVEEIGRGGFGVVYRCVQPSLDRAVAVKVLSTDLDRDNLERFLREQR
AMGRLSGHPHIVTVLQVGLAGGRPFIVMPYHAKNSLETIRRHGPLDWRETLISIGVKLAGALEAAHRVGLTH
RDVKPGNILLTDYGEPLTDFGIARIAGGFETATGVIAGSPAFTAPEVLEGASPTPASDVYSLGATLFCALTGHAAY
ERRSGERVIAQFLRITSQPIPLDKQGLPADVAAAIERAMARHPADRATAADVGEELRDVQRRNGVSVDEMPL
PVELGVERRRSPEAHAHRHTGGGTPTVPTPTPATKYRPSVPTGSLVTRSRLTDILRAGGRRRLILIHAPSGFGK
STLAAQWREELSRDGA AVAWLTIDNDNNEVWFLSHLLESIRRVPTLAESLGHVLEEHGDDAGRYVLTSLIDEI
HENDDRIAVVIDDWHRVSDSRTQAALGFLLDNGCHHLQLIVTSWSRAGLPVGRRLRIGDELAEIDSAALRFDTDE
AAALLNDAGGLRPLRADVQALTTSTDGWAAALRLAALSRLGGGDATQLLRGLSGASDVIHEFLSENVLDLLEPE
LREFLLVASVTERTCGGLASALAGITNGRAMLEEAHRGLFLQRTEDDPNWFRFHQMFADFLHRRLERGGSHR
VAELHRRASAWFAENGYLHEAVDHALAAGDPARAVDLVEQDETNLPEQSKMTLLAIVQKLP TSMVVSRLR
QLAIWANILLQRPAATGALNRFETALGRAELPEATQADLRAEADVLRVAEVEFADRVERVDDLLAEAMSRPD
TLPPRVPGTAGNTAALAAICRFEFAEVYPLLDWAAPYQEMMGPFQTVYAQCLRGMAARNRLDIVAALQNFRT
AFEVGTAVGAHSHAARLAGSLLAELLYETGDLGAGRLMDESYLLGSEGGAVDYLAARYVIGARVKAQGDHE
GAADRLSTGGDTAVQLGLPRLAARINNERIRLGIAPAAVAADLLAPRTIPRDNGIATMTAELEDESAVRLSAGD
SADRQACQQRAGALAAAIDGTRRPLAALQAQILHIETLAATGRES DARNELAPVATKCAELGLSRLLDVAGLA

>sp|P9WIU5|ARFA_MYCTU Peptidoglycan-binding protein ArfA OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=arfA PE=1 SV=1

MASKAGLGQTPATTDARRTQKFYRGSPGRPWLIGAVVIPLLIAIGYGAFERPQSVTGPTGVLPTLTPTSTRGAS
ALSLSLLSISRSGNTVTLIGDFPDEAKAALMTALNGLLAPGVNVIDQIHVDPVVRSLDFSSAEPVFTASVPIPDFG
LKVERDVTTLGTAPSEHKDAVKRAATSTWPD MKIVNNEIVTGQAPP GPPASGPCADLQSAINAVTGGPIAFG
NDGASLIPADYEILNRVADKLGKACPDARVTINGYTDNTGSEGINIPLSAQRAKIVADYLVARGVAGDHIATVGLGS
VNPIASNATPEGRAKNRRVEIVVN

>sp|P9WIR7|APA_MYCTU Alanine and proline-rich secreted protein Apa OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=apa PE=1 SV=1

MHQVDPNLTRRKGRLAALAIAMASASLVTVAVPATANADPEPAPPVPTTAASPPSTAAAPPAPATPVAPPPPA
AANTPNAQPGDPNAAPPADPNAPPPPIAPNAPQPVRIIDNPVGGFSFALPAGWVESDAAHFYDGSALLSKT
TGDPPFPQQPPVANDTRIVLGRDLQKLYASAEATDSKAAARLGSDMGFEFYPYGPTRINQETVSLDANGVSG
SASYEYVKFSDPSKPNGQIWTGVIGSPAANAPDAGPPQRWFVWVWLTANNPVDKGA AKALAESIRPLVAPPPA
PAPAPAEAPAPAPAGEVAPTPTTPQRTLPA

>sp|P9WIB9|SCMU_MYCTU Secreted chorismate mutase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv1885c PE=1 SV=1

MLTRPREIYLATAVSIGILLSLIAPLGPPLARADGTSQLAELVDAAAERLEVADPVAAAFKWRAQLPIEDSGRVEQQ
LAKLGEDARSQHIDPDYVTRVFDDQIRATEAIEYSRFSWDKLN PASAPPEPPDLSASRS AIDSLNNRMLSQIWSH
WSLLSAPSCAAQLDRAKRDIVRSRHLSLYQRALTATQSYCQALPPA

>sp|P9WNK7|ESXA_MYCTU 6 kDa early secretory antigenic target OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=esxA PE=1 SV=1

MTEQQWNFAGIEAAASAIQGNVTSIHSLLDEGKQSLTKLAAWGGSGSEAYQGVQKQKWDATATELNNALQN
LARTISEAGQAMASTEENVTGMFA

>sp|P9WMK7|DBH_MYCTU DNA-binding protein HU homolog OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=hup PE=1 SV=1

MNKAELIDVLTQKLGSDRRQATAAVENVVDITVRAVHKGDSVTITGFGVFQRRRAARVARNPRTGETVKVKPT
SVPAFRPGAQFKAVVSGAQRLPAEGPAVKRGGVGSAAKKVAKKAPAKKATKAAKKAATKAPARKAATKAPAKK
AATKAPAKKAVKATKSPAKKVTKAVKKTAVKASVRKAATKAPAKKAAAKRPATKAPAKKATARRGRK

>sp|P9WMK1|ACR_MYCTU Alpha-crystallin OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=hspX PE=1 SV=1

MATTLPVQRHPRSLFPEFSELFAAFPSFAGLRPTFDTRLMRLEDEMKEGRYEVRAELPGVDPDKDVDIMVRDG
QLTIKAERTEQKDFDGRSEFAYGFSFVRTVSLPVGAEDEDDIKATYDKGILTVSVAVSEGKPTKHIQIRSTN

>sp|P9WJA3|HRP1_MYCTU Hypoxic response protein 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=hrp1 PE=1 SV=1

MTTARDIMNAGVTCVGEHETLAAAQYMREHDIGALPICGDDDRHLHGMLTDRDIVIKGLAAGLDPNTATAGEL
ARDSIYYVDANASIQEMLNVMEEHQVRRVPISEHRLVGIVTEADIARHLPEHAIVQFVKAICSPMALAS

>sp|P9WG65|MPT53_MYCTU Soluble secreted antigen MPT53 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=mpt53 PE=1 SV=1

MSLRLVSPIKAFADGIVAVAVVLMFGLANTPRAVAADERLQFTATTLSGAPFDGASLQGKPAVLWFWTPWC
PFCNAEAPSLSQVAANPAVTFVGIATRADVGAMQSFVSKYNLNFNLNDADGVIWARYNVPWQPAFVRYRA
DGTSTFVNNPTAAMSQDELSGRVAALTS

>sp|P9WHR5|CAEB_MYCTU Carboxylesterase B OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=caeB PE=1 SV=1

MAAMWRRRPLSSALLSFGLLGGLPLAAPPLAGATEEPGAGQTPGAPVVAPQQSWNSCREFIADTSEIRTARC
ATVSVVDYDQPGGTQAKLAVIRVPATGQRFGALLVNPGGPGASAVDMVAAMAPAIADTDILRHFDLVGFDP
RGVGHSTPALRCRTDAEFDAYRRDPMADYSPAGVTHVEQVYRQLAQDCVDRMGFSFLANIGTASVARDMD
MVRQALGDDQINYLGYSGTELGTAYLERFGTHVRAMVLDGAIDPAVSPIEESISQMAGFQTAFNDAADCARS
PACPLGTDSAQWVNRYHALVDPLVQKPGKTS DPRGLSYADATTGTINALYSPQRWKYLTSGLLGLQRGSDAGD
LLVLADDYDGRDADGHYSNDQDAFNAVRCVDAPTPADPAAWVAADQIRIQVAPFLSYGQFTGSAPRDLCAL
WPVPATSTPHPAAPAGAGKVVVVSTTHDPATPYQSGVDLARQLGAPLITFDGTQHTAVFDGNQCVD SAVMHY
FLDGTLPPTSLRCAP

>sp|P9WNF5|MP70_MYCTU Immunogenic protein MPT70 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=mpt70 PE=1 SV=1

MKVKNITIAATSFAAAAGLAALAVAVSPPAAAGDLVGPAGCAEYAAANPTGPASVQGMSPVAVAAASNNPELTTL
TAALSGQLNPQVNLVDTLNSGQYTVFAPTNAAFSKLPASTIDELKTNSSLLTSILTYHVVAGQTSPANVVGTRQTL
QGASVTVTGQGNLSKVGNDVVCVGGVSTANATVYMIDSVLMPPA

>sp|P9WNL1|ENO_MYCTU Enolase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=eno PE=1 SV=1

MPIIEQVRAREILDSRGNPTVEVEVALIDGTFARAAPVSGASTGEHEAVELRDGGDRYGGKGVQKAVQAVLDEI
GPAVIGLNADDQRLVDQALVDLDGTPDKSRLGGNAILGVSLAVAKAAADSALPLFRYVGGPNAHILPVPMMN
ILNGGAHADTAVDIQEFMVAPIGAPSFVEALRWGAEVYHALKSVLKKKEGLSTGLGDEGGFAPDVAGTTAALDLI
SRAIESAGLRPGADVALALDAAATEFFTDGTGYVFEGTTRTADQMTEFYAGLLGAYPLVSIEDPLSEDDWDGWA
ALTASIGDRVQIVGDDIFVTNPERLEEGIERGVANALLVKVNQIGTLTETLDAVTLAHHGGYRTMISHRSGETEDT

MIADLAVAIGSGQIKTGAPARSERVAKYNQLLRIEALGDAARYAGDLAFPRFACETK
>sp|P9WIR1|CFP6_MYCTU Low molecular weight protein antigen 6 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=cfp6 PE=1 SV=1
MAHFAVGFLTGLLVPVLTWPVSAPLLVIPVALSASIIRLRTLADERGVTVRTLVGSRAVRWDDIDGLRFHRGSW
ARATLKDGTLELRLPAVTFATLPHLTEASSGRVNPYPYR
>sp|P9WP39|CUT3_MYCTU Probable cutinase cut3 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=cut3 PE=1 SV=1
MNNRPIRLLTSGRAGLGAGALITAVLLIALGAVWTPVAFADGCPDAEVTFARGTGEPPGIGRVGQAFVDSLRLQ
QTGMEIGVYPVNYAASRLQLHGGDGANDAISHIKSMASCPNTKLVGGYSQGATVIDIVAGVPLGSISFGSPLP
AAYADNVAAVAVFGNPSNRAGGSSLSPLFGSKAIDL CNPTDPICHVGPNEFSGHIDGYIPTTYTQAASFVVQ
RLRAGSVPHLPGSVPQLPGSVLQMPGTAAPAPESLHGR
>sp|P9WP28|DAGK_MYCTO Diacylglycerol kinase OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=dagK PE=1 SV=1
MSAGQLRRHEIGKVTALTNP LSGHGA AVKAAHGA IARLKH RGV DVVEIVGG DAHDARHLLAAAVAKGTDAV
MVTGGDGVVSNALQVLGTDIPLGIIPAGTGNDHAREFGLPTKNPKAAADIVVDGWTETIDLGRIQDDNGIEK
WFGTVAATGFDSL VNDRANRMRWPHGRMRYIAMLAE LSRLRPLPFR LVLVDGTEEIVADLT LADFGNTRSYGG
GLLICPNADHSDGLLDITMAQSDSRTKLLRLFPTIFKGAHVELDEVSTTRAKTVHVECPGINVYADGDFACPLPAE
ISAVPAALQVLRPRHG
>sp|P9WJE1|ESPA_MYCTU ESX-1 secretion-associated protein EspA OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=espA PE=1 SV=1
MSRAFIIDPTISAI DGLYDLLGIGIPNQGGILYSSLEYFEKALEELAAAFPGDGWLGSAADKYAGKNRNHVNFQ E
LADLDRQLISLIHDQANAVQTRDILEGAKKGLEFVRPVAVDLTYIPVVGHALSAAFQAPFCAGAMAVVGGALA
YLVVKT LINATQLLKLAKLAELVAAAIA DIISDVADI IKTGLGEVWEFITNALNGLKELWDKLTGWV TGLFSRGWS
NLEFFAGVPGLTGATSGLSQVTGLFGAAGLSASSGLAHADSLASSASLPALAGIGGGSGFGGLPSLAQVHAAS T
RQALRPRADGPGVGA AAEEQVGGQSQLVSAQGSQGMGGPVGMGGMHPSSGASKGTTTKKYSEGAAAGTEDA
ERAPVEADAGGGQKVLVRNVV
>sp|P9WJD9|ESP B_MYCTU ESX-1 secretion-associated protein EspB OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=espB PE=1 SV=1
MTQSQT VTV DQQEILNRANEVEAPMADPPTDVPITPCELTA AKNAAQQLVLSADNMREYLAAGAKERQRLAT
SLRNAAKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDSSAELTDTPRVATAGEPNFMDLKEAARKLETGDQ
GASLAHFADGWNTFNLT LQGDVKRFRGFDN WEGDAATACEASLDQQRQWILHMAKLSAAMAKQAQYVAQ
LHVWARREHPTYEDIVGLERLYAENPSARDQILPVYAEYQRSEKVLTEYNNKAALEPVNPPKPPPAIKIDPPPPP
QEQGLIPGFLMPPSDGSGVTPGTGMPAAMPVPTGSPGGGLPADTAAQLTSAGREAAALSGDVAVKAASLGG
GGGGVPSAPLGS AIGGAESVRPAGAGDIAGLGQGRAGGGAALGGGGMGMPMGA AHQGGGAKSKGSQ
QEDEALYTEDRAWTEAVIGNRRRQDSKESK
>sp|P9WJD7|ESPC_MYCTU ESX-1 secretion-associated protein EspC OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=espC PE=1 SV=1
MTENLTVQPERLGLV LASHHDNA AVDASSGVEAAA GLGESVAITHG PYCSQFNDTLNVYLTAHNALGSSSLHTAG
VDLAKSLRIA AAKIYSEADEAWRKAIDGLFT
>sp|P9WK37|LPQB_MYCTU Lipoprotein LpqB OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=lpqB PE=1 SV=1
MERLMRLTILLFLGAVLAGCASVPSTSAPQAIGTVERPVPSNLPKPSPGMDPDVLLREFLKATADPANRH LAAR
QFLTESASNAWDDAGSALLIDHVVFVETRSAEKVSVTMRADILGSLSDVGVFETAEGQLPDPGPIELVKTS DGW
RIDRLPNGVFLDWQQFQETYKRNTLYFADPTGKTVVDP RYVAVSDRDQLATELVSKLLAGPRPEMARTVRNLL

APPLRLRGPVTRADGGKSGIGRGGYGGARVDM EKLSSTDPHSRQLLAAQIIWTLARADIRGPYVINADGAPLED
RFAEGWTTSDVAATDPGVADGAAAGLHALVNGSLVAMDAQRVTPVPGAFGRMPEQTAAAVSRSGRQVASV
VTLGRGAPDEAASLWVGD LGGEAVQSADGHSLRPSWSLDDAVWVVVD TNVVLRAIQDPASGQPARIPVDS
TAVASRFPGAINDLQLSRDGTRAAMVIGGQVILAGVEQTQAGQFALTYPRRLGFLGSSVVLSWRTGDDIVVT
RTDAAHPVSYVNL DGVNSDAPSRGLQTP LTAIAANPSTVYVAGPQGVLMYSASVESRPGWADVPGLMVPGA
APVLPG

>sp|A0QPU4|MSPB_MYCS2 Porin MspB OS=Mycobacterium smegmatis (strain ATCC 70084 /
mc(2)155) GN=mspB PE=1 SV=1

MTAFKRVLIAMISALLAGTTGMFVSAGAAHAGLDNELSLVDGQDRTLTVQQWDTFLNGVFPLDRNRLTREFW
HSGRAKYIVAGPGADEFEGTLELGYQIGFPWSLGVGINFSYTTPNILIDDGDITAPPFGLNSVITPNLFPVGSISAD
LGNPGIQEVATFSVDVSGPAGGVAVSNAHGTVTGAAGGVLLRPFARLIASGTGDSVTTYGEPWNMN

>sp|P9WIN7|MTB12_MYCTU Low molecular weight antigen MTB12 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=mtb12 PE=1 SV=1

MKMVKSIAGLTA AAAAGVTSIMAGGPVVYQMQPVVFGAPLPLDPASAPDVPTAAQLTSLNLSLADP
NVSFANKGSLVEGGIGGTEARIADHKLKAAEHGDLPLSFSVTNIQAAAAGSATADVSVSGPKLSSPVTQNVTFV
NQGGWMLSRASAMELLQAAGN

>sp|P9WHW9|PPE68_MYCTU Uncharacterized PPE family immunogenic protein PPE68
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ppe68 PE=1 SV=1

MLWHAMPPELNTARLMAGAGPAPMLAAAAGWQTLAALDAQAVELTARLNSLGEAWTGGGSDKALAAATP
MVVWLQTA STQAKTRAMQATAQAAAYTQAMATTPSLPEIAANHITQAVLTATNFFGINTIPIALTEMDYFIRM
WNQAALAMEVYQAETAVNTLFEKLEPMASILDPGASQSTTNPIFGMPSPGSSTPVGQLPPAATQTLGQLGEM
SGPMQQLTQPLQQVTSLFSQVGGTGGGNPADEEAAQMGLLGTSPLSNHPLAGGSGPSAGAGLLRAESLPGA
GGSLTRTPLMSQLIEKPVAPSVMPAAAAGSSATGGAAPVGAGAMGQGAQSGGSTRPGLVAPAPLAQEREED
DEDDWDEEDDW

>sp|A0QX22|RIPA_MYCS2 Peptidoglycan endopeptidase RipA OS=Mycobacterium smegmatis
(strain ATCC 70084 / mc(2)155) GN=ripA PE=1 SV=1

MRRTVRALATRVHGRVCAVPLVVGMLLATALYGGPAAADPAAPDNLATLVAKVASADQKLQELGAAIQTQQE
TVNKAIVDVQAARDA AAAAQRELEAGQRGVADANAAIEAAQKRFD SFAAATYMNGPSRSYLTATDPADIVNTT
ATGQALIASSQQVMAKLQRARTEQVNRESAARLAKEKADQAARDAESSQDNVAALKQAQQT FNAQQGELE
RLAAERAAAQAE LDSVRKVSATGNAAPAAAPAAAPAPAAAPVPNSAPAPVPGAQPNPQAAAGNWDRAPS
GPASSGQNWAVWDPTLPAIPSAFVSGDPIA IINAVLGIAS TSAQVTADMGRSFLQKLGILPTPTGFTNGAIPRVY
GREAVEYVIRRGMSQIGVPYSWGGGNAAGPSRGIDSGAGTVGFDCSGLMLYMFAGVGIKLDHYSQSQYNAG
RKIPSSQMRRGDMIFYGPNASQHVAMYLGNQMLEAPYTGSHVKVSPVRTSGMTPYVTRLIEY

>sp|H8F3N4|RPFC_MYCTE Resuscitation-promoting factor RpfC OS=Mycobacterium tuberculosis
(strain ATCC 35801 / TMC 107 / Erdman) GN=rpfc PE=2 SV=1

MTRIAKPLIKSAMAAGLVTASMSLSTAVAHAGPSPNWDVAQCESGGNWAANTGNGKYGGLQFKPATWAAF
GGVGNPAAASREQQIAVANRVLAEQGLDAWPTCGAASGLPIALWSKPAQGIKQIINEI IWAGIQASIPR

>sp|P9WLN2|Y2004_MYCTO Uncharacterized protein MT2060 OS=Mycobacterium tuberculosis
(strain CDC 1551 / Oshkosh) GN=MT2060 PE=2 SV=1

MDSPTNDGTCDAPVTDPEFIDVRETHAVVVLAGDRAFKAKKPVVTD FCFDRTAEQRERACIREFELNSRLAA
QSYLGHIAHSDPSGGHAEPVVVMRRYRDKQRLASMV TAGLPVEGALDAIAEVLARFHQRAQRNRCIDTQGEV
GAVARRWHENLAELRHHADKVVSGDVIRRIEHMVDEFVSGREVLFAGRIKEGCIVDGHADLLADDIFLVDGEP
ALLDCLEFEDELRYLDRIDDA AFLAMDLEFLGRKDLGDYFLAGYAVRSGDTAPASLRDFYIAYRAVVRAKVECVRF
SQGKPEAAADAVRHLLIATQHLQHATVRLALVGGNPGTGKSTLARGVAELVGAQVISTDDVRRRLRDCGVITGE

PGVLDSGLYSRANVVAVYQEALRKARLLGSGHVSILDGTWGDQPQRACARRLAADTHSAIVEFRCSATVDVM
ADRIVARAGGNSDATAEIAAALAARQADWDTGHRIDTAGPRERSVGQAYHIWRSI

>sp|P9WL75|Y2588_MYCTU Uncharacterized protein Rv2588c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv2588c PE=1 SV=1

MESFVLFLLPFLIMGGFMYFASRRQRAMQATIDLHDSLQPGERVHTTSGLEATIVAIADDTIDLEIAPGVVTTW
MKLAIRDRIIPDDDDIDEELNEDLDKDVDDVAGERRVTNDS

>sp|P9WKW5|Y3835_MYCTU Uncharacterized membrane protein Rv3835 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv3835 PE=1 SV=1

MLDAPEQDPVDPGDPASPPHGAEQPLPGPRWPRALRASATRRALLLTALGGLLIAGLVTAIPAVGRAPERLAG
YIASNPVPSTGAKINASFNRVASGDCLMWPDGTPESAAIVSCADEHRFEVAESIDMRTFPGMEYGQNAAPPSP
ARIQQISEEQCEAAVRRYLGTKFDPNSKFTISMLWPGDRAWRQAGERRMLCGLQSPGPNQQLAFKGVADI
DQSKVWPAGTCLGIDATTNQPIDVPVDCAAPHAMEVSGTVNLAERFPDALPSEPEQDGFIKDACTRMTDAYL
APLKLRTTTLTIYPTLTLPSWSAGSRVVACSIGATLGNGGWATLVNSAKGALLINGQPPVPPPDIPEERLNLPIPI
LQLPTPRPAPPAQQLPSTPPGTQHLPAAQPVVTPTRPPESHAPASAAPAETQPPPPDAGAPPATQSPEATPPGP
AEPAPAG

Non-secretory protein

>sp|P9WPY3|AROK_MYCTU Shikimate kinase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=aroK PE=1 SV=1

MAPKAVLVGLPGSGKSTIGRRLLAKALGVLLDQVIEQRTGRSIADIFATDGEQEFRRIEEDVVRAALADHDGV
LSLGGGAVTSPGVRAALAGHTVVYLEISAAEGVRRGTGGNTVRPLLAPDRAEKYRALMAKRAPLYRRVATMRV
DTNRRNPGAVVRHLSRLQVPSPEAAT

>sp|P9WVGK3|DEVS_MYCTU Redox sensor histidine kinase response regulator DevS OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=devS PE=1 SV=1

MTTGGLVDENDGAAMRPLRHTLSQLRLHELLVEVQDRVEQIVEGRDRLDGLVEAMLVVVTTAGLDLEATLRAIVH
SATSLVDARYGAMEVHQRHRVLFVYEGIDEETVRRIGHLPKGLGVIGLLIEDPKPLRLDDVSAHPASIGFPPYH
PPMRTFLGVVVRVDESFGTLYLTDKTNQPFSDDEVLVQALAAAAGIAVANARLYQQAKARQSWIEATRDLA
TELLSGTEPATVFRVLAEEALKLTAADAALVAVPVDEMPAADVGEVLLVIETVGSASIVGRTIPVAGAVLREVFV
NGIPRRVDRVDLEGLDELADAGPALLPLRARGTVAGVVVLSQGGPGAFTEQLEMMAAFADQAALAWQL
ATSQRRMRELDVLTDRDRIARDLHDHVIQRLFAIGLALQGAVPHERNPEVQQRLSDVVDDLQDVQIERTTIYDL
HGASQGITRLRQRIDAAVAQFADSLRQSVQFVGPLSVVDSALADQAEAVVREAVSNAVRHAKASTLTVRVKV
DDDLCEIVTDNDRGLPDEFTGSGLTNLRQRAEQAGGEFTLASVPGASGTVLRWSAPLSQ

>sp|P9WI81|PKNB_MYCTU Serine/threonine-protein kinase PknB OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pknB PE=1 SV=1

MTTPSHLSDRYELGELGFGGMSEVHLARDLRLHRDVAVKVLRLADLARDPSFYLRFRREAQNAALNHPAIVAV
YDTGEAETPAGPLPYIVMEYVDGVTLRDIVHTEGPMTPKRAIEVIADACQALNFSHQNGIIHRDVKPANIMISAT
NAVKVMDFGIARAIADSGNSVTQTAAVIGTAQYLSPEQARGDSVDARSVYSLGCVLYEVLTEGPPFTGDSPPV
VAYQHVREDPIPPSARHEGLSADLDAVVLKALAKNPENRYQTAAEMRADLVRVHNGEPPEAPKVLTDARTSL
SSAAGNLGPRTDPLRQDLDDTDRDRSIGSVGRWVAVVAVLAVLTVVTIAINTFGGITRDVQVPDVRGQSSA
DAIATLQNRGFKIRTLLQKPDSTIPPDHVIGTDPAAANTSVSAGDEITVNVSTGPEQREIPDVSTLTAYEAVKLLAAG
FGRFKQANSPSTPELVGKVIGTNPANQTSAITNVVIVGSGPATKDIPDVAGQTVDAQKLNLVYGFTKFSQA
SVDSPRPAGEVTGTNPPAGTTVPVDSVIELQVSKGNQFVMPDLSGMFWVDAEPRLRALGWTGMLDKGADV
DAGGSQHNRVVYQNPAGTGVRDGIITLRFQ

>sp|P9WMF9|DEVR_MYCTU Transcriptional regulatory protein DevR (DosR) OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=devR PE=1 SV=1

MVKVFLVDDHEVRRGLVDLLGADPELDVVGEGSVAEAMARVPAARPDVAVLDVRLPDGNGIELCRDLSR
MPDLRCLITSYTSDEAMLDAILAGASGYVVKDIKGMELARAVKDVGAGRSLLDNRAAALMAKLRGAAEKQD
PLSGLTDQERTLLGLLSEGLTNKQIADRMFLAEKTVKNYVSRLAKLGMERRTQAAVFATELKRSPPGDGP

>sp|P9WPP9|CP51_MYCTU Lanosterol 14-alpha demethylase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=cyp51 PE=1 SV=1

MSAVALPRVSGGHDEHGHLEEFRTDPIGLMQRVRDECGDVGTFQLAGKQVVLLSGSHANEEFFRAGDDDDLD
QAKAYPFMTPIFGEGVVFDAASPERRKEMLNHAALRGEQMKGHAATIEDQVRRMIADWGEAGEIDLLDFFAEL
TIYTSSACLIGKKFRDQLDGRFAKLYHELERGTDPPLAYVDPYLPESFRRRDEARNGLVADVADIMNGRIANPPTDK
SDRDMLDVLIKAVKAETGTPRFSADEITGMFISMMFAGHHTSSGTASWTLIELMRHRDAYAAVIDELDELYGDGR
SVSFHALRQIPQLENVLKETLRLHPLIILMRVAKGEFEVQGHRIHEGLVAASPAISNRIPEDFPDPHFVDPARYE
QPRQEDLLNRWTWIPFGAGRHRVCGAAFAIMQIKAIFSULLREYEFEMAQPPESYRNDHSMVQVLAQACV
RYRRRTGV

>sp|P9WFF7|DPDS_MYCTU Decaprenyl diphosphate synthase OS=Mycobacterium tuberculosis

(strain ATCC 25618 / H37Rv) GN=uppS PE=1 SV=1

MARDARKRTSSNFPQLPPAPDDYPTFPDTSTWPVVFPELPAAPYGGPCRPPQHTSKAAAPRIPADRLPNHVAI
VMDGNRWATQRLARTEGHKMGAEVVIDIACGAIELGIKWLSLYAFSTENWKRSPPEVRFMLMGFNDRDVRR
RRDTLKKLGVRRVWVGSRPLWRSVINELAVAEEMTKSNDVITINYCVNYGGRTTEITREIAREVAAGRLNPE
RITESTIARHLQRPDIPDVLFLRTSGEQRSSNFMLWQAAYAEIFQDKLWPDYDRRDLWAACEEYASRTRRFG
SA

>sp|P9WQ37|FAC13_MYCTU Long-chain-fatty-acid--CoA ligase FadD13 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=fadD13 PE=1 SV=1

MKNIGWMLRQRATVSPRLQAYVEPSTDVRMTYAQMNALANRCADVLTALGIAKGDRVALLMPNSVEFCCLFY
GAAKLGAVAVPINTRLAPEVSFILSDSGSKVVIYGAPSAPVIDAIRAQADPPGTVTDWIGADSLAERLSAAAD
EPAVECGDDNLFIMYSGTTGHPKGVVHTHESVHSAASSWASTIDVRYRDRLLLPLPMFHVAALTTVIFSAMR
GVTLISMPQFDATKVWVSLIVEERVCIGGAVPAILNFMQRQVPEFAELDAPDFRYFITGGAPMPEALIKIYAAKNIEV
VQGYALTESCGGGTLLLEDALRKAGSAGRATMFTDVAVRGDDGVIREHGEVVIKSDILLKEYWNRPEATRD
AFDNGWFRTGDIGEIDDEGYLIKDRDKDMIISGGENVYPAEIESVIIGVPGVSEVAVIGLPDEKWGEIAAAIVVA
DQNEVSEQQIVEYCGTRLARYKLPKKVIFAEAI PRNPTGKILKTVLREQYSATVPK

>sp|O53585|GLFT2_MYCTU Galactofuranosyl transferase GlfT2 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=glt2 PE=1 SV=1

MSELAASLLSRVILPRGPELDVRKLYLEESTTNARRAHAPTRTSLQIGAESEVSFATYFNAPASYWRRWTTCKS
VVLRVQVTGAGRVDVYRTKATGARIFVEGHDFGTEDQPAAVETEVLQPFEDGGVWVFDITTDVAVTLHSG
GWYATSPAGTANIAVGIPTFNRPADCVNALRELTADPLVDQVIGAVIVPDQGERKVRDHPDFAAAAARLGSRL
SIHQPNLGGSGGYSRVMEALKNTDCQQILFMDDIRLEPDSILRVLAMHRFAKAPMLVGGQMLNLQEPSH
LHIMGEVDRSIFMWTAAAPHAEDHDFAEYPLNDNNSRSKLLHRRIDVDYNGWWTMIPRQVAEELGQPLP
LFIKWDDADYGLRAAEHGYPVTLPGAIIWHMAWSDKDDAIDWQAYFHLRNRLVVAAMHWDGPKAQVIGL
VRSHLKATLKLACLEYSTVAIQKAIDDFLAGPEHIFSILESALPQVHRIRKSYPDVAVLPAASELPPPLHKNKAM
KPPVNPLVIGYRLARGIMHNLTAANPQHRRRPEFNVPTQDARWFLCTVDGATVTTADGCGVVYRQRDRAK
MFALLWQSLRRQRQLKRFEEEMRRIYRDALPTLSSKQKWETALLPAANQEPEHG

>sp|P9WPZ3|ARGJ_MYCTU Arginine biosynthesis bifunctional protein ArgJ OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=argJ PE=1 SV=1

MTDLAGTTRLLRAQGVTAAGFRAAGVAAGIKASGALDLALVFNEGPDYAAAGVFTRNQVKAAPVLWTQQVL
TTGRLRAVILNSGGANACTGPAGFADTHATAEAVAAALS DWGTETGAIEVAVCSTGLIGDRLPMDKLLAGVAHV
VHEMHGGLVGGDEAAHAIMTTDNVPKQVALHHHDNWTVGGMAKGAGMLAPSLATMLCVLTTDAAEPA
ALERALRRAAAATFDRLDIDGSCSTNDTVLLSSGASEIPPAQADLDEAVLRVCDDLCAQLQADAEGVTKRVTVT
VTGAATEDDALVAARQIARDSLVKTALFGSDPNWGRVLAAVGMAPITLDPDRISVSFNAAVCVHGVGAPGA
REVDLSADADITVDLGVGDGQARIRTTDLSHAYVEENSAYSS

>sp|P71590|FHAA_MYCTU FHA domain-containing protein FhaA OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=fhaA PE=1 SV=1

MGSQKRLVQRVERKLEQTVGDAFARIFGGIVPQVEEALLRREAADGIQSLQGNRLLAPNEYIITLGVHDFEKL
ADPELKSTGFARDLADYIQEQGWQTYGDVVVRFQSSNLHTGQFRARGTVNPDVETHPPVIDCARPQSNHAF
GAEPGVAPMSDNSSYRGGQGQGRPDEYDDRYARPQEDPRGGPDPOGGSDPRGGYPPETGGYPPQPGYPR
PRHPDQGDYPEIQYDPDQGGYPEQRGYPEQRGYPDQGRGYDQGRGYDQGGYPPYEQRPPVSPGPA
GYGAPGYDQGYRQSGGYGSPGGGQPGYGGYGEYGRGPARHEEGSYVPSGPPGPEQRPAYPDQGGYDQ
YQQGATTYGRQDYGGGADYTRYTESPRVPGYAPQGGGYAEPAGRDYDYGQSGAPDYGQPAPGGYSGYGGG
YGSAGTSVTLQLDDGSGRTYQLREGSNIIGRQDAQFRLPDTGVSRRHLEIRWDGQVALLADLNSTNGTTVNN
APVQEWQLADGDVIRLGHSEIIVRMH

>sp|P9WIT9|OTC_MYCTU Ornithine carbamoyltransferase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=argF PE=1 SV=1

MIRHFLRDDDLSPAEQAEVLELAAELKDPVSRRLQGPGRGVAVIFDKNSTRTRFSFELGIAQLGGHAVVVDSGS
TQLGRDETLQDTAKVLSRYVDAIVWRTFGQERLDAMASVATVPVINALSDEFHPCQVLADLQTI AERK GALRGL
RLSYFGDGANNMAHSLLLGGVTAGIHVTVA APEGFLPDPSVRAAAERRA QDTGASVTVTADAHAAAAGADVL
VTDTWTSMGQENDGLDRVKPFRPFQLNSRLLALADSDAIVLHCLPAHRGDEITDAVMDGPASAVWDEAENR
LHAQKALLVWLLERS

>sp|P9WIL5|PANC_MYCTU Pantothenate synthetase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=panC PE=1 SV=1

MTIPAFHPGELNVYSAPGDVADVSRALRLTGRRVMLVPTMGALHEGHLALVRAAKRVPGSVVVVSIFVNPMQ
FGAGEDLDAYPRTPDDDLAQLRAEGVEIAFTPTTAAMYPDGLRRTTVQGPLAAEELEGGPRPTHFAGVLTVVLK
LQIVRPDRVFFGEKDYQQLVLRQLVADFNLDAVAVGVPTVREADGLAMSSRNRYLDPAQRAAAVALSAALTA
AHAATAGAQAALDAARAVLDAAPGVAVDYELRDIGLGPMLNGSGRLLVAARLGTTRLLDNIAIEIGTFAGTD
RPDGYRAILESHWRN

>sp|P9WHR9|Y3671_MYCTU Serine protease Rv3671c OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv3671c PE=1 SV=1

MTPSQWLDIAVLAVAFIAAISGWRAGALGSMLSFGGVLLGATAGVLLAPHIVSQISAPRAKLF AALFLILALVVVG
EVAGVVLGRAVRGAI RNRP IRLIDSIVIGVGVQLVVVLTAAWLLAMPLTQSKEQPELAAAVKGSRLARVNEAAP
TWLKTVPKRLSALLNTSGLPAVLEPFSRTPVIPVASPDALVNNPVVAATEPSVVKIRSLAPRCQKVLEGTGFVISP
DRVMTNAHVVAGSNNVTVYAGDKPFEATVVSYPDSDVAILAVPHLPPPPLVFAAEPAKTGADVVLGYPGGG
NFTATPARIREAIRLSGPDYGDPEPVTRDVY TIRADVEQDGGPLIDLNGQVLGVVFGAAIDDAETGFVLTAGE
VAGQLAKIGATQPVGTGACVS

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

MSTTFAARLNRLFDTVYPPGRGPHTSAEVIAALKAEGITMSAPYLSQLRSGNRTNPSGATMAALANFFRIKAAY
FTDDEYEEKLDKELQWLCTMRDDGVRRIAQRAHGLPSAAQKQVLDRIDELRRAEGIDA

>sp|P9WI79|PKND_MYCTU Serine/threonine-protein kinase PknD OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pknD PE=1 SV=1

MSDAVPQVGSQFGPYQLLRLLGRGGMGVEYEAEDTRKHRVVALKLISPOYSDNAVFRARMQREADTAGRLTE
PHIVPIHDYGEINGQFFVEMRMIDGTSRLALLKQYGPLTPARAVAIVRQIAAALDAAHANGVTHRDKPENILVT
ASDFAYLVDFGIARAASDPGLTQTGTAVGTYNMAPERFTGDEVYRADIYALACVLGECLTGAPPYRADSVERLI
AAHLMDPAPQPSQLRPGRVPPALDQVI AKGMAKNPAERFMSAGDLAIAAHDALTSEQHQA T TILRRGD NAT
LLATPADTGLSQSESGIAGAGTGPPTPGAARWSPGDSATVAGPLAADSRRGGNWPSTGHSPAVPNALQASLG
HAVPPAGNKRKVVAVVGGAAIVLVAIAAAGYLVLRPSWSPTQASGQTVLPFTGIDFRLSPSGVAVDSAGNVY
VTSEGM YGRVVKLATGSTGTTVLPFNGLYQPQGLAVDGAGTVYVTD FNNRVVTLAAGSNNQTVLPFDGLNYP
EGLAVDTQGAVYVADRGNRRVVKLAAGSKTQTVLPFTGLNDPDGVAVDNSGNVYVTD T DNNRVVKLEAESN
NQVVL PFTDITAPWGIAVDEAGTVYVTEHNTNQVVKLLAGSTTSTVLPFTGLNTPLAVAVDSDRTVYVADRGN
DRVVKLTS

>sp|P9WN23|TRHBO_MYCTU Group 2 truncated hemoglobin G1bO OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=g1bO PE=1 SV=1

MPKSFYDAVGGAKTFDAIVSRFYAQA EDEVLRVYPEDDLAGAEERLRMFLEQYWGGPRTYSEQRGHPRLR
MRHAPFRISLIERDAWLRCMHTAVASIDSETLDDEHRRELLDYLEMAAHSVNSPF

>sp|P9WGF7|Y1739_MYCTU Probable sulfate transporter Rv1739c OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv1739c PE=1 SV=1

MIPTMTSAGWAPGVVQFREYQRRWLRGDVLAGLTVAAYLIPQAMAYATVAGLPPAAGLWASIAPLAIYALLGS
SRQLSIGPESATALMTAAVLAPMAAGDLRRYAVLAATLGLLVGLICLLAGTARLGFLASLSRSPVLVGYMAGIALV
MISSQLGTITGTSVEGNEFFSEVHSFATSVTRVHWPTFVLAMSVLALLTMLTRWAPRAPGPIIIVLAATMLVAV
MSLDAKGIAIVGRIPSGLPTPGVPPVSVEDLRALIIPAAGIAIVTFTDGVLTARAFARRGQEVNANAELRAVGAC
NIAAGLTHGFVSSSSSRTALADVGGRTQLYSLIALGLVIVMVFASGLLAMFPIAALGALVVYAALRLIDLSEFR
RLARFRRESEMLALATTAAVLGLGVFYGVLAVALSILELLRRVAHPHDSVLGFVPGIAGMHDDIDDPQAKRVPG
LVVYRYDAPLCFANAEDFRRRALTVDQDPGQVEWFLNAESNVEVDLTALDALDQLRTELLRRGIVFAMARV
KQDLRESLRAASLLDKIGEDHIFMTLPTAVQAFRRR

>sp|P9WIR9|34KD_MYCTU 34 kDa antigenic protein homolog OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv0954 PE=1 SV=1

MTYSPGNPGYPQAQPAQSYGGVTPSFAHADEGASKLPMYLNIAVAVLGLAAYFASFGPMFTLSTELGGGDGAV
SGDTGLPVGVALLAALLAGVALVPKAKSHVTVAVLGLVGLVFLMVSATFNKPSAYSTGWALWVVLAFIVFQAVA
AVLALLVETGAITAPAPRPKFDYPYQYGRYQYQYGVQPGGYGQQAAGLQSPGPQQSPQPPGYGS
QYGGYSSSPSQSGSYTAQPPAQAQSGSQSHQGPSTPPTGPFSPPPPVSAGTGSQAGSAPVNYSNPSG
GEQSSSPGGAPV

>sp|P9WQP7|3BHS_MYCTU 3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv1106c PE=1 SV=1

MLRRMGDASLTTELGRVLVTGGAGFVGANLVTLLDRGHVRSFDRAPSLLPAHPQLEVLQGDITDADVCAA
AVDGIDTIFHTAAIIELMGGASVTDEYRQRSFAVNVGGTENLLHAGQRAGVQRFVYTSSNSVVMGGQNIAGG
DETLPYTDRFNDLYTETKVVAERFVLAQNGVDGMLTCAIRPSGIWNGDQTMFRKLFESVLKGHVKVLVGRKS
ARLDNSYVHNLHGFILAAHLVPDGTAPGQAYFINDAEPINMFEFARPVLEACGQRWPKMRISGPAVRWVM
TGWQRLHFRFGFPAPLLEPLAVERLYLDNYFSIAKARRDLGYEPLFTTQQALTECLPYVVSLEFQMKNEARA EKTA
ATVKP

>sp|O65934|ABC1_MYCTU ABC transporter ATP-binding/permease protein Rv1747
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv1747 PE=1 SV=1

MPMSQPAAPPVLTVRYEGSERTFAAGHDVVGRDLRADVRVAHPLISRAHLLRFDQGRWVAIDNGSLNGLY
LNNRRVPVVDIYDAQRVHIGNPDGPALDFEVRHRGSAGRPPQTTSIRLPNLSAGAWPTDGPPTGTGLGSGQ
LQQLPPATTRIPAAPPSPGPQPRYPYTGQQLWPPSPGQRPAPQYRPPAAPPAGARGGTEAGNLATSMMKILR
PGRLTGELPPGAVRIGRANDNDIVPEVLASRHHATLVPTPGGTEIRDNRSINGTFVNGARVDAALLHDGDVVTI
GNIDLVFADGTLARREENLETRVGGDLVRGVTWTIDGDKTLLDGLSITARPGMLTAVIGPSGAGKSTLARLVAG
YTHPTDGTVTFEGHNVAEYASLSRIGMVPQDDVVHGQLTVKHALMYAAELRLPPDTTKDDRTQVVARVLE
ELEMASKHIDTRVDKLSGGQRKRASVALELLTGPSLLILDEPTSGLDPALDRQVMTMLRQLADAGRVLVVTHTSLT
YLDVCDQVLLAPGGKTAFCGPPTQIGPVMGTTNWADIFSTVADDPDAAKARYLARTGPTPPPPVEQPAELG
DPAHTSLFRQFSTIARRQLRLIVSDRGYFVFLALLPFIMGALSMSVPGDVGFGFPNPMGDAPNEPGQILVLLNV
GAVFMGTALTIRDLIGERAIFRREQAVGLSTTAYLIAKVCVYTVLAVVQSAIVTVIVLVGKGGPTQGAVALSKPDLE
LFVDVAVTCVASAMLGLALSIAKSNEQIMPLLVAVMSQLVFSGGMIPVTGRVPLDQMSWVTPARWGFAAS
AATVDLIKLVPGPLTPKDSHWHHTASAWWFDMAMLVALSVIYVGFVRWKIRLKAC

>sp|P9WMB5|ACYLT_MYCTU Phosphatidylinositol mannoside acyltransferase
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2611c PE=1 SV=1

MIAGLKGLKLPKDRSSVTRTATDWAYAAGWMAVRALPEFAVRNAFDTGARYFARHGGPEQLRKNLARVLGV
PPAAVPDPLMCASLESYGRYWREVFRLPTINHRKLARQLDRVIGGLDHLDAALAAGLAVLALPHSGNWDMA
GMWLVRHGTFTTVAERLKPELYQRFIDYRESLGFVLPSSGGERPPFEVLSERLRNNRVVCLMAERDLTRTG
VEVDFFGEPTRMPVGPAPKAVETGAALLPTHCFEGRGWGFQVYPALDCTSGDVAAITQALADRFAQNIAAH
PADWHMLQPQWLADLSESRAQLRSR

>sp|P9WN03|AFTA_MYCTU Arabinofuranosyltransferase AftA OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=aftA PE=1 SV=1

MPSRRKSPQFGHEMGAFTSARAREVLVALGQLAAAVVVAVGVAVVSLAIARVEWPAFPSSNQLHALTTVGQ
VGCLAGLVGIGWLWRHGRFRRLARLGGVLVSAFTVVTLGMPLGATKLYLFGISVDQQFRTEYLRLTDAAALRD
MTYIGLPPFPYPPGWFWIGGAAAALGTPAWEMFKPWAITSMAIAVAVALVWWRMIRFEYALLTVATAAVM
LAYSSPEPYAAMITVLLPPMLVLTWSGLGARDRQGWAAVVGAGVFLGFAATWYLLVAYGAFTVVLMAALLAG
SRLQSGIKAADVPLCRLAVVGAIAAAIGSTTWLPHYLLRAARDPVSDTGSQAQHYLPADGAALTFPMLQFSLGAIC
LLGTLVLMRARRSSAPAGALAIGVLAVYLWLSLMLATLARTLLSFRLQPTLSVLLVAAGAFGFVEAVQALGKR
GRGVIPMAAAIGLAGAIAFSQDIPDLRDLTIAYTDTDGYGQRGDRRPPGSEKYPAIDAAIRRVTKRRDRTV
VLTADYSFLSYYPYWGFGQLTPHYANPLAQFDKRAQIDSWGLSTADEFIAALDKLPWQPPTVFLMRHGAHN
SYTLRLAQDVYPNPQNVRRYTVDLRTALFADPRFVVEDIGPFVLAIRKPQESA

>sp|O53582|AFTB_MYCTU Terminal beta-(1->2)-arabinofuranosyltransferase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=aftB PE=1 SV=3

MVRVSLWLSVTAVAVLFGWGSWQRRWIADDGLVLRVLRNLLAGNGPVFNQGERVEANTSTAWTYLLVGG
WVGGPMRLEYVALALAMVLSLLGMVLLMLGTGRLYAPSLRGRRAIMLPAGALVYIAVPPARDFATSGLESGLV
AYLGLLWMMVCWSQPLRARPDSQMFLGALAFVAGCSVLRPEFALIGGLALIMMLIAARTWRRRVLIVLAG
GFLPVAYQIFRMGYGLLPSTALAKDAAGDKWSQGMIIYVSNFNRPYALWVPLVLSVPLGLLLMTARRRPSFLR
PVLAPDYGRVARAVQSPPAVAVFIVGSGVLQALYWIRQGGDFMHGRVLLAPLFCLLAPVGVIPILLPDGKDFSRE
TGRWLVGALSGLWLGIAGWSLWAANSPGMGDDATRVTYSGIVDERRFYAQATGHAHPLTAADYLDYPRMAA
VLTALNNTPEGALLPSGNYNQWDLVPMIRPSSGTAPGGKPAKPKQHAVFFTNMGMLGMNVGLDVRVIDQI
GLVNPLAAHTERLKHARIGHDKNLFDPDWVIADGPVWKWYPGIPGYIDQQWVTQAEALQCPATRAVLNSVR
APITLHRFLSNVLHSYEFTRYRIDRVPRYELVRCGLDVPDGPDPGPPRE

>sp|P9WMZ7|AFTC_MYCTU Alpha-(1->3)-arabinofuranosyltransferase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=aftC PE=1 SV=1

MYGALVTAADSIRTGLGASLLAGFRPRTGAPSTATILRSALWPAAVLSVLHRSIVLTTNGNITDDFKPVYRAVLNFR
RGWDIYNEHFDYVDPHYLPPGGTLLMAPFGYLPFAPSRYLFISSINTAAILVAAYLLRMFNFTLTSVAAPALILAM
FATETVTNTLVFTNINGCILLLEVLFLRWLLDGRASRQWCGGLAIGLTLVLPKPLGPLLLPLLNQRWRALVAAVV
VPVVVNVAALPLVSDPMSFFTRTLPYILGTRDYFNSSILNGVYFGLPTWLILFLRILFTAIFGALWLLRYRYRTGD
PLFWFTTSSGVLLLWSWLVMSLAQGYSSMMLFPFLMTVVLPNSVIRNWPWALGVYGFMTLDRWLLFNWM
RWGRALEYLKITYGWSLLIVTFTVLYFRYLDKADNRDLGGIDPAWLTPEREGQR

>sp|AOQPD4|AFTD_MYCS2 Alpha-(1->3)-arabinofuranosyltransferase OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=aftD PE=1 SV=1

MVAAATLVLTFAQSPGQISPDTKLDLTANPLRFLARAFNLWNSDLPGQAQNAQYGLFPHGTFFLLGDVLGVP
GWVTQRLWWALLLTVGFVGVLRVAEALGIGSTPSRLIGAAAFALSPRVLTTLGAISSETLPMMLAPWVLLPVIL
ALRGQHSVRLMAARSAGAVALMGAVNAVATLTGCLAAVIWWACHRPNRLWWRFTAWWLLCGALAVTWW
VVALLMLGRISPPFLDFIESSGVTTQWMSLTEMRLRGTMSWTPFVAPSATAGASLVTSTTAVLATTVAAAAGLAG
LALRTMPARGRLITMLLIGVLLGLGYSGGLGSPVALQVQAFLDGSGTPLRNLAKLEPVIRLPLALGLVHLLGRIPL
PGSAPRAVWVSAFAHPERDKRVAVAIVLSALAAGTSLAWTARLTPPGSFTAIPQHWHDAAAWLDEHNTDRG
RVLVAPGAPFATQVWGNSHDEPLQVLGDNPWGVRDSIPLTPPETIRALDSVQRLFASGRPSPGLADTLARQGIS
YVVVRNDLDPDTSRSARPILVHRAVEGSPGLTKVAEFGDPVPGTLEGFVADSGLRPRYPAVEIFRVEPADAGSS
QQRSPMHPYLVDSAMTRVAGAPEALLRLDERRRLNGEPLGPMMLAADARRAGLPVDGVIVTDTPTAREIDY
GRVDDHASAIRTPDDARHTYNRVDPYPSDGADLVYKWTGGRLSVSSAADSTALPYVAPATGPAAAIDSST
AWVSNALQAAVQWLQVDFDHPVTNATLTITPSATAVGAQVRRIEIATATGTSSLRFDTAGKPLIPLVGETPW
VRVTAVATDDGSPGVQFVTDLAITQYDASGFAHPVTLRHTVEVPVGGPPAGSVVQQWDLGTELLGRPGCADSP

VGVRCAAAMALASEEPVNLSTLTPQDTEVQPTVWIRGRQGNLADLVAQPDTTTRAFGSDPIDVLGSAYAA
TDGDPRTSWTAPQRVVQFQTPPTLTLKLRPTEVSGMRIVPGDTEPPAHTLVAIDLGDGPQMHRLPADGEPR
TVTLKPRVTDVTVSLLAWNDIIDRTSLGFDQLKPPGLAELTVLDGRGAPVGAADAANKRSRAVALPCGQGPIIA
VAGQFIQTSVHTTVGALLDGEPIPARPCRSEPVKLPAGQQELVSPGAAAFIVDGVLELPTAADEIRSAPTTSAETG
TWTADRREVRVSAQAQRVLVVPESVNRGWSAHDPAQELQSVTVNGWQQGWVVPAGTEGTVTLTFASN
MPYRVGLIGGLALLPLALLALIPVRRPVRAAAPARPWNPVLTGAAALVAGTAISGVAGLLVGAAMGVRILL
NRRGAAGEKVDNVTVVVAAGGLLAGSVLSQYPWRSVDGYVGHTPGVQFLALLSVAFLAASAVRLVNRPEP
SEDGRSAKPEHTGASAHAG

>sp|P9WQM7|ANSP2_MYCTU L-asparagine permease 2 OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) GN=ansP2 PE=1 SV=1

MPPLDITDERLTREDTGYHKGLHSRQLQMIALGGAIGTGLFLGAGGRLASAGPGLFLVYGICGIFVFLILRALGELV
LHRPSSGSFVSYAREFYGEKVAFVAGWMYFLNWAMTGIVDTTAAIAHYCHYWRAFQPIQWTLALIALLVLSM
NLISVRLFGELEFWASLIKVIALVTLVGTVFLAGRYKIDGQETGVSLWSSHGGIVPTGLLPIVLVTSQVVFAYAAIE
LVGIAAGETAEPKIMPRAINSVLRIACFYVGSTVLLALLPYTAYKEHVSPFVTFFSKIGIDAAGSVMNLVLTAA
LSSLNAGLYSTGRILRSMANGSGPRFTAPMSKTGPYPYGGILLTAGIGLLGILNAIKPSQAFEIVLHIAATGVIAAW
ATIVACQLRLHRMANAGQLRQPKFRMPLSPFSGYLTLAFLAGVLILMYFDEQHGPWMIATVIGVPALIGGWY
LVRNRVTAVAHHAIDHTKSVAVVHSADPI

>sp|P9WQ05|ARCA_MYCTU Arginine deiminase OS=Mycobacterium tuberculosis (strain ATCC
25618 / H37Rv) GN=arcA PE=1 SV=1

MGVELGSNSEVGALRVVILHRPGAELRRLTPRNTDQLLFDGLPWVSRAQDEHDEFAELLASRGAEVLLSLLT
EALHHSGAARMQGIAAAVDAPRLGLPLAQELSAYLRSLDPGRLAHVLTAGMTFNELPSDTRTDVSLVLRMHG
GDFVIEPLPNLVFTRDSSIWIGPRVVIPSLALRARVREASLTDLIYAHHPRTGVERRAYESRTAPVEGGDVLAPG
VVAVGVGERTTPAGAEALARSLFDDDLAHTVLAVPIAQQAQMHLDTVCTMVDTDMVMYANVVDLTLEAFT
IQRTPDGVITGDAAPFAEAAKAMGIDKLRVIHTGMDPVVAEREQWDDGNNTLALAPGVVYVERNVTQNA
RLQDAGIEVLTIAAGSELGTGRGGPRCMSCPAARDPL

>sp|A1KH32|ARFB_MYCBP Uncharacterized membrane protein ArfB OS=Mycobacterium bovis
(strain BCG / Pasteur 1173P2) GN=arfB PE=2 SV=1

MDFVIQWSCYLLAFLGGSAAVAVVVVTLSEIKRSTRDEGAAEPSAAETGAQ

>sp|A1KH33|ARFC_MYCBP Uncharacterized membrane protein ArfC OS=Mycobacterium bovis
(strain BCG / Pasteur 1173P2) GN=arfC PE=2 SV=1

MEHVHWWLAGLAFTLGMVLTSTLMVRPVEHQVLVKKSVRGSSAKSKPPTARKPAVKSGTKREESPTAKTKVAT
ESAAEQIPVAGEPAEPIPVAGEPAARIPVVPYAPYGPGSARAGADGSGPQGWLVKGRSDTRLYTPEPTYDP
TVAQVWFQDEESAARAFFTPWRKSTRRT

>sp|P9WPZ7|ARGD_MYCTU Acetylornithine aminotransferase OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=argD PE=1 SV=1

MTGASTTTATMRQRWQAVMMNNYGTPIALASGDGAVVTDVDGRTYIDLLGGIAVNVLGHRHPAVIEAVTR
QMSTLGHTSNLYATEPGIALAEELVALLGADQRTRVFFCNSGAEANEAFLKLSRLTGRTKLVAHDAFHGRTMG
SLALTGQPAKQTPFAPLPGDVTHVGYGDVDAALAAVDDHTAAVFLPEIMGESGVVPPAGYLAAARDITARRG
ALLVLDEVQTMGRTGAFFAHQHDGITPDVVTLAKGLGGGLPIGACLAVGPAEELLTPGLHGSTFGGNPVCAA
AALAVLRVLASDGLVRRAEVLGKSLRHGIEALGHPLIDHVRGRGLLLGIALTAPHAKDAEATARDAGYLVNAAAP
DVIRLAPPLIAEAQLDGFVAALPAILDRAVGAP

>sp|P9WPX5|ASPG_MYCTU Probable L-asparaginase OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) GN=ansA PE=1 SV=1

MARLVITTTGGTISTTAGPDGVLRPETHCGATLIAGLMDSDIEVVLDLMLDSSKLT PADWDRIGA AVQEA FRGG

ADGVVITHGTDLTLEETALWLDLTYAGSRPVVLTGAMLSADAPGADGPANLRDALAVAADPAARDLGVVLSFGG
RVLQPLGLHKVANPDLGCFAGESLGFTSGGVRLTRTKTRPYLGDGAAVAPRVDIVAVYPGSDAVAMDACVAA
GARAVVLEALGSGNAGAAVIEGVRRHCRDGDSPVVIIVSTRVAGARVGGAGYGPGHDLVEAGAVMVPRLPPSQ
ARVLLMAALAANSPVADVIDRWG

>sp|P43315|BFR_MYCLE Bacterioferritin OS=Mycobacterium leprae (strain TN) GN=bfr PE=1
SV=1

MQGDPDVLRLNEQLTSELTAINQYFLHSMQENWGFTELAERTRVESFDEMRAEAITDRILLDGLPNYQRI
GSLRVGQTLREQFEADLAIEYEVMSRLKPGIIMCREKQDSTSAVLLKIVADEEEHIDYLETQLALMGQLGEELYS
AQCVRPPS

>sp|P9WMJ5|BLAI_MYCTU Transcriptional regulator Blai OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) GN=blai PE=1 SV=1

MAKLTRLGLERAVMDHLWSRTEPQTVRQVHEALSARRDLAYTTVMTVLQRLAKKNLVLQIRDDRAHRYAPV
HGRDELVAGLMVDALQAEDSGSRQAALVHFVERVGADEADALRRALAELEAGHGNNRPPAGAATET

>sp|P9WPG9|CDH_MYCTU Probable CDP-diacylglycerol pyrophosphatase OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=cdh PE=1 SV=1

MPKSRRAVSLVIGAVIAALAGALIAVTVPARPNRPEADREALWKIVHDRCEFGYRRTGAYAPCTFVDEQSGTA
LYKADFDYPYQFLLIPLARITGIEDPALRESAGRNLYDAWAARFLVTARLNNLSPESDVVLTINPKNARTQDQLHIH
ISCSSPTTSAALRNVDTSEYVGWKQLPIDLGGRRFQGLAVDTKAFESRNLFRDIYLVKVTADGKKMENASIAVANV
AQDQFLLLAEGTEDQPVAEATLQDHDCSITKS

>sp|P9WPF7|CDSA_MYCTU Phosphatidate cytidyltransferase OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=cdsA PE=1 SV=1

MTTNDAGTGNPAEQPARGAKQQPATETSRAGRDLRAAIVVGLSIGLVLI AVLVFVPRVWVAIVAVATLVATHEV
VRRLEAGYLIPVIPLIGGQAAVWLTWPFVAVGALAGFGGMVVVCMIWRLFMQDSVTRPTTGGAPSPGNYL
SDVSATVFLAVWVPLFCFSGAMLVYPENSGWVFCMMIAVIASDVGGYAVGVLFKHPMVPTISPKKSWEGF
AGSLVCGITATIITATFLVGKTPWIGALLGVLFVLTALGDLVESQVKRDLGIKDMGRLLPGHGGGLMDRLDGILPSA
VAAWIVLTLPP

>sp|P9WIC1|CHMU_MYCTU Intracellular chorismate mutase OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv0948c PE=1 SV=1

MRPEPPHHENAELAAMNLEMLESQPVPEIDTLREEIDRLDAEILALVKRRAEVSKAIGKARMASGGTRLVHSRE
MKVIERYSELGPDGKDLAILLRLGRGRGLGH

>sp|P9WPD1|CLPB_MYCTU Chaperone protein ClpB OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) GN=clpB PE=1 SV=1

MDSFNPTTKTQAALTAALQAASTAGNPEIRPAHLLMALLTQNDGIAAPLLEAVGVEPATVRAETQRLLDRLPQA
TGASTQPQLSRESLAAITTAQQLATELDDEYVSTEHVMVGLATGSDVAKLLTGHGASPOALREAFVKVRSAR
VTSPEEATYQALQKYSTDLTARAREGKLDPVIGRDNEIRRVVQVLSRRTKNNPVLIGEPGVGKTAIVEGLAQRIV
AGDVPESLRDKTIVALDLGSMVAGSKYRGEFEERLKAVLDDIKNSAGQIITFIDELHTIVGAGATGEGAMDAGN
MIKPM LARGELRLVGATTLEDEYRKHIEKDAALERRFQQVYVGEPSVEDTIGILRGLKDRYEVHGHVRITDSALVA
AATLSDRYITARFLPKAIDLVDAAASRLRMEIDSRPVEIDEVERLVRRLIEEMALSKEEDEASAERLAKRSELAD
QKEKLAELTTRWQNEKNAIEIVRDLKEQLEALRGESERAERDGLAKAAELRYGRIPEVEKKLDAALPQAQARE
QVMLKEEVGPDADIADVSAWTGIPAGRLLEGETAKLLRMEDELGKRVIGQKAAVTAVSDAVRRSRAGVSDPNR
PTGAFMFLGPTGVGKTELAKALADFLDDERAMVRIDMSEYGEKHTVARLIGAPPGYVGYEAGGQLTEAVRRR
PYTVVLFDEIEKAHPDVFVLLQVLDEGRITDGHGRTVDFRNTILILTSNLGSGGSAEQVLA AVRATFKPEFINRL
DDVLIFEGLNPEELVRIVDIQLAQLGKRLAQRRLQLQVSLPAKRWLAQRGFDPVYGARPLRRLVQQAIGDQLAK
MLLAGQVHDGDTVPVNVSPDADSLILG

>sp|P9WP93|COBD_MYCTU Cobalamin biosynthesis protein CobD OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=cobD PE=1 SV=1

MFASTWQTRAVGVVIGLLDVFVFGDPKRGHPVALFGRAAAKLEQITYRDGRVAGAVHVGLLVGAVGLLGAAL
QRLPGRSWPVAATATATWAAALGGTSLARTGRQISDLLERDDVEAARRLLPSLCGRDPAQLGGPGLTRAALESVA
ENTADAQVVPLLWAASSGVPVAVLGYRAINTLDSMIGYRSPRYLRFGWAAARLDDWANYVGARATAVLVVICAP
VVGGSPPRGAVRAWRRDAARHPSNAGVVEAAFAGALDVRLLGGPTRYHHELQIRPTLGDGRSPKVADLRRRAV
LSRVVQAGAAVLAVMLVYRRRP

>sp|P9WP71|COX1_MYCTU Probable cytochrome c oxidase subunit 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaD PE=1 SV=1

MTAEAPPLGELEAIRPYPARTGPKGSLVYKLITTTDHKIMIGIMYCVACISFFFIGLLALLMRTELAAPGLQFLSNE
QFNQLFTMHGTIMLLFYATPIVFGFANLVLPLQIGAPDVAFPRLNAFSFWLFFVFGATIGAAGFITPGGAADFGW
TAYTPLTDAIHSPGAGGDLWIMGLIVAGLGTILGAVNMITTVCMRAPGMTMFRMPIFTWNIMVTSILILIAFP
LLTAALFGLAADRHLAGHIYDAANGVLLWQHLFWFFGHPEVYIIALPFFGIVSEIFPVFSRKPFGYTTLVYATLSI
AALSVAVWAHHMFATGAVLLPFFSFMTYLIAPTGIKFFNWIGTMWKGQLTFETPMLFSVGFMTVFLGGLTG
VLLASPLDFHVTDSYFVVAHFHYVLFGTIVFATFAGIYFWFKMTGRLLDERLGLKHLFWLTFIGFHTTFLVQHW
LGDEGMPPRYADYLPDGFQGLNVVSTIGAFILGASMPFVWVNFKSWRYGEVVTVDDPWGYSNSLEWATS
CPPPRHNFTLPRISRPAFELHYPHMMVERLRAEAHVGRHHDEPAMVTSS

>sp|P9WP69|COX2_MYCTU Cytochrome c oxidase subunit 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaC PE=1 SV=1

MTPRGPGRLQRLSQCRPQRGSGGPARGRLQLALAAMLGALAVTVSGCSWSEALGIGWPEGITPEAHLNREL
WIGAVIASLAVGVVWGLIFWSAVFHRKKNDDTELPRQFGYNMPELVLTVIPFLIISVLFYFTVVVQEKMLQIAK
DPEVVIDITSFQWNWKFQYQRVNFKDGLTYDGADPERKRAMVSKPEGKDKYGEELVGPVRLNTEDRTYLN
FDKVELTGTSTEIVLVLPSGKRIEFQMASADVIHAFWVPEFLFKRDVMPNPVANNVSVNFQIEEITKGFVVG
HCAEMCGTYHSMNFEVRVVTNDFKAYLQQRIDGKTNAEALRAINQPPLAVTTHPFDRRRELAPQPVG

>sp|P9WP67|COX3_MYCTU Probable cytochrome c oxidase subunit 3 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctaE PE=1 SV=1

MTSAVGTSGTAITSRVHSLNRPNMVS SVGTIVWLSELMMFFAGLFAFYFSARAQAGGNWPPPTELNLYQAVPV
TLVLIASSTFCQMGVFAAERGDIFGLRRWYVITFLMGLFFVLGQAYEYRNLM SHGTSIPSSAYGSVFLATGFHGL
HVTGGLIAFIFLLVRTGMSKFTPAQATASIVVSYWVHFVDIVWIALFTVIYFIR

>sp|P9WPL7|CP141_MYCTU Putative cytochrome P450 141 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=cyp141 PE=1 SV=1

MTSTSIPTFPFDRPVPTSPMLSELNRNSCPVAPIELPSGHTAWLVTRFDDVKGVLSDKRFSCRAAAHPSSPPFV
PFVQLCPSLLSIDGPQHTAARRLLAQGLNPGFIARMRPVQVQVNDALDDLAAAEPVDFQIEVSVPIGEQLMA
KLLGVEPKTVHELAHVDAAMSVCIEGDEEVSRRWSALCTMVIDILHRKLAEPGDDLSTIAQANRQSTMTD
EQVVGMLLTVVIGGVDTPIAVITNGLASLLHHRDQYERLVEDPGRVARAVEEIVRFNPATEIEHLRVVTEVDVIAG
TALSAGSPAFTSITSANRSDQFLDPDEFDVERNPNHEIAFGYGPACPASAYSRMCLTFFFTSLTQRFPQLQLAR
PFEDLERRGKGLHSVGIKELLVTWPT

>sp|P9WP49|CSOR_MYCTU Copper-sensing transcriptional repressor CsoR OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=csoR PE=1 SV=1

MSKELTAKKRAALNRLKTVRGHLDGIVRMLES DAYCVDVMKQISAVQSSLERANRVMLHNHLETCTFSTAVLDG
HGQAAIEELIDAVKFTPALTGPHARLGGAAVGESATEEPPMPDASNM

>sp|P9WPU1|CTPA_MYCTU Cation-transporting P-type ATPase A OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctpA PE=1 SV=1

MTTAVTGEHHASVQRIQLRISGMSCSACAHRVESTLNKLPGVRAAVNFGTRVATIDTSEAVDAAALCQAVRRA

GYQADLCTDDGRSASDPDADHARQLLIRLAIAAVLFVPPVADLSVMFGVVPATRF TGWQWVLSALALPVVTTWA
AWPFHRVAMRNARHHAASMETLISVGITAATIWSLYTVFGNHSPHERSGIWQALLGSDAIYFEVAAGVTVFVLV
GRYFEARAKSQAGSALRALAALSAKEVAVLLPDGSEMVIPADELKEQRFVVRPGQIVAADGLAVDGSAAVDM
SAMTGEAKPTRVRPGGQVIGGTTVLDGRLIVEAAAVGADTQFAGMVRLVEQAQAQKADAQRLADRISSVFP
AVLVIAALTAAGWLIAGGQPDRAVSAAALVLIACPCALGLATPTAMMVASGRGAQLGIFLKGYKSLEATRAVD
VVFDKTGLTTGRLQVSAVTAAPGWEADQVLALAAATVEAASEHSVALAIAAATRRDAVTFRAIPGRGVS
SGRAVRVVGKPSWIGSSSCHPNMRAARRHAESLGETAVFVEVDGEPGVIADAVKDSARDAVAALADRGLR
TMLLTGDNPEAAAATRVGIDEVIADILPEGKVDVIEQLRDRGHVVMVGDGINDGPALARADLGMIAIGRT
DVAIGAADIILVRDHLDDVPLALDLARATMRTVKLNMVWAFGYNIAAIPVAAAAGLLNPLVAGAAMAFSSFFVVS
NSLRRLKFGRYPLGCGTVGGPQMTAPSSA

>sp|P9WPT1|CTPE_MYCTU Probable cation-transporting ATPase E OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=ctpE PE=1 SV=1

MTRSASATAGLTDAAEVAQRVAEGKSNIPERVTRTVGQIVRANVFRINAILGVLLLVLATGSLINGMFGLLIAN
SVIGMVQEIRAKQTLDKLAIIGQAKPLVRRQSGTRTRSTNEVLDIIELGPGDQVVVDGEVVEENLEIDESLLT
GEADPIAKDAGDVMGSGFVVSAGAYRATKVGSEAYAAKLAEEASKFTLVKSELNGINRILQFITYLLVPAGLLT
IYTQLFTTHVWRESVLRMVGALVPMVPEGLVLMTSIAFAVGVVRLGQRQCLVQELPAIEGLARVDVVCADKT
GTLTESGMRVCEVEELDAGRQESVADVLAALAAADARNASMQAIAEAFHSPPGWVVAANAPFKSATKWS
GVSFRDHGNWVIGAPDVLLDPASVAARQAERIGAQGLRVLLAAGSVAVDHAQAPGQVTPVALVVLEQKVRP
DARETLDYFAVQNVSVKVISGDNVSVGAVADRGLHGEAMDARALPTGREELADTLDSTYTSFGRVRPDQKRA
IVHALQSHGHTVAMTGDGVNDVLALKDADIGVAMGSGSPASRAVAQIVLLNNRFATLPHVVGEGRRVIGNIER
VANLFLTKTVYSVLLALLVGIECLIAIPLRRDPLLPFQPIHVTIAAWFTIGIPAFILSLAPNNERAYPGFVRRVMTSA
VPFGLVIGVATFVTYLAAYQGRYASWQEQEQASTAALITLLMTALWVLAVIARPYQWWRLALVLASGLAYVVIFS
LPLAREKFLLDASNLATTSIALAVGVGAATIEAMWWIRSRMLGVKPRVWR

>sp|P9WPS8|CTPF_MYCTO Probable cation-transporting ATPase F OS=Mycobacterium
tuberculosis (strain CDC 1551 / Oshkosh) GN=ctpF PE=2 SV=1

MSASVSATTAHGLPAHEVVLLLESDPYHGLSDGEEAQRLEFRGPNLAVVTRASLLARILRQFHHPLIYVLLVA
GTITAGLKEFVDAAVIFGVVINAIVGFIQESKAEALQGLRSMVHTHAKVVREGHEHTMPSEELVPGDLVLLAA
GDKVPADRLVRQTGLSVNESALTGESTPVHKDEVALPEGTPVADRRNIAYSGTLVTAGHGAGIVVATGAETELG
EIHRLVGAAEVVATPLTAKLAWFSKFLTIAILGLAALTFGVGLLRRQDAVETFTAIALAVGAIPEGLPTAVTITLAIG
MARMARRAVIRRLPAVELGSTTVICADKTGTLTENQMTVQSIWTPHGEIRATGTGYAPDVLLCDDTDDAPVP
VNANAALRWSLLAGACSNDAALVRDGTWQIVGDPTEGAMLVVAKAGFNPERLATTLPQVAAIPFSSERQY
MATLHRDGTGDHVVLAKGAVERMLDLGTEMGADGALRPLDRATVLRATEMLTSRGLRVLATGMGAGAGTPD
DFDENVIPGSLALTGLQAMSDPPRAAAASAVAACHSAGIAVKMITGDHAGTATAIATEVGLLDNTEPAAGSVLT
GAELAALSADQYPEAVDTASVFARVSPEQKLRLVQALQARGHVAMTGDGVNDAPALRQANIGVAMGRGGT
EVAKDAADMVLTDDDFATIEAAVEEGRGVFDNLTKFITWTLPTNLGEGLVILAAIAGVVALPILPTQILWINMTTA
IALGLMLAFEPKEAGIMTRPPRPDQPLLTGWLVRRTLLVSTLLVASAWWLFWEWDNGAGLHEARTAAALNLFV
VVEAFYLFSCRSLTRSARWRLGMFANRWIILGVSQAIAQFAITYLPAMNMVFDTAPIDIGVWVRIFAVATAITIVV
ATDTLLPRIRAQPP

>sp|P9WPS7|CTPG_MYCTU Probable cation-transporting ATPase G OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=ctpG PE=1 SV=1

MTTVVDAEVQLTVVSDAAGRMRVQATGFQFDAGRAVAIEDTVGKVAGVQAVHAYPRTASIVIWYSRAICDTA
AILSIIIDAETVPAAAVPAYASRSASNRKAGVVQKIIDWSTRTLGVRDDVAAQPSGETSDACCDGEDNEDREPE
QLWQVAKLRRAAFSGVLLTASLVAAWAYPLWPVVLGLKALALAVGASTFVPSLKRLEAGRVGVTLMTIAALG
AVALGELGEAATLAFLSISEGLEEYATARRRGLRALLSLVPDQATVLRREGTETIVASTELHVGDMIVKPERLA

TDGIIRAGRTALDVSAITGESVPVEVGPDEVFAGSINGLVLQVGVGTATAANNSLARIVHIVEAEQVRKGASQR
LADCIARPLVPSIMIAAALIAGTGSVLGNPLVWIERALVVLVAAAPCALAIAPVTVVASIGAASRLGVLIKGGAAAL
ETLGTIRAVALDKTGTLTANRPVVIDVATTNGATREEVLAVAAALEARSEHPLAVAVLAATQATTAASDVQAVPG
AGLIGRLDGRVVRGRPGWLDAEELADHVACMQQAGATAVLVERDQQLLGAIAVRDELREPEAAEVVAGLRTG
GYQVTMLTGDNHATAAALAAQAGIEQVHAELRPEDKAHLVAQLRARQPTAMVGDGVNDAPALAAADLGIAM
GAMGTDVAIETADVALMGQDLRHLRHPQALDHARRSRQIMVQNVGLSLSIITVLMPLALFGILGLAAVVLVHEFTE
VIVIANGVVGRAGRIKPLAGPPKTPDRTIPG

>sp|P9WPS5|CTPI_MYCTU Probable cation-transporting ATPase I OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ctpI PE=1 SV=1

MKIPGVATVGGVTNGVAQTVRAGARLPGSAAAQVTLASPVLELTGPVVQSVVQTTGRAIGVVRGSHNESPD
GMTPPVRWRSRRVHFDLPLLPFRWHEHAAMVEEPVRRIPGVAEAHVEGSLGRLVLEPEADSDIAVDE
VRDVVSAVAADIFLAGSVSSPNSAPFADPGNPLAILVPLTAAAMDVAMGATVTGWVARLPAAPQTTRALAALI
NHQPRMVSLMESRLGRVGTDIALAATTAANGTLQSLGTPLLDLVQRSQISEAAAHRVWRDREPALASPRR
PQAPVVPIISSAGAKSQEPRHSWAAAAAGEASHVVVGGSIDAAIDTAKGSRAGPVEQYVNVQAANGSLIAAASA
LVAGGGTEDAAGAILAGVPRAAHMGRQFAAVLGRGLANTGQLVLDPGALRRLDRVRVVIDGAALRGDNR
AVLHAQGDEPGWDDDRVYEVADALLHGEQAPEPDPDELATGARLRWAPAQGPSATPAQGLEHADLVVDG
QCVGSVDVGVWEVDPYAIPLQTAHRTGARVVRHVAGTEDLSASVSTHPPGTPLLLKLVREL RADRGPVLLITAV
HRDFASTDLAALAIADVGVALDDPRGATPWTADLITGDLAAAVRILSALPVARAASESAVHLAQGGTTLAGLL
LVTGEQDKTTPASFRRWLNPNVAAAATLVSGMWSAAKVL RMPDPTPQPLTAWHALDPEIVYSRLAGGSRP
LAVEPGIPAWRRILDDLSYEPVMAPLRGPARTLAQLAVATRHELADPLTPILAVGAAAASAIVGSNIDALLVAGVM
TVNAITGGVQRLRAEAAAAELFAEQDQLVRRVVPAVATRRRLEAARHATRTATVSAKSLRVGDVIDLAAPEV
VPADARLLVAEDLEDESFLTGESLPVDKQVDPVAVNDPDRASMLFEGSTIVAGHARAIVVATGVGTAAHRAISA
VADVETAAGVQARLRELTSKVLPMTLAGGAAVTALALLRRASLRQAVADGVAIAVAAPVPEGLPLVATLSQLAAA
QRLTARGALVRSPTIEALGRVDTICFDKTGTLTENRLRVVLCALPSSTAAERDPLPQTDDAPSAEVLRRAARASTQ
PHNGEGHAHATDEAILAAASALAGSLSSQGDSEWVVLAEVPESSRGYAAAIGRVGTDGIPMLMLKGAPETILP
RCRLADPGVDHEHAESVVRHLAEQGLRVLAVAQRTWDNGTTHDDETDADAVIDAVAHDELIGYVGLADTARS
SSRPLIEALLDAERNVVLITGDHPITARAIAIARQLGLPADARVVTGAELAVLDEEAHAKLAADMVQVFARVSPEQKV
QIVAALQRCGRVTAMVGDGANDAAAIRMADVIGVSGRGSSAARGAADIVLTDLDDLVLLDALVEGRSMWA
GVRDAVTILVGGNVGEVLFVIGTAFGAGRAPVGT RQLLLVNLITDMFPALAVAVTSQFAEPDDAEYPTDDAAE
RAQREHRRAVLIGPTPSLDAPLLRQIVNRGVVTAAGATAAWAIGRWTPGTERRTATMGLTALVMTQLAQTLLTR
RHSPLVIATLGSAGVLVGIITPVIHFSGVPRWDRSPGRASSAPRQEPQSQRWHRSGWQAQSVSCNLMN
ALTRKTLTRVDRTYRRPR

>sp|P9WJF3|CWSA_MYCTU Cell wall synthesis protein CwsA OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=cwsA PE=1 SV=1

MSEQVETRLTPRERLRLGLAYSAVGPVDVTRGLLELGVGLGLQ SARSTAAGLRRRYREGRLAREVAAAQETLAQ
ELTAAQDVVANLPQALQDARTQRRSKHHLWIFAGIAAAILAGGAVAFSIVRRSSRPEPSRPPSVEVQPRS

>sp|P9WPZ5|DAPC_MYCTU Probable N-succinyl diaminopimelate aminotransferase DapC OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=dapC PE=1 SV=1

MTVSRLRPYATTVFAEMSALATRIGAVNLGQGFPEDEGPPKMLQAAQDAIAGGVNQYPPGPGSAPLRRRAIAA
QRRRHFGVDYDPETEVLVTVGATEAIAAAVLGLVEPGSEVLLIEPFYDSYSPVAMAGAHRTVPLVPDGRGFAL
DADALRAVTPRTRALIINSPHNPTGAVLSATELAAIEIAVAANLVVITDEVYEHVFDHARHLPLAGFDGMAE
RTITISSAAKMFNCTGWKIGWACGPAELIAGVRAAKQYLSYVGGAPFQPAVALALDTEDAWVAALRNSLRARR
DRLAAGLIEIGFAVHDSYGTYFLCADPRPLGYDDSTEFCAALPEKVGVAaipMSAFCDPAAGQASQQADVWNH
LVRFTFCKRDDTLDEAIRRLSVLAERPAT

>sp|P9WNZ3|DESA3_MYCTU Stearoyl-CoA 9-desaturase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=desA3 PE=1 SV=1

MAITDVDVFAHLTDADIENLAAELDAIRRDVEESRGERDARYIRRTIAAQRALVSGRLLLAGSSRRRLAWWTGAL
TLGVAKIENMEIGHNVMHGQWDWMNDPEIHSSTWEWDMMSGSSKHWRYPHNFVHHKYTNILGMDDDVG
YGMLRVTRDQRWKRYNIFNVVWNTILAIGFEWGWALQHLEIGKIFKGRADREAAKTRLREFSAKAGRQVFKDY
VAFPALTSLSPGATYRSTLTANVVANVIRNVWSNAVIFCGHFPDGAEKFTKDMIGEPKGQWYLRQMLGSANF
NAGPALRFMSGNLCHQIEHHLYPDLPSNRLHEISVRVREVCDDRYDLPYTTGSFLVQYGKTWRTLAKLSLPDKYLR
DNADDAPETRSEMFAGLPGFAGADPVTGRRRGLKTAIAAVRGRRRSKRMAKSVTEPDDLAA

>sp|P9WNE9|DESET_MYCTU Stearoyl-CoA 9-desaturase electron transfer partner OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv3230c PE=1 SV=1

MSKKHTTLNASHIDTRRPTVAGADRHPGWHALRKAARITPLLPDDYLHLANPLWSARELRGRILGVRRETEDS
ATLFIKPGWGFSDYQPGQYIGIGLLVDGRWRWRSYSLTSSPAASGSARMVTVTKAMPEGFLSTHLVAGVKP
GTIVRLAAPQGNFVLPDPAPLILFLTAGSGITPVMSMLRTLVRNRNQTDDVHLSAPTAADVMFGAELAAALAA
DHPGYRLSVRETRAQGRDLTRIGQQVPDWRETRQWACGPEGLNQADKVVSSAGASDRLHLERFAVSKTA
PAGAGGTVTFARSGKVAADAATSLMDAGEGAGVQLPFGCRMGICQSCVVDLVEGHVRDLRTGQRHEPGTR
VQTCVSAASGDCVLDI

>sp|AOQVQ8|DHA_MYCS2 Alanine dehydrogenase OS=Mycobacterium smegmatis (strain ATCC 70084 / mc(2)155) GN=ald PE=1 SV=1

MLVGIPTEIKNNEYRVAITPAGVAELTRRGHEVIIQAGAGEGSAISDRDFKAAGAEIVNTADQVWSEAELLKVK
EPIEPEYSRMRKQTLFTYLHLAASKPCTDALLASGTTSIAYETVQTAEGALPLLAPMSEVAGRLSAQVGAHYLM
RSYGGRGVLMMGGVPGVAPAEVVVIGAGTAGYNAARVAAGMGAVTVFDLNINTLRRVDGEGGRIETRYSSS
LELEEAVKKADLVIGAVLPGAKAPKLVNTSTVAHMKPGAVLVDIAIDQGGCFEDSRPTTHDEPTFKVHDTIFYC
VANMPGAVPRTSTFALTNSTMPYVCLKLADKGWQAACASDSALAKGLSTHDGKLLSEAVAKDLDPFTDAAQFL
A

>sp|P9WG63|DIPZ_MYCTU Protein DipZ OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=dipZ PE=1 SV=1

MVESRRAAAAASAYASRCGIAPATSQRSLATPPTISVPSGEGRCRCHVARGAGRDPRRRRLRRRRWCGRCGYHS
HLTGGEFDVNRLCQQRSRERSCQLVAVPADPRPKRQRITDVLTLALVGFGLGITGISCILPVLPIFFSQAQSV
AAQVAKPEGAVAVRRKRALSATLRPYRVIGGLVLSFGMVTLLGSALLSVLHLPQDAIRWAALVALVAIGAGLIFPR
FEQLLEKPFSTRIPQKQIVTRSNFGLGLALGVLYVPCAGPILAAIVVAGATATIGLTVVLTATFALGAALPLFFALA
GQRIAERVGAFRRRQREIRIATGSVTILLAVALVFDLPAALQRAIPDYASLQQQISTGTEIREQLNLGGIVNAQNA
QLSNCSDGAAQLESCGTAPDLKGITGWLNTPGNKPIDLKSRLGKVVLDIFWAYSINCQRAIPHVVGWYQAYK
DSGLAVIGVHTPEYAFKVPGNVAKGAANLGISYPIALDNNYATWTNRYRNYWPAEYLIDATGTVRHIKFGEGD
YNVTTTLVRQLLNDKPGVKLPQPSSTTPDLTPRAALTPETYFGVGVVNYGGGGAYDEGSAVFDYPPSLAAN
SFALRGRWALDYQGATSDGNDAAIKLNYHAKDVYIVVGGTGLTVVRDGGKPATLPISGPPTTHQVVAGYRLASE
TLEVRPSKGLQVFSFTYG

>sp|P9WHH9|DLDH_MYCTU Dihydrolipoyl dehydrogenase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=lpdC PE=1 SV=1

MTHYDVVVVGAGPGGYVAAIRAAQLGLSTAIVEPKYWGGVCLNVGCIPSKALLRNAELVHIFTKDAKAFGISGE
VTFDYGIAYDRSRKVAEGRVAGVHFLMKKNKITEIHGYGTFADANTLLVDLNDGGTESVTFDNIATGSSTRLLVP
GTSLSANVVYEEQILSRELPKSIIAGAGAIGMEFGYVLKNYGVDTVIVEFLPRALPNEDADVSKEIEKQFKKLG
TILTATKVESIADGGSQVTVTKDGVQELKAEKVLQAIGFAPNVEGYGLDKAGVALTDRKAIGVDDYMRTNV
GHIYAIGDVNGLLQLAHVAEAQGVVAAETIAGAETLTLGDHRMLPRATFCQPNVASFGLTEQQARNEGVDVVV
AKFPFTANAKAHGVGDPSGFVKLVADAKHGELLGGHVLVGHDAELLPELTLAQRWDLTASELARNVHTHTPTMS

EALQECFHGLVGHMINF

>sp|P9WFR5|DPPRS_MYCTU Decaprenyl-phosphate phosphoribosyltransferase
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv3806c PE=1 SV=1
MSEDEVVTQPPANLVAGVVKAIRPRQWVKNVLAAPLAALGGGVRYDYVEVLSKVSMFVVFSLAASAVYLV
NDVRDVEADREHPTKRFRPIAAGVVPEWLAYTVAVVLGVTSLAGAWMLTPNLALVMVVYLAMQLAYCFGLKH
QAVVEICVSSAYLIRAIAGGVATKIPLSKWFLLIMAFGSLFMVAGKRYAELHLAERTGAAIRKSLESYTSYLRV
WTLSATAVVLCYGLWAFERDGYSGSWFAVSMIPFTIAILRYAVDVGGLAGEPEDIALRDRVLQLLALAWIATVG
AAVAFG

>sp|P9W153|DPRP_MYCTU Putative decaprenylphosphoryl-5-phosphoribose phosphatase
Rv3807c OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv3807c PE=1 SV=1
MVAVQSALVDRPGMLATARGLSHFGEHCIGWLILALLGAIALPRRRREWLVAGAGAFVAHAIAVLKRLVRRQR
PDHPAIAVNVDTPSQLSFPSAHATSTTAAALLMGRATGLPLPVVLPMPALSRIILGVHYPSTVAVGVALGATVG
AIVDSVGGGRQRARKR

>sp|P9WQL9|DRRA_MYCTU Doxorubicin resistance ATP-binding protein DrrA
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=drrA PE=1 SV=1
MRNDDMAVVVNGVRKTYGKGIKIVALDDVSFKVRRGEVIGLLGPNAGKTTMVDILSTLRPDAGSIIAGYDV
VSEPAVRRSIVMTGQQVAVDDALSGEQNLVLFGRWLWLSKSAARKRAAELLEQFSLVHAGKRRVGTYSGGM
RRRIDACGLVVQPQVAFLEPTTGLDPRSRQAIWDLVASFKLGIATLLTQYLEEADALSDRIILDHGIIAEGTA
NELKHRAGDTFCEIVPRDLKDLDAIVAALGSLLPEHHRAMLPDSDRITMPAPDGIRMLVEAARRIDEARIELADI
ALRRPSLDHVFLAMTTDPTESLTHLVSGSAR

>sp|P9WG23|DRRB_MYCTU Doxorubicin resistance ABC transporter permease protein DrrB
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=drrB PE=1 SV=1
MSGPAIDASPALTFNQSSASIQRRSTGRQMWWVLYRRFAAPSLNNGEVLTTVGAPIIFMVGFYIPFAIPWNQFV
GGASSGVASNLGQYITPLVTLQAVSFAAIGSGFRAATDSSLGNRRFQSMPPMAPLTPLLARVWVAVDRCFTGLV
ISLVCGYVIGFRFHRGALYIVGFCLLVIAIGAVLSFAADLVGTVTRNPDAMLPLLSLPILIFGLLSIGLMPKLKPHWI
HPFVRNQPIQSQVFAALRALAGDTTKTASQVSWPVMAPTTLWLFVAVVILALSSTIVLARRP

>sp|P9WG21|DRRC_MYCTU Probable doxorubicin resistance ABC transporter permease protein
DrrC OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=drrC PE=1 SV=1
MITTTSQEIELAPTRLPGSQNAARLFVAQTLTQNRLLTRWARDYITVIGAVLPILFMVVLNIVLGNLAYVVTHD
SGLYSIVPLIALGAAITGSTFVAIDLMRERSFGLLARLWVLPVHRASGLISRILANAIRTLVTTVLMLGTGVVLGFRF
RQGLIPSLMWISVPVILGIAIAAMVTTVALYTAQTVVVEGVELVQAIAIFFSTGLVPLNSYPGWIQPFVAHQPVSY
AIAAMRGFAMGGPVLSPMIGMLVWTAGICVVCAPLAIGYRRASTH

>sp|P9WPH7|ECCA2_MYCTU ESX-2 secretion system protein EccA2 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=eccA2 PE=1 SV=1
MSRMVDTMGDLLTARRHFDRAMTIKNGQGCVAALPEFVAATEADPSMADAWLGRIACGDRDLASLKQLNA
HSEWLHRETRIGRTLAAEVQLGPSIGITVDASQVGLALSSALTIAGEYAKADALLANRELLDSWRNYQWHQL
ARAFLMYVTQRWPDVLSAAEDLPPQAIVMPAVTASICALAAHAAHLGQGRVALDWLDRVDVIGHSRSSLER
FGADVLTAAIGPADIPLLVADLAYVRGMVYRQLHEEDKAQIWLKATINGVLTDAAKEALADPNRLRIVTDERTIA
SRSDRWDASTAKSRDQLDDNAAQRRGELLAEGRELLAKQVGLAAVKQAVSALEDQLEVRMMRLEHGLPVE
GQTNHMLLVGPPGTGKTTTAEALGKIYAGMGIVRHEIREVRRSDFCGHYIGESGPKTNELIEKSLGRIIFMDEFY
SLIERHQDGTDPDMIGMEAVNQLLVQLETHRFDFCFIGAGYEDQVDFLTVNPLAGRFNRKRFESYSPVEIVEI
GHRYATPRASQLDDAAREVFLDAVTTIRNYTTSPGQHIGIDAMQNGRFARNVIERAEGFRDTRVVAQKQKAGQP
VSVQDLQIITATDIDAIRSVCSNDRDMAIIVW

>sp|P9WPI3|ECCA3_MYCTU ESX-3 secretion system protein EccA3 OS=Mycobacterium

tuberculosis (strain ATCC 25618 / H37Rv) GN=eccA3 PE=1 SV=1
MAGVGEEDSGGVERDDIGMVAASPVASRVNGKVDADVGRFATCCRALGIAVYQRKRPPDLAAARSGFAALT
RVAHDQCDAWTGLAAAGDQSIGVLEAASRTATTAGVLQRQVELADNALGFLYDTGLYLRFATGPDFFHLAYA
AALASTGGPEEFAKANHVVSGITERRAGWRAARWLAVVINYRAERWSDVVKLLTPMVNDPDLDEAFSHA
TLGTALARLGMFAPALSYLEEPDGPVAVAAVDGALAKALVLAHVDEESASEVLQDLYAAHPENEQVEQALS
SFGIVTTTAGRIEARTDPWDPAEPGAEDFVDPAAHERKAALLHEAELQLAEFIGLDEVKRVSRKSSVAMELV
RKQRGLTVAQRTHHLVAFAGPPGTGKTTIARVVAKIYCGLLKRENIREVHRADLIGQHIGETEAKTNAIIDS
GVLFLDEAYALVATGAKNDFGLVAIDTLLARMENDRDLRVVIIAGYRADLDFKLDTNEGLRSRFRTRNIDF
SYTSH ELVEIAHKMAEQRDSVFEQSALHDLEALFAKLAESTPDTNGISRRSLDIAGNGRFVRNIVERSE
EERFRLDHSE HAGSGEFSDEELMTITADDVGRSVEPLLRGLGLSVRA

>sp|P9WNR3|ECCB3_MYCTU ESX-3 secretion system protein eccB3 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=eccB3 PE=1 SV=1

MTNQQHDHDFDHRRSFASRTPVNNPNPKVVYRRGFVTRHQVTGWRFVMMRRIAAGIALHDTRMLVDPLRT
QSRVLMGVLVITGLIGSFVFLIRPNGQAGSNAVLADRSTAALYVRVGEQLHPVLNLSARLIVGRPVSPPTVK
STELDQFPRGNLIGIPGAPERMVQNTSTDANWTVCDGLNAPSRGGADGVGVTVIAGPLEDTGARAAALGPG
QAVLVDSGAGTWLLWDGKRSPIDLADHAVTSGGLGADVPAPRIIASGLFNAIPEAPLTAIIPDAGNPASFGV
PAPIGAVVSSYALKDSGKTISDTVQYYAVLPDGLQQISPVLAAILRNNSYGLQQPRLGADEVAKLPVSRVLDTR
RYPSEPVSLVDVTRDPVTCAYWSKPVGAATSSLLAGSALPVPDAVHTVELVGAGNGGVATRVALAAGTYFT
QTVGGGPDAPGAGSLFWVSDTGVRYGIDNEPQGVAGGGKAVEALGLNPPPPIPWSVLSLFPVPGPTLSRADA
LLAHDTLVPDSRPARPVSAEGGYR

>sp|P9WNA5|ECCC5_MYCTU ESX-5 secretion system protein EccC5 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=eccC5 PE=1 SV=1

MKRGFARPTPEKPPVIKPENIVLSTPLSIPPEGKPWVWLVVGVVGLLGGMVAMVFASGSHVFGGIGSIFPL
FMMVGMIMMMFRMGGGQQMSRPKLDAMRAQFMLMLDMLRETAQESADSMANRWFHPAPNTL
AAAVGSPRMWERKPDGKDLNFGVVRVGVGMTRPEVTWGEPQNMPTDIELEPVTGKALQEFGRYQSVVYNL
PKMVSLLEPWPYALVGEREQVLGLMRAIICQLAFSHGPDHVQMIVVSSDLQWDWVVKWLPHFGDSRRHDA
AGNARMVYTSVREFAAEQALFAGRGSFTPRHASSAQTPPTHTVIIADVDDPQWEYVISAEGVDGVTFFDLT
GSSMWTIDIPERKLQFDKTVIEALPRDRDTWVIDDKAWFFALTDQVSIAEAEFAQKLAQWRLAEAYEEIGQ
RVAHIGARDILSYGIDDPGNIDFDSLWASRTDTMGRSRLRAPFGNRSNDELLFLDMKSLDEGGDGPBGVM
SGTTGSGKSTLVRTVIESLMLSHPPEELQFVLADLKGSAVKPFAGVPHVSRITDLEEDQALMERFLDALWGEIA
RRKAICDSAGVDDAKEYSVRARMRARGQDMAPLMLVVVIDEFYEFWRIMPTAVDVLDSIGRQGRAYWIH
LMMASQTIESRAEKLMMENMGYRLVVKARTAGAAQAAGVNAVNLPAQAGLYFRKSLEDIRFQAEFLWRDYF
QPGVSDIGEEAPALVHSIDYIRPQLFTNSFTPLEVSVGGPDIEPVVAQPNGEVLESDDIEGGEDEDEEVRTPKV
GTVIIDQLRKIKFEPYRLWQPPLTQVPAIDDLVNRFLGRPWKEYGSACNLVFPIGIIDRPYKHDQPPWTVDTSG
PGANVLILGAGSGKTTALQTLICSAALHTPQQVQFYCLAYSSTALTTSRIPHVGEVAGPTDPYGVRRRTVAELL
ALVRERKRSFLECGIASMEMFRRRKFGGEAGVPDDGFGDVYLVIDNYRALAEENEVLIEQVNVIIINQGPSFGV
HVVVTADRESELPPVRSFGSRIELRLAAVEDAKLVRSRFAKDVPVKPGRGMVAVNYVRLSDPQAGLHTLVA
RPALGSTPDNVFECDSVVAASRLTSAQAPPVRRRLPARFGVEQVRELASRDTRQGVGAGGIWAISELDLAPVY
LNFAENSHLMVTGRRECGRTTTTLATIMSEIGRLYAPGASSAPPAPGRPSAQVWLVDP RRQLLTALGSDYVERFA
YNLDGVVAMMGEALAAAGREPPPLSAEELLSRSWWSGPEIFLIVDDIQLPPGFDSPLHKAVPFVNRAADV
GLHVIVTRTFGGWSSAGSDPMLRALHQANAPLLVMDADPDEGFIRGKMKGGPLPRGRGLLMAEDTGVFVQV
AATEVRR

>sp|P9WNQ7|ECCD1_MYCTU ESX-1 secretion system protein eccD1 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=eccD1 PE=1 SV=1

MSAPAVAAGPTAAGATAARATTRVTILTGRRMTDLVLPAAVPMETYIDDTVAVLSEVLEDTPADVLGGDFDFTA
QGVWAFARPGSPPLKLDQSLDDAGVVDGSLTLVSVSRTERYRPLVEDVIDAIAVLDESPEFDRTALNRFVGA
PLLTAPVIGMAMRAWWETGRSLWWPLAIGILGIAVLVGSFVANRFYQSGHLAECLLVTTYLLIATAAALAVPLPR
GVNSLGAPQVAGAATAVFLTLMTTRGGPRKRHELASFVITAIAVIAAAAAFGYGYQDWVPAGGIAFGLFIVTNA
AKLTVAVARIALPPIPVPGETVDNEELLDPVATPEATSEETPTWQAIIASVPASAVRLTERSKLAKQLLIGYVTSGLI
LAAGAIAVVVRGHFFVHSLVAVGLITTVCGFRSRLYAERWCAWALLAATVAIPTGLTAKLIWYPHYAWLLLSVYLT
VALVALVVVGSMAHVRRVSPVVKRTLELIDGAMIAAIPMLLWITGVYDTRNIRF

>sp|P9WNQ5|ECCD2_MYCTU ESX-2 secretion system protein eccD2 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=eccD2 PE=1 SV=1

MTAPHKVAFPARCAVNICYDKHLCSQVFPAGIPVEGFFEGMVLELFDADLKRKGFDDGVALPAGSYELHKINGVRL
DINKSLDELGVQDGDTLVLPVAVGESFEPQYESLSTGLAAMGKWLGRDGGDRMFAPVTSLTAAHTAMAIAM
AVGVVLLALTRTRITDSPAAMAGGIGVLLVIGALVWWGWRRERDLFSFGWLAVLLAVAAACAPPGAL
GAAHALIGLVVVVVGAITIGVATKRWQTAVVAVTVCGILAAVAARMFRPVSQVLAICVLVGLLVLIRMTP
TVALWVARVRPPHFGSITGRDLFARRAGMPVDTVAPVSEADADDEDNELTDITARGTAIAASARLVNAVQVGM
CVGVSLVLPAAVWGVLTTPRQPWAWLALLVAGLTVGLFITQGRGFAAKYQAVLVCGASAAVCAGVLKYALDTPK
GVQTGLLWPAIFVAAFAALGLAVALVVPATRFRIIRLTVIEWLEVLAMIALPAAAAALGGLFAWLRH

>sp|P9WNQ3|ECCD3_MYCTU ESX-3 secretion system protein eccD3 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=eccD3 PE=1 SV=1

MSGTVMQIVRVAILADSRLTEMALPAELPLREILPAVQRLVPSAQNGDGGQADSGAAVQLSLAPVGGQPFSL
DASLDTGVVVDGDLVLPVAGPAAPGIVEDIAAAMIFSTSRKLPWGIAHIQRGALAAVIAVALLATGLTVTY
RVATGVLAGLLAVAGIAVASALAGLLITIRSPRSIALSIAALVPIGAALALAVPGKFGPAQVLLGAAGVAAWSIAL
MIPSAERERVVAFFTAAAVGASVALAAGAQLLWQLPLLSIGCGLIVAALLVTIQAAQLSALWARFPLVPVAPGD
PTPSAPPLRLLLEDLPRRVRVSDAHQSGFIAAAVLLSVLGSVAIAVRPEALSVVGWYLVAATAAAATLRARVWDSA
ACKAWLLAQPYLVAGVLLVFYATGRYVAAFAGAVLVAVLMLAWVVVALNPGIASPESYSLPLRLLGLVAAGLD
VSLIPVMAYLVGLFAWVLNR

>sp|P9WNP9|ECCD5_MYCTU ESX-5 secretion system protein eccD5 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=eccD5 PE=1 SV=1

MTAVADAPQADIEGVASQAVVVGVMAGEGVQIGVLLDANAPVSVMTDPLLKVVNSRLRELGEAPLEATGRG
RWALCLVDGAPLRATQSLTEQDVYDGDRLWIRFIADTERRSQVIEHISTAVASDLSKRFARIDPIVAVQVGSMV
ATGVVLTATGVLGWWRWHHNTWLTTIYAVIGVLVAVAMLLLMRAKTDADRRVADIMLMSAIMPVTVAAAA
APPGPVGSPQAVLFGFVLTVAALALRFTGRRLGIYTTIVIGALTMLAALARMVAATSAVTLSSLLICVVAYHA
APALSRRLAGIRLPVFPATSRRWVFEARPDLPPTVVVSGGSAPVLEGPSSVRDVLQAERARSFSLGLTGLGVM
VVVCMTSLCDPHTGQRWLPLILAGFTSGFLLRGRSYVDRWQSITLAGTAVIAAAVVCVRYALESSPLAVSIVAAI
LVLLPAAGMAAAAHVPHTIYSPLFRKFVEWIEYLCLMPIFPLALWLMNVYAAIRYR

>sp|P9WJE9|ECCE1_MYCTU ESX-1 secretion system protein EccE1 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=eccE1 PE=1 SV=1

MRNPLGLRFSTGHALLASALAPPCIIAFLETRYWWAGIALASLGIVATVTFYGRRITGWVAAVYAWLRRRRRPP
DSSSEPVVGVATVKPGDHVAVRWQGEFLVAVIELIPRPFTPTVIVDQQAHTDDMLDTGLVEELLSVHCPDLEADV
SAGYRVGNTAAPDVVSLYQQVIGTDPAPANRRTWIVLRADPERTRKSAQRRDEGVAGLARYLVASATRIADRLA
SHGVDAVCGRSFDDYDHATDIGFVREKWSMIKGRDAYTAAYAAPGGPDVWWSARADHTITRVRVAPGMAP
QSTVLLTTADKPKTPRGFARLFGGQRPALQGQHLVANRHCQLPIGSAGVLVGETVNRCPVYMPFDDVDIALNL
GDAQFTTQFVVRAAAAGAMVTVGPQFEFARLIGAHIGQEVKVAWPNATTYLGPHPGIDRVILRHNVIGTPRH
RQLPIRRVSPPEESRYQMALPK

>sp|P9WJE7|ECCE2_MYCTU ESX-2 secretion system protein EccE2 OS=Mycobacterium

tuberculosis (strain ATCC 25618 / H37Rv) GN=eccE2 PE=1 SV=1
MTSKLTGFSPRSARRVAGVWTVFVLASAGWALGGQLGAVMAVVVGVVALVFVQWWGQPAWSWAVLGLRGR
RPVKWNPITLANNRSGGGVVRVQDGVAVVAVQLGRAHRATTVTGSVTVESDNVIDVVELAPLLRHPLDLELD
SISVVTFGSRTGTVDYPRVYDAEIGTPPYAGRRETWLMRLPVIGNTQALRWRTSVGAAAISVAQRVASSLRC
QGLRAKLATATDLAELDRRLGSDAVAGSAQRWKAIRGEAGWMTTYAYPAEAISSRVLSQAWTLRADEVIQNV
VYPDATCTATITVRTPTPAPTPPSVILRRLNGEQAAAAANMCGPRPHLRGQRRCLPAQLVTEIGPSGV
LIGKLS
NGDRLMIPVTDAGELSRVFAADDTIKRIVIRVVGAGERVCVHTRDQERWASVRMPQLSIVGTPRPAPRTTV
GVVEYVRRRKNKGDDGKSESGVDVAISPTPRPASVITIARPGTSLSESDRHGFVETIEQIDRATVKVGAAGQNW
LVEMEMFRAENRYVSLEPVTMSIGR

>sp|P9WJE5|ECCE3_MYCTU ESX-3 secretion system protein EccE3 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=eccE3 PE=1 SV=1

MNPIPSWPGRGRVTLVLLAVVPVALAYPWQSTRDYVLLGVAAAVVIGLFGFWRGLYFTTIARRGLAILRRRRRIA
EPATCTRTTVLVWVGPPASDTNVLPLTLIARYLDRYGIRADTIRITSRVTASGDCRTWVGLTVVADDNLAALQARS
ARIPLQETAQVAARRLADHLREIGWEAGTAAPDEIPALVAADSRETWRGMRHTDSYVAAAYRVSANAELPDTL
PAIRSRPAQETWIALEIAYAAGSSTRYTVAACALRTDWRPGGTAPVAGLLPQHGNHVPALTALDPRSTRRLDG
HTDAPADLLRLHWPTPTAGAHRAPLTNAVSR

>sp|P9WJE3|ECCE5_MYCTU ESX-5 secretion system protein EccE5 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=eccE5 PE=1 SV=1

MKAQRSFGLALSWPRVTAVFLVDVLLAVASHCPDSWQADHHVAWWWVGVGVAAVTLLSVVSYHGITVISGL
ATWVRDWSADPGTTLGAGCTPAIDHQRFRDRTVGVREYNGRLVSVIEVTCGESGPSGRHWHRKSPVPMPLP
VVAVADGLRQFDIHLGDIDIVSVLVRGGVDAKASASLQEWEPQGWKSEERAGDRTVADRRRTWLVRMNP
QRNVAACRDSLASTLVAATERLVQDLDGQSCARPVTADDELTEVDSAVLADLEPTWSRPGWRHLKHFNGYA
TSFVWTPSDITSETLDELCLPDSPEVGTTVVTRLTRVGPALSAAWVRYHSDTRLPEVAAGLNRLTRGQLAAV
RASLPAPTHRPLLVIPSRNLRDHDELVLPVQGELEHATSSFFVGQ

>sp|P9WJY5|EFPA_MYCTU Uncharacterized MFS-type transporter EfpA OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=efpA PE=1 SV=1

MTALNDTERAVRNWTAGRPHRPAPMRPPRSEETASERPSRYPTWLPSSFIAAVIAIGGMQLLATMDSTVAI
VALPKIQNELSLSDAGRSWVITAYVLTFGGLMLLGGRLGDTIGRKRFTIVGVALFTISSVLCVAWDEATLVIARLS
QGVGSAIASPTGLALVATTFPKGPARNAAVFAAMTAIGSVMGLVVGALTEVSWRWAFVNVPIGLVMIYLA
RTALRETNKERMKLDATGAILATLACTAAVFAFSIGPEKGWMSGITIGSGLVALAAAVFVIVERTAENPVVPHL
FRDRNRLVTFSAILLAGGVMSLTVICIGLYVQDILGYSALRAGVGFIPFVIAMGIGLVSSQLVSRFSPRVLTIGGG
YLLFGAMLYGSFFMHRGVYPFNLVMPVIVGGIGIGMAVPLTLSAIAAGVGFQIGPVSAIALMLQSLGGPLVLA
VIQAVITSRTLYLGGTTPVKFMNDVQLAALDHAYTYGLLWVAGAAIIVGGMALFIGYTPQQVAHAQEVKEAID
AGEL

>sp|P9WKH1|EFPP_MYCTU (2E,6E)-farnesyl diphosphate synthase OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv3398c PE=1 SV=1

MRGTDEKYGLPPQPSDRMTRRRLPVLGLAHELITPTLRQMADRDPHMRPVVSYHLGWSDERGRPVNNNC
GKAIRPALVFVAAEAAGADPHSAIPGAVSVLVHNFSLVHDDLMDRDEHRRHRPTVWALWGDAMALLAGDA
MLSLAHEVLLDCDSPHVGAALRAISEATRELIRGQAADTAFESRTDVALDECLMAEGKTAALMAASAIEVGALL
AGAPRSVREALVAYGRHIGLAFQLVDDLLGIWGRPEITGKPVYSDLRSRKKTLPTVTVAHGGSAGRRLAAWL
DETGSQTASDDELAVAELIECGGRRWASAEARRHVQIGDMVARIGIPDRPAAELQDLAHYIVDRQA

>sp|P9WNL7|EMBB_MYCTU Probable arabinosyltransferase B OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=embB PE=1 SV=1

MTQCASRRKSTPNRAILGAFASARGTRWVATIAGLIGFVLSVATPLLPVVQTTAMLDWPQRGQLGSVTAPLISLT

PVDFTATVPCDVVRAMPPAGGVVLGTAPKQGDANLQALFVVVSAQRVDVTDNRNVVILSVPREQVTSPPQCQR
IEVTSTHAGTFANFVGLKDPSPGAPLRSGFPDPNLRPQIVGVFTDLTGAPPGLAVSATIDTRFSTRPTTLKLLAIIGA
IVATVVALIALWRLDQLDGRGSIAQLLLRPFPPASSPGGMRRILPASWRTFTLTDVAVIFGFLWHVIGANSSDD
GYILGMARVADHAGYMSNYFRWFGSPEDPFGWYYNLLALMTHVSDASLWMRLPDLAAGLVCWLLLSREVLV
RLGPAVEASKPAYWAAAMVLLTAWMPFNGLRPEGIIALGSLVTVLIERSMRYSRTPAALAVVTAFTLGVQP
TGLIAVAALVAGGRPMLRILVRRHRLVGTLPVSPMLAAGTVILTUVFADQTLSTVLEATRVRKIGPSQAWYTEN
LRYYYLILPTVDGSLRFRGFLITALCLFTAVFIMLRRKRIPSVARGPAWRMLMGVIFGTMFFLMFTPTKWVHHFGL
FAAVGAAMAALTTVLVSPSVLRWSRNRMAFLAALFFLLALCWATTNGWVYVSSYGVFNSAMPKIDGITVSTI
FFALFAIAAGYAAWLHFAPRGAGEGRILALTTAPVPIVAGFMAAVFVASMVAGIVRQYPTYSNGWSNVRAFV
GGCGLADDVLVEPDTNAGFMKPLDGDGSGSWGPLGGLGGVNPVGFPTNGVPEHTVAEAIVMKPNQPGTDYD
WDAPTKLTSPGINGSTVPLPYGLDPARVPLAGTYTTGAQQQSTLVSAWYLLPKPDDGHPLVVTAAGKIAGNSV
LHGYPGQTVVLEYAMPGPALVPAGRMVPDDLYGEQPKAWRNLRFARAKMPADAVAVRVAEDLSLTPED
WIAVTPPRVPLRSLQEYVGSTQPVLDDWAVGLAFPCQQPMLHANGIAEIPKFRITPDYSAKKLDTDWEDGT
NGGLLGITDLLLRAHVMAATYLSRDWARDWGLSRKFDTLVDAPPAQLELGTATRSGLWSPGKIRIGP

>sp|P9W1Q7|ERP_MYCTU Exported repetitive protein OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=erp PE=1 SV=1

MPNRRRRKSTAMSAVAALAVASPCAYFLVYESTETTERPEHHEFKQAAVLTDLPGELMSALSQGLSQFGINIPP
VPSLTGSGDASTGLTGPGLTSPGLTSPGLTSPGLTDPALTSPLTLPGLSLAAPGTTLAPTGVGANPALTNPALTS
PTGATPGLTSPTGLDPALGGANEIPITTPVGLDPGADGTYPILGDPTLGTIPSSPATTSTGGGGLVNDVMQVANE
LGASQAIDLLKGVLMPSIMQAVQNGGAAAPASPPVPIAAAAVPTDPITVPVA

>sp|P9WJD3|ESPE_MYCTU ESX-1 secretion-associated protein EspE OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=espE PE=1 SV=1

MASGSGLCKTTSNFIWGLQLLLGEGIPDPGDIFNTGSSLFKQISDKMGLAIPGTNWIGQAAEAYLNQNIQQLR
AQVMGDLKLTGNMISNQAKYVSDTRDVLRAMKKMIDGVYKCKGLEKIPLLGHLSWELAIPIMSGIAMAV
VGGALLYLTIMTLMNATNLRGILGRLEMLTTLKPKFPLGPLSLPDIIDGLWPPKLPDIPGLPDIPGLPDFKWP
PTPGSPLFPDLPSPFGPFGEFPAIPGFPALPGLPSIPNLFPLGLGDLGKLPWTELAALPDFLGGF
AGLPSLGFNLLSFASLPTVGQVTATMGQLQQLVAAGGGPSQLASMGSSQAQLISSQAQQGGQQHATLVSD
KKEDEEGVAEERAPIDAGTAASQRGQEGTVL

>sp|P9WJC1|ESPK_MYCTU ESX-1 secretion-associated protein EspK OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=espK PE=1 SV=1

MSITRPTGSYARQMLDPGGWVEADEDTFYDRAQEYSQVLQRVTDVLDTCRQKQGHVFEGGLWSGGAANAA
NGALGANINQLMTLQDYLATVITWHRHIAGLIEQAKSDIGNNVGDAQREIDILENDPSLDADERHTAINSLVTAT
HGANVSLVAETAERVLESKNWKPKNALEDLLQKSPPPDVPTLVVPSGTPGTPTITPGTPTITPGTPTIP
GAPVTPITPTPGTPTVTPGKPVTPVTPKPGTPEPTITVTPPVAPATPATPATVTPAPAPHPQPAPAPAP
SPGQPVTPTATPGSPGATPGTGGEPAPHVKAALAEQPGVPGQHAGGGTQSGPAHADESAASVTPAAASG
VPGARAAAAAPSGTAVGAGARSSVGTAAASGAGSHAATGRAPVATSDKAAAPSTRAASARTAPPARPPSTDHI
DKPDRSESADDGTPVSMIPVSAARAARDAATAAASARQRGRGDALRLARRIAAALNASDNNAGDYGFFWITA
VTTDGSIVVANSYGLAYIPDGMELPNKVYLASADHAIPVDEIARCATYPVLAVQAWAAFHDMTLRAVIGTAEQL
ASSDPGVAKIVLEPDDIPESGKMTGRSRLEVVDPSAAAQLADTTDQRLLDLLPAPVDVNPVPPGDERHMLWFEL
MKPMTSTATGREAHLRAFRAAAHSQEIALHQAHTATDAAVQRVAVADWLYWQYVTGLLDRALAAAC

>sp|P9WNF9|ETHA_MYCTU FAD-containing monooxygenase EthA OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ethA PE=1 SV=1

MTEHLDVVIVGAGISGVSAAWHLQDRCPTKSYAILEKRESMGGTWDLFRYPGIRSDSDMYTLGFRFRPWTR
QAIADGKPILEVYKSTAAMYGIDRHIRFHKKVISADWSTAENRWTVHIQSHGTLTCEFLFLCSGYNNYDEGY

SPRFAGSEDFVGPPIHPQHWPEDLDYDAKNIVVIGSGATAVTLVPALADSGAKHVMTLQRSPTYIVSQPDRDZIA
EKLNRWLPETMAYTAVRWKNVLRQAAVYSACQKWPRRMRKMFLSLIQRQLPEGYDVRKHFGPHYNPWDQ
RLCLVPNGDLFRAIRHGKVEVVTDTIERFTATGIRLNSGRELPADIIITATGLNLQLFGGATATIDGQQVDITTTMAY
KGMMLSGIPNMAYTVGYTNASWTLKADLVSEFVCRLLNMYDDNGFDTVVVERPGSDVEERPFMEFTPGYVL
RSLDELPKQGSRTPWRLNQNYLRDIRLIRRGKIDDEGLRFAKRPAVGV

>sp|P9WQD7|FAB2_MYCTU 3-oxoacyl-[acyl-carrier-protein] synthase 2 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=kasB PE=1 SV=1

MTELVTKAFPYVVVTGIAMTTALATDAETTWKLLDRQSGIRTLDDPFVEEFDLPVRIGGHLLLEFDHQLTRIEL
RRMGYLQRMSTVLSRRLWENAGSPEVDTNRLMVSIGTGLGSAEELVFSYDDMRARGMKAVSPLTVQKYMPN
GAAAAVGLERHAKAGVMTPVSACASGAEAIARAWQQIVLGEADAAICGGVETRIEAVPIAGFAQMRIVMSTN
NDDPAGACRPFDRDRDGFVFGEGGALLIETEEHAKARGANILARIMGASITSDGFHMVAPDPNGERAGHAIT
RAIQLAGLAPGDIDHVNAHATGTQVGDLAEGRAINNALGGNRPAVYAPKSALGHSVGA VGAVESILTVLALRD
QVIPPTNLVNLDPIDLDV VAGEPRPGNYRYAINNSFGFGGHNVAIAFGRY

>sp|P9WQ47|FAC23_MYCTU Probable long-chain-fatty-acid--CoA ligase FadD23
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=fadD23 PE=1 SV=1

MVLSLIPSMRLRQCVNLHPDGTAFYTYIDYERDSEGISLTSWSQVYRRTLNVAAEVRRHAAIGDRAVILAPQGLDY
IVAFGLAQGLIAPVLSAPLGGASDERVDAVVRDAKPNVLTSSAIMGDVVPRVTPPPGIASPPTVAVDQLDL
DSPIRSNIVDDSLQTTAYLQYTSGSTRTAGVMITYKNILANFQQMISAYFADTGAVPPLDLFIMSWLFPYHDMG
LVLGVCAPIIVGC GAVLTSPVAF LQRPARWLQLMAREGQAFSAAPNF AFELTAAKAIDDDLAGLDLGRIKTILCGS
ERVHPATLKRFRVDRFSRNLREFAIRPAYGLAEATVYVATSQAGQPPEIRYFEPHEL SAGQAKPCATGAGTALVSYP
LPQSPIVRIVDPNTNTECPPGTIGEIVVHGDNVAGGYWEKPEDETERTFGGALVAPSAGTPVGPWLRTGDSGFV
SEDKFFIIGRIKDLLIVYGRNHSPDDIEATIQEITRGRCAAIAVPSNGVEKLV AIVELNNRGNL DTERLSFVTREVTS
AISTSHGLSVSDLVLVAPGSIPITTSKGKVRRAECVKLYRHNEFTRLD APLQASDL

>sp|P9WQ55|FAD10_MYCTU Putative fatty-acid--CoA ligase FadD10 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=fadD10 PE=1 SV=1

MGGKKFQAMPQLPSTVLDRVFEQARQQPEAIALRRC DGSALRYRELVAEVGGLAADLRAQSVSRGSRVLVIS
DNGPETYSVLACAKLGAIVMADGNLPIAAIERFCQITDPAALVAPGSKMASSAVPEALHSIPVIAVDIAAVTR
ESEHSLDAASLAGNADQGS EDP LAMI FTSGTTGEPKAVLLANRTFFAVPDILQKEGLN WVTWVVG ETTYSPLPA
THIGGLWWILTCLMHGGLCVTGGENTTSLEILTNAVATTCLVPTLLSKLVSELKSANATVPSLRVLVGYGGSRAIA
ADVRFIEATGVRTAQVYGLSETGCTALCLPTDDGSIVKIEAGAVGRPYPGVDVYLAATDGIGPTAPGAGPSASFG
TLWIKSPANMLGYWNNPERTAEVLIDGWVNTGDLLEREDGFFYIKGRSSEMIICGGVNIAPDEVDRIAEGVSG
VREAACYEIPDEEFGLVGLAVVASAELDESAARALKHTIAARFRRESEPMARPSTIVIVTDIPRTQSGKVMRASL
AAAATADKARVVVRG

>sp|P9WJB5|FHAB_MYCTU FHA domain-containing protein FhaB OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=fhaB PE=1 SV=1

MQGLVLQLTRAGFLMLLWVFIWSVLRILKTDIYAPTGA VMRRGLALRG TLLGARQRRHAARYLVVTEGALTG
ARITLSEQPVLIGRADDSTLVLTDDYASTRHARLSMRGSEWYVEDLGSTNGTYLDRAKVTTAVRVPIGTPVRIGKT
AIELRP

>sp|P9WJB3|FLQE2_MYCTU Fluoroquinolones export permease protein Rv2686c
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2686c PE=1 SV=1

MRAISSLAGPRALAAFGRNDIRGTYRDP LLVMLVIAPVIWTTGVALLT PLFTEMLARRYGF DLVGYYP LILTAFLLL
TSIIVAGALAAFLVLD DVDAGTMTALRVTPVPLSVFFGYRAATVMVVT TIYVVATM SC SGILEPGLVSSLIPIGLVA
GLSAVV TLLLILAVANNKIQLG LAMV RALGMLIAGL PCLPWFISSNWNLAFGVLPPYWA AKAFVWASDHGTW
WPYLVGGAVYNLAIWVWLFRRFRAKHA

>sp|P9WJB1|FLQE3_MYCTU Fluoroquinolones export permease protein Rv2687c
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2687c PE=1 SV=1

MTRLVPALRLELTQVRQKFLHAAVFSGLIWLAVLLPMPVSLRPAEPYVLVGDIAIIGFFVGGTVFFEKQERTIG
AIVSTPLRFWEYLAAKLTVLLAISLFVAVVVATIVHGLGYHLLPLVAGIVLGTLLMLLVGFSSSLPFASVTDWFLAAVI
PLAIMLAPPVVHYSGLWPNPVLYLIPTQGPLLLLGAAFDQVSLAPWQVGYAVVYPIVCAAGLCRAAKALFGRYV
VQRSGVL

>sp|P9WQN3|FTSH_MYCTU ATP-dependent zinc metalloprotease FtsH OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=ftsH PE=1 SV=1

MNRKNVTRTITAIIVVLLGWSFFYFSDDRGYKPVDTSSVAITQINGDNVKSQIIDDREQLRLILKKGNNETD
GSEKIVITKYPTGYAVDLFNALSAKNAKSTVNVNQQSILGELLVYVLPLLLLVGLFVMFMRMQGGARMGFGFGKS
RAKQLSKDMPKTTFFADVAGVDEAVEELYEIKDFLQNPSTRYQALGAKIPKGVLLYPPGTGKTLARAVAGEAGVP
FFTISGSDVEMFVGVGASRVRDLFEQAKQNSPCIIFVDEIDAVGRQRGAGLGGGHDEREQLNQLLVEMDGF
GDRAGVILIAATNRPDILDALLRPRGRFDRQIPVSNPDLARRAVLRVHSGKPMMAADADLDGLAKRTVGMTG
ADLANVINEAALLTARENGTVITGPALAEAVDRVIGGPRRKGRIIESEQEKKITAYHEGGHTLAAWAMPDIEPIYKV
TILARGRTGGHAVAVPEEDKGLRTRSEMIAQLVFAMGGRAAEELVFREPTTGAVSDIEQATKIARSMVTEFGMS
SKLGAVKYGSEHGDPFLGRMTGTPDYSHEVAREIDEVVRKLIIEAAHTEAWEILTEYRDVLDLAGELEKETH
RPELESIFADVEKRPLTMFDDFGGRIPSDKPPIKTPGELAIERGEPWPQVPEPAFKAAIAQATQAAEAARSDA
GQTGHGANGSPAGTHRSGDRQYGSTQPDYAGAPAGWHAPGWPPRSSHRPSYSGEPAPTYPGQPYPTGQADP
GSESSAEQDDEVSRTPAHG

>sp|P9WN97|FTSW_MYCTU Putative lipid II flippase FtsW OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=ftsW PE=1 SV=1

MLTRLLRRGTSDDTGSQTRGAEPVEGQRTGPEEASNPGSARPRTRFGAWLGRPMTSFHLIIAVAALLTTLGLIM
VLSASAVRSYDDGSAWVIFGKQVLWTLVGLIGGYVCLRMSVRFMRRIAFSGFAITIVMLVLVLPVIGKEANGS
RGWVAVAGFSMQPSELAKMAFAIWGAHLLAARRMERASLREMLIPLVPAAVVALALIVAQPDLGQTVSMGIIL
LGLLWYAGLPLRVFLSSLAAVVVSAAILAVSAGYRSDRVRSWLNPENDPQDSGYQARQAKFALAQGGIFGDGL
GQGVAKWNYLNAHNDIFAIIGEELGLVGALGLLGLFLFAYTGMRIASRSADPFLRLLTATTLWVLGQAFINI
GYVIGLLPVTGLQLPLISAGGTSTAATLSLIGIIANAARHEPEAVAALRAGRDDKVNRLRLPLPEPYLPPRLEAFRD
RKRRANPQAQTQPARQTPRTAPGQPARQMGLPPRPGSPRTADPPVRRSVHHGAGQRYAGQRRTRRRVRALEG
QRYG

>sp|P9WMX3|GLFT1_MYCTU Galactofuranosyl transferase GlfT1 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=glt1 PE=1 SV=1

MTESVFAVVVTHRRPDELAKSLDVLTAQTRLDPDHLIVVDNDGCGDSPVRELVAGQPIATTYLGSRRNLGGAGGF
ALGMLHALAQGADWVWLADDDGHAQDARVLATLLACAKEYSLAEVSPMVCNIDDPTLAFPLRRGLVWRR
RASELRTEAGQELLPGIASLFGALFRASTLAAIGVPLRFLFIRGDEVEMHRRRLIRSGLPFGTCLDAAYLHPCGSD
EFKILCGRMHAQYPDDPGKRFFTYRNRGYVLSQPGLRKLKLAQEWLRFGWFFLVTRRDPKGLWEWIRLRLRGR
REKFGKPGGSA

>sp|P9WGI9|GLYA1_MYCTU Serine hydroxymethyltransferase 1 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=glyA1 PE=1 SV=2

MTAAPDARTTAVMSAPLAEVDPDIAELLAKELGRQRDTLEMIASENFVPRAVLQAQGSVLTNKYAEGLPGRRY
GGCEHVDVVENLARDRAKALFGAEFANVQPHSGAQANA AVLHALMSPGERLLGLDLANGGHLTHGMRLNFS
GKLYENGFYGVDPATHLIDMDAVRATALEFRPKVIIAGWSAYPRVLDFAAFRSIADEVGAKLLVDMAHFAGLVAA
GLHPSPVPHADVSTTVHKTLLGGGRSGLIVGKQYAKAINSAVFPQQGGPLMHVIAGKAVALKIAATPEFAD
RQRRTLSGARIADRLMAPDVAKAGVSVVSGGTDVHLVLDLRDSDPLDGQAAEDLLHEVGITVNRNAVNPDP
PPMVTSGLRIGTPALATRGFGDTEFTEVADIATLATGSSVDVSALKDRATRLARAFPLYDGLEEWSLVGR

>sp|P9WMX5|GLYTR_MYCTU Putative glycosyltransferases OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pimF PE=1 SV=1

MRLSIVTTMYMSEPYVLEFYRRARAAADKITPDVEIIFVDDGSPDAALQQAVSLLDSDPCVRVIQLSRNFGHHK
AMMTGLAHATGDLVFLIDSDLEEDPALLEPFYEKLISTGADVVFVGCHARRPGGWLRFNFGPKIHYRASALLCDPPL
HENTLTVRLMTADYVRSVLQHQERELSIAGLWQITGFYQVPM SVNKAWKGTTTYTFRRKVATLVDNVTFSFNK
PLVFIFYLGAIFISSAAGYLIIDRIFFRALQAGWASVIVSIWMLGGVTIFCIGLVGIYVSKVFIETKQRPYTIIRRIYG
SDLTTREPSSLKTAFPAAHLSNGKRVTSEPEGLATGNR

>sp|P9WMN9|GSA_MYCTU Glutamate-1-semialdehyde 2,1-aminomutase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=hemL PE=1 SV=1

MGSTEQATSRVGAARTSAQLFEAACSVIPGGVNSPVRAFTAVGGTPRFITEAHGCWLIDADGNRYVDLVCSW
GPMILGHAHPAVVEAVAKAAARGLSFGAPTPAETQLAGEIIGRVAPVERIRLVNSGTEATMSAVRLARGFTGRA
KIVKFSGCYHGHVDALLADAGSGVATLGLCDDPQRPASPRSQSSRGLPSSPGVTGAAAADTIVLPYNDIDAVQQ
TFARFGEQIAAVITEASPGNMGVPPGPGFNAALRAITAEHGALLILDEVMTGFRVSRSGWYIDPVPADLFAF
GKVMSSGMPAAAFGGRAEVMQRLAPLGPVYQAGTLSGNPVAVAAGLATLRAADDAVYALDANADRLAGLL
SEALDAVVPHQISRAGNMLSVFFGETPVTFASARASQWRYPAFFHAMLDAAGVYPPCSAFEAWFVSAALD
DAAFGRANALPAAARAAAQERPA

>sp|P72065|GYRA_MYCXE DNA gyrase subunit A (Fragment) OS=Mycobacterium xenopi GN=gyrA PE=1 SV=2

RPDRSHAKSARSVAETMGNYHPHGDASIYDTLVRMAQPWSMRYPLVDGQGNFGSPGNDPPAAMRYCITGD
ALVALPEGESVRIADIVGARPNSDNAIDLKVLDRHGPNVLADRLFHSGEHPVYTVRTVEGLRVGTANHPDLLL
VDVAGVPTLLWKLIDEIKPGDYAVIQRSAFSVDCAGFARGKPEFAPTTYTVGVPGLVRFLEAHRDPDAQIAIDE
LTDGRFYAKVASVTDAGVQPVYSLRVDTADHAFITNGFVSHNTEAPLPLAMEMLREIDEETVDFIPNYDGRV
QEPTVLPSTRFPNLLANGSGGIAVGMATNIPPHN

>sp|A5TZK3|HBHA_MYCTA Heparin-binding hemagglutinin OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=hbhA PE=1 SV=1

MAENSNIDDIKAPLLAALGAADLALATVNELITNLRERAETRTDTRSRVEESRARLTKLQEDLPEQLTELREKFTA
EELRKAAGYLEAATSRYNELVERGEAALERLRSQSFEEVSARAEGYVDQAVELTQEALGTVASQTRAVGERAA
KLVGIELPKKAAPAKKAAPAKKAAPAKKAAKKAPAKKAAKKVQK

>sp|P9WHQ9|HPRT_MYCTU Hypoxanthine-guanine phosphoribosyltransferase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=hpt PE=1 SV=1

MHVTSQSSAITPGQTAELYPGDIKSVLLTAEQIQARIAELGEQIGNDYRELSATTGQDLLLLITVKGAVLFVTDLAR
AIPVPTQFEFMAVSSYGSSTSSSGVVRILKDLDRDIHGRDVLIVEDVVD SGLTSLWLSRNLTSRNPRSLRVCTLLRK
PDAVHANVEIAYVGFDFIPNDFVVG YGLDYDERYRDSYIGTLDPRVYQ

>sp|P9WJ99|INIA_MYCTU Isoniazid-induced protein IniA OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=iniA PE=1 SV=1

MVPAGLCAYRDLRRKRARKWGDTVTQPDDPRRVGVIVELIDHTIAIAKLN ERGDLVQRLTRARQRITDPQVRV
IAGLLKQGSQLLNSLLNLPAAARVGDDEATVVITVVSYSQAQPSARLVLAAGPDGTTAAVDIPVDDISTDVRRA
AGGREVLRVEVGAPSPLLRGGLAFIDTPGVGGLQPHLSATLGLLPEADAVLVSDTSQEFTEPEMWFVRQAH
QICPVGAVVATKTDLYPRWREIVNANAHLQRARVPMPIIAVSSLLRSHAVTLNDKELNEESNFPAIVKFLSEQVL
SRATERVRAGVLGEIRSATEQLAVSLGSELSVNDPNLDRDLASDLERRKREAAVQQTALWQQVLGDFND
LTADVHDHLRTRFRVTEDAERQIDSCDPTAHWAEIGNDVENAIATAVGDNFVWAYQRSEALDDVARSFADA
GLDSVLSAELSPHVMGTDFGRLKALGRMESKPLRRGHKMIIGMRGSYGGVVMIGMLS SVVGLGLFNPLSVGA
GLILGRMAYKEDKQNRLLRVRSEAKANVRRFVDDISFVSKQSRDRLKMIQRLLRDHYREIAEEITRSLTESLQATI
AAAQVAETERDNRIRELQRQLGILSQVNDNLAGLEPTLTPRASLGRA

>sp|P9WGL3|KDPD_MYCTU Sensor protein KdpD OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=kdpD PE=1 SV=1

MTLLFADLCAIFTPYRWMIEHVTTKRGQLRIYLGAAPGVGKTYAMLGEAHRRLERGTDVVAAVVETHGRNKTA
KLEGIEMIPPRYVEYRGARFPELDVEAVLRRHPQVVLVDELAHTNTPGSKNPKRWQDVQEILDAGITVISTVNI
QHLEGLNDVVEQITGIEQKEKIPDEIVRAADQVELVDITPEALRRRLAHGNVYAAERVDAALSNYFRTGNLTALR
EIALLWLADQVDAALEKYRADKKITATWEARERVVAVTGGPESETLVRRASRIASKSSAELMVVHVIRGDGLA
GVSAPQLGRVRELATSLGATMHTVVGDDVPTALLDFAREMNATQLVVGTSRRSRWARLFDGIGARTVQEPG
GIDVHMVTHPAASRASGWSRVSPRERHIASWLAALVPSVICAITVAWLDRFMGIGGESALFFIGVLIVALLGG
VAPAALSALLSGMLLNYFLTEPRYTWTIAEPDAAVTEFVLLAMAVAVAVLVDGAASRTREARRASQEAELLALFA
GSVLRGADLTLQRVRETYSQRAVTMLRVRQGASTGETVACVGTNPCRVDVSADTAIEVGDDEFWMLMAG
RKLAARDRRVLTAVATQAAGLVKQRELAEEAGQAEAIARADELRRSLLSAVSHDLRTPLAAAQVAVSSLRTEDVA
FSPEDTAELLATIEESIDQLTALVANLLDSSRLAAGVIRPQLRRAYLEEAVQRALVSIGKGATGFYRSGIDRVKVDVG
DAVAMADAGLLERVLANLIDNALRYAPDCVVRVNAGRVRERVLINVIDEGPGVPRGTEEQLFAPFQRPDHD
NTTGVLGMSVARGFVEAMGGTISATDTPGGGLTVVIDLAAPEDRP

>sp|O53638|LDT1_MYCTU L,D-transpeptidase 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ldtA PE=1 SV=1

MRRVVRYLSVVVAITMLTAESVSIATAAVPPLQPIPGVASVSPANGAVVGVVHPVVVFTTPVTDRAVERSIRI
STPHNTTGHFEVVASNVVRWVPHRYWPPHTRVSVGVQELTEGFETGDALIGVASISAHTFTVSRNGEVLRTM
PASLGKPSRPTPIGSFHAMSKERTVVMDSRTIGIPLNSSDGYLLTAHYAVRVTWSGVYVHSAPWSVNSQGYAN
VSHGCINLSPDNAAWYFDAVTVGDPIEVVG

>sp|P9WK81|LPPA_MYCTU Putative lipoprotein LppA OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=lppA PE=1 SV=1

MIAPQPISRTLPRWQRIVALTMIGISTALIGGCTMDHNPDTSRRLTGEQKIQILIDSMRNKGSYEAARERLTATARI
ADRVSAAIPGQTWKFDDDPNIQQSDRNGALCDKLTADIARRPIANSVMFGATFSAEDFKIAANIVREEAAKYGA
TTESLNFESAKRDYDVQNGYEFRLQIKFATLNTGDCFLQKVLDPAGQLPPEPPIWPTTSTPH

>sp|P9WK77|LPPJ_MYCTU Putative lipoprotein LppJ OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=lppJ PE=1 SV=1

MPHSTADRRLRLTRQALLAAAVVPLLAGCALVMHKPHSAGSSNPWDDSAHPLTDDQAMAQVVEPAKQIVAA
ADLQAVRAGFSFTSCNDQGDPPYQGTVRMAFLQGDHDAYFQHVRAAMLSHGWDGPPPGQYFHGITLHK
NGVTANMSLALDHSYGEMILDGECRNTTDHHHDETTNITNQLVQP

>sp|P9WK71|LPPO_MYCTU Putative lipoprotein LppO OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=lppO PE=1 SV=1

MTDPRHTVRIAVGATALGVSALGATLPACSAHSGPGSPSAPSAPAAATVMVEGHTHTISGVVECRTSPAVRTA
TPSESGTQTRVNAHDDASVTLSDSTPPDVNGFGISLKIGSVQMPYQPVQSPTQVEATRQGKSYTLTGT
GHAVIPGQTGMRELPGVHVTC

>sp|P9WK61|LPQH_MYCTU Lipoprotein LpqH OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=lpqH PE=1 SV=1

MKRGLTAVAGAAAILVAGLSGSSNKSTTGSGETTTAAGTTASPGAASGPKVVIDGKDQNVGTGSVVCTTAAGN
VNIAIGGAATGIAAVLTDGNPPEVKSGLGNVNGVTLGYTSGTGQGNASATKDGSHYKITGTATGVDMANPM
SPVNKSFEIEVTCS

>sp|P9WK49|LPRE_MYCTU Putative lipoprotein LprE OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=lprE PE=1 SV=1

MPGVWSPPCPTTRVGVVAALVAATLTGCGSGDSTVAKTPEATPSLSTAHPAPPSSEPPSATAAPPSNHSAAP
VDPCAVALASPTIAKVVSELPRDPRSEQPWNPEPLAGNYNECAQLSAVVIKANTNAGNPTRAVMFMHLGKYIP

QGVPTDYGFTGIDTSQCTGDTVALTYASGIGLNNVVKFRWNGGGVELIGNTTGG

>sp|P65315|LPRF_MYCBO Putative lipoprotein LprF OS=Mycobacterium bovis (strain ATCC BAA-935 / AF2122/97) GN=lprF PE=1 SV=1

MNGLISQACGSHRPRRPSLGAVALIAATLFATVVAGCGKKPTTASSPSPGSPSPAQQILQDSSKATKGLHSVH
VVVTVNNLSTLPFESVDADVTNQPQNGQAVGNAKVRMKPNTPVVATEFLVTNKMTYTKRGGDYVSVGPAE
KIYDPGIILDKDRGLGAVVQVQNPQTIQGRDAIDGLATVKVSGTIDAAVIDPIVQLGKGGGRLPITLWIVDTNAS
TPAAPANLVRMVIDKDKQGNVDITLSNWGAPVTIPNPAG

>sp|P9WIP7|LSR2_MYCTU Nucleoid-associated protein Lsr2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=lsr2 PE=1 SV=1

MAKKVTVTLVDDFDGSGAADETFEFLDGVTYEIDLSTKNATKLRGDLKQWVAAGRRVGGRRRGRSGSGRGR
GAIDREQSAAIREWARRNGHNVSTRGRIPADVIDAYHAAT

>sp|P9WFU7|LYSX_MYCTU Lysylphosphatidylglycerol biosynthesis bifunctional protein LysX OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=lysX PE=1 SV=1

MGLHLTVPLRRDGRGVQSNSHDTSKTTADISRCQHTDAGLQRAATPGISRLGISSRSVTLTKPRSATRGNS
RYHWVPAAGWTVGVIATLSLLASVSPLIRWIKVPREFINDYLFNFPDTNFAWSFVLALLAAALTARKRIAWLVL
LANMVLAAVVNAEEAAGGNTAAESFGENLGFVHVVAIVLVLYGREFWAKVRRGALFRAAAVWLAGAVVG
IVASWGLVELFPGSLAPDERLGYAANRVVGFALADPDFTGRPHVFLNAIFGLFGAFALIGAAIVFLSQRADNAL
TGEDESAIRLLDLYGKDDSLGYFATRRDKSVVFASSGRACITYRVEVGVCLASGDPVGDHRAWPQAVDAWLRL
CQTYGWAPGVMGASSQGAQTYREAGLTALELGDAILRPADFKLSGPEMRGVRQAVTRARRAGLTVRIRRRHR
DIAEDEMAQTITRADSWRDTETERGFMSALGRLGDPADSDCLLVEAIDPHNQVLAMLSLVPWGTTGVSLDLM
RRSPQSPNGTIELMVSELALHAESLITRISLNFVAFRAAFEQGAQLGAGPVARLWRGLLVFFSRWWQLETLYRS
NMKYQPEWVPRYACEDARVIPRVGASVIAEGFLVLPFSRRNRVHTGHHPAVPERLAATGLLHHDGSAPDVS
GLRQVGLTNGDGVERRLEQVRVRFDKLEKLRSSGIDAFVGRPPSHTVAQALAADHQASVSVSGRIMRIRNY
GGVLFALQRDWSGEMQVLLDNSRLDQGCAADFNAATDLGDLVEMTGHMGASKTGTPSLIVSGWRILIGKCLR
PLPNKWKGLLDPEARVTRYLDLAVNAESRALITARSSVLRAVRETLFAKGFVEVETPIQQQLHGGATARPFVTHI
NTYSMDLFLRIAPELYLKRCLCVGGVERVFELGRAFRNEGVDVFSHNPEFTLLEAYQAHADYLEWIDGCRELIQNA
QAANGAPIAMRPRTDKGS DGRHHLEPVDISGIWPVRTVHDAISEALGERIDADTGLTTLRKLCAAGVPYRTO
WDAGAVVLELYEHLVECRTEQPTFYIDFPTSVSPLTRPHRSKRGAERWDLVAVWGIELGTAYSELDPVEQRRRL
QEQSLLAAGGDPEAMELDEDFLQAMEYAMPPTGGLGMGIDRVVMLITGRSIRETLPPFLAKPH

>sp|P9WJ83|MCTB_MYCTU Copper transporter MctB OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=mctB PE=1 SV=1

MISLRQHAVSLAAVFLALAMGVVLGSGFFSDTLSSLRSEKRDLYTQIDRLTDQRDALREKLSAADNFDIQVGSRI
VHDALVGKSVVIFRTPDAHDDIAAVSKIVGQAGGAVTATVSLTQEFVEANSAEKLRVSVNSSLPAGSQLSTKLV
DQGSQAGDLLGIALLSNADPAAPTVEQAQRDTVLAALRETGFITYQPRDRIGTANATVVVTGGALSTDAGNQG
VSVARFAAALAPRSGTLLAGRDGSANRPAAVAVTRADADMAAEISTVDDIDAEPGRITVILALHDLINGGHVG
HYGTGHGAMSVTVSQ

>sp|P9WMX1|MFTF_MYCTU Putative mycofactocin biosynthesis glycosyltransferase MftF OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=mftF PE=1 SV=1

MTATRLPDGFAVQVDRRVRVLGDGSALLGGSPTLLRLAPAARGLLCDGRLKVRDEVSAELARILLDATVAHPRP
PSGPSHRDVTVVIPVRNNASGLRRLVTSRGLRVIVVDDGSACPVESDDFVGAHCDIEVLHHPHSGPAAARNT
GLAACTTDFVAFDSDVTPRRGWLESLLGHFCDPVALVAPRIVSLVEGENPVARYEALHSSLDLQREAPVLP
STVSYVPSAAIVCRSSAIRDVGGFDETMHSGEDVLCWRLEAGARLRYEPIALVAHDHRTQLRDWIARKAFYG
GSAAPLAVRHPDKTAPLVISGGALMAWILMSIGTGLGRLASLVIAVLTGRRIARAMRCAETSFLDVLAVATRGLW
AAALQLASAI CRHYWPLALLAAILSRRCRRVVLIAAVDGVVDWLRRREGADDDAEPIGPLYLVLRVDDLAYG

AGLWYGVVRENRIGALKPQIRT

>sp|P46841|MMP1_MYCLE Major membrane protein I OS=Mycobacterium leprae (strain TN)
GN=mmp1 PE=1 SV=2

MTSAQNESQALGDLAAGQLANATKTPQLSTITPRWLLHLLNWVPEAGVYRVNRVVNPERVAVKAEAGAG
TEAPLPETFVDYETSPREYTLRTISTLLDIHTRVSDLYSSPHDQITQQLRLTIETIKERQECELVNSPEFGLLAQVTPE
QTIRTFAGAPTPDDLDALITKVKMPSFFLTHPQGIAAFGREATYRGVPPVVVSLFGAQFITWRGIPLIPSDKVP
VQDGETKFILVRTGEERQGVVGLFQPGVGEQAPGLSVRFTGINQAAIATYLVTLTSLAVLTDALAVLDNVAV
DQFHEYK

>sp|P9WJV7|MMPL2_MYCTU Putative membrane protein mmpL2 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=mmpL2 PE=1 SV=1

MSEHHAALSLPILPRLIRFAVVIVLLWLGFTAFVNLAVPQLEVVGKAHSVMSPSDAASIQAIRVGVQVFGEF
DSDNAVITIVLEGDQPLGGDAHRFYSDLMRKLSADTRHVAHIQDFWGDPLTAAGSQSADDRAAYVVVYLVGN
NETEAYDSVHAVRHMVDTPPPHGVKAYVTGPAALNADQAEAGDKSIAKVTAITSMVIAAMLLVIYRSVITAVL
VLIMVGDILGAIRGFIALADHNIFSLSTFATNLLVMAIAASTDYAIFMLGRYHESRYAGEDRETAFTMFHGTAH
VILGSGLTIAGAMYCLSFARLPYFETLGAPIAIGMLVAVLAALTLGPAVLTVGSFFKLFDPKRRMNTRRWRVGTAI
VRWPGPVLAATCLVASIGLLALPSYRTTYDLRKFMPASMPNSVGDAAAARRFRARLNPEVLLIETHDMRNP
VDMVLVDKVAKNYHSPGIEQVKAITRPLGTTIKHTSIPFIISMQGVNSSEQMEFMKDRIDDILVQVAAMNTSIET
MHRMYALMGEVIDNTVMDHLTHDMSDITATLRDHLADFEDFFRPIRSYFYWEKHCFDVPLCWSIRSIFDMF
DSVDQLSEKLEYLVKMDILITLLPQMRAQMPPMISAMTTMRDMMLIWHGTLGAFYKQQERNKDPGAM
GRVFDAAQIDDSFYLPQSAFENPDFKRGLKMFSPDGKAARFVIALEGDPATPEGISRVEPIKREAREAIKGTPLQ
GAAIYLGTAATFKDIREGARYDILLIAGVAAISLILIMMIITRSVVAAVVIVGTVVLSMGASFGSLVWQDILGIE
LYWMLAMSVILLAVGSDYNLLISRLKEEIGAGLNTGIIRAMAGTGGVVTAAGMVFAVTMSLFFVSDLRIGQI
GTTIGLGLLFDLTVRSFMTPSIAALLGRWFWWPLRVRPRPASQMLRPFAPRRLVRAALLPSGQHPSATGAHE

>sp|P9WJV5|MMPL3_MYCTU Putative membrane protein mmpL3 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=mmpL3 PE=1 SV=1

MFAWWGRTVYRYRFIVGVMVALCLGGGVFGLSLGKHVTQSGFYDDGSQSVQASVLGDQVYGRDRSGHIVAI
FQAPAGKTVDDPAWSKVVDELNRFQDHPDQVLGWAGYLRASQATGMATADKKYTFVSIPLKGGDDDDTIL
NNYKAIAPDLQRLDGGTVKLAGLQPVAEALTGTIATDQRRMEVLALPLVAVVLFVFGGVIAAGLPVMVGGLCI
AGALGIMRFLAIFGPVHYFAQPVVSLIGLGIADYGLFIVSRFREEIAEGYDTETAVRRTVITAGRTVTFSAVLIVASA
IGLLFPQGFLKSLTYATIASVMLSAILSITVLPACLGILGKHVDALGVRTLFRVPFLANWKISAAYLNWLADRLQRT
KTREEVEAGFWGKLVNRVMKRPVFAAPIVIMILLIIPVKGKLSLGGISEKYLPTNSVRQAQEEFDKLPFGYRTNP
LTLVIQTSNHQPVTDAQIADIRSKAMAIGGFIEPDNDPANMWQERAYAVGASKDPSVRVLQNGLINPADASKKL
TELRITPPKGITVLVGGTPALELDSIHGLFAKMLMVVILLTTTIVLMFLAFGSVVLPIKATLMSALTLGSTMGILT
WIFVDGHFSKWLNFPTPTAPVIGLIIALVFLSTDYEVFLVSRMVEARERGMSTQEAIRIGTAATGRIITAAALIV
AVVAGAFVSDLVMMKYLAFLMAALLLDATVVRMFLVPSVMKLLGDDCWVAPRWARRLQTRIGLGEIHL
DERKRPVSNRPARPPVTAGLVAARAAGDPRPPHDPHTPLAESPRPARSSPASPELTPALEATAAPAAPSGAST
TRMQIGSSTEPTTRLAAAGRSVQSPASTPPPTPTPPSAPSAGQTRAMPLAANRSTDAAGDPAEPTAALPIIRS
GDDSEATEQLNARGTSDKTRQRRRGGGALSQAQDLLRREGRL

>sp|P9WJU7|MMPL7_MYCTU Putative membrane protein mmpL7 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=mmpL7 PE=1 SV=1

MPSPAGRLHRIRYIRLKKSSPDCRATITSGSADGQRRSPRLTNLLVVAWVAAVIANLLTFTQAEPHDTSPALL
PQDAKTAATSRIAQAFPGTGSNAIAYLVVEGGSTLEPQDQPPYDAAVGALRADTRHVGSVLDWVSDPVTAPL
GTSPDGRSATAMVWLRGEAGTTQAAESLDAVRSVLRQLPPEGLRASIVVPAITNDMPMQITAWQSATIVTVA
AVIAVLLLLRARLSVRAAAIVLLTADLSLAVAWPLAAVVRGHDWGTDSVFSWTLAAVLTIGTITAATMLAARLGS

DAGHSAAPTYRDSLPAFALPGACVAIFTGPLLLARTPALHGVGTAGLGVFVALAASLTVLPALIALAGASRQLPAP
TTGAGWTGRLSLPVSSASALGTAAVLAICMLPIIGMRWGVVAENPTRQGGAAQVLPGNALPDVVVIKSARDLRDP
AALIAINQVSHRLVEVPGVRKVESAAWPAGVPWTDASLSSAAGRLADQLGQQAGSFVPAVTAIKSMKSIIEQM
SGAVDQLDSTVNVTLGARQAQQYLDPMLAAARNLKNKTTELSEYLETIHTWIVGFTNCPDDVLCTAMRKVIE
PYDIVVTGMNELSTGADRISAISTQTMSALSSAPRMVAQMRSALAQVRSFVPKLETTIQDAMPQIAQASAMLK
NLSADFADTGEFFHLSRKDLADPSYRHVRESMFSSDGTATRLFLYSDGQLDLAAAARAQQLEIAAGKAMKYG
SLVDSQVTVGGAAQIAAAVRDALIHDAVLLAVILLTVVALASMWRGAVHGAAVGVGLASYLAALGVSIALWQ
HLLDRELNALVPLVSFAVLASCGVPYLVAGIKAGRIADEATGARSKGAVSGRGAVAPLAALGGVFGAGLVLVSGG
SFSVLSQIGTVVVLGLGLVITVQRAWLPTTPGRR

>sp|P9WJU5|MMPL8_MYCTU Membrane transport protein mmpL8 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=mmpL8 PE=1 SV=1

MCDVLMQPVRTPRPSTNLRKPLRPTGDGGVFPRLGRLVRRPWVVIAFWVALAGLLAPTVPSLDAISQRHPV
AILPSDAPVLVSTRQMTAAFREAGLQSVAVVLSDAKGLGAADERSYKELVDALRRDTRDVVLMQDFVTTPLR
ELMTSKDNQAWILPVGLPGDLGSTQSKQAYARVADIVEHQVAGSTLTANLTGPAATVADNLNTGQRDRSRIEFAI
TILLVILLIYGNPITMVLPLITIGMSVVVAQRLVAIAGLAGLGIANQSIIFMSGMMVGAGTDYAVFLISRYHDYLR
QGADSDQAVKKALTSIGKVIAASAATVAITFLGMVFTQLGILKTVGPMLGISVAVVFFAAVTLPALMVLTRRRG
WIAPRRDLTRRFWRSSGVHIVRRPKTHLLASALVLVILAGCAGLARYNYDDRKTLPASVESSIGYAALDKHFPSNL
IPEYLFISSTDLRTPKALADLEQMVRVSVQVPGVAMVRGITRPAGRSLEQARTSWQAGEVSGSKLDEGSKQIA
VHTGDIDKLAGGANLMSKLGDVRAQVNRAISTVGGIDALAYLQDLLGGRVNLGELEGAEKLGSMRALGDTI
DADASFVANTEWASPVLGALDSSPMCTADPACASARTELQRLVTARDDGTLAKISELARQLQATRAVQTLAAT
VSGLRGALATVIRAMGSLGMSSPGGVRSKINLVNKGVNDLADGSRQLAEGVQLLVDQVKMGFGLGEASAF
LAMKDTATTPAMAGFYIPPELLSYATGESVKAETMPSEYRDLLGGLNVDQLKKVAAAFISPDGHSIRYLIQTDLNP
FSTAAMDQIDAATAARGAQNTALADAKVSVVGLPVVLKDTRDYSHDHLRLIIMTVCIVLILVLLRAIVAPLY
LIGSVIVSYLAALGIGVIVFQFLGQEMHWSIPGLTFVILVAVGADYNMLLISRLREEAVLGVRSVIRTAVSTGGVI
TAAGLIMAASMYGLVFASLGSVVQGAFLVLTGLLLDTFLVRTVTPAIAVLVQANWWLPSSWRPATWWPLG
RRRGRAQRTRKPKLLPKEEEEQSPDDDDLIGLWLHDGLRL

>sp|P9WJT9|MMPLB_MYCTU Putative membrane protein mmpL11 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=mmpL11 PE=1 SV=1

MMRLSRNLRRCRWLVTGWLLALVPAVYLAMTQSGNLTGGGFVAGSQSLLVHDQLDAHYPDRGAPALALVA
APRPDASYQDIDNAVALLRQIASLPGVTEAPNPTQRPPQDPDRPYVVSRLDARNAGTSDVAKKLRDRIGVKGD
QSGQTANGKVRVLYVIGQGALSAAAAANTKHDIANAERWNLPIILMVLVAVFGSLAAAIPALAVCTVITMGL
VFLVLSMHTTMSVFTSTVSMFGIALAVDYSFILMRYREELRCGRRPPDAVDAAMATSGLAVVLSGMTVIASLT
GIYLINTPALRSMATGAILAVAVAMLTSAITPAVLATFARAAAARSAVHWSRRPASTQSWFWSRWVGVWVWR
RPWITALAASTVLLVMAAPATLMVLGNSLLRQFDSSEIIRTGAAAAAQALGPGALGPVQVLVRFDAGGASAPE
HSQTIAAIRHRIAQAPNVVSVAPPRFADDNGSALLSAVLSVDPEDLGARDTITWMRTQLPRVAGAAQVDVGG
PTALIKDFDDRVSATQPLVLVFAVIAFLMLLISIRSVFLAFKGVLMTLLSVAAAYGSLVMVFQWGWARGLGFAL
HSIDSTVPPLVLAMTFGLSMDYEIFLLTRIRERFLQTGQTRDAVAVGVRTSARTITSAALIMIAVFCGFAFAGMPLV
AEIGVACAVAIADVATVRLVLPALMAMFDRWNWWLPRWLAHILPSVDFDRPLPKVDLGDVVIPDDFAAA
IPPSADVRMVLKSAKLRKRLAPDAICVTDPLAFTGCGCDGKALDQVQLAYRNGIARAIWSGQRPVHPVTVWR
KRLAVALDALQTTTWECCGVQTHRAGPGYRRRSPVETTNVALPTGDRLQIPTGAETLRFKGYLIMSRNSSHDYA
DFADLVDTMAPETAAAVLAGMDRYSCQAPGRQWMATQLVGRADPQPSDLGDQSPGADAQAKWEEVRR
RCLSVAVAMLEEAR

>sp|P9WJT3|MMPS2_MYCTU Putative membrane protein mmpS2 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=mmpS2 PE=1 SV=1

MISVSGAVKRMWLLLAIVVAVVGGGLGIYRLHSIFGVHEQPTVMVKPDFDVPLFNPKRVTYEVFGPAKTAKIAYL
DPDARVHRLDSVSLPWSVTVETTLPAVSVNLMAQSNADVISCRIIVNGAVKDERSETSPRALTSCQVSSG

>sp|P9WJT1|MMP53_MYCTU Putative membrane protein mmpS3 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=mmpS3 PE=1 SV=1

MSGPNPPGREPDEPESEPVSDTGDERASGNHLPVAGGGDKLPSDQTGETDAYSRAYSAPESHTGGPYVPA
DLRLYDYDDYEESDLDELAAPRWVWVGVAAIIAVALVSVSLVTRPHTSKLATGDTTSSAPPVQDEITTTK
PAPPPPPAPPPTTEIPTATETQTVTVTPPPPPPPATTTAPPATTTTAAAPPPTTTTPTGPRQVTVSVTGKAPGD
IISVTVYDAAGRRRTQHNVYIPWSMTVTPISQSDVGSVEASSLFRVSKLNCISITSDGTVLSSNSNDGPQTSC

>sp|P9WGF1|MMR_MYCTU Multidrug resistance protein Mmr OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=mmr PE=1 SV=1

MIYLYLLCAIFAEVVATSLKSTEGFTRLWPTVGLVGYGIAFALLALSISHGMQTDVAYALWSAIGTAAIVLVAFLF
LGSPISVMKVVGVGLIVGVVTLNLAGAH

>sp|P9WIZ5|MNTH_MYCTU Divalent metal cation transporter MntH OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=mntH PE=1 SV=1

MAGEFRLSHLCSRGSKVGELAQDTRTSLKTSWYLLGPAFVAIIAYVDPGNVAANVSSGAQFGYLLLWVIVAAN
VMAALVQYLSAKLGLVTGRSLPEAIGKRMGRPARLAYWAQAEIVAMATDVAEVIAGGAIALRIMFNLPPIGGIIT
GVVSLLLTIQDRRGQRLFERVITALLLVIAIGFTASFFVVTPPNAVLGGLAPRFQGTESVLLAAAIMGATVMPH
AVYLHSGLARDRHGHPDPGPQRRRLRVTRWDVGLAMLIAGGVNAAMLLVAALNMRGRGDTASIEGAYHAV
HDTLGATIAVLFVGLLASGLASSVGGAYAGAMIMQGLLHWSVPMLVRRILITLGPALAILTLGFDPTRTLVLVSQVV
LSFGIPFAVLPLVKTGSPAVMGGDTNHRATTWVGWVAVMVSLNVMMLIYLTVTG

>sp|P9WGU3|MODA_MYCTU Molybdate-binding protein OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=modA PE=1 SV=1

MRWIGLSTGLVSAMLVAGLVACGSNSPASSPAGPTQGARSIVVFAAASLQSAFTQIGEQFKAGNPGVNVNFAF
AGSSELATQLTQGATADVFAADTAQMDSVAKAGLLAGHPTNFATNTMVIVAAAGNPKKIRSFADLTPGLNV
VVCQPSVPCGSATRRIEDATGIHLNPVSEELSVTDVLNKVITGQADAGLVYVSDALSVATKVTCVRFPEAAGVVN
VYAIKRTSQPALARQFVAMVTAAGRRILDQSGFAKP

>sp|P9WMN7|MOEZ_MYCTU Probable adenylyltransferase/sulfurtransferase MoeZ OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=moeZ PE=1 SV=1

MSTSLPPLVEPASALSREEVARYSRHLIIPDLGVDGQKRLKNARVLVIGAGGLGAPTLVLAAGVGTIGIVDFDV
VDESNLQRQVIHGVADVGRSQAQSARDSIVAINPLIRVRLHELRLAPSNAVDLQYDLILDGTDNFATRYLVND
AAVLGKPYVWGSYRFEGQASVFWEDAPDGLGVNYRDLYPEPPPPGMVPSCAEGGVLIICASVASVMGTE
AIKLITGIGETLLGRLLVYDALEMSYRTITIRKDPSTPKITELVDYEQFCGVVADDAQAAGSTITPRELRDWLDS
GRKLALIDVRDPVEWDIVHIDGAQLIPKSLINSGEGLAKLPQDRTAVLYCKTGVRSAEALAAVKKAGFSDAVHLQ
GGIVAWAKQMOPDMVMY

>sp|Q7UOX3|MPRB_MYCBO Signal transduction histidine-protein kinase/phosphatase MprB OS=Mycobacterium bovis (strain ATCC BAA-935 / AF2122/97) GN=mprB PE=1 SV=1

MWWFRRRDRAPLRATSSLSLRWRVMLLAMSVMAMVVVLMVAVYAVISAALYSDIDNQLQSRAQLLIASGSL
AADPGKAIEGTAYSDVNAMLVNPQGQSIYTAQQPGQTLVPGAEEKAVIRGELFMSRRTTADQRVLAIRLTNGSSL
LISKSLKPTAVMKNLRRWVLLVGGIGVAVAAVAGGMVTRAGLRPVGRLEAAERVARTDDLRRPIPVFGSDELA
RLTEAFNLMLRALAESRERQARLVTDAGHELRTPLTSLRTNVLLMAMAPGAPRLPKQEMVDLRADVLAQIEE
LSTLVGDLVDSLGRDAGEVVEHPVDMADVDRSLERVRRRRNDIHFVVEVIGWQVYGDVAGLSRMALNLMMD
NAAKWSPPGGHVGVRSLQLDASHAELVSDRGPVQERRLVFERFYRSASARALPGSGLGLAIVKQVVLNH
GGLRIEDTDPGGQPPGTSIYVLLPGRMPQPQLPGATAGARSTDIENSRSANVISVESQSTRAT

>sp|P9WGK9|MTRB_MYCTU Sensor histidine kinase MtrB OS=Mycobacterium tuberculosis

(strain ATCC 25618 / H37Rv) GN=mtrB PE=1 SV=1

MIFGSRIRRRIRRRGRSGPMTRGLSALSRAVAVAWRRSLQLRVVVALTLGLSLAVILALGFVLTSQVTNRVLDIKVRA
AIDQIERARTTVSGIVNGEETRSLDSSLQLARNTLTSKTD PASGAGLAGAFDAVLMVPGDG PRAASTAGPVDQV
PNALRGFVKAGQAAYQYATVQTEGFSGPALIIIGTPTLSRVANLELYLIFPLASEQATITLVRGTMATGGLVLLVLLAG
IALLVSRQVVVPVRSASRIAERFAEGHLSERMPVVRGEDDMARLAVSFNDMAESLSRQIAQLEEFGNLQRRFTSD
VSHELRTPLTTVRMAADLIYDHSADLDPTLRRSTELMVSELDRFETLLNDLLEISRHDAGVAELSVEAVDLRTTVN
NALGNVGH LAEEAGIELLVDLPAEQVIAEVDARRVERILRNLIANAIDHAEHKPV RIRMAAEDTVAVTVRDYG
VGLRPGEEKLVFSRFRWSDPSRVRSSGGTGLGLAISVEDARLHQGRLEAWGEPGEGACFRLLP MVRGHKVT
SPLPMKPIQPVLQPV AQPNPQMPPEYKERQRPREHA EWSG

>sp|P9WJM1|MURA_MYCTU UDP-N-acetylglucosamine 1-carboxyvinyltransferase
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=murA PE=1 SV=1

MAERFVVTGGNRLSGEVAVGGAKNSVLKMAATLLAEGTSTITNCPDILDVPLMAEVL RGLGATVELDGDVARI
TAPDEPKYDADFAAVRQFRASVCVLGPLVGRCKRARVALPGGDAIGSRPLDMHQAGLRQLGAHCNIEHGCVV
ARAETLRGAEIQLEFPVSGATENILMAAVVAEGVTIHNAAAREPDVVDLCTMLNQMG AQVEGAGSPTMTITG
VPRLHPTEHRVIGDRIVAATWGIAAAMTRGDISVAGV DPAHLQLVLHKLHDAGATVTQTDASFRVTQYERPKA
VNVATLPFPGFPTDLQPMIALASIADGTSMITENVFEARFRFVEEMIRLGADARTDGHHAVVRGLPQLSSAPV
WCSDIRAGAGLVLAGLVADGDTEVHDV FHDVHIDRGYPLFVENLVSLGAEIERVCC

>sp|P9WJL1|MURF_MYCTU UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=murF PE=1 SV=1

MIELTVAQIAEIVGGAVADISPQDAHRRVTGTVEFDSRAIGPGGLFLALPGARADGHDHAASAVAAGA AVVL
AARPVGVPAIVVPPVAAPNVLAGVLEHDNDGSGAAVLAALAKLATAVAAQLVAGGLTIIGITGSSGKTSTKDL M
AAVLAPLGEVVAPPGSFNNELGHPWTVLRATRRTDY LILEMAARHHGNIAALAEIAPPSIGVVLNVGTAHLGEF
GSREVIAQTKAELPQAVPHSGAVVLNADDPAVAAMAKLTAARVVRVSRDNTGDVWAGPVSLDELARPRFTLH
AHDAQAEVRLGVCGDHQVTNALCAA VALECGASVEQVAAALTAAPPVSRHRMQVTTRGDGVTVIDDAYNA
NPDSMRAGLQALAWIAHQPEATRRSWAVLGEMAELGEDAIAEHDRIGRLAVRLDVSRLVVVGTGRSISAMHH
GAVLEGAWGSGEATADHGADRTAVNVADGDAALALLRAELRPGDVVLVKASNAAGLGAVADALVADDT CGS
VRP

>sp|P9WJK3|MVIN_MYCTU Probable peptidoglycan biosynthesis protein MviN
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=mviN PE=1 SV=1

MRPSPGEVPTASQRQPELSDAALVSHSWAMAFATLISRITGFARIVLLAAILGAALASSFSVANQLPNLVAALVLE
ATFTAIFVPVLARAEQDDPDGGA AFVRRVLTATLLLGATLSVLAAPLLVRLMLGTNPQVNEPLTTAFAYLLLPQ
VLVYGLSSVFMALNTRNVFGPPAWAPV VNNVVAIATLAVYLAVPGELSVD PVRMGNAKLLVLGIGTTAGVFAQ
TAVLLVAIRREHISLRPLWGIDQRLKRFGAMAAAMVLYVLISQLGLVGNRIASTAAASGPAIYNTWLVLM LPF
GMIGVTVLTVM PRLSRNAAADDTPAVLADLSLATRLTMITLIPTVAFMTVGGPAIGSALFAYGNFGD VDAGYL
GAAIALSAFTLIPYALVLLQLRVFYAREQPWTPITII VITGVKILGSL LAPHITGDPQLVAAYLGLANGLGFLAGTIV
GYIILRRALRPDGGQLIGVGEARTVLTVAASLLAGLLAHVADRLLGLSELTAHAGSVGSLRLSVLALIMLPILAA
VTLCARVPEARAALDAVRARIRSRRLKTGPQTQNVLDQSSRPGPV TYPERRRLAPPRGKSVVHEPIRRRPPEQV
ARAGRAKGPEVIDRPSENASFGAASGAELPRVADELQLDAPAGRDPGPVSRPHPSDLQNGDLPADAARGPIA
FDALREPDRESSAPPDDVQLVPGARIANGRYRLLIFHGGVPP LQFWQALD TALDRQVALTFVDPQGVLPDDVL
QETLSRTLRLSRIDKPGVARVLDVVHTRAGGLVVAEWIRGGSLQEVA DTSPSPVGAIRAMQSLAAAADA AHRA
GVALSIDHPSRVRSIDGDVVLAYPATMPDANPQDDIRGIGASLYALLVNRWPLPEAGVRSGLAPAERDTAGQPI
EPADIDRDIPFQISAVAARSVQGDGGIRSASTLLNLMQQATAVADRTEVLGPIDEAPVSAAPRTSAPNSETYTRR
RRNLLIGIGAGAAVLMVALLVLSVLSRIFGDVSGGLNKDELGLNAPTASTSAASSAPPGSVVKPTKVTFSPDG
GADNPGEADLAIDGNPATSWKTDIYTD PVPFPFSKNGVGLMLQLPQATVVGTV AIDVASTGKVEIRSASTPTP

ATLEDTAVLTSATALRPGHNTISVEAAAPTSNLLVWISTLGTTDGKSQADISEITIYAAS

>sp|P9WJY6|NARK2_MYCTO Probable nitrate/nitrite transporter NarK2 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=narK2 PE=2 SV=1

MRGQAANLVLATWISVWNFWAWNLIPLSTSYARDMSLSSAEASLLVATPILV GALGRIVTGPLTDRFGGRAML
IAVTLASILPVLAVGVAATMGSYALLVFFGLFLGVAGTIFAVGIPFANNWYQPARRGFSTGVFGMGMVGTALSAF
FTRPFVRWFGLFTTHAIVAAALASTAVVAMVVLRDAPYFRPNADPVLPRLKAAARLPVTWEMSFLYAIVFGGFV
AFSNYLPTYITTIYGFSTVDAGARTAGFALAAVLARPVGGWLSDRAPRHVVLASLAGTALLAFAAALQPPPEVW
SAATFITLAVCLGVTGGVFAWVARRAPAASVGSVTGIVAAAGGLGGYFPPLVMGATYDPVDNDYTVGLLLLVA
TALVACTYTALHAREPVSEEASR

>sp|O53857|NARS_MYCTU Probable sensor histidine kinase NarS OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=narS PE=1 SV=3

MPSYGNLGRLLGRHEYGVLVAMTSSAELDRVRWAHQRLSYRIASVLRIGVVGLMVAAMVVGTSRSEWPQQI
VLIGVYAVAALWALLAYSASRRFFALRRFRSMGRLEPFATAVDVLIITGFQLLSTDGIYPLLIIMILLPVLGLDVST
RRAAVVLACTLVGFAVAVLGDVPLMLRAIGWPETIFRFALYAFLCATALMVVRIEERHTRSVAGLSALRAELLAQT
MTASEVLQRRIAEAIHDGPLQDVLAAARQELIELDAVTPGDERVGRALAGLQSASERLRQATFELHPAVLEQVGLG
PAVKQLAASTAQRSGIKISTDIDYPIRSGIDPIVFGVVRELLSNVVRHSGATTASVRLGITDEKCVLDVADDGVGVT
GDTMARRLGEHGHLASHRARVDAAGGVLFVFLATPRGTHVCVELPLKR

>sp|P9WJQ0|NARX_MYCTO Nitrate reductase-like protein NarX OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=narX PE=2 SV=1

MTVTPRTGSRIEELLARSGRFFIPGEISADLRVTTRRGRDGDV FYRDRWSDKVVVRSTHGVNCTGSCSWKIYV
KDDIITWETQETDYPVSGPDRPEYEPGRCPRGAAFSWYTYSPTRVRHPYARGVLEMYREAKARLGDVPAAW
ADIQADPRRRRRYQRARGKGLVRVSWAEATEMIAAAHVHTISTYGPDRVAGFSPIPAMSMVSHAAGSRFVE
LIGGVMTSFYDWYADLPVSPQVFGDQTDVPESGDWWDVWVWQCASVLLTYPNSRQLGTAEELLAHIDGPAA
DLLGRTVSELRRADPLTAATRYVDTFDLRGRATLYLYWTAGDTRNRGREMLAFAQTYRSTDVAPPRGETPDFLP
VVLEFAATVDPEAGRRLLSGYRVPIAALCNALTEALPYAHTVAAVCRTGDMMGELFWTVVYPYVMTIVAVGS
WWRYRYDKFGWTRSSQLYESRLLRIASPMFHFGILVVIVGHGIGLVIPQSWTQAAGLSEGAYHVQAVVLGSIA
GITLAGVTLIIYRRRTRGPVFMATTVNDKVMYLVVAAIVAGLGATALGSGVVEAYNYRETVSVWFRSVVWL
QPRGDLMAEAPLYQIHVLIGLALFALWPFTRLVHAFSAPIGYLFRPYIIRSREELVLRPRRRGW

>sp|P9WIW1|NUOL_MYCTU NADH-quinone oxidoreductase subunit L OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=nuoL PE=1 SV=1

MTTSLGTHYTWLLVALPLAGAAILLFGRRRTDAWGHLLGCAAALAAFVGVGAMLLADMLGRDGLERAIHQQVF
TWIPAGGLQVDFGLQIDQLSMCFVLLISGVGSLIHIYSVGYMAEDPDRRRFFGYLNLFLASMLLLVADNYVLLY
VGWEGVGLASYLIGFWYHKPSAATAAKKAFVMNRVGDAGLAVGMFLTFSTFGTLYSAGVFAGVPAASRAVLT
AIGLLMLLGAOKSAQVPLQAWLGDAMEGPTPVSAIHAATMVTAGVYLIVRSGPLYNLAPTAQLAVVIVGAVT
LLFGAIIIGCAKDDIKRALAASTISQIGYMVLAAGLPAGYAFAIMHLLTHGFFKAGLFLGSGAVIHAMHEEQDMR
RYGGLRAALPVTFATFGLAYLAIIGVPPFAGFFSKDAIIEAALGAGGIRGSLGGAALLGAGVTA FYMTRVMLMTF
FGEKRWTPGAHPHEAPAVMTWPMILLAVGVSFSGGLLAVGGTLRHWLQPVVGSHEEATHALPTWVATTLLAL
GVVAVGIAVAYRMYGTAPIPRVAPVRVSALTAARADLYGD AFNEEVFMRPGAQLTNAVVAVDVAGVDGSVN
ALATLVSQTSNRLRQMGTGFARNYALSMLVGAVLVAAALLVVQLW

>sp|P9WIW5|NUOM_MYCTU NADH-quinone oxidoreductase subunit M OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=nuoM PE=1 SV=1

MNNVPWLSVLWLVLPLAGAVLIILLPPGRRRLAKWAGMVVSVLTLAVSIVVAAEFKPSAEPYQFVEKHSWIPAFG
AGYTLGVDGIAVVLVLLTTLVLIPLLLVAGWNDATDADDLSPASGRYPQRAPPRLRSSGGERTRGVHAYVALTLAI
ESMVLMSVIALDVLLFYVFFEAMLIPMYFLIGGFGQAGRSRAAVKFLLYNLFGGLIMLAAVIGLYVTAQYDSG

TFDFREIVAGVAAGRYGADPAVFKALFLGFMFAFAIKAPLWPFHRWLPDAAVESTPATAVLMMMAVMDKVGTF
GMLRYCLQLFPDPSTYFRPLIVTLAIIGVIYGAIVAIGQTDMMRLIAYTSISHFGFIIAGIFVMTTQGGSGSTLYML
NHGLSTA AVFLIAGFLIARRGSRSIADYGGVQKVAPILAGTFMVSAMATVSLPGLAPFISEFLVLLGTFSTRYWLAA
AFGV TALVLSAVYMLWLYQRVMTGPVAEGNERIGDLVGREMIVVAPLIALLLVGVYKPKVLDIINPAVENTMTT
IGQHDPAPSV AHPVPAVGASRTAEGPHP

>sp|P9WIL7|PANB_MYCTU 3-methyl-2-oxobutanoate hydroxymethyltransferase
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=panB PE=1 SV=1

MSEQTIYGANTPGGSGPRTKIRTHHLQRWKADGHKWAMLTAYDYSTARIFDEAGIPVLLVGD SAANVVYGYDT
TVPISEIDELIPLVRGVVRGAPHALVVADLPFGSYEAGPTAALAAATRFLKDGGAHAVKLEGGERVAEQIACLTAAAG
IPVMAHIGFTPQSVNTLGGFRVQGRGDAAEQTIADAIVAEAGAFVVMEMVPAELATQITGKLIPTVIGIGAG
PNCDGQVLVWQDMAGFSGAKTARFVKRYADVGGELRRAAMQYAEVAGGVFPADEHSF

>sp|P9WIL1|PANE_MYCTU Putative 2-dehydropantoate 2-reductase OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2573 PE=1 SV=1

MATGIALVGP GAVGTTVAALLHKAGYSPLLCHGTPRAGIELRRDGADPIVVP GPVHTSPREVAGPVDVLILAVKA
TQNDAARPWLTRLCDERTVVAVLQNGVEQVEQVQPHCPSSAVVPAIVWCSAETQPQGWVRLRGEAALVVPT
GPAAEQFAGLLRGAGATVDCDPDFTTAAWRKLVLNALAGFMVLSGRRSAMFRRDDVAALSRRYVAECLAVAR
AEGARLDDD VVDEVVRLVRSAPQDMGTSMLADRAAHRPLEWDLRNGVIVRKARAHGLATPISDVLVPLAAA
SDGPG

>sp|P71707|PBP1A_MYCTU Penicillin-binding protein 1A OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) GN=ponA1 PE=1 SV=3

MNSDGRHHQSSSGAPRGPANPGQRGQVPPDDRILTALPPVTD DR SAPHADSIEAVKAALDGAPPMPPPRDP
LEEVTAAALAPP GKPPRGDQLGGRRRPPGPPGSSGQPAGRLPQPRVDLPRVGQINWKWIRRSLYLTA AVV
ILLPMVTF TMAYLIVDVPKPGDIRTNQVSTILASDGSEIAKIVPPEGNRVDVNL SQVPMHVRQAVIAAEDRNFYS
NPGFSFTGFARAVKNNLFGGDLQGGSTITQQYVKNALVGS AQHGW SGLMRKAKELVIATKMSGESKDDVL
QAYLNIIYFGRGAYGISAASKAYFDKPVEQLTVAEGALLAALIRRPSTL DPAVDPEGAHARWNWVLDGMVETKA
LSPNDRAAQVFPETVPPDLARAENQTKGPNGLIERQVTRELLELFNIDEQTLNTQGLVTTTTIDPQAQRAAEKA
VAKYLDGQDPDMRAAVVSIDPHNGAVRAYYGGDNANGFDFAQAGLQTGSSFKVFALVAAL EQIGLGYQVDS
SPLTVDGKITNVEGEGCGTCNIAEALKMSLNTSYRLMLKLN GGPQAVADAAHQAGIASSFPGVAHTLSE DGK
GGPPNNGIVLGQYQTRVIDMASAYATLAASGIYHPPHFVQKVVSANGQVLF DASTADNTGDQRIPKAVADNVT
AAMEPIAGYSRGNLAGGRDSA AKTGTTQFGDTTANKDAWMVGYTPSLSTAVVWGT VKGDEPLVTASGAAIY
GSGLPSDIWKATMDGALKGTSNETFPKPTVEGGYAGVPPPPPPPEVPPSETVIQPTVEIAPGITIPIGPPTTITLAP
PPPAPPAATPTPPP

>sp|P9WKD1|PBPA_MYCTU Penicillin-binding protein A OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) GN=pbpA PE=1 SV=1

MNASLRRISVTVMALIVLLLLNATMTQVFTADGLRADPRNQRVLLDEYSRQRGQITAGGQLLAYS VATDGRFRF
LRVYPNPEVYAPVTGFYSLRYSSTALERAEDPILNGSDRRLFGRR LADFFTG RDPRGGNVDTTINPRIQQAGWD
AMQQGCYGPCKGAVVALEPSTGKILALVSSPSYDPNLLASHNPEVQAQAWQRLGDN PASPLTNRAISETYPPG
STFKVITTAALAAAGATEQEQLTAAPTIPLPGSTAQLENYGGAPCGDEPTVSLREAFVKSCNTAFVQLGIRTGADA
LRSMARAFGLD SPPRPTPLQVAESTVGPIDSAALG MTSIGQKDVALTPLANAEIAATIANGGITMRPYLVGSLK
GPDLANISTTVGYQQRRAVSPQVA AKTELMVGAEKVAQKGAIPGVQIASKGTAEHGTDPRH TTPHAWYIA
FAPAQAPKVAVAVLVENGADRLSATGGALAAPIGRAVIEAALQGEP

>sp|L0T911|PBPB_MYCTU Penicillin-binding protein PbpB OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=pbpB PE=1 SV=1

MSRAAPRRASQSQSTRPARGLRPPGAQEVGQRKRPGKTKARQAQAEATKSRPATRS DVAPAGRSTRARRTR

QVVDVGTRGASVFRHRTGNAVILVLMVAATQLFFLQVSHAAGLRAQAAGQLKVTDVQPAARGSIVDRNND
RLAFTIEARALTFQPKRIRRLQLEEARKKTSAAPDPQQLRDIAQEVAGKLNNKPDAAVLLKKLQSDETFVYLARA
VDPVASAICAKYPEVGAERQDLRQYPGGS LAANVVGIDWDGHLLGLEDSLDAVLAGTDGSVTVYDRGSDG
VVIPGSYRNHRKAVHGSTVVLTDNDIQFYVQQVQVQAKNLSGAHNVS AVVLD AKTGEVLAMANDNTFDPS
QDIGRQGDQKQLGNPAVSSPFEPGSVNKIVAASAVIEHGLSSPDEVLQVPGSIQMGGVTVHDAWEHGVMPYTT
TGVFGKSSNVGTLMLSQRVGPERRYDMLRKFGLGQRTGVGLPGESAGLVPPIDQWSGSTFANLPIGQGLSMT
LLQMTGMYQAIANDGVRVPPRIKATVAPDGSRTTEPRPDDIRVVSAQTAQTVRQMLRAVVQRDPMGYQQG
TGPTAGVPGYQMAGKTGTAQQINPGCGCYFDDVYWITFAGIATADNPRYVIGIMLDNPARNSDGAPGHSAAAP
LFHNIAGWLMQRENVPLSPDPGPPLVLQAT

>sp|P9WP99|PDUO_MYCTU Cob(l)yrinic acid a,c-diamide adenosyltransferase
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv1314c PE=1 SV=1

MAVHLTRIYTRTGDDGTTGLSDMSRVAKTDARLVAYADCDEANAAIGAALALGHPTDQITDVLRLQIQNDLFDA
GADLSTPIVENPKHPPLRIAQSYIDRLEGWCDAYNAGLPALKSFVLPGGSPSALLHVARTVVRRAERSAWAAVD
AHPEGVSVLPAKYLNRLSDLLFILSRVANPDGDVLRWPGGDRTAS

>sp|P9WIG9|PE23_MYCTU Uncharacterized PE family protein PE23 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=PE23 PE=1 SV=1

MQFLSVIPEQVESAAQDLA GIRSALSASAAAAAGPTTAVVSAAEDEVSTAIASIFGAYGRQCQVLSAQASAFHDE
FVNLLKTGATAYRNTEFANAQSNVLNAVNPAPARSLGHPSAAESVQNSAPTLGGGHSTVTAGLAAQAGRAVAT
VEQQAAAAVAPLPSAGAGLAQVVNGVVTAGQGSAAKLATALQSAAPWLAKSGGEFIVAGQSALTGVALLQPA
VVGVVQAGGFTLAGTSAATGLGLLTLAGVEFSQGVGNLALASGTAATGLGLLGSAGVQLFSPAFLAVPTALGG
VGS LAI AVVQLVQGVQHLSLVVPPNVVAGIAALQTAGAQFAQGVNHTMLAAQLGAPGIAVLQTAGGHFAQGIG
HLTTAGNAAVTVLIS

>sp|P9WHS7|PEPE_MYCTU Probable dipeptidase PepE OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) GN=pepE PE=1 SV=1

MGSRRFDAEVYARRLALAAAATADAGLAGLVITPGYDLCYLIGSRAETFERLTALVLPAA GAPAVVLPRLLEAALK
QSAAAELGLRVCDWVDGDDPYGLVSAVLGGAPVATAVTDSMPALHMLPLADALGVLPVLTDLVLRRLRMVKE
ETEIDALRKAGAAIDRVHARVPEFLVPRTEADVAADIAEIVAEGHSEVAFVIVGSGPHGADPHHGYSDRELRE
GDIVVVDIGGTYPGYHSDSTRYSIGEPDSDVAQSYMLQRAQRAAFEAIRPGVTAEQVDAAARDVLAEAGL
AEYFVHRTGHGIGLCVHEEPIYVAGNDLVLPGMAFSIEPGIYFPGRWGARIEDIVIVTEDGAVSVNNCPHELIV
VPVS

>sp|P9WID1|PGK_MYCTU Phosphoglycerate kinase OS=Mycobacterium tuberculosis (strain ATCC
25618 / H37Rv) GN=pgk PE=1 SV=1

MSVANLKDLLAEGVSGRGLVRSDLNVLDEDDGTTDAGRIIASAPTLKALLDADAKVVVA AHLGRPKDGPDPPT
LSLAPVAVALGEQLGRHVQLAGDVVGADALARAEGLTGGDILLENI RFDKRETSKNDDRRALAKQLVELVGT
GGV FVSDGFGVVHRKQASVYDIATLLPHYAGTLVADEMVRLEQLTSSTQRPYAVVLLGGSKVSDKLGVIESLATKA
DSIVIGGGMCFTFLAAQGFVSGTSLLEDDMIEVCRGLLETYHDVLRPLVLDLVVTEKFAADSPPQTVDVGAVPNG
LMGLDIGPGSIKRFSTLLSNAGTIFWNGPMGVFEFPAYAAGTRGVAEIVAATGKGAFSVVGGGDSAAAVRAM
NIPEGAFSHISTGGGASLEYLEGKTLPGIEVLSREQPTGGVL

>sp|P9WPG5|PGSA1_MYCTU Putative CDP-diacylglycerol--glycerol-3-phosphate
3-phosphatidyl-transferase 1 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv)
GN=pgsA1 PE=1 SV=1

MEPVL TQNRVLTVPNMLSVIRLALIPAFVYVLSAHANGWGVAILVFSGVSDWADGKIARLLNQSSRLGALLDP
AVDRLYMVTVPVIFGLSGIVPWVFLTLTRDALLAGTLPLLSRGLSALPVTVYGKAATFGFMVGFPTILLGQC
DPLWSHVLLACGWAFWIWGMAYLWAFVLYAVQMTMVVRQMPKLGRAHRPAAQNA GERG

>sp|P9WPG3|PGSA2_MYCTU Putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyl-transferase 2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pgsA2 PE=1 SV=1

MSRSTRYSVAVSAQPETGQIAGRARIANLANILTLRLVMVPVFLALFYGGGHSAARVVAWAIFATACITDRF
DGLLARNYGMATEFGAFVDPIADKTLIGSALIGLSMLGDLPWVWTVLILTRELGVTVLRLAVIRRGVIPASWGGK
LKTFVQAVAIGLFLPLSGPLHVAVVVMAAAILLTVITGVVDYVARALRDIGGIRQTAS

>sp|AOQQ72|PHNF_MYCS2 HTH-type transcriptional repressor PhnF OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=phnF PE=1 SV=2

MTAGAAPRILKHQVRAELDRMLDGMRIGDPPFAERIEAQFEVARETVRQALRELLIDGRVERRGRRTTVVAR
PKIRQPLMGSYTEAKAQGLSAGRILVAWSDLTADEVLAGVLGVDVGAPVLQLERVLTDDGVRVGLLETTKLP
QRYPLRETFDHEASLYAEIRSRGIAFTRTVDITDLPDAREAAALLGADARTPMFLLNRVSYDQDDVAIEQRSL
YRGDRMTFTAVMHAKNSAIVS

>sp|P9WIA3|PHOL_MYCTU PhoH-like protein OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2368c PE=1 SV=1

MTSRETRAADAAGARQADAQVRSSIDVPPDLVVGLLGSADENLRALERTLSADLHVRGNAVTLCEPADVALA
ERVISELIAIVASGQSLTPEVVRHSVAMLVGTGNESPAEVLTDILSRRGKTIRPKTLNQRVYDAIDANTIVFGIGP
AGTGKTYLAMAKAVHALQTKQVTRIIILTRPAVEAGERLGLPGLTSEKIDPYLRPLYDALYDMMDPPELIPKLMSA
GVIEVAPLAYMRGRRTLNDAFIVLDEAQNTTAEQMKMFLTRLGFGSKVVVTGDVTQIDLPGGARSGLRAAVDILE
DIDDIHIAELTSDVVRHRLVSEIVDAYARYEPEGSGLNRAARRASGARGRR

>sp|A5U7Y7|PILIN_MYCTA Pilin OS=Mycobacterium tuberculosis (strain ATCC 25177 / H37Ra) GN=ntp PE=1 SV=1

MYRFACRTLMLAACILATGVAGLVGAQSAQTAPVPDYWCPGQPFDPAWGPNWDPYCHDDFHRDSGD
PDHSRDYGPPILEGPVLDPPGAAPPPAAGGGA

>sp|AOQWG6|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

MRIGMVCPSYFDPVGGVQSHVLQLAEVLRDAGHEVSVLAPASPHVKLPDYVVS GGKAVPIPYNGSVARLRFGP
ATHRKVKKWAIEGDFDLHIHEPNAPSLMLALQAAEGPIVATFHTSTTKSLTSLVVFQGILRPYHEKIIIGRIAVSDL
ARRWQMEALGSDAVEIPNGVDVASFADAPLLDGYPREGRTVFLGRYDEPRKGMVLLAALPKLVARFPDVEIL
IVGRGDEDELREQAGDLAGHLRFLGQVDDATKASAMRSADVYCAPHLGGESFGIVLVEAMAAGTAVVASDLD
AFRRVLADGDAGRLVPVDDADGMAAALIGILEDDQLRAGYVARASERVHRYDWSVVSQAQIMRVYETVSGAGI
KVQVSGAANRDETAGESV

>sp|P9WN01|PIME_MYCTU Polyprenol-phosphate-mannose-dependent alpha-(1-2)-phosphatidylinositol pentamannoside mannosyltransferase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pimE PE=1 SV=1

MCRTLIDGPVRSIAIKVRQIDTTSSTPAAARRVTSPARETRAALLVLSVGARLAWTYLAPNGANFVDLHVYV
SGAASLDHPGTYLYGVYADQTPDFPLPFTYPPFAAVVFYPLHLVFPGLIALLWQVVTMAALYGAVRISQRLMGGT
AETGHFAAMLWTAIAIWIPLRSTFDYQGINVLLMLAALWAVYTPRWWSGLLVGVASGVKLTAPITAVYLVGV
RRLHAAAFSVVFLATVGVSLLVGDEARYYFTDLLGDAGRVGPIATSFNQSWRGAISRILGHDAGFGPLVLAAL
ASTAVLAILAWRALDRSDRLGKLLVVELFGLLLSPISWTHHWVWLVPMLMIWLIDGPARERPGARILGWGWLVLT
IVGVPWLLSFAQPSIWQIGRPWYLAWAGLVYVATLATLGWIAASERYVRIRPRRMAN

>sp|AOR036|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

MLEMSKRQSPRGAGLAPTIAWRVFQLLLTAGVLVWVGWVWVLLGRVYRVIDVYRMGGRAWLDGRPLYADGAIF
HTQGGLDLPFTYPPPLAAIAFAPFAWLSLPLASSAITATTLVLLIVATTIVLTRLVDVWPHTTVTSEPAWMRRAWLAA
AMVAPAVIYLEPIRNSFEFGQINVVLMTLVIADCVPRRTPWPRGLLLGLAIALKLTPAVFLLYFLRRDIHTLLRTAA
TAVVASLAGFALAWSDSVEYWTETVRNTDRIGTATLNTNQNAGALARLGLGESPRFILVWLACFAVLALTVWA
ARRALRGDTADQTTEAPVLALVCVALFGLVVSPVSWSHHWVWMLPVLVVTAVLAYRRRSVWFTALTAAGLALT
VWTPITLLPEHRETTASLWRQLAGGSYVWVAFVIVVIGLVSSSRHTHTGDAHETDEPLVPLARGEAG

>sp|Q9F7Y9|PISA_MYCSM CDP-diacylglycerol--inositol 3-phosphatidyltransferase
OS=Mycobacterium smegmatis GN=pgsA PE=1 SV=1

MSNVYLMTRAAYVKLSRPVAKAALRAGLTPDIVTLAGTAAVIGALTLFPIGQLWWGAVVVSFFVLADMLDGA
MAREQGGGTRFGAVLDATCDRLGDGAVFAGLTWWAAFGLDSPSLVVATLCLVTSQVVISYIKARAEASGLRGDG
GIIERPERLVIVLIGAGLSLDPFFPLPWLHVAMWVLAVASVVTLLQRVHAVRTSPGAMEPLHPANGKEPETSEP

>sp|P9WI69|PKNI_MYCTU Serine/threonine-protein kinase PknI OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=pknI PE=1 SV=1

MALASGVTFAGYTVRMLGCSAMGEVYLVQHPGFPGWQALKVLSPAMAADDEFRRRFQRETEVAARLFHP
HILEVHDRGEFDGQLWIAMDYVDGIDATQHMADRFPVLPVGEVLAIVTAVAGALDYAHQRGLLHRDVNPAN
VVLTSQSAGDQRILLADFGIASQPSYPAPELSAGADVDGRADQYALALTAIHLFAGAPPVDRSHTGPLQPPKLSA
FRPDLARLDGVSRLATAPADRFGSCREFADAMNEQAGVAIADQSSGGVDASEVTAAAGEEAYVVDYPAYG
WPEAVDCKEPSARAPAPAAPTQRRGSMQSAAGVLARRLDNFSTATKAPASPTRRRPRRILVGAVALLLAGL
FAVGIVGRKTNNTATEVARPPTSASAVPSAPTTTAVTAPVPLDGTYRIEIQRSKQTYDYTPTPQPPDVNTWWA
FRTSCTPTECLAATMLDDNDHTQAKTPVPRPFLMQFEGEQWKSREPVTQFPCVGPNGSPSTQATTQLLALR
PQPQGDVLGEMVVTVHSNECGQQGAVIRIPAVASRSGDLPPAVTVDPATIPDTPDPTTSTATLPTPTTAPGPG
R

>sp|P9WI66|PKNJ_MYCTO Serine/threonine-protein kinase PknJ OS=Mycobacterium
tuberculosis (strain CDC 1551 / Oshkosh) GN=pknJ PE=1 SV=1

MAHELSAGSVFAGYRIERMLGAGGMGTVYLARNPDLPSEALKVLAELSRDLDFRARFVREADVAAGLDHP
NIVAVHQRGQFEGRLWIAMQFVDGGNAEDALRAATMTTARAVYVIGEVAKALDYAHQQGVIHRDIK PANFLL
SRAAGGDERVLLSDFGIARALGDTGLTSTGSVLATLAYAAPEVLAGQGFDGRADLYSLGCALFRLLTGEAPFAAGA
GAAVAVVAGHLHQPPPTVSDRVPGLSAAMDVIATAMAKDPMRRFTSAGEFAHAAAAALYGGATDGWVPPS
PAPHVISQGAVPGSPWWQHPVGSVTALATPPGHGWPPGLPPLRRRPRYRRGVAAVAAMVVAAA AVTAVT
MTSHQPRTATPPSAAALSPTSSSTPPQPPIVTRSRLPGLLPLDDVKNFVGIQNLVAHEPMLQPQTPNGSINPA
ECWPAVGGGVPSAYDLGTVIGFYGLTIDEPTGTAPNQGQLIVAFRDAATAQRHLADLASIWRRCGGRTVTLF
RSEWRRPVELSTSVPEVVDGITTMVLTAQGPVLRVREDHAI AAKNNVLDVDIMTPDTSRGQQAVIGITNYILA
KIPG

>sp|P9WN05|PMT_MYCTU Probable dolichyl-phosphate-mannose--protein mannosyltransferase
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pmt PE=1 SV=1

MVPVVSPPGLPVVADFGPLDRLRGWIVTGLITLLATVTRFLNLGSLTDAGTPIFDEKHYAPQAWQLNNHGVED
NPGYGLVHPPVGKQLIAIGEAIIFYNGFGWRFTGALLGVVLVALVVRIRRRISRTLVAIAIGVLLICDGVSFVTA
RTALLDGLFTFFVAAFGALIVDRDQVRERMHIALLAGRSAATVWGPRVGRVWRFRGAGVLLGLACATKWSG
VYFVLFFGAMALAFDVAARRQYVQRPWLGTVRRDVLPSGYALGLIPFAVYLATYAPWFASETAIDRHAVGQA
VGRNSVVPLDAVRSLWHYAKAFHFHAGLNSAGNYHPWESKPWTWPMSLRPVLYAIDQQDVAGCGAQS
CVKAEMLVGTPAMWWLAVPVLAYAGWRMFVRRDWRVAVLVGYCAGWLPWFADIDRQMYFFYAATMAP
FLVMGISLVLDILYHPGQGSERRTLGLIVCCYVALVVTNFAWLYPVLTPISQQTWNLEIWLP SWR

>sp|P9WI43|PPE04_MYCTU Uncharacterized PPE family protein PPE4 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=ppe4 PE=1 SV=1

MAAPIWMASPEVHSALLSNGPGPSLVAAATAWSQLSAEYASTAAELSGLLGAVPGWAWQGPSAEWYVAA
HLPYVAWLQASADAAGAAAQHEAAAAAYTTALAAMPTLAELAANHVIHTVLVATNFFGINTIPITLNEADYVR
MWLQAAAVMGLYQAASGAALASAPRTVPAPTVMNPGGGAASTVGAVNPWQWLLALLQQLWNAYTGFYQ
WMLQLIWQFLQDPIGNSIKIIIAFLTNPIQALITYGPLLFALGYQIFFNLVWPTWGMILSSPFLLPAGLGLLAAI
AFLPIVLPAVIPPASTPLAAAABAAGSVWPAVSMVAVTGAGTAGAATPAAGAAPSAGAAPAPAPATASFAYAV
GGSGDWGPSLGPVTGGRGGIKAPAATVAAAAAATRGQSRARRRRRSELRDYGFDEFDMDSDSGFGPSTG
DHGAQASERAGTGLFAGTATKERRVRAVGLTALAGDEFNGPRMPMPVPGTWEQGSNEPEAPDGSGRGGG
DGLPHDSK

>sp|P9WI01|PPE36_MYCTU Uncharacterized PPE family protein PPE36 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=ppe36 PE=1 SV=1

MPNFWALPPEINSTRILYLPVGGPILAAAQGWALASELEKTKVGLQSALDTLLESYRGQSSQALIQQLPYVQ
WLTTTAEHAHKTAIQLTAAANAYEQARAAMVPPAMVVRANRVQTTVLKAINWFGQFSTRIADKEADYEQMWF
QDALVMENYWEAVQEAIQSTSHFEDPPEMADDYDEAWMLNTVFDYHNENAKEEVIHLVDPVNERGPIELV
TKVDKEGTIRLVYDGEPTFSYKEHPKF

>sp|P9WGK7|PRRB_MYCTU Sensor-type histidine kinase PrrB OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=prb PE=1 SV=1

MNILSRIFARTPSLRTRVVATAIGAAIPVLIVGTVVVWGITNDRKERLDRRLDEAAGFAIPFVPRGLDEIPRSPND
QDALITVRRGNVIKNSDITLPLKQDDYADTYVRGVRYRVRTVEIPGPEPTSVAVGATYDATVAETNNLHRRVLLI
CTFAIGAAAVFAWLLAAFAVRPFKQLAEQTRSIDAGDEAPRVEVHGASEAIEAIEAMRGMLQRIWNEQNRTKE
ALASARDFAAVSSHELRTPLTAMRTNLEVLSTLDLPDDQRKEVLNDVIRTQSRIEATLSALERLAQGELSTSDDHV
PVDITDLLDRAAHDAAIRYDLDVSLVPSPTCIIVGLPAGLRRAVDNAIANAVKHGGATLVQLSAVSSRAGVEIAID
DNGSGVPEGERQVVFERSRGSTASHSGSGLLALVAQQAQLHGGTASLENSPLGGARLVLRPLPGPS

>sp|P9WG09|PSTA2_MYCTU Phosphate transport system permease protein PstA 2
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pstA2 PE=1 SV=1

MGESAESGRQLPAMSPRRSVAYRRKIVDALWAAACVCLAVVITPTLWMLIGVVSRAVPVFHWSVLVQDS
QGNNGGLRNAIIGTAVLAIGVILVGGTVSVLTGIYLSEFATGKTRSLRGAYEVLGIPISIVLGYVGYLALVVYFDWG
FSLAAGVLVLSVMSIPYIAKATESALAQVPTSYREAAEALGLPAGWALRKIVLKTAMPGIVTGMLVALALAIGETA
PLLYTAGWSNSPPTGQLTDSVGYLTYPIWTFYNQPSKSAQDLSYDAALLLIVFLLLIFIGRLINWLSRRRWDV

>sp|P9WHW5|PSTP_MYCTU PP2C-family Ser/Thr phosphatase OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=pstP PE=1 SV=1

MARVTLVLRYAARSDRGLVRANNEDSVYAGARLLALADGMGGHAAGEVASQLVIAALAHLDDEPGGDLLAK
LDAAVRAGNSAIAAQVEMEPDLEGMGTTLTAILFAGNRLGLVHIGDSRGYLLRDGELTQITKDDTFVQTLVDEG
RITPEEAHSHPPQRSLIMRALTGHEVEPTLTMREARAGDRYLLCSDGLSDPVSDETILEALQIPEVAESAHRILIELAL
RGGGPDNVTVVADVVDYDYGQTPILAGAVSGDDQLTLPNTAAGRASAIQRKEIVKRVPQADTFSRPR
WSGRRLAFVVALVTLMTAGLLIGRAIIRSNIYVADYAGSVSIMRGIQGSLLGMSLHQPYLGMCLSPRNELSQIS
YGQSGGLDCHLMKLEDLRPPERAQVRAGLPAGTLDDAIGQLRELAANSLPPCAPRATSPGRPAPPTTSET
TEPNTVSSPASPSTTSAPAPTGTTPAIPTSASPAAPASPTPWPVTSPTMAALPPPPQPGIDCRAAA

>sp|P9WGU1|PST1_MYCTU Phosphate-binding protein PstS 1 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=pstS1 PE=1 SV=1

MKIRLHTLLAVLTAAPLLAAAGCGSKPPSGSPETGAGAGTVATTPASSPVTLAETGSTLLYPLFNLWGPFAHERY
PNVTITAQGTGSGAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISAQQVNYNLPGVSEHLKLNKG
VLAAMYQGTIKTWDDPQIAALNPGVNLPGTAVVPLHRSDGSGDTFLFTQYLSKQDPEGWKGSPGFGTTVDFP
AVPGALGENGNGGMVGTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNSSGNFLLPDAQSIQAAAAGFASKTP
ANQAISMIDGPAPDGYPIINYEYAIVNNRQKDAATAQTLQAFLHWAITDGNKASFLDQVHFQPLPPAVVKLSDA

LIATISS

>sp|P9WGT6|PSTS3_MYCTO Phosphate-binding protein PstS 3 OS=Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh) GN=pstS3 PE=1 SV=1

MKLNRFGAAVGVLAAGALVLSACGNDDNVTGGGATTGQASAKVDCGGKTLKASGSTAQANAMTRFVNVF
EQACPGQTLNYTANGSGAGISEFNQNTDFGGSDVPLSKDEAAAAQRRCGSPAWNLPVVFVGFPIAVTYNLSV
SSLNLDGPTLAKIFNGSITQWNNPAIQALNRDFTLPGERIHVVFRSDESGTTDNFQRYLQAASNGAWGKAGK
SFQGGVGEARGNDGTSAAAKNTPGSITYNEWSFAQAQHLTMANIVTSAGGDPVAITIDSVGQTIAGATISGV
GNDLVLDTSFYRPKRPGSYPIVLATYEIVCSKYPDSQVGTAVKAFLLQSTIGAGQSGLDNGYIPIPDEFKSRLSTA
VNAIA

>sp|P9WHP1|PTA_MYCTU Phosphate acetyltransferase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=pta PE=1 SV=1

MADSSAIYLAAPESQTKSTIALGLLHRLTAMVAKVGVFRPITRLSAERDYILELLLAHTSAGLPYERCVGVTYQQL
HADRDDAIAEIVDSYHAMADECDVAVVVGSDYTDVTSPTELSVNGRIAVNLGAPVLLTVRAKDRTPDQVASV
EVCLAELDTQRAHTAAVVANRCELSAIPAVTDALRRFTPPSYVPEEPLLSAPTVAELTQAVNGAVVSGDVALRE
REVMGVLAAGMTADHVLERLTDGMAVITPGDRSDVVLAVASAHAAEGFPLSCIVLNGGFQLHPAIAALVSG
RLRLPVIATAGTYDTASAAASARGLVLTATSQRKIDTALELMDRHVDVAGLLAQLTIPIPTVTPQMFTYRLLQQA
RSDLMRIVLPEGDDDRILKSAGRLLQRGIVDLTILGDEAKVRLRAAELGVDLDGATVIEPCASELHDQFADQYQ
LRKAKGITVEHAREIMNDATYFGTMLVHNCHADGMVSGAAHTTAHTVRPALEIIKTVPGISTVSSIFLMCLPDR
VLAYGDCAIIPNPTVEQLADIAICSARTAAQFIEPRVAMLSYSTGDSGKGADVVKVRAATELVREPREPQLPVEG
PIQYDAAVEPSVAATKLDRSPVAGRATVLIFFDLNTGNNTYKAVQRSAGAIAIGPVLQGLRKPVNDLSRGALVDD
IVNTVAITAIQAQGVHE

>sp|P9WIA1|PTPA_MYCTU Probable low molecular weight protein-tyrosine-phosphatase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=ptpA PE=1 SV=1

MSDPLHVTFVCTGNICRSPMAEKMFQAQLRHRGLGDAVRVTSAGTGNWHVHGSCADERAAGVLRAGHYPTD
HRAAQVGTTEHLAADLLVALDRNHARLLRQLGVEAARVRLRSFDRSGTHALDVEDPYYGDHSDFEVFAVIE
SALPGLHDWVDERLARNGPS

>sp|P9WH23|QCRA_MYCTU Ubiquinol-cytochrome c reductase iron-sulfur subunit OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=qcrA PE=1 SV=1

MSRADDVAVGPPTCGGRSDEEERRIVPGPNPQDGAKDGAKATAVPPREPDEAALAAMSNOELLALGGKLDG
VRIAYKEPRWPVEGKAEKRAERSVAVWLLGGVFLGALLLIFLFWPWEFKAADGESDFIYSLTTPYGLTFGLSIL
SIAIGAVLYQKRPIPEEISIQERHDGASREIDRKTVVANLTDAFEGSTIRRRKLIQLSFGVGMGAFGLTLVAFAGGL
IKNPWKPVVPTAEGKKAVLWTSWTPRYQGETIYLARATGTEDGPPFIKMRPEDMDAGGMETVFPWRES
DGTTVESHHKLQEIAMGIRNPVMLIRIKPSDLGRVVKRKGQESFNFGFEFFAFTKVCSHLGCPSLSYEQQSYRILCP
CHQSQFDALHFAKPIFGPAARALAQLPITIDTDGYLVANGDFVEPVGPAFWERTTT

>sp|P9WP37|QCRB_MYCTU Ubiquinol-cytochrome c reductase cytochrome b subunit OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=qcrB PE=1 SV=1

MSPKLSPPNIGEVLARQAEDIDTRYHPSAALRRQLNKVFPHTWSFLLGEIALYSFVLLITGVYLLTFDPSMVDV
TYNGVYQPLRGVEMSRAQSALDISFEVRGGLFVRQIHHWAALMFAAAIMVHLARIFFTGAFRRPRETNWVIG
SLLLILAMFEGYFGYSLPDDLSSGLGLRAALSSITLGMPIVIGTWLHWALFGGDFPGTILIPRLYALHILLPGIILALIG
LHLALVWFQKHTQFPGRTEHNVVGVRVMPVFAFKSGAFFAAIVGLGLMGGLLQINPIWNLGPYKPSQVS
AGSQPDFYMMWTEGLARIWPPWEFYFWHHTIPAPVWVAVIMGLVFLPAYPFLEKRFRTGDYAHHNLQRP
RDVPVRTAIGAMAIAFYMLTLAAMNDIALKFHISLNATTWIGRIGMVILPPFVYFITYRWCIGLQRSDRSVLEH
GVETGIKRLPHGAYIELHQPLGPVDEHGHPIPLQYQGAPLPKRMNKLGSAGSPGSGSFLFADSAAEDAALREA
GHAAEQRALAALREHQDSIMGSPDGEH

>sp|P9WP35|QCRC_MYCTU Ubiquinol-cytochrome c reductase cytochrome c subunit OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=qcrC PE=1 SV=1

MTKLGFTSRGGSKSGRTRRRRLRRRLSSGGVLLLIALTIAGGLAAVLTPTPQVAVADESSALLRTGKQLFDTSCVSC
HGANLQGVDPDHGPSLIGVGEAAVYFQVSTGRMPAMRGEAQAPRKDPIDFAEQIDAIGAYVQANGGGPTVVR
NPDGSIATQSLRGNDLGRGGDLFRLNCASCHNFTGKGGALSSGKYAPDLAPANEQQILTAMLTGPQNMFKFSN
RQLSFEAKKDIIAYVKVATEARQPGGYLLGGFGPAPEGMAMWIIIGMVAAIGLALWIGARS

>sp|P9WHI1|RECX_MYCTU Regulatory protein RecX OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=recX PE=1 SV=1

MTVSCPPPSTSEREEQARALCLRLLTARSRTRAELAGQLAKRGYPEDIGNRVLDRLAAGVLDVDDTDFAEQWVQS
RRANAASKRALAAELHAKGVDDDVTTLVGGIDAGAERGRAEKLVRARLRREVLIDDGTDEARVSRRLVAMLA
RRGYGQTLACEVVIAELAAERERRRV

>sp|A1KML4|RIP1_MYCBP Zinc metalloprotease Rip1 OS=Mycobacterium bovis (strain BCG / Pasteur 1173P2) GN=rip1 PE=1 SV=1

MMFVTGIVLFALAILISVALHECGHMMVARRTGMKVRRYFVGFPGPTLWSTRGETEYGVKAVPLGGFCDIAG
MTPVEELDPDERDRAMYKQATWKRVAVLFAGPGMNLAICLVLIYAIALVWGLPNLHPTRAVIGETGCVAQEV
SQGKLEQCTGPGPAALAGIRSGDVVVKVGDTPVSSFDEMAAAVRKSHGSVPIVVERDGTAVTYVDIESTQRWI
PNGQGGELOPATVGAIGVGAARVGPVRYGVFSAMPATFAFTGDLTVEVGKALALPTKVAGLVRAIGGGQRD
PQTPISVVGASIIIGDVTVDHGLWVAFWFFLAQLNLILATINLLPLLPFDGGHIAVAVFERIRNMVRSARGKVAAA
PVNYLKLIPATYVVLVLVVGYMLLTVTADLVNPIRLFQ

>sp|L0T550|RIP2_MYCTU Putative zinc metalloprotease Rip2 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=rip2 PE=1 SV=1

MSETGQRESVRPSIFLGLLGLTAVGGALAWLAGETVQPLAYAGVFMVIAGWLVSCLLHEFGHAFTAWRFGD
HDVAVRGYLTDRRYSHPMLSLGLPMLFIALGGIGLPGAAYVHTWFMTTARRTLVSLAGPTVNLALAMLLLA
ATRLFDPIHAVLWAGVAFLAFLQLTALVLNLLPIPGLDGYAALEPHLRPETQRALAPAKQFALVFLVFLAPTNG
WFFGVVYWLFDLSGVSHRLAAAGSVLARFWSIWF

>sp|H8EUF2|RIP3_MYCTE Putative zinc metalloprotease Rip3 OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) GN=rip3 PE=2 SV=1

MRDAIPLGRIAGFVNVHWSVLVILWLFWSLATMLPGTVGGYPVVYVLLGAGGAVMLLASLHAHELAHAV
VARRAGVSVESVTLWLFGGVVLTALGGEAKTPKAAFRIAFAGPATSLALSATFGALAITLAGVRTPAIVISVAWWLAT
VNLLGLFNLLPGAPLDGGRLVRAYLWRRRHGDSVRAGIGAARAGRVALVLIALGLAEFVAGGLVGGVWLAFIG
WFIFAAAAREEETRISTQQLFAGVRVADAMTAQPHTAPGWINVEDFIQRYVLGERHSAYPVADRDSITGLVALR
QLRDVAPSRRTTSVGDIALPLHSVPTARPQEPLTALLERMAPLGPSSRALVTEGSAVVGIVTPSDVARLIDVYRL
AQPEPTFTTSPQDADRFS DAG

>sp|P9WH01|RNH2_MYCTU Ribonuclease HII OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=rnhB PE=1 SV=1

MTKTWPPRTVIRKSGGLRGMRTLESALHRGGLGPVAGVDEVGRGACAGPLVVAACVLGPGRIASLAALDDSK
KLSEQAREKLFPLICRYAVAYHVVFIPSAEVDRRGVHVANIEGMRRRAVAGLAVRPGYVLSDFRVPGLPMPPLPV
IGGDAACIAAASVLAKVSRDRVMVALDADHPGYGFAEHKGYSTPAHSRALARLGPQHRYSFINVRRVAS
GSNTAEVADGQPDPRDGTAGTGEGRWSKSSHPATMRATGRAQGT

>sp|P9WG27|RPFD_MYCTU Resuscitation-promoting factor RpfD OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=rpfd PE=1 SV=1

MTPGLLTAGAGRPRDRCARIVCTVFIETAVVATMFVALLGLSTISSKADDIDWDIAIAQCESGGNWAANTGNGL
YGGLQISQATWDSNGGVGSPAAASPQQQIEVADNIMKTQGPAGWPKCSCSQGDAPLGLSLHILFLAAETG
GCSGSRDD

>sp|P9WJ71|RSDA_MYCTU Anti-sigma-D factor RsdA OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=rsdA PE=1 SV=1

MREFGNPLGDRPPLDELARTDLLLDALAEREVEVDFADPRDDALAALLGQWRDDLWPPASALVSQDEAVAAL
RAGVAQRRRARRSLAAVGSVAAAALLVLSGFGAVVADARPGDLYGLHAMMFNRSRVSDQIVLSAKANLAKV
EQMIAQGGWAEAQDELAEVSSTVQAVTDGSRQDLINENLLNTKVETRDPNATLRPGSPSNPAAPGSGVNS
WTPLAPVVEPTPTPASAAEPSMSAGVSESPMPNSTSTVAASPSTPSSKPEPGSIDPSLEPADEATNPAGQPAP
ETPVSPTH

>sp|L0T905|RSEA_MYCTU Anti-sigma-E factor RseA OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=rseA PE=1 SV=1

MADPGSVGHVFRRAFSLWPAQFASQSDAPVGAQRFRSTEHLSEIAIAAFVDGELRMNAHLRAAHLSLCAQ
CAAEVDDQSRARAALRDSHPPIRIPSTLLGLLSEIPRCPEGSPKSGSSGSSQGPPDGAAAGFGDRFADGDGGNR
GRQSRVRR

>sp|Q7U1Z7|RSKA_MYCBO Dysfunctional anti-sigma-K factor RskA OS=Mycobacterium bovis (strain ATCC BAA-935 / AF2122/97) GN=rskA PE=1 SV=1

MTEHTDFELLELATPYALNAVSDDERADIDRRVAAAPSPVAAAFNDEVRAVRETMAVVSAAATTAEPHAHLRTAIL
DATKPEVRRQRWRRTAAAFASAAIAVGLGAFDLGLVLRPSPPPTVAEQVLTAPDVRTVSRPLGAGTATVVFSDRDR
NTGLLVMNNVAPSRGTVYQMWLLGGAKGPRSAETMGTAAVTPSTTATLTDLGASTALAFVTEPGTGPQPT
GTILAEPLG

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

MTMPLRGLGPPDDTGVREVSTGDDHHYAMWDAAYVLGALSAADRREFEAHLGACPECRGAVTELGVDPALL
SQLDRDEVA AIS EAPT VVASGLSPELLPSLLAAVHRRRRRRLITWVASSAAA VLAIGVLVGVQGHSAAPQRA
AVSALPMAQVGTQLLASTVSISGEPWGTFINLRCVCLAPPYASHDTLAMVVVGRDGSQTRLATWLAEPGHAT
PAGSISTPVDQIAAVQVVAADTGQVLLQRSL

>sp|H8F2P5|RSMAF_MYCTE Anti-sigma-M factor RsmA OS=Mycobacterium tuberculosis (strain ATCC 35801 / TMC 107 / Erdman) GN=rsmA PE=1 SV=1

MSAADKDPDKHSADADPPLTVELLADLQAGLLDDATAARIRSRVSDPQAQQILRALNRVRRDVAAMGADPA
WGPAARPAVVDISAAALSARPNSSPGAAHAARPHVHPVRMIAGAAGLCAVATAIGVGAVVDAPPPAPSAPT
AQHITVSKPAPVIPLSRPQVLDLLHHTPDYGGPGLGDPSSRRTSCLSGLYPASTPVLGAQPIDIDARPAVLLVIP
ADTPDKLAVFAVAPHCSAADTGLLASTVVPRA

>sp|P9WGN5|SECG_MYCTU Probable protein-export membrane protein SecG OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=secG PE=1 SV=1

MELALQITLIVTSVLVLLVLLHRAKGGGLSTLFGGGVQSSLSGSTVVEKNLDRLLTFVTGIWLVSIIGVALLIKYR

>sp|A0QR01|SENX3_MYCS2 Signal-transduction histidine kinase senX3 OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=senX3 PE=1 SV=1

MSLLTIAGVAVGVTVPRIVARRQRRAAAYAAGMTVSQMLQHITSLSPMGVAVVDTFNDVVYSNDRAVELNV
VRDRILDDRAWQAAQRVFETGQDVEVDLSPLKVANPGRSGISVRGKVRLLTDDRRFAVVYIDDQSEHARME
ATTRDFVANVSHELKTPVGAMSVLAEALLASADDPDTVRRFAEKMVAESHRLADMIGELIELSRLQGAERLPDL
DAVDVDSIVSEAVSRHKVAADNSQISITTDAPTGYRVLGDEGLLVTAIANLVSNIAIAYSPNGTDVVISRRKRGGNIE
IAVTDRGIGIAKDDQERVFERRFRVDKARSRATGGTGLGLAIVKHVAANHNGSIRLWSQPSTGTFSTLSIPEYDP
PESHSDEREDQRER

>sp|P9WG91|STP_MYCTU Multidrug resistance protein Stp OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=stp PE=1 SV=1

MNRTQLLTIATGLGLFMIFLDALIVNVALPDIQRSFAVGEDGLQWVVASYSGLMAVFIMSAAATLADLDGRRRW

YLIGVSLFTLGSACGLAPSIIVLTTARGAQQGLGAAVSVTSLALVSAAFPEAKEKARAIGIWTAIASIGTTTGPTLG
GLLVDQWGWRSIFYVNLPMGALVFLTLCYVEESCNERARRFDLSGQLLFIVAVGALVYAVIEGPQIGWTSVQTI
VMLWTAAVGCALFVWLERSSNPMDLTLFRDTSYALAIATICTVFFAVYGM LLLTTQFLQNVRGYTPSVTGL
MILPFSAAVAIVSPLVGHVGRIGARVPILAGLCMLMLG LLLMIFSEHRSSALVLVGLGCGSGVALCLTPITTVAM
TAVPAERAGMASGIMSAQRAIGSTIGFAVLGSVLAAWLSATLEPHLERAVPDPVQRHVLA EIIIDSANPRAHVG
GIVPRRHIEHRDPVAIAEEDFIEGIRVALLVATATLAVVFLAGWRWFPRDVHTAGSDLSERLPTAMTVECAVSHM
PGATWCRLWPA

>sp|P9WQI3|SUGC_MYCTU Trehalose import ATP-binding protein SugC OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=sugC PE=1 SV=1

MAEIVLDHVNKSYPDGHTAVRDLNLTADGEFLILVGPSCGKTTTLNMIAGLEDISSGELRIAGERVNEKAPKD
RDIAMVFQSYALPHMTVRQNIAPLTLAKMRKADIAQKVSETAKILDLTNLLDRKPSQLSGGQRQVRAMGRAI
VRHPKAFLMDEPLSNLDAKLRVQMRGEIAQLQRRLLGTTTVVTHDQTEAMTLGDRVVV MYGGIAQQIGTPE
ELYERPANLFVAGFIGSPAMNFFPARLTAIGLTLPFGEVTLAPEVQGVIAAHPKPVNIVGVRPEHIQDAALIDAYQ
RIRALTQVKVNLVLESLGADKYLYFTTESPAVHSVQLDELAEEVEGESALHENQFVARVPAESKVAIGQSVELAFDT
ARLAVFDADSGANLTI PHRA

>sp|O07776|TCRA1_MYCTU Transcriptional regulatory protein TcrA OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=tcrA PE=1 SV=1

MADETTMRAGRGPGRACGRVSGVRILVVEDEPKMTALLARALTEEGHTVDTVADGRHAVA AVDGGDYDAVV
LDVMLPGIDGFEVCARLRRQRVWTPVLM L TARGAVTDRIAGLDGGADDYLT KPFNLDEL FARLRALSRRGPIPR
PPTLEAGDLRLDPSEHRVWRADTEIRLSHKEFTLLEALIRRP GIVHTRAQLLERCWDAAYEARSNIVDVYIRYLRD
KIDRPFVTSLETIRGAGYRLRKDGGRHALPR

>sp|O69729|TCRY_MYCTU Probable sensor histidine kinase TcrY OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=tcrY PE=1 SV=1

MGITAATEMALRRHLVAQLDNQLGGTSYRSVLMYPEKMPRPPWRHETHNYIRSGPGRFLDAPGQPAGMVA
AVVSDGTTVAAGYLTGSGSRAALTSTGRS QLERIAGSRTPLTLDL DGLGRYRVLAA PSRNGHDVIVTGLSMGNV
DATMLQMLIIFGIVTVIALVAATTAGIVI KRALAPLRRVAQTASEVV DLPLDRGEVKLPVRVPEPDANPSTEVGQL
GSALNRMLDHIAAALSARQASETCVRQFVADASHELRTPLAAIRGYTEL TQRIGDDPEAVAHAMSRVASETERIT
RLVEDLLLLLARLD SGRPLERGPVDM SRLAVDAVSDAHVAGPDHQWALDLPPEPVVIPGDAARLHQVVTNLLA
NARVHTGPGTIVTTRLSTGPTHVVLQVIDNGPGIPAALQSEVFERFARGDTSRSRQAGSTGLGLAIVSAVKAHN
GTITVSSSPGYTEFAVRLPLDGWQPLESSPR

>sp|P9WFY7|TRMD_MYCTU tRNA (guanine-N(1)-)-methyltransferase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=trmD PE=1 SV=1

MRIDIVTFPACLDPLRQSLPGKAIESGLVDLNVHDLRRWTHDVHHSVDDAPYGGGPGMVMKAPVWGEALD
EICSSETLLIVPTAGVLF TQATAQRWTTESH LVFACGRYEGIDQRVVQDAARRMRVEEVSGIDYVLP GGESAAV
VMVEAVLRLLAGV LGNPASHQDDSHSTGLDGLLEGPSYTRPASWRGLDVPEVLLSGDHARIAAWRREVSLQRT
RERRPDL SHPD

>sp|P9WGC9|TSAC_MYCTU Putative threonylcarbamoyl-AMP synthase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv1301 PE=1 SV=1

MTETFDCADPEQSRGIVSAVGAIKAGQLVVMPTDTVYGIGADAFDSSAVAALLSAKGRGRDMPVGVLVGSW
HTIEGLVYSMPDGARELIRAFWPGALSLVVVQAPSLQWDLGDAHGTVM LRMPLHPVAIELLREVGPMAVSSA
NISGHPPPVD AEQARSQ LGDHVAVYLDAGPSEQQAGSTIVDLTGATPRVLRPGPVSTERIAEVLGVDAASLFG

>sp|A0R006|WAG31_MYCS2 Cell wall synthesis protein Wag31 OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=wag31 PE=1 SV=1

MPLTPADVHNVAFSKPPIGKRGYNEDEVDAFLDLVENELTRLIEENADLRQRVAELDQELAAARSGAGASSQAT

SSIPLYEPEPEPAPPQPVYEAPAQPAAPQSEDTAVRAARVLSLAQDTADRLTSTAKAEADKLLSDARAQAEAM
VSDARQTAETTVEARQRADAMLADAQTRSEAQLRQAQEKADALQADAERKHSEIMGTINQRTVLEGRLE
QLRTFEREYRTRLKTYLESQLEELGQRGSAAPVDSSANS DASFGQFNRRNN

>sp|AOR211|WECA_MYCS2 Decaprenyl-phosphate N-acetylglucosaminophosphotransferase
OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=wecA PE=1 SV=1

MLQYGAPVITATRETGMDSQVVLALS DTGAGVPLRELALVGLTAAIITYFATGWVVRVLAIRFGAVAYPRERDVHV
QPTPRMGG LAMYIGVASAVLLASQLPALTRGFVYSTGMPAVVVAGGLIMAIGLIDDRWGLDALT KFAGQITAAS
VLVTMGVAWSVLYIPIGGVGTIVLDQVSSILLTALT VSIINAMNFVDGLDGLAAGLGLITALAICVFSVGLLRDHG
GDVLFYPPAVISVVLGACLGLPHNFHRAKIFMGDSGSM LIGLMLGAASTTAAGPISQ NAYGARDV FALLSPFL
LVVAVMLVPALDTLLAIVRRTRAGRSPLSPDKMHLHRLQLIGHSHRRAVLLIYLWVGIIA FGAASTIFFDPGQTA
MVMGVAIVVAIVVTLIPLLRGPDGAQEP

>sp|Q9S426|WHIB2_MYCSM Transcriptional regulator WhiB2 OS=Mycobacterium smegmatis
GN=whmD PE=1 SV=1

MSYESGDFDRVVRFDNRLLGSVSHAPHIDTGSTPTGAAGRPQLSLVPDSFDVAPEAEEDQWQERALCAQTDP
EAFFPEKGGSTREAKRICQGCEVRDACLEYALAHDERFGIWGGLSERERRRLKRGII

>sp|P9WMA7|Y007_MYCTU Uncharacterized protein Rv0007 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv0007 PE=1 SV=1

MTAPNEPGALS KGDGPNADGLVDRGGAHRAATGPGRIPDAGDPPPWQRAATRQSQAGHRQPPPVSHPEGR
PTNPPAAADARLNRFISGASAPVTGPAAAVRTPQDPDASLGC GDGSPA EAYASELPDLSGPTPRAPQRNPAPA
RPAEGGAGSRGDSAAGSSGGRSITAESRDARVQLSARRSRGPVRASMQIRRIDPWSTLKVSLLSVALFFVWMI
TVAFLYLVGGMGVWAKLNSNVGDLLNNASGSSAELVSSGTIFGG AFLIGLVNIVLMTALATIGAFVYNLITDLIG
GIEVTLADRD

>sp|P9WJY1|Y037_MYCTU Uncharacterized MFS-type transporter Rv0037c OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv0037c PE=1 SV=1

MPRVEVGLVIHSRMHARAPVDVWRSVRSPLDFWRLQLVRVASQFGDGLFQAGLAGALLFNP DRAADPMAIA
GAFAVLFLPYSL LGPFAGALMDRWD RRWV LVGANTGRLALIAGVGTILAVGAGDV PLLV GALVANGLARFVAS
GLS AALPHVVPREQVVTMNSVAIASGAVSAFLGANFM LPRWLLGSGDEGASAI VFLVAIPVSIALLW SLRFGPR
VLGPDDTERAIHGS AVYAVVTGWLHGARTV VQLPTVAAGLSGLAAHRMVVGINSL LILLV RHTARAVGGLGT
ALLFFAATGLGAFLANVLTPTAIRRWGRYATANGALAAA TIQVAAAGLLVPVMV VCGFLLGVAGQVVKCADS
AMQMDVDDALRGHVFVAVQDALFWVSYILSITVAAAL IPEHGHAPV FVFLFGSAIYLAGLVVHTIVGRRRQPVIGR

>sp|P9WM87|Y048_MYCTU Uncharacterized protein Rv0048c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv0048c PE=1 SV=1

MAKWLGA PLARGVSTATRAKDS DRQDACRILDALRDGELSM EHRERVSAATKAVTLGDLQRLVADLQVESA
PAQMPALKSRAKRT ELGLLAAAFVASVLLGVGIGWGVYGNTR SPLDFTSDPGAKPDGIAPV VLTTPRQLHSLGG
LTG LLEQTRKRF GDTMGYRLVIPEYASLDRVDPADDRVLAYTYRGGWGDATSSAKSIADVSVDLSKFDAKTA
VGIMRGAPETLGLKQSDVKSMYLIVEPVKDPTT PAALSLSLVSSDYGGGYLVFAGDGTIKHVSYPS

>sp|P9WG17|Y072_MYCTU Uncharacterized ABC transporter permease Rv0072
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv0072 PE=1 SV=1

MLFAALRDMQWRKRRLVITII STGLIFGMTLVLTGLANGFRVEARHTVDSMGVDV FVVRSGAAGPFLGSIPFPD
VDLARVAAEPGVMAAAPLGSVGTIMKEGTSTRNVT VFGAPEHGPMPRVSEGRSPSPKPEVAASSTMGRHL
GDTVEVGARRLRVGVIPNSTALAKIPNVFLTTEGLQLKAYNGQPNITSIGIIGMPRQLPEGYQTFDRVGAVNDL
VRPLKVAVNSISIVAVLLWIVAVLIVGSVVYLSALERLRDFAVFKAIGTPTRSIMAGLALQALVIALLA AVGVVLAQ
VLAPLFPMIVAVPVGAYLALPVA AIVIGLFASVAGLKRVTVDPAQAFGGP

>sp|P9WM71|Y090_MYCTU Uncharacterized protein Rv0090 OS=Mycobacterium tuberculosis

(strain ATCC 25618 / H37Rv) GN=Rv0090 PE=1 SV=1

MAKNQNRIRNRWELITCGLGGHVITYAPDDAALAARLRASSTGLGEVWRCLRCGDFALGGPQGRGAPEDAPLI
MRGKALRQAIIRALGVERLVRALVLALAAWAVWEFRGARGAIQATLDRDLPVLAAGFKVDQMTVIHALEKA
LAAKPSTLALITGMLAAYAVLQAVEGVGLWLLKRWGEYFAVVATSIFLPLEVHDLAKGITTRRVVTF SINVAVVY
LLISKRLFGVRGGRKAYDVERRGEQLDLERAAMLT

>sp|P9WM69|Y093_MYCTU Uncharacterized protein Rv0093c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv0093c PE=1 SV=1

MLAQATTAGSFNHASTVLQGCGRVPAAMWSEPAIRRHACATIDGMDCEVAREALSARLDGERAPVPSAR
VDEHLGEC SACRAWFTQVASQAGDLRRLAESRPVPPVGR LGIRRAPRRQHSPMTWRRWALLCVGIAQIALG
TVQGFGLDVGLTHQHPTGAGTHLLNESTWSIALGVIMVGAALWPSAAAAGLAGVLTAFVAITGYVVIDALSGA
VSTTRILTHLPVIGAVLAIMVWRSASGPRPRPDAAAEPDIVLPDNASRGRRRGHLWPTDGSAA

>sp|P9WM63|Y102_MYCTU Uncharacterized protein Rv0102 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv0102 PE=1 SV=1

MGTHGATKSATS AVPTPRNSMAMVRLAIGLLGVCVAAAFGLVSGARRYAEAGNPYPGAFVSVAEVPGFFAA
SLAGALCLGALIHVVM TAKPEPDGLIDAAAFRIHLLAERV SGLWLGLAATMVVIQAAHDTGVGPARLLASGALS
DSVAASEMARGWVAAICALVVATALRLYTRWLGHVLLVPTVLAVVATAVTGNPGQGPDDHYATSAAIVFAVA
FATLTGLKIAAALAGTTPSRAVLVTQVTCGALALAYGAMLLYL FIPGWAVDSDFARLGLLAGVILTSVWLFDCWRL
LVRPPHAGRRRGGGSGAALAMMAAMASIAAMAVMTAPRFLTHAFTAWDVFLGYELQPPTIARVLTVWRFD
SLIGAAGVVAIGYAAGFAALRRRGNSWPVGR LIAWLTGCAALVFTSGSGVRAYGSAMFSVHMAEHMTLNMF
IPVLLVLGGPVT LALRVLPVTGDGRPPGAREWLTWLLHSRVTTFLSH PITAFVLFVASYIVYFTPLFDTFVRYHW
GHEFMAIHFLVVG YLYFWAII GIDPGPRRLPYPGRIGLLFAVMPFHAF FGIALMTMSSTVGATFYRSVNL PWLSS
IIADQHLGGGIAWSLTELPMVIMVIVALVTQWARQDRR VASREDRHADSDYADDELEAYNAMLRELSRMRR

>sp|P9WFM3|Y1101_MYCTU UPF0118 membrane protein Rv1101c OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv1101c PE=1 SV=1

MNTEFTLTQKRALAILT LIALLLFGAYFLRNYFVLIVVAAV GAYLFTPLFKWFTKRFNTGLSAACTLLSALAAVVVPV
GALVGLAIVQIARMVDSVADWVRTD LSTLGDKILQFVNGLFD RVPFLHITVTADALRKAMISVAQNVGEWLL
HFLRDAAGSLAGVITS AIIFFVYFVALLVNREKRLT LIGQLNPLGEDVTDLYLQKMGSMV RGTVNGQFVIAACQG
VAGAASIYIAGFHGGFFIFAI VLTALSIPLGGGIVTIPFGIGMIFYGNIAGGIFVLLWHLVVTNIDNVL RPILVPRDA
RLNSALMLLSVFAGITMFGPWGIIIGPVL MILIVTTIDVYLAVYK GVELEQFEAPPVRRRWLPRRGPATSRNAPP
STAE

>sp|P9WJX9|Y1258_MYCTU Probable multidrug-efflux transporter Rv1258c OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv1258c PE=1 SV=1

MRNSNRGP AFLILFATLMAAAGDGV SIVAFPWLVLQREGSAGQASIVASATMLPLL FATLVAGTAVDYFGRRRV
SMVADALSGAAVAGVPLVAWGYGGDAVNV LVLAVLAALAAAFGPAGMTARDSMLPEAAARAGW SLDRING
AYEAILNLA FIVGPAIGGLMIATVGGITM WITATAFGLSILAI AALQLEGAGKPHHTSRPQGLVSGIAEGLRFVW
NLRVLR TLMIDLTVTALYLPME SVLFPKYFTDHQQPVQLGWALMAIAGGGLV GALGYAVLAI RVP RRVTMSTA
VLTGLAS MVIAFLPPLPVIMVLC AVVGLVYGPIQPIYNYVIQ TRAAQH LRGRVVGVM TSLAYAAGPLG LLLAGPL
TDAAGLHATFLALALPIVCTGLVAIRLPALRELDLAPQADIDR PVGSAQ

>sp|P9WGU5|Y1280_MYCTU Uncharacterized protein Rv1280c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv1280c PE=1 SV=1

MADRGQRRGCAPG IASALRAS FQGKSRPWTQTRYWAFALLT PLVVAMVLTGCSASGTQLELAPTAD RRAAVG
TTSDINQQDPATLQDGGNLRSLTDFPPNFN I LHIDGNNAEVAAMMKATLPRAFIIIGPDG STTVDTNYFTSIELT
RTAPQVVY TINPEAVWSDGTPITWRDIASQIHAISGADKA FEIASSSGAERVASVTRGVDDRQAVVTF AKPYAE
WRGMFAGNGM LLLPASMTATPEAFNKGQLDGP GSPAGPFVVSALDRTAQRIVLTRNPRWWGARPR LDSITYL

VLDDAARLPALQNNTIDATGVGTLDQLTIAARTKGISIRRAPGPSWYHFTLNGAPGSILADKALRLAIKIDRYTI
ARVAQYGLTSDPVPLNNHVFVAGQDGYQDNSGVVAYNPEQAKRELDALGWRRSGAFREKDGRQLVIRDLFYD
AQSTRQFAQIAQHTLAQIGVKLELQAKSGSGFFSDYVNVGAFDIAQFGWVGDAFPLSSLTQIYASDGESNFGKI
GSPQIDAAIERTLAELDPGKARALANQVDELIWAEGFSLPTQSPGTVAVRSTLANFGATGLADLDYTAIGFMRR

>sp|P9WM35|Y1290_MYCTU Uncharacterized protein Rv1290c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv1290c PE=1 SV=1

MLQRSGLGVNKRKLAMSARSARKRERKNASTAASKCYVPPSARGWVHAYSVTATSMLNRRKAILDYLGAVVW
LPTFGVAIGLGSAGVLSMIPVKSGLTIDKLMFQGTGPDARGVLIVVSATMITTIGIVFSLTVLSLQIASSQFSVRLLR
TFLRDVPNQVLAIFACTFAYSTGGLHTVGEHRDGGAFIPKVAVTGSLALAFVSI AALIYFLHHLMHSIQIDTIMD
KVRLRTLGLVDQLYPESDTADRQVETPPSPPADAVPLLAPHSGYLQTVDDVDDIAELAAASRYTALLVTFVGDYVTA
GGLLGWCWRRGTAPGAPGSDFPQRCLRHVHIGFERTLQQDIRFGLRQMVDIALRALSPALNDPYTAIQVVHHL
SAVESVLASRALPDDVRRDRAGELLFWLPYPSFATYLVHGCAQIRRYGSREPLVLTALLQLLSAVAQNCVDPSSRRV
AVQTQIALVVRAAQREFADESDRAMVLGAAARATEVVERPGTLAPPSTFGQVAAAQAAASTIRSADR DG

>sp|P9WM31|Y1303_MYCTU Uncharacterized protein Rv1303 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv1303 PE=1 SV=1

MTTPAQDAPLVFPSVAFRPVRLFFINVGAAVAMLVAGVFGHLTVGMFLGLGLLLGLLNALLVRRSAESITAKEH
PLKRSMALNSASRLAIITILGLIAYIFRPAGLGVVFGLAFFQVLLVATTALPVLKKLRTATEEPVATYSSNGQTGGSE
GRSASDD

>sp|P9WM29|Y1312_MYCTU Uncharacterized protein Rv1312 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv1312 PE=1 SV=1

MSAPMIGMVVLLVVLGLAVLALSRYRLWKLKRGGTAGIMRDIPAVGGHGWHRGVIRYRGGEAAFYRLSSLRLW
PDRRLSRRGVEIISRRAPRGDEFDIMTDEIVVVELCDSTQDRRVGYEIALDRGALTAFLSWLESRPSRARRRSM

>sp|P9WQ29|Y1320_MYCTU Uncharacterized protein Rv1320c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv1320c PE=1 SV=1

MPSEKATTRHLPGAVETLSPRTGRRPETPAYGSWLLGRVSESPRMRRVRIQGMLTVAILVTNVIGLIVGAMLLTV
AFPKPSVILDAPHWVSFGIVPGYCVLAFILGTYWLTRQTARALRWAIEERTPSHDEARS AFLVPLRVALAVLFLWG
AAAALWTIYGLANRLFIPRFLFSMGVIGVVAATSCYLLTEFALRPMAAQALEVGATPRSLVRGIVGRTMLVWLLC
SGVPNVGVALTAIFDDTFWELSNDQFMITVLILWAPLLIFGFILMWILAWLTATPVRVREALNRVEQGDLSGDL
VVFDTGTELGELQRGFNRMVEGLRERERVRDLFGRHVGREVAAAERERPKLGGEERHVAVVFDIVGSTQLVT
SRPAAEVVMLLNRFVTIVDEVNHHRGLVNKFQGDASLAVFGAPNRLSHPEDAALATARAIAADRLASEMPECC
AGIGVAAGQVVAGNVGAHERFEYTVIGEPVNEAARLCELAKSYPSRLLASSQTLRGASENECARWSLGETVTLR
GHDQPIRLTSPVQQLQMPAQSA DIVGGALGDHQHTIYRGAHPTD

>sp|P9WM23|Y1333_MYCTU Uncharacterized aminopeptidase Rv1333 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv1333 PE=1 SV=1

MNSITDVGGIRVGHYQRLDPDASLGAGWACGVTVVLPPTGTVGAVDCRGGAPGTRETDLLDPANSRVFVDAL
LLAGGSAYGLAAADGVMRWLEEHRRGVAMDSGVVPIVPGAVIFDLPVGGWNCRPTADFGYSACAAAGVDVA
VGTVGVGVGARAGALKGGVGTASATLQSGVTGVLAVVNAAGNVVDPATGLPWMADLVGEFALRAPPAEQI
AALAQLSSPLGAFNTPFNNTTIGVIACDAALSPAACRRRIAIAHDGLARTIRPAHTPLDGD TVFALATGAVAVPPEA
GVPAALSPETQLVTAVGAAAADCLARAVLAGVLNAQPVAGIPTYRDMFPGAFGS

>sp|P9WM19|Y1342_MYCTU Uncharacterized protein Rv1342c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv1342c PE=1 SV=1

MTAPETPAAQHAEPAAIVERIRTALLGYRIMAWTTGLWLIALCYEIVVRYVVKVDNPPTWIGVVHGWVYFTYLL
LTLNLAVKVRWPLGKTAGVLLAGTIPLLGIVVEHFQTK EIKARFGL

>sp|P9WM01|Y1362_MYCTU Uncharacterized protein Rv1362c OS=Mycobacterium tuberculosis

(strain ATCC 25618 / H37Rv) GN=Rv1362c PE=1 SV=1
MTDDVRDVNTETTTDATEVAEIDSAAGEAGDSATEAFDTSATESTAQKGQRHRDLWRMQVTLKPVVILILLM
LISGGATGWLYLEQYRPDQQTDSGAARAATAASDGTIALLSYSPDLDQDFATARSHLAGDFLSYYDQFTQQIV
APAAKQKSLKTTAKVVRAAVSELHPDSAVVLFVDQSTTSKSDPNPSMAASSVMVTLAKVDGNWLITKFTPV
>sp|P9WLZ9|Y1363_MYCTU Uncharacterized protein Rv1363c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv1363c PE=1 SV=1

MAETTEPPSDAGTSQADAMALAAEAEAEAEALAAAARARARAARLKREALAMAPAEDENVPEEYADWEDA
EDYDDYDDYEAADQEAARSASWRRRLRVRLPRLSTIAMAAAVVVICGFTGLSGYIVWQHHEATERQQRAAFA
AGAKQGVINMTSLDFNKAKEDVARVIDSSTGEFRDDFQQRAADFTKVVEQSKVVTEGTVNATAVESMNEHSA
VVLVAATSRVNSAGAKDEPRAWRLKVTVTEEGGQYKMSKVEFVP

>sp|P9WLY1|Y1417_MYCTU Uncharacterized protein Rv1417 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv1417 PE=1 SV=1

MTAAPNDWDVVLPRHWTPLFAYAAAFLIAVAHVAGGLLLKVGSSGVVFQADQVAMGALGLVLAGAVLLFAR
PRLRVGSAGLSVRNLLGDRIVGWSEVIGVSFPGGSRWARIDLADDEYIPVMAIQAVDKDRAVAAMDTVRSLLA
RYRPDLCAR

>sp|P9WLX9|Y1419_MYCTU Uncharacterized protein Rv1419 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv1419 PE=1 SV=1

MGELRLVGGVLRVLLVVGAVFDVAVLNAGAASADGPVQLKSRLGDVCLDAPSGSWFSPVINPCNGTDFQRW
NLTDQRQVESVAFPGECVNIGNALWARLQPCVNWISQHWTVQPDGLVKSDLDACTVLGGPDPGTWVSTR
WCDPNAPDQQWDSVP

>sp|O53150|Y1459_MYCTU Alpha-(1->6)-mannopyranosyltransferase Rv1459c
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv1459c PE=1 SV=1

MAARHHTLSWSIASLHGDEQAVGAPLTTTELALARTLFGATGTVLMALGAGARPVVQDPTFGVRLNL
PSRIQTVSLTMTTGTAVMMALAWMLGRFTLGRRRMSRGKLDRTLLWMLPLLIAPPMYSKDVYSYLAQSEIG
RDGLDPYRVGPASGLGLGHVFTLSVPSLWRETPAPYGPLFLWIGRIGISLTGENIVA AVLCHRLVVLIGVTLIVWA
TPRLAQRGVAEVSALWLGAANPLIMHLVAGIHNEALMLGLMLTGVFEFALRGLDMANTPRPSPETWRLGPAT
IRASRRPELGASPRAGASRAVKPRPEWGPLAMLLAGSILITSSQVKLPSLLAMGFVTTVLAYRWGGNLRALLA
AAVMASLTAIMAILGWASGLGFGWINTLGTANVVRSWMSPTLLALGTGHVIGILLGLGDHTTAVLSLTRAIGV
LIITVMVCWLLLAVLRGRLHPIGGLGVALAVTVLLFPVVPWYLLWAIPLAAWATRPGRVAAAILATLIVGIFGPT
ANGDRFALFQIVDATAASAIIVILLIALLYTRLPWRPLAAEQVVTAAESASKTPATRRPTAAPDAYADST

>sp|P9WPR9|Y1488_MYCTU Uncharacterized protein Rv1488 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv1488 PE=1 SV=1

MQGAVAGLVFLAVLVFAIIVVAKSVALIPQAEAAVIERLGRYSRTVSGQLTLLVFPFIDRVRRVLDLRRVVSFPQ
PVITEDNLTLNIDTVVYFQVTVPQAAVYEISNYIVGVEQLTTTTLRNVVGGMTLEQLTSTRDQINAQLRGVLDEA
TGRWGLRVARVELRSIDPPPSIQASMEKQMKADREKRAMILTAEGTREAAIKQAEQKQAQILAAEGAKQAAI
LAAEADRQSRMLRAQGERAAAYLQAQGGAKAIEKFAAIKAGRPTPEMLAYQYLQTLPEMARGDANKVWVV
PSDFNAALQGFTRLLGKPGEDGVFRFEPSPVEDQPKHAADGDDAEVAGWFSTDTDPDIARAVATAEAIARKPV
EGSLGTPPRLTQ

>sp|P9WLW1|Y1510_MYCTU Uncharacterized protein Rv1510 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv1510 PE=1 SV=1

MYERRHERGMCDRAVEMTDVGATAAPTGPARGSVARVGAATALAVACVYTVIYLAARDLPPACFSIFAVFWG
ALGIATGATHGLLQETTREVWVRSTQIVAGHRTHPLRVAGMIGTVAAVVIAGSSPLWSRQLFVEGRWLSVGLL
SVGAGFCAQATLLGALAGVDRWTQYGSLMVTDAVIRLAVAAA VVIGWGLAGYLWAAATAGAVAWLLMLM
ASPTARSAASLLTPGGIATFVRGAHSITAAGASAILVMGFPVLLKVTSDQLGAKGGAVILAVTLTRAPLLVPLSA

MQGNLIAHFVDRRTQRLRALIAPALVGGIGAVGMLAAGLTGPWLLRVGFGPDYQTGGALLAWLTAATAVAIA
MLTLTGAAAVAAALHRAYLLGWVSATVASTLLLLPMPLETRTIVALLFGPTVGIAIHVAALARRPD

>sp|P9WLT5|Y1591_MYCTU Uncharacterized protein Rv1591 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv1591 PE=1 SV=1

MLGLSATGVLVGGWLWAWIAPPIHAVVAITRAGERVHEYLGSESNFFIAPFMLLGLLSVLAVVASALMWQWRE
HRGPQMVAAGLSIGLTTAAIAAGVGVVRLRYGALDFDTVPLSRGDHALTYVTQAPPVFFARRPLQIALTLMW
PAGIASLVYALLAAGTARDDLGGYPAVDPPSSNARTEALETPQAPVS

>sp|P9WJX3|Y1634_MYCTU Probable multidrug-efflux transporter Rv1634 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv1634 PE=1 SV=1

MTETASETGSWRELLSRYLGTSLVLAGGVALYATNEFLTISLLPSTIADIGGSRLYAWVTTLVVGSVVAATTVNTML
LRVGARSSYLMGLAVFGLASLVCAAAPSMQILVAGRTLQGIAGGLLAGLGYALINSTLPKSLWTRGSALVSAMW
GVATLIGPATGGLFAQLGLWRWAFGVMTLLTALMAMLVPVALGAGGVGPGGETPVGSTHKVPVWSLLMGA
AALASVAALPNYLVTAGLLAAALLVAVFVVVDWRIHAAVLPPSVFVSGPLKWIYLTMSVQMIAMVDTYVP
LFGQRLGHLPVAAGFLGAALAVGWTVEVASASLNSARVIGHVVAAPLVMASGLALGAVTQRADAPVGIIA
LWALALLIIGTGIGIAWPHLTVRAMDSVADPAESSAAAAAINVVQLISGAFGAGLAGVNVNTAKGGEVAAARGL
YMAFTVLAAGVIASYQATHRRRLPR

>sp|P9WLS8|Y1733_MYCTO Probable membrane protein MT1774 OS=Mycobacterium
tuberculosis (strain CDC 1551 / Oshkosh) GN=MT1774 PE=2 SV=1

MIATTRDREGATMITFRLRLPCRTILRVFSRNSLVRGTDRLVAVMMLAVTVSLLTIPFAAAAGTAVHDSRSHVYA
HQAQTRHPATATVIDHEGVDSNTTATSAPPRTKITVPARVWVNGIERSGEVNAKPGTKSGDRVGIWVDSAGQ
LVDEPAPPARAIADAALALGLWLSVAAVAGALLALTRAILIRVNASWQHHDIDSLFCTQR

>sp|P9WLS4|Y1735_MYCTO Uncharacterized membrane protein MT1776 OS=Mycobacterium
tuberculosis (strain CDC 1551 / Oshkosh) GN=MT1776 PE=2 SV=1

MFLYVAVGSLVVARLLYPLRPADLTPPYWVAMGATAITVLAGAHIVEMADAPMAIVTSGLVAGASVVFVAFG
PWLIPPLVAASIWKHVHRVPLRYEATLWSVVFPLGMYGVGAYRLGLAAHLPIVESIGEFEGWVALAVWTITFV
AMLHHLAATIGRSGRSSHAIGAADDTHAIICRPPRSFDHQVRAFRRNQPM

>sp|P9WMC9|Y1816_MYCTU Uncharacterized HTH-type transcriptional regulator Rv1816
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv1816 PE=1 SV=1

MCQTCRVGKRRDAREQIEAKIVELGRRQLLDHGAAGLSLRAIARNLGMVSSAVYRYVSSRDELLTLLVDAYS
DLADTVDRARDTVDADSWDDVIAIARAVRGWAVTNPARWALLYGSPVPGYHAPPDRTAGVATRVVGAFFDAIA
AGIATGDIRLTDVAPQPMSSDFEKIRQEFQFPGDDRVTCKFLLWAGVVGAISSLEVFGQYGADMLTDPGVVF
DAQTRLLVAVLAEH

>sp|P9WFG1|Y1823_MYCTU UPF0749 protein Rv1823 OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) GN=Rv1823 PE=1 SV=1

MAESDRLGGYDPNAGYSAHAGAQPQRIPVPSLLRALLSEHLDAGYAAVAERERAAAAPRCWQARAVSWM
WQALAATLVAAVFAAQAARSVAPGVRAAQQLLVASVRSTQAAATTLAQRSTLSAKVDDVRRIVLADDAEG
QRLRLDLVLSLAAASAPVVGPLTVTDPGASPNSLSDVSKQRVSGSQIILDRDLQLVNSLWESGAEAISID
GVRIGPNVTIRQAGGAILVDNNTSSPYTILAVGPPHAMQDVFDRSAGLYRLRLLLETSYGVGVSVNVGDGLALP
AGATRDVKFAKQIGP

>sp|P9WFG3|Y1825_MYCTU UPF0749 protein Rv1825 OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) GN=Rv1825 PE=1 SV=1

MSENRPEPVAEAETSAATTARHSQADAGAHDAVRRGRHELPADHPRSKVGPLRRTRLTEILRGGRSRLVFGTLAIL
LCLVLGVAVTQVRQTDSDGSLETARPADLLVLLDSLRLQREATLNAEVIDLQNTLNALQASGNTDQAALESAQAR
LAALSILVGAVGATGPGVMITIDDPGPGVAPEVMIDVINELRAAGAEAIQINDAHRVSRVGVDTWVVVGPVGS

VDTKVLSPYSILAIGDPPTLAAAMNIPGGAQDGVKRVGGRMVVQQADRVDVTALRQPKQHQAQPVK
>sp|P9WLQ9|Y1836_MYCTU Uncharacterized protein Rv1836c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv1836c PE=1 SV=1

MGRHSPDPEDSVDDLSDGHAAEQHWEDISGSYDYPGVDQPDGGLSSEGHYSAVGGYSASGSEDPDIP
PRPDWEPTGAEPAAAAAPPPLFRFGHRRGPGDWQAGHRSADGRRGVSIGVIVALVAVVVMVAGVILWRRFFGDAL
SNRSHTAAARCVGGKDTVAVIADPSIADQVKESADSYNASAGPVGDRCAVAVTSAGSDAVINGFIGKWPTTEL
GGQPGLWIPSSSISAARLTGAAGSQAISDSRSLVISPVLLAVRPELQQALANQNWAAALPGLQTNPNLSGLDLPA
WGSRLRAMPSSNGDAAYLAGEAVAAASAPAGAPATAGIGAVRTLMGARPKLADDSLTAAAMDTLLKPGDVAT
APVHAVVTTEQQLFQRGQSLSDAENTLGSWLPPGPAAVADYPTVLLSGAWLSQEQTSAASAFARYLHKPEQLA
KLARAGFRVSDVKPPSSPVSFPALPSTLSVGDDSMRATLADTMVTASAGVAATIMLDQSMNPDEGGNSRSLN
VVAALENRIKAMPSSVVLWTFDQREGRETEVPAGPLADPVNGQPRPAALTAALGKQYSSGGGAVSFTTLRLIY
QEMLANYRVGQANSVLVITAGPHTDQTLDGPGQLQDFIRKSADPAKPIAVNIIDFGADPDRAWEAVAQLSGGS
YQNLETSASPDLATAVNIFLS

>sp|P9WFP3|Y1842_MYCTU UPF0053 protein Rv1842c OS=Mycobacterium tuberculosis (strain
ATCC 25618 / H37Rv) GN=Rv1842c PE=1 SV=1

MNLTDTVATILAILALTAGTGVFVAAEFSLTALDRSTVEANARGGTSRDRFIQRAHHRLSFQLSGAQLGISITTLAT
GYLTEPLVAELPHPLVAVGMSDRVADGLITFFALVIVTSLSMVFGELVPKYLAVARPLRTARSVAVAGQVLFSLLT
PAIRLTNGAANWIVRRLGIEPAEELRSARTPQELVSLVRSSARSGALDDATAWLMRRSLQFGALTAELMTPRSKI
VALQTDITADLVAAAAASGFSRFPVVEGDLDATVGIVHVQVFEVPPGDRAHTLLTTVAEPVAVPSTLDGDA
VMAQVRASALQTMVVDEYGGTAGMVTLEDLIEIVGDVRDEHDDATPDVVAAGNGWRVSGLLRIDEVASA
TGYRAPDGPYETIGGLVRELGHIPVAGETVELTALDQDGLPDDSMRWLATVIQMDGRRIDLLELIKMGGHAD
PGSGRGR

>sp|P9WQM5|Y1979_MYCTU Uncharacterized transporter Rv1979c OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv1979c PE=1 SV=1

MVGPRTRGYAIHKLGFCSVVMGINSIIGAGIFLTPGEVIGLAGPFAPMAYVLAGIFAGVVAIVFATAARYVRTNG
ASYAYTTAAFRRIGIYGVTHAITASIAWGVLASFFVSTLLRVAFPDKAWADAEQLFSVKTLTFLGFIGVLLAINLF
GNRAIKWANGTSTVGKAFALSAFIVGGLWIITQHVNNYATAWSAYSATPYSLLGVAEIGKGTSSMALATIVALLY
AFTGFESIANAAEMDAPDRNLPRAIPIAIFSVGAIYLLTVMALLGSNKIAASDDTVKLAALAAIGNATFRTIIVVG
ALISMFGINVAASFGAPRLWTALADSGVLPTRLSRKNQYDVPMSFAITASLALAFPLALRFDNLHLTGLAVIARF
VQFIIVPIALIALARSQAVEHAARRNAFTDKVLPVAIVSVGLAVSYDYRCIFLVRGGPNYFSIALIVITFIVVPAM
AYLHYYRIIRRVGDRPSTR

>sp|P9WLP9|Y1989_MYCTU Uncharacterized protein Rv1989c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv1989c PE=1 SV=1

MSDALDEGLVQRIDARGTIEWSETCYRYTGAHRDALSSEGARRFGGRWNPPLLPALYLAADSAQACMVEVER
AAQAASTTAEKMLEAAYRLHTIDVTDLAVLDLTPQAREAVGLENDIYGDDWSGCQAVGHAAWFLHMQGV
LVPAAGGVGLVVTAYEQRTRPGQLQLRQSVDLTPALYQELRAT

>sp|P9WQM3|Y1999_MYCTU Uncharacterized transporter Rv1999c OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv1999c PE=1 SV=1

MRRPLDPRDIPDELRRRLGLLDVAVIGLGS MIGAGIFAALAPAAYAAGSGLLLGLAVA AVVAYCNAISSARLAARY
PASGGTYVYGRMRLGDFWGYLAGWGFVVGKTASCAAMALTVGFYVWPAQAHAVAVAVVVALTAVNYAGIQ
KSAWLTRSIVAVVVLVAVVVAAYGSGAADPARLDIGVDAHVVWGMQLAAGLLFFAFAGYARIATLGEVVRDPA
RTIPRAIPLALGITLAVYALVAVAVIAVLGPQRLARAAAAPLSEAMRVAGVNWLPVQVIGAAVAALGSLALILGVS
RTTLAMARDRHLPRWLA AVHPRFKVPFRAELVVGAVVAALAAATADIRGAIGFSSFGVLVYAIANASALTGLDE
GRPRRLIPLVGLIGCVLAFALPLSSVAAGAAVLGVGVAAYGVRRITRRARQTDSGDTQRS GHPSAT

tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2235 PE=1 SV=1
MPRLAFLLRPGWLALALVVVAFYLCFTVLAPWQLGKNAKTSRENQQRIRYSLDTPPVPLKTLPPQQDSSAPDAQ
WRRVTATGQYLPDQVQLARLRVVEGDQAFEVLAPFVVDGGPTVLVDRGYVRPQVGSHPPIRPLPVQTVTITA
RLRDSEPSVAGKDPFVRDGFQVYSINTGQVAALTGVQLAGSYLQIEDQPGGLGVLPVHLDPGPFLSYGIQ
WISFGILAPIGLGYFAYAEIRARRREKAGSPPDPKPMTEVQKLADRYGRRR
>sp|P9WLH1|Y2237_MYCTU Uncharacterized protein Rv2237 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv2237 PE=1 SV=1
MLLPAANVIMQLAVPGVGYGVLESPVDSGNVYKHPFKRARTTGTYLAVATIGTESDRALIRGAVDVAHRQVRST
ASSPVSYNAFDPKLQLWVAACLYRYFVDQHEFLYGPLEDATADAVYQDAKRLGTTLQVPEGMWPPDRVAFDEY
WKRSLDGLQIDAPVREHLRGVASVAFLPWPLRAVAGPFNLFATTGFLAPEFRAMMQLEWSQAQQRRFEWLL
SVLRLADRLIPHRAWIFVYQYLWDMRFRARHGRRIV
>sp|P9WLG7|Y2240_MYCTU Uncharacterized protein Rv2240c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv2240c PE=1 SV=1
MLIGWRAVPRRHGGELPRRGALALGCIALLMGIVGCTTVDGTAMPDTNVAPAYRSSVSASVSASAATSSIRE
SQRQQSLTTKAIRTSCDALAATSKDAIDKVNAYVAAFNQGRNTGPTGPAIDALNNSASTVSGSLSAALSAQLG
DALNAYVDAARAVANAIGAHASTAEFNRRVDRLNDTKTKALTMCVAAF
>sp|P9WLF5|Y2272_MYCTU Uncharacterized protein Rv2272 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv2272 PE=1 SV=1
MADDSNDTATDVEPDYRFTLANERTFLAWQRTALGLLAAVALVQLVPELTIPGARQVLGVVLAAILTSGMGL
LRWQQADRAMRRHLPLRHPTPGYLAVGLCVVGVVALALVVAKAITG
>sp|P9WJ13|Y2287_MYCTU Uncharacterized Na(+)/H(+) exchanger Rv2287 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2287 PE=1 SV=1
MNGRRITIGEDGLVFLVIVALVAVVVGTVLGHRYRVGPPVLLILSGSLLGLIPRFGDVQIDGEVVLLFLPAILY
WESMNTSFREIRWNLRVIVMFSIGLVIATAVAVSWTARALGMESHAAVAVLAVLSPTDAAVAVGLAKRLPRRAL
TVLRGESLINDGTALVFAVTVAVAEGAAGIGPAALVGRFVVSYLGGIMAGLLVGLVTLRRRIDAPLEEGALSLL
TPFAAFLLAQLKCSGVAVLVSALVLTIVGPTVIRARSRLQAHAFWDIATFLINGSLWVFGVQIPGAIDHIAGE
DGGLPRATVLAVALVTVIATRIAWVQATTVLGHTVDRVLKPKTRHVGFQRQCVTSWAGFRGAVSLAAALAVP
MTTNSGAPFPDRNLIIFVSVVILVTVLQGTSLPTVVRWARMPEVAHANELQLARTRSAQAALDALPTVAD
ELGVAPDLVKHLEKEYEERAVLVMADGADSATSDLAERNDLRRVRLGVLQHQHQAVTTLRNQNLIDDIVLREL
QAAMDLEEVQLLDPADAE
>sp|P9WLC7|Y2307_MYCTU Uncharacterized protein Rv2307c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv2307c PE=1 SV=1
MSLKRCRALPVVAIVALVASGVIMFIWSQQRRLIYFPSAGPVPSASSVLPAGRDVVVETQDGMRLGGWYFPHT
SGGSGPAVLVCNGNAGDRSMRAELAVLHGLGLSVLLFDYRGYGGNPGRPSEQGLAADARAAQEWLSGQSD
VDPARIAYFGESLGAAVAVGLAVQRPPAALVLRSPFTSLAEVAVHYPWLPLRRLLDHYPSEIRIASVHAPVLVIA
GGSDDIVPATLSERLVAAAAEPKRYVVVPGVGHNDPELDDGRVMLDAIRRFLTETAVLGQ
>sp|P9WPI7|Y2325_MYCTU Uncharacterized protein Rv2325c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv2325c PE=1 SV=1
MTTTSAPARNGTRRPSRPVLLIPVPGSSVIHDLWAGTKLLVVFVGLVLLTFYPGWVTIGMMAALVLAARIAHIP
RGALPSVPRWLWVLAIGFLTAALAGGTPVAVGGVQLGLGGALHFLRITALSVLLALGAMVSWTTNVAEISP
AVATLGRPFVRLRIPVDEWAVLALALRAFPMILIDEFQVLYAARRLRPKRMPPSRKARRQRHARELIDLLAAAIT
VTLRRADEMGDITARGGTGQLSAHPGRPKLADWVTLAITAMASGTAVAIESLILHS
>sp|P9WQI7|Y2326_MYCTU Uncharacterized ABC transporter ATP-binding protein Rv2326c
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2326c PE=1 SV=1

MCCAUCGPEPGRIGEVTPLGPCPAQHRGGPLRPSSELAQASVMAALCAVTAIISVVVFAAGLALLGTVPTGLLAY
RYRLRVLAAATVAAGMIAFLIAGLGGFMGVVHSAYIGGLTGIVKRRGRGTPTVVVSSLIGGFVFGAAMVGM
AMVRLRHLIFKVMANVDGIAATLARMHMQGAAADVCRYFAEGLQYWPWVLLGYFNIGIMIVSLIGWWALS
RLLERMRGIPDVHKLDPPPDDVDALIGPVPVRLDKVRFYPRAGQDALREVSLDVRAGEHLAIIGANGSGKTT
LMLILAGRAPTSVDRPGTVGLGKLGTAVVVLPQHPESQVLGTRVADDVVWGLPLGTTADVGRLLSEVGL
AERDTGSLSGGELQRLALAAALAREPAMLIADVVTDQQRDALLAVLSGLTQRHRTALVHITHYDNEADS
ADRTLSLSDSPDNTDMVHTAAMPAPVIGVDQPQHAPALELVGVGHEYASGTPWAKTALRDINVFVEQGDGVL
IHGGNGSGKSTLAWIMAGLTIPTTGACLLDGRPTHEQVGAVALSFQAARLQLMRSRVDLEVASAAGFSASEQD
RVAAALTVVGLDPALGARRIDQLSGGQMRRVVLGALLARAPRALILDEPLAGLDAASQRGLLRLLDLRRARGL
TVVVVSHDFAGMEELCPRTLHLRDGVLESAAASEAGGMS

>sp|P9WFJ5|Y2345_MYCTU UPF0603 protein Rv2345 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2345 PE=1 SV=1

MRLVRLGMLVTLAAGLLGPPAGAQPFRLSNYVTDNAGVLTSSGRTAVTAAVDRLYADRRIRLWVVYVENFS
GQSALNWAQRTRTSELGNYDALLAVATTGREYAFVPSAMPGVSEGQVDNVRRYQIEPALHDGDYSGAAVA
AANGLNRSPSSSRVLLVTVGIIVVAVLLVVMRHRNRRADELAARRVDPTNVMALAAVPLQALDDLSR
SMVVDVNAVSTNELALAEIEFGERRTAPFTQAVNNAKAALSQAFTVRQQLDDNTPETPAQRRELLTRVIVS
AAHADRELASQTEAFEKLRDLVINAPARLDTLQYVELTRIGPTQQRALHTEFDAAAMTSIAGNVTTATERL
AFADRNIASAARDLADQAVSGRQAGLVDAVRAAESALGQARALLDAVDSAATDIRHAVASLPVVADIQTGIKRA
NQHLQQAQQPQTGRGDLIAARDAARALDRARGAADPLTAFDQLTKVDADLDRLLATLAEQATADRLNRS
EQALFTAESRVAVSEYIDTRRGSIGPEARTRLAEAQRQLEAAHDRKSSNPTEAIAYANAASTLAAHAQSLANAD
VQSAQRAYTRRGNNAGAILGGIIGDLSGGTRGGLGGWIPTSFSGSSNAPGSSPDGGFLGGGGRF

>sp|P9WFP1|Y2366_MYCTU UPF0053 protein Rv2366c OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2366c PE=1 SV=1

MTGYYQLGSIVLIGLGLFAAIDAAISTVSPARVDELVRDQRPAGSLRKMADRPRYVNLVLLRTSCEITATAL
LVVFIRYHFSMVWGLYLAAGIMVLASFVVVGVGPRTLGRQNAYSISLATALPLRLISWLLMPISRLVLLGNALTP
GRGFRNGPFASEIELREVVDLAQQRGVVAADERRMIESVFELGDTAPREVMVPRTEMIWIESDKTAGQAMTL
AVRSGHSRIPVIGENVDDIVGVVYLKDLVEQTFCSTNGGRETTRVARVMRPAVFPDPSKPLDALLREMQRDRNH
MALLVDEYGAIAGLVSIEDVLEEIVGEIADEYDQAETAPVEDLGDKRFRVSARLPIEDVGEYGVFEFDDLDVDTV
GGLLALGLRVPPLGAEVISHGLRLHAEGGTDHRGRVTRIGTVLLSPAEPDGADEEADHPG

>sp|O53176|Y2449_MYCTU Putative trans-acting enoyl reductase Rv2449c OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2449c PE=1 SV=3

MTATPREFDIVLYGATGFVGLKTAEYLARAGGDARIALAGRSTQRLAVREALGESAQTPILTADASLPSTLQA
MAARAQVVVTVGPYTRYGLPLVAACAAAGTDYADLTGEPMFMNRNSIDLYHKQAADTGARIVHACGFDSVPS
DLSVYALYHAAREDGAGELDTNVCVRSFKGGFSGGTIASMLEVLSTASNDPDARRQLSDPYMLSPDRGAPEL
GPQPDLPSSRRRLAPELAGVWTAGFIMAPTNRIVRRSNALLDWAYGRRFRYSETMSVGSVTLAPVSVVVG
GGVGNAMFGLASRYIRLLPRGLVKRVVPGTGPASAAARERGGYRIETYTTTTTGARYLARMAQDGDGPYKAT
SVLLGECGLALALDRDKLSDMRGVLTAAAMGDALLERLPAAGVSLQTTTLAS

>sp|P9WJX1|Y2456_MYCTU Uncharacterized MFS-type transporter Rv2456c OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2456c PE=1 SV=1

MSGTVVAVPPRVARALDLLNFSADVRDGLPYSIYLLIHDWDQASIGFVMAVGGIAAIVAQTPIGALVDRTT
AKRALVAVAVLVTAAVAMPLFAGLYSISVLQAVTGIASSVFAPALAAITLGAVGPQFFARRIGRNEAFNHAGN
ASAAGATGALAYFFGPVVVFWVLAGMALISVLATLRIPPDAVDHDLARGMDHAPGEPHPQPSRFTVLAHNREL
VIFGAAVAVFHANAAMLPLVGELLALHNRDEGTALMSSCIVAAQVVMVPVAVVVGTRADAWGRKPIFLVGF
VLTARGFLYTLSDNSYWLGVQQLDGGIGAGIFGALFPLVVDVTHGTGHFNISLGAVTATGIGAALSNLVAGWI

VVVAGYDAAFMSL GALAGAGFLLYLVAMPETVDS DVRVRSRPTLGGK

>sp|P9WLA1|Y2560_MYCTU Uncharacterized protein Rv2560 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2560 PE=1 SV=1
MSQPPEHPGNPADPQGGNQGAGSYPPPGYGAPPPPGYGGPPPGTYLPPGYNAPPPPGYGGPPPGPPPGYP
THLQSSGFSVGD AISWSWNRFTQNAVTLVVPVLAYAVALA AVIGATAGLVVALSDRATTAYTNTSGVSSSEVDIT
MTPAAGIVMFLGYIALFALVLYMHAGILTGCLDIADGKPVTIATFFRPRNLGLVLTGLLIVAVTFIGGLLCVIPGLIF
GFVAQFAVAFVDRSTSPIDSVKASIE TVGSNIGGSVLSWLAQLTAVLVGELLCFVGMLIGIPVAALIHVYTYRKLKLS
GGQVVEAVRPAAPPVGVWPPGPQLA

>sp|P9WL89|Y2571_MYCTU Uncharacterized protein Rv2571c OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2571c PE=1 SV=1
MSASLLVRTACGGRAVAQRLRTVLWPITQTSV VAGLAWYLTHDVFNHPQAFFAPISAVVCMSATNVLRARRAQ
QMIVGVALGIVLGAGVHALLGSGPIAMGVVVFIALSVAVLCARGLVAQGLMFINQAAVSAVLVLFASNGSVVF
ERLFDALVGGGLAIVFSILLFPDPVVMLCSARADVLA AVRDILAELVNTVSDPTSAPPDWPM AAADRLHQQLN
GLIEVRANAAMVARRAPRRWGV RSTVRDLQQA VYLALLVSSVHLARTIAGPGGDKLP TPVHAVLTDLAAGT
GLADADPTAANEHAAAARATASTLQSAACGSNEVVRADIVQACVTDLQRVIERPGPSGMSA

>sp|P9WL85|Y2575_MYCTU Uncharacterized protein Rv2575 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2575 PE=1 SV=1
MTFNEGVQIDTSTSTSGSGGRR LAIGGGLGLLVVVAMLLGVDPGGVLSQQPLDTRDHVAPGFDLSQCR
TGADANRFVQCRVVATGNSVDAVWKPLLPGYTRPHMRLFSGQVGTGCGPASSEVGPFPYCPVDKTAYFD TDF
QVLVTQFGSSGPF AE EYVVAHEYGHVQNL LGLVGRAQQGAQGAAGSGVRTELQADCYAGVWAYYASTVK
QESTGVPYLEPLSDKDIQDALAAAAAVGDDRIQQQTTRTNPETWTHGSAAQRQKWFTVGYQTGDPNICDTF
SAADLG

>sp|P9WL83|Y2576_MYCTU Uncharacterized protein Rv2576c OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2576c PE=1 SV=1
MPAGVGNASGSVLDMTSVRTVPSAVALVTFAGAALS GVIPAIARADPVGHQVITYVT TTTSDLMANIRYMSAD
PPSMAAFNADSSKYMITLHTPIAGGQPLVYTATLANPSQWAIVTASGGLRVNPEFHCEIVVDGQVVVSQDGGG
GVQCSTRPW

>sp|P9WL77|Y2585_MYCTU Uncharacterized lipoprotein Rv2585c OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2585c PE=1 SV=1
MAPRRRRHTRIAGLRVVGATLVAATTLTACSGSAAAQIDYVVDGALVYNTNTVIGAASAGAQA FARTLTGFG
YHGPDGGQV VADRDFGTVSVVEGSPLILDYQISDDAVYSDGRPVTCDDLVLAWAAQSGRFPGFDAATQAGYVDI
ANIECTAGQKKARVSFIPDRSVVDHSQLFTATSLMP SHVIADQLHIDVTAALLSNNVSAVEQIARLWNSTWDLK
PGRSHDEVRSRFPSSGPYKIESVLDDGAVVLVANDRWWGTKAITKRITVWPQGADIQDRVNNRSVDVVDVAA
GSSGSLVTPDSYQRTDYP SAGIEQLIFAPQGS LAQSRRRALALCVPRDAIARDAGVPIANSRLSPATDDALTDAD
GAAEARQFGRVDPAAARDALGGTPLTVRIGYGRPNARLAATIGTIADACAPAGITVSDVTVDTPGPQALRDGKI
DVLLASTGGATGSGSSGSCAMDAYDLHSGNGN NLSGYANAQIDGIISALAVSADPAERARLLAEAAPVLWDEM
PTLPLYRQQRLLMSTKMYAVSRNPTRWGAGWNMDRWALAR

>sp|P9WL73|Y2597_MYCTU Uncharacterized protein Rv2597 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2597 PE=1 SV=1
MGNLLVVI AVALFIAAIVLVVAIRRPKTPATPGGRRDPLAFDAMPQFGPRQLGPGAIVSHGGIDYVVRGSVTFR
EGPFVWWEHLLEGDTPTWLSVQEDDGRLELAMWVKRTDLGLQPGGQHVIDGVTFQETERGHAGYTTEGT
TGLPAGGEMDYVDCASAGQGADESMLLSFERWAPDMGWEIATGKSVLAGELTVYPAPPVSA

>sp|P9WL69|Y2599_MYCTU Uncharacterized protein Rv2599 OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2599 PE=1 SV=1

MSRNRLFLVAGSLAVAAAVSLISGITLLNRDVGSYIASHYRQESRDVNGTRYLCTGSPKQVATTLVKYQTPAARAS
HTDTEYLRYRNNIVTVGPDGTYPCCIIRVENLSAGYNHGAYVFLGPGFTPGSPSGSGSGSPGGPGGSK

>sp|P9WP07|Y2637_MYCTU Uncharacterized membrane protein Rv2637 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2637 PE=1 SV=1

MDVEALLQSIPPLMVYLVVGAVVGIESLGIPLPGEIVLVSAAVLSHPPELAVNPIGVGGAAVIGAVVGDSDIGYSIGR
RFGLPLFDRLGRRFPKHFPGHVALAERLFNRWGVRAVFLGRFIALLRIFAGPLAGALKMPYPRFLAANVTGGIC
WAGGTTALVYFAGMAAQHWLERFSWIALVIAVIAGITAAILLRERTSRAIAEAEHCRKAGTTAA

>sp|P9WPD7|Y2685_MYCTU Uncharacterized transporter Rv2685 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2685 PE=1 SV=1

MSIIAIVFVAGYALIASDRVSKTRVALTCAAIMVGVAGIVGSDDFYSHEAGIDWDVIFLLGMMIIVSVLRHTGV
FEYVAIWAVKRANAAPLRIMILLVLTALGSALLDNVTTVLLIAPVTLVCDRLGVNSTPFLVAEVFASNVGGAATL
VGDPPNIIASRAGLTFNDFLIHMAPAVLVVMIALIGLLPWLLGSVTAEPDRVADVLSLNEREAIHDRGLLIKCGVV
LVLVFAAFIAHPVLHIQPSLVALLGAGVLRFSGLERSDYSSVEWDTLLFFAGLFVMVGVKTVVEQLARAAT
ELTGGNELLTVGLILGISAPVSGIIDNIPYVATMTPIVELVAAMPGHVHPDTFWWALALSADFGGNTLTAASA
NVVMLGIARRSGTPISFWKFRKGAVVTAVSLVSAVYLWLRVYFVFG

>sp|P9WG93|Y2723_MYCTU Uncharacterized membrane protein Rv2723 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2723 PE=1 SV=1

MGASGLVWTLTIVLIAGLMLVDYVLHVRKTHVPTLRQAVIQSATFVGIAILFGIAVVVFGGSELAVEYFACYLTDE
ALSVDNLFVFLVISSFGVPRLAQKQVLLFGIAFALVTRTGFIIVGAALIENFNNSAFYLFGLVLLVMAGNLARPTGLE
SRDAETLKRSVIIRLADRFLRTSQDYNGDRLFTVSNNKRMMPDLLVMIAVGGTDILFAFDSIPALFGLTQNVYLV
FAATAFSLGLRQLYFLIDGLLDRLVYLSYGLAVILGFIGVKLMLEALHDNKIPFINGGKPVPTVEVSTTQSLTVIIIVLL
ITTAASFWSARGRAQNAMARARRYATAYLDLHYETESAERDKIFTALLAAERQINTLPTKYRMQPGQDDDLMT
LLCRAHAARDAHM

>sp|P9WJW7|Y2994_MYCTU Uncharacterized MFS-type transporter Rv2994 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv2994 PE=1 SV=1

MSRDPTGVGARWAIMIVSLGVTASSFLFINGVAFLIPRELNARGTPLSHAGLLASMPVSWGLVVTMFAWGYLLD
HVGERMVMVAVGSALTAAYAAASVHSLWIGVFLFLLGMAAGGCNSAGGRLVSGWFPPQQRGLAMGIRQ
TAQPLGIASGALVIPELAERGVHAGLMFPAVVCTLAASVSVLGVDPKRKSRKASEQELASPYRGSSILWRIHAA
SALLMMPQTVTVTFMLVWLNHHGWSVAQAGVLTISQLLALGRVAVGRWSDHVGSRMRPVRLIAAAAAA
TLFLAAVDNEGSRYDVLMLIAISVIAVLDNGLEATAITEYAGPYWVSGRALGIQNTTQRLMAAAGPPLFGSLITTA
AYPTAWALCGVFPAAVPLVPVRLPPGLETRARRQSVRRHRWWQAVRCHAWPNGPRRPPGPPGQPRRVRQ
GGTAITPPT

>sp|P9WKZ9|Y3395_MYCTU Uncharacterized protein Rv3395c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv3395c PE=1 SV=1

MTAAFASDQRENGAEQLESRRQMALLSEKVSGGPSRSGDLVPAGPVSLPPGTGVVLSGARSLLSMVASVTA
AGGNAAIVGQPDIGLLAAVEMGADLSRLAVIPDPGTDPVEVAVLIDGMDLVVGLGGRRVTRARARAVVAR
ARQKGTLLVTDGDWQGVSTRLAARVCGYEITPALRGVPTPGLGRISGVRLQINGRGR

>sp|P9WP09|Y364_MYCTU Uncharacterized membrane protein Rv0364 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv0364 PE=1 SV=1

MSTAVTAMPDILDPMYWLGVANGVFGSAVLPGLIIVFIETGLLFPPLPGESLLFTGGLLSASPAPPVTIGVLAPCVA
LVAVLGDQYAYFIGRRIGPALFKKEDSRFFKHYVTESHAFFEKYGKWTIILARFVPIARTFVPIAGVSYMRYPVFL
GFDIVGGVAWGAGVTLAGYFLGSVPFVHMNFQLIILAIVFVSLPALVSAARVYRARRNAPQSDPDPLVPE

>sp|P9WMT3|Y3659_MYCTU Putative conjugal transfer protein Rv3659c OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv3659c PE=2 SV=1

MLGDTEVLANLRVLQTELTGAGILEPLLSADGTTDLVLTAPDSVWVDDGNGLRRSQIRFADES AVRRLAQRLLA
AAGRRLDDAQPWVDGQLTGIGVGGFAVRLHAVLPPVATQGTCLSLRVL RPATQDLAALAAAG AIDPAAAAALVA
DIVTARLAFVLCGGTGAGKTTLLAAMLGAVSPDERIVCVEDAAELAPRHPHLV KLVARRANVEGIGEVTVRQLVR
QALRMRPDRIVVGEVRGAEVVDLLAALNTGHEGGAGTVHANNPGEV PARMEALGALGGLDRAALHSQLAA
AVQVLLHVARDRAGRRRLAEIAVLRQAEGRVQAVTVWHADRGMSDDAAALHDLLRSRASA

>sp|O69659|Y3691_MYCTU Uncharacterized membrane protein Rv3691 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv3691 PE=1 SV=4

MGAGVPVIPTRLATVRRRRPWRGVLLTAAVAVVASIGTYLTAPRPGGAMAPASTSSTGGHALATLLGNHGV
VVADSIADVEAAARPDSL LLAQ TQYLVDNALLDRLAKAPGDLLVAPTSRTRTALTPQLRIAAASPFNSQPNCTL
REANRAGSVQWGPSDTYQATGDLVLTSCYGGALVRFRAEGRTITVVGSSNFMTNGGLLPAGNAALAMNLAG
NRPRLVWYAPDHIEGEMSSPSSLDLIPENVHWTIWQLWLVLVLLVALWKRRIGPLVAEELPVVIRASETVEGR
GRLYRSRRARDRAADALRTATLQRLRPRLGVGAGAPAPAVVTIAQRSKADPPFVAYHLFGPAPATDNDLLQLAR
ALDDIERQVTHS

>sp|O69726|Y3760_MYCTU Uncharacterized membrane protein Rv3760 OS=Mycobacterium
tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv3760 PE=1 SV=4

MTSNPSSSADQPLSGTTVPGSVPGKAPEEPPVKFTRAAAVWSALIVGFLILILLIFIAQNTASAQFAFFGWRWS
LPLGVAILLA AVGGGLITVFAGTARILQLRRAAKKTHAAALR

>sp|P9WMS9|Y3789_MYCTU Uncharacterized protein Rv3789 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv3789 PE=1 SV=1

MRFVVTGGLAGIVDFGLYVVLYKVAGLQVDLSKAISFIVGTITAYLINRRWTFQAEPSTARFVAVMLLYGITFAVQV
GLNHLCLALLHYRAWAIPVAFVIAQGTATVINFIVQRAVIFRIR

>sp|P9WKV7|Y479_MYCTU Uncharacterized protein Rv0479c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv0479c PE=1 SV=1

MTNPQGGPPNDPSPWARPGDQGPLARPPASSEASTGRLRPGEPAGHIQEPVSPPTQPEQQPQTEHLAASHAH
TRRSGRQAAHQAWDPTGLLAAQEEPAAVKTKRRARRDPLTVFLVLIIVFSLVLAGLIGGELYARHVANSKVAQA
VACVVKDQATASFGVAPLLLWQVATRHFTNISVETAGNQIRDAKGMQIKLTIQNVRLKNTPNSRGTIGALDATIT
WSSEGIKESVQNAIPILGAFVTSSVVTHPADGTVELKGLLNNITAKPIVAGKGLELQIINFNTLGFSLPKETVQSTLN
EFTSSLTKNYPLGIHADSVQVTSTGVVSRFSTRDAAIPTGIQNPCFSHI

>sp|P9WKU3|Y497_MYCTU Uncharacterized protein Rv0497 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv0497 PE=1 SV=1

MTGPHPETESSGNRQISVAELLARQGVGTGAPARRRRRRRGSDAITVAELTGEIPIIRDH HHAGPDAHASQSP
AANGRVQVGEAAPQSPAEPVAEQVAEEPTRTVYWSQPEPRWPKSPPQDRRESGPELSEYPRPLRH THSDRAP
AGPPSGAEHMSPDPVEHYPDLWVDVLDTEVGEAEAE TEVREAQPGRGERHAAAAAGTDVEGDGAAEARV
ARRALDVVPTLWRGALVVLQ SILAVAFGAGLFIAFDQLWRWNSIVALVLSVMVILGLVSVRAVRKTEDIASTLIA
VAVGALITLGPLALLQSG

>sp|A5TZU0|Y567_MYCTA Uncharacterized protein MRA_0567 OS=Mycobacterium tuberculosis
(strain ATCC 25177 / H37Ra) GN=MRA_0567 PE=1 SV=1

MSTVLTYIRAVDIYEHMTESLDLEFESAYRGESVAFGEGVRPPWSIGEPQPELAALIVQGGKFRGDVLDVGCGEAA
ISLALAERGH TTVGLDLSPAAVELARHEAAKRLANASFEVADASSFTGYDGRFDTIVDSTLFHSMPVESREGYL
QSIVRAAAPGASYFVLVFDRAA IPEGPINA VTEDELRAAVSKYWIIDEIKPARLYARFPAGFAGMPALLDIREPNG
LQSIGGWLLSAHLG

>sp|P9WFS5|Y625_MYCTU TVP38/TMEM64 family membrane protein Rv0625c
OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=Rv0625c PE=1 SV=1

MSTHNSAPTSSRRRHIVRLVVFAGFLVGMFYLVAATDVIDVA AVRGAVSATGPAAPLTYVVVSAVLGALFVPGPI

LAASSGLLFGPLVGVFVTLGATVGTAVVASLVGRRAGRASARALLGGERADRTDALIERCGLWAVVGQRFVPGIS
DAFASYAFGTFGVPLWQMAVGAFIGSAPRAFAYTALGAAIGDRSPLLASCAIAVWCVTAIIGAFARHGYRQWR
AHARGDGADGGVEDPDREVGAR

>sp|P9WKS7|Y628_MYCTU Uncharacterized protein Rv0628c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv0628c PE=1 SV=1

MRIGVGVSTAPDVRRAAAEAAAHAAREELAGGTPALAVLLGSRSHDQAVDLLAAVQASVEPAALIGCVAQGIV
AGRHELENEPAVAVWLASGPPAETFHLDFVRTGSGALITGYRFDRTAHDHLHLLLPDPYSFPSNLLIEHLNTDLPGT
TVVGGVSVSGRRRGRDTRLFRDRDVLTSGLVGVRLPGAHSVSVVSQGCRPIGEPYIVTGADGAVITELGGRPLH
RLREIVLGMAPDEQELVSRGLQIGIVVDEHLAVPGQGDFLIRGLLGADPTTGAIGIGEVVEVGATVQFQVRDAA
AADKDLRLAVERAAAELPGPPVGGLLFTCNRRGRMMFGVTDHDASTIEDLLGGIPLAGFFAAGEIGPVAGHNA
LHGFTASMAFVD

>sp|P9WKR5|Y876_MYCTU Uncharacterized protein Rv0876c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv0876c PE=1 SV=1

MSGRRGDHPGRMAPTPGRRTRNGSVNGHPGMANYPPDDANYRRSRRPPMPSANRYLPPLGEQPEPERSR
VPPRTTRAGERITVTRAAAMRSREMGSRMYLLVHRAATADGADKSGLTALTWPVMANFAVDSAMAVALANT
LFFAAASGESKSRVALYLLITIAFVIAPIGLPALDRLQHRRVALALSFGLRTALAVVLIMNYDGATGSFSPSWVLY
PCALAMMVFSKSFSVLSAVTPRVMPPTIDLVRVNSRLTVFLLGGTIAGGAIAGVEFVCTHLFQLPGALFVVV
AITIAGASLSMRIPRWVEVTSGEVPATLSYHRDRGRLLRRRWPEEVKNLGGTLRQPLGRNIITSLWGNCTIKVMV
GFLFLYPAFVAKAHEANGWVQLGMLGLIGAAAAGNFAGNFTSARLQLGRPAVLVVRCTVLVTVLAIAAVAGS
LAATAIATLITAGSSAIAKASLDASLQHDLPESRASGFRSESTLQLAWVLGGAVGVLVYTELWVGFTAVSALLIL
GLAQTIVSFRGDSLIPGLGGNRPVMAEQETTRRGAAPQ

>sp|P9WKQ5|Y885_MYCTU Uncharacterized protein Rv0885 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv0885 PE=1 SV=1

MDRTRIVRRWRRNMDVADDAEYVEMLATLSEGSVRRNFNPYTDIDWESPEFAVTDNDPRWILPATDPLGRH
PWYQAQSRERQIEIGMWRQANVAKVGLHFESILIRGLMNYTFWMPNGSPEYRYCLHESVEECNHTMMFQE
MVNRVGADVPGLPRRLRWVSPLVPLVAGPLPVAFFIGVLAGEEPIDHTQKNVLRGKSLHPIMERVMSIHVAEE
ARHISFAHEYLRKRLPRLTRMQRFWISLYFPLTMRSLCNAIVVPPKAFWEEFDIPREVKKELFFGSPESRKWLCD
MFADARMLAHDGTGLMNPIARLVWRLCKIDGKPSRYRSEPQRQHAAAPAA

>sp|P9WKQ1|Y888_MYCTU Uncharacterized protein Rv0888 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv0888 PE=1 SV=1

MDYAKRIGQV GALAVVLGVAAVTTHAIGSAAPTDSSSSTDSVPDACSPLGGSASSLAAIPGASVPQVGVRQ
VDPGSI PDDL NALIDFLAAVRNGLVPIIENRTPVANPQQVSVPEGGTVGPVRFDACDPDGNRMTFAVRERGA
PGGPQH GIVTVDQRTASFIYTADPGFVGTDTFSVNVSDDTSLHVHGLAGYLGPFHGHDDVATVTVFVGNTPD
TISGDF SMLTYNIAGLPFLSSAILPRFFYTKEIGKRLNAYVANVQEDFAYHQFLIKKSKMPSQTPPEPPTLLWPI
GVPFSDGLNTLSEFKVQLDRQTWYECTSDNCLTKGFTYSQMRLPGGDTV DVYNLHTNTGGGPPTNANLAQ
VANYIQNSAGRAVIVTGDFNARYSDDQSALLQFAQVNGLTDAAVQVEHGPTT PPFAPT CMVGN ECELLDKI
FYRSGQGVTLQAVSYGNEAPKFFNSKGEPLSDHSPAVVGFHYVADNVAVR

>sp|P9WKP7|Y897_MYCTU Uncharacterized protein Rv0897c OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv0897c PE=1 SV=1

MSDHDRDFDVVVVGGGHNGLVAAAYLARAGLRVRLLELAQTGGAAVSIQAFDGV E VALSRYSYLV SLLPSRIV
ADLGAPVRLARRPFSSYTPAPATAGRSGLLIGPTGEPRAAH LAAIGAAPDAHGF AAFYRRCRLVTARLWPTLIEPL
RTREQARRDIVEYGGHEAAA WQAMVDEPIGHAIAGAVANDLLRGIATDALIGTFARMHEPSLMQNICFLYH
LVGGGTGVVHVPIGGMGSVTSALATAAARHGAEIVTGADV FALDPDGT VRYHSDGSDGAEHLVRGRFVLVGV
TPAVLASLLGEPVAALPGAQVKVNMVVRRLPRLRDDS VTPQQAFAGTFHVNETWSQLDAAYSQAASGRLPD

PLPCEAYCHSLTDPSILSARLRDAGAQLTVFGLHTPHSVFGDTEGLAERLTAAVLASLNSVLAEPIQDVLWTDQAQ
SKPCIETTTTLDLQRTLGMTGGNIFHGALSWPFFADNDDPLDTPARQWGVATDHERIMLCGSGARRGGAVSGI
GGHNAAMAVLACLASRRKSP

>sp|P9WKN3|Y955_MYCTU Uncharacterized protein Rv0955 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv0955 PE=1 SV=1

MNRVSASADDRAAGARPARDLVRVAFGPGVVALGIIAAVTLQLLIANSMDTGAWGAIASMWLGVHLVPISIG
GRALGVMPLLPVLLMVWATARSTARATSPQSSGLVVRWVVASALGGPLLMAAIALAVIHDASSVTELQTPSAL
RAFTSVLVVHSVGAATGVWSRVGRRALAATALPDWLHDSMRAAAAAGVLALLGLSGVVTAGSLVVHWATMQE
LYGITDSIFGQFSLTVLSVLYAPNVIVGTSIAIVGSSAHIGFATFSSFAVLGGDIPALPILAAAPTPLGPAWVALLIVG
ASSGVAVGQQCARRALPFVAAMAKLLVAAVAGALVMAVLGYGGGGRLGNFGDVGVDGALVGLVLFWFTFV
GWVTVVIAGGISRRPKRLRPAPPVELDADESSPPVDMFDGAASEQPPASVAEDVPPSHDDIANGKAPTADDE
ALPLSDEPPPRAD

>sp|P9WKL7|Y970_MYCTU Uncharacterized protein Rv0970 OS=Mycobacterium tuberculosis
(strain ATCC 25618 / H37Rv) GN=Rv0970 PE=2 SV=1

MIHDLMLRWVVTGLFVLTAAECGLAIIAKRRPWTLIVNHGLHFAMAVAMAVMAWPWGARVPTTGPAVFLL
AAVWFGATAVVAVRGATATRGLYGYHGLMMLATAWMYAAMNPRLLPVRSCTEYATEPDGSMAMPAMDMTAMN
MPPNSGSPWFSAVNWIGTVGFAVAVFWACRFVMERRQEATQSRLPGSIGQAMMAAGMAMLFFAMLFP
V