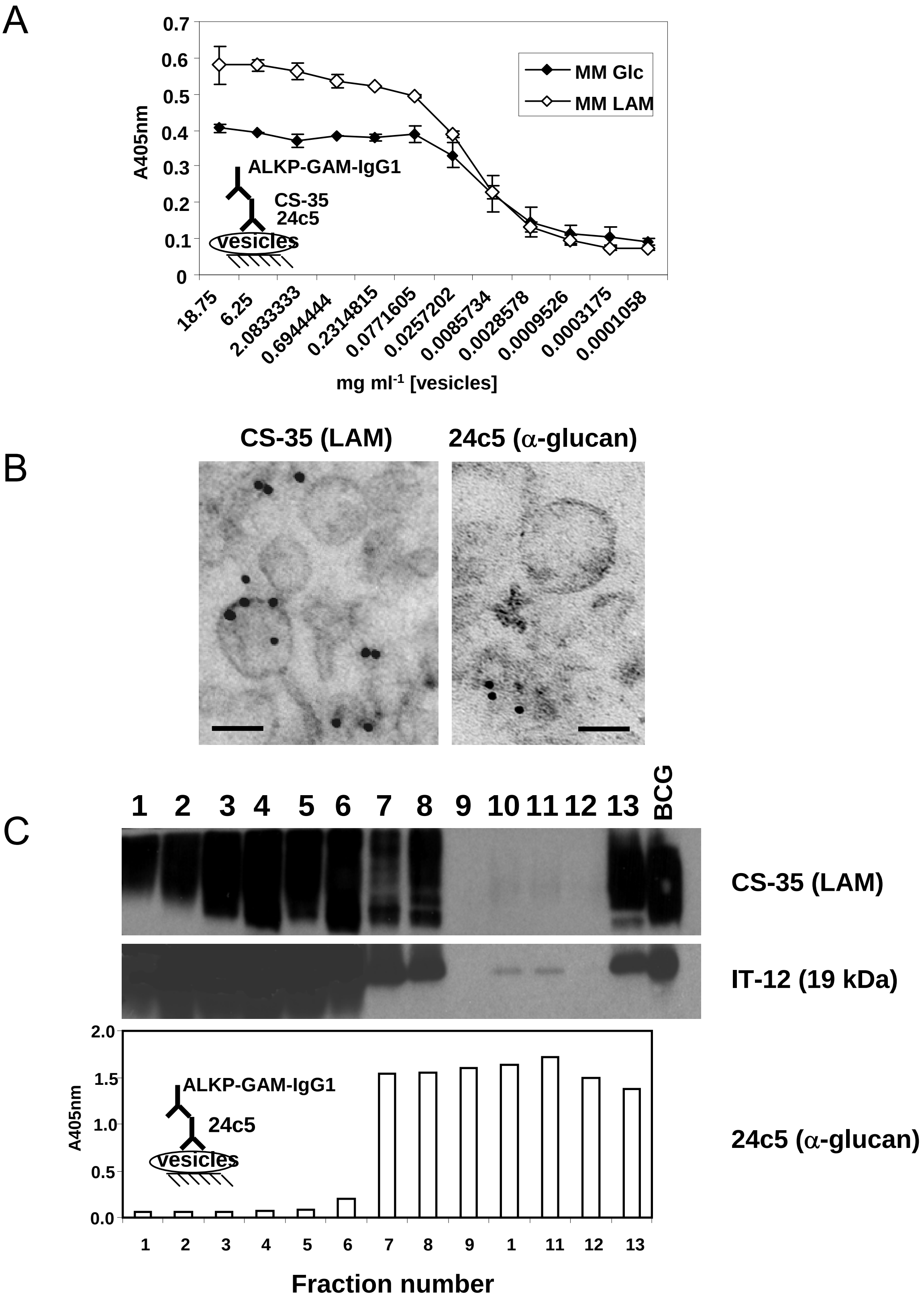
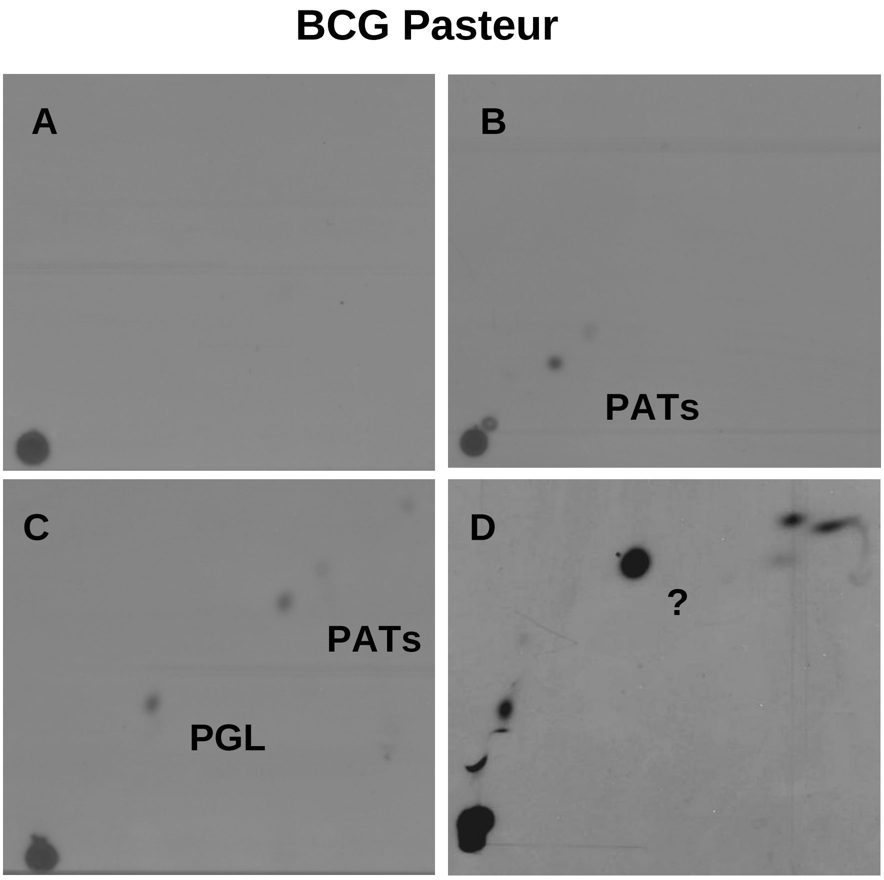
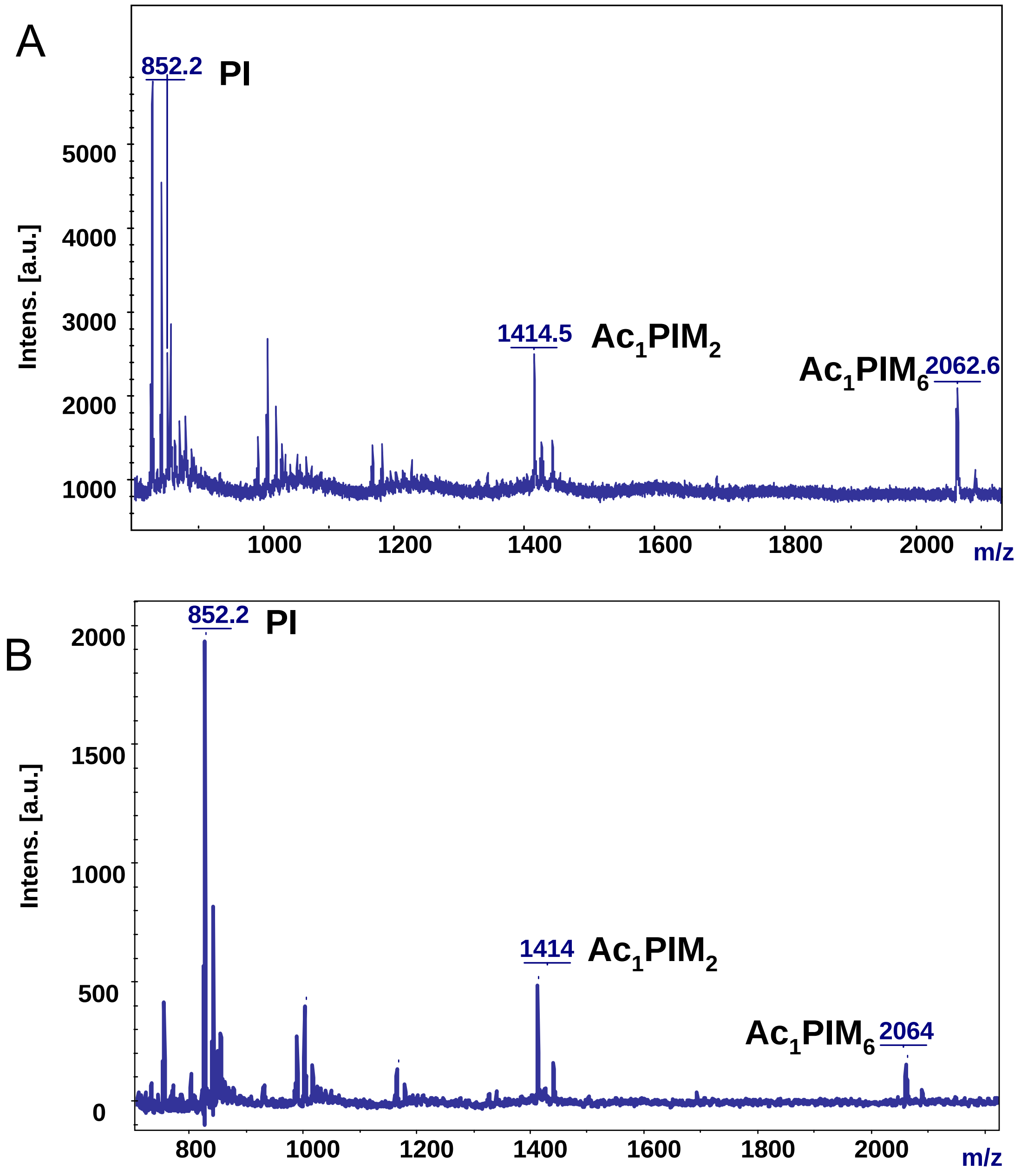


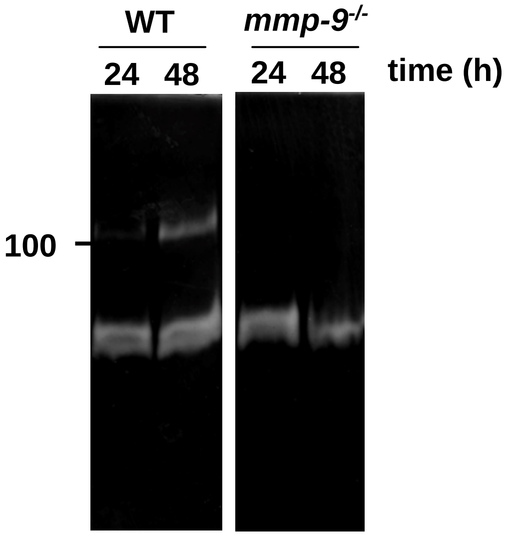
Supplementary Figure 1. Analysis of LAM and α-glucan in vesicle preparations. (A) ELISA of BCG vesicles for LAM and α-glucan, using the monoclonal antibodies CS-35 and 24c5 for LAM and α-glucan, respectively. (B) Thin sections of BCG vesicles Immunolabeled for LAM and α-glucan. Bar 100 nm. (C) Western blot analysis of the fractions of an Optiprep density gradient for LAM and α-glucan.



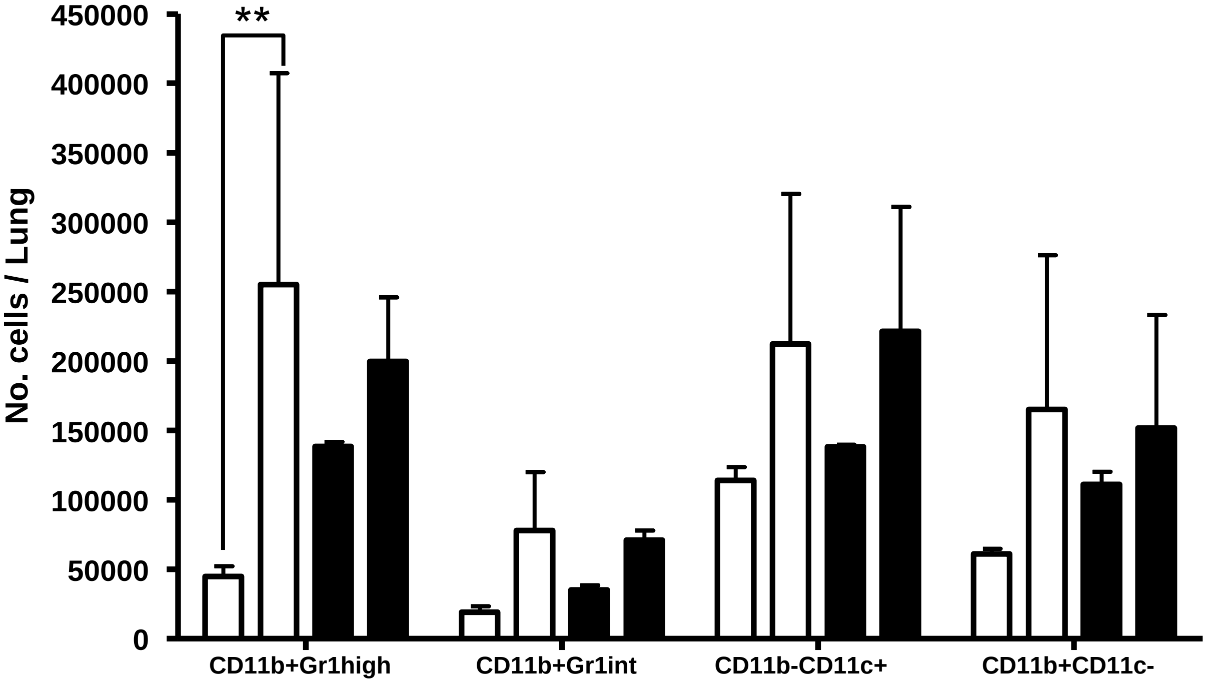
Supplementary Figure 2. 2D-HPTLC analysis of apolar lipids of BCG and *M. tuberculosis* vesicles. Total lipids of vesicles isolated from 14C-acetate-labeled cells were extracted with chloroform: methanol (2:1, vol/vol). Lipid extracts were separated by 2-D TLC by applying an amount of lipids corresponding to 10,000 DPM per TLC plate and by using the solvent systems A-D for separation of apolar lipids. PGL, phenolglycolipid; PAT, poly-acyltrehaloses



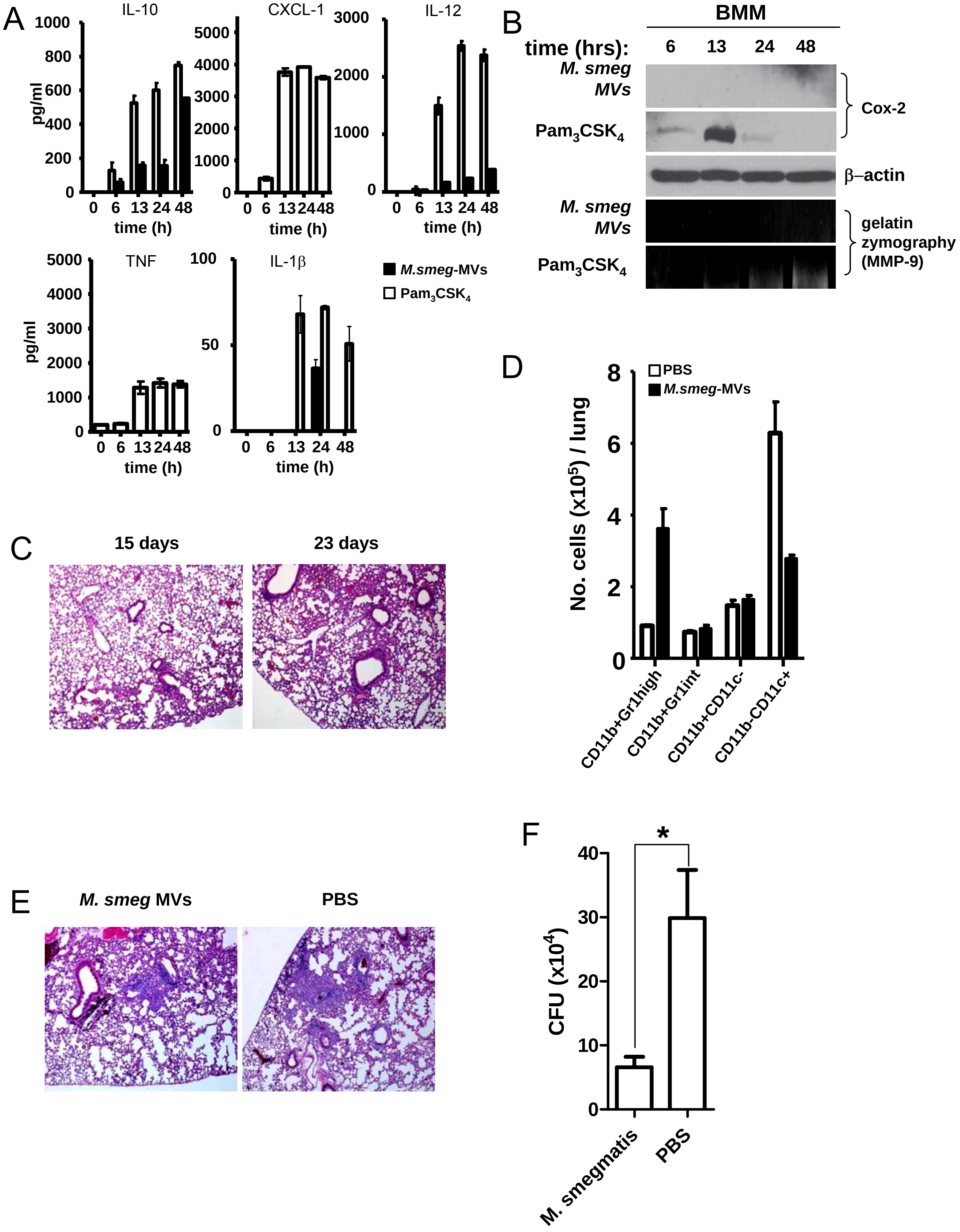
Supplementary Figure 3. MALDI-TOF-MS of BCG and H37Rv vesicles for polar lipid analysis. The various PIM species and their relative abundances were determined by matrix-assisted laser-desorption/ionization time of flight mass spectrometry in the negative mode.



Supplementary Figure 4. Validation of gelatinolytic activity of MMP-9. The levels of MMP-9 activity in culture supernatants from macrophage treated with vesicles were analyzed by zymography after 24 and 48 h. The gelatinolytic activity corresponding to MMP-9 was absent in *mmp9* knockout isolated BMMs.



Supplementary Figure 5. Myeloid cells in the lungs after 23 days. Bar graphs indicate the mean absolute numbers of the different populations of lung cells of WT (open bars) and TLR2-/- (filled bars) after 23 days.


A
IL-10
1000
800
600
400
200
0
pg/ml
0 6 13 24 48
time (h)
CXCL-1
5000
4000
3000
2000
1000
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0 6 13 24 48
time (h)
IL-12
3000
2000
1000
0
0 6 13 24 48
time (h)
TNF
5000
4000
3000
2000
1000
0
pg/ml
0 6 13 24 48
time (h)
IL-1β
100
50
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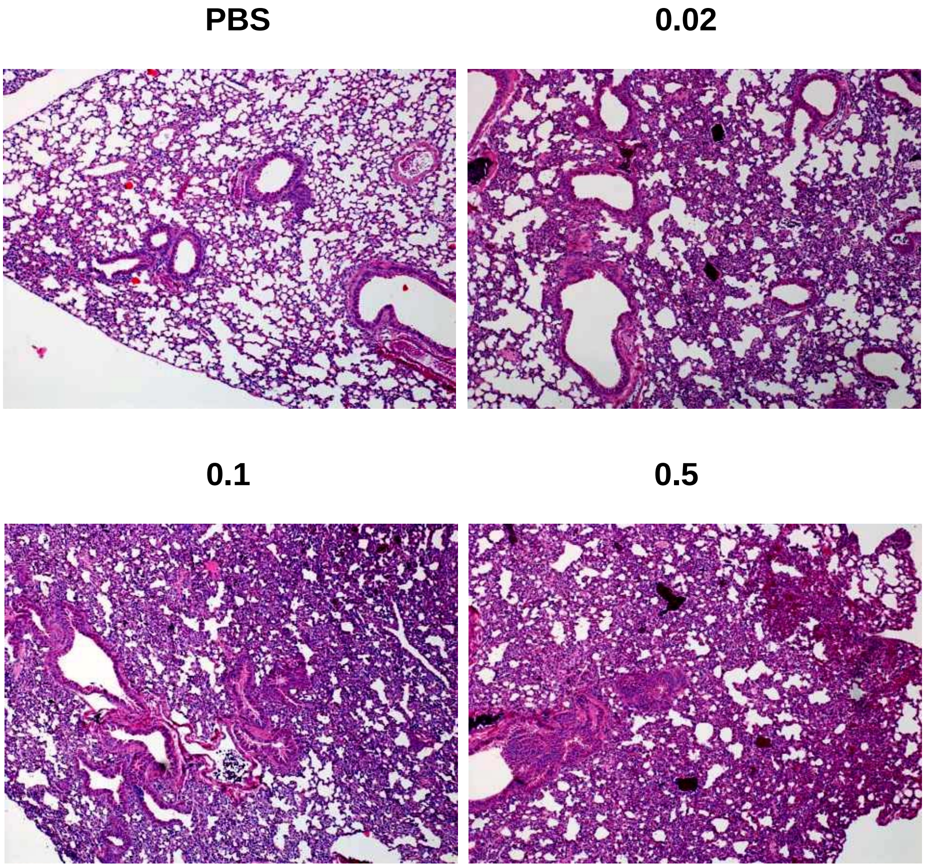
0 6 13 24 48
time (h)
■ M.smeg-MVs
☐ Pam3CSK4
B
BMM
time (hrs): 6 13 24 48
M. smeg MVs
Pam3CSK4
Cox-2
β–actin
M. smeg MVs
Pam3CSK4
gelatin zymography (MMP-9)
C
15 days
23 days
D
☐PBS
■M.smeg-MVs
No. cells (x10^5) / lung
8
6
4
2
0
CD11b+Gr1high
CD11b+Gr1int
CD11b+CD11c-
CD11b-CD11c+
E
M. smeg MVs
PBS
F
*
CFU (x10^4)
40
30
20
10
0
M. smegmatis
PBS

Supplementary Figure 6. Analysis of the response to *M. smegmatis* MVs. Freshly isolated BMM were stimulated with MVs and with Pam3CSK4 *in vitro* (500,000 cells/500 μl of media). Macrophage supernatants and cell lysates were collected at time intervals ranging from 0 to 48 hours after stimulation (X-axes of all graphs indicate time in hours). (A) The supernatants of cultures *M. smegmatis* MVs (black bars) or Pam3CSK4 (white bars) -stimulated macrophages were assayed for cytokines including IL-1β, IL-10, IL-12p70, TNF-α and chemokine CXCL1 by multiplex ELISA (MSD Systems). Cytokines IL-6 and MIP-1a were analyzed by standard ELISA. (B) The levels of Cox-2 and MMP-9 were analyzed by Western blot and zymography, respectively. For Cox-2 analysis lysates were made from BMM cells and collected at the indicated times, ranging from 0 to 48 hours after addition Pam3CSK4 or *M. smegmatis* MVs. For measurement of MMP-9 activity, culture supernatants were collected at the indicated times following stimulation as shown. (C) Analysis of lung pathology in mouse lungs after injection of *M. smegmatis* MVs. Representative images of H&E stained lung sections of intratracheally vesicle treated WT C57BL/6 mice. Lungs were analyzed at 15 and 23 days after treatment. The images are representative of five lungs. The experiment was done twice. (D) Analysis of myeloid cells in the lungs following intratracheal injection of *M. smegmatis* MVs. Bar graphs indicating the mean absolute numbers of the different populations of lung cells of mice treated with PBS (white bars) or *M. smegmatis* MVs (black bars). (E) Representative images of H&E stained lung sections of WT C57BL/6 mice infused with *M.smegmatis* MVs or PBS and challenged with a low dose of H37Rv (50-100 CFUs). Lungs were analyzed at 30 days after the challenge. (F) Colony forming units in lungs of mice receiving the indicated treatments followed by Mtb H37Rv challenge. Analysis was done at day 30 after challenge. The experimental data is representative of two independent experiments.



Supplementary Figure 7. Dose dependent inflammatory response in the lungs after infusion of MVs. Representative images of H&E stained lung sections of intratracheally vesicle treated WT C57BL/6 mice. Lungs were analyzed histologically at 15 days after treatment. The images are representative of five lungs. The experiment was done twice. The number indicates the dilution factor of the MV suspensions that were injected intratracheally.

Supporting table 1. *M. bovis* BCG Pasteur vesicles-associated proteins

Accesion number	Protein name	Unique peptides[a]	Score[b]	TMD[c]	SP[d]	Functional category[e]
gi|31792657	ABC transporter ATP-binding protein	3	223	+	-	cell wall and cell processes
gi|31794087	D-alanyl-D-alanine carboxypeptidase	3	85	-	+	cell wall and cell processes
gi|31792982	hypothetical protein Mb1822 putative ABC transporter	1	68	+	-	cell wall and cell processes
gi|31793701	possible conserved membrane protein	1	73	+	-	cell wall and cell processes
gi|31794764	possible conserved membrane protein	2	122	+	-	cell wall and cell processes
gi|31794976	hypothetical protein Mb3832c	1	125	+	-	cell wall and cell processes
gi|149974	immunogenic protein MPB57	1	60	-	+	cell wall and cell processes
gi|31792158	metal cation transporter P-type ATPase CtpV	2	121	+	-	cell wall and cell processes
gi|31792544	phosphate ABC transporter, phosphate-binding protein	2	96	+	-	cell wall and cell processes
gi|31792229	putative ESAT-6 like protein ESXI (ESAT-6 like protein 1)	3	299	-	-	cell wall and cell processes
gi|121639584	putative membrane-associated serine protease	2	209	-	+	cell wall and cell processes
gi|31794055	soluble secreted antigen MPB53 precursor	1	57	-	+	cell wall and cell processes
gi|31794066	30S ribosomal protein S2	7	501	-	-	information pathways
gi|31791892	30S ribosomal protein S3	3	215	-	-	information pathways
gi|31794634	30S ribosomal protein S4	5	324	-	-	information pathways
gi|31791869	elongation factor Tu	9	566	-	-	information pathways
gi|61224549	alpha-amylase family protein	2	230	-	-	intermediary metabolism and respiration
gi|31793066	bacterioferritin	6	337	-	-	intermediary metabolism and respiration
gi|31795015	bacterioferritin BfrB	5	420	-	-	intermediary metabolism and respiration
gi|31793702	bacterioferritin comigratory protein BCP	1	85	-	-	intermediary metabolism and respiration
gi|31793400	glutamine synthetase GLNA1 (glutamine synthase) (GS-I)	21	911	-	-	intermediary metabolism and respiration
gi|31794841	membrane-associated serine protease	3	133	+	-	intermediary metabolism and respiration
gi|121635956	myo-inositol-1-phosphate synthase INO1	1	67	-	-	intermediary metabolism and respiration
gi|31794220	phosphoserine phosphatase	2	55	+	-	intermediary metabolism and respiration
gi|31791708	thioredoxin protein	1	66	-	+	intermediary metabolism and respiration
gi|31794453	transmembrane carbonic anhydrase	1	69	+	-	intermediary metabolism and respiration
gi|31794978	secreted antigen 85-A FBPA (fibronectin-binding protein A)	3	119	-	-	lipid metabolism
gi|121637790	secreted antigen 85-B	2	114	-	-	lipid metabolism
gi|31792330	acetyl-CoA acetyltransferase	2	164	-	-	lipid metabolism
gi|31792287	acyl-[acyl-carrier protein] desaturase	2	177	-	-	lipid metabolism
gi|31792542	acyl-CoA dehydrogenase	2	147	-	-	lipid metabolism
gi|31791332	acyl-CoA dehydrogenase FADE2	1	74	-	-	lipid metabolism
gi|31794454	acyl-CoA dehydrogenase FADE25	1	55	-	-	lipid metabolism
gi|31791393	acyl-CoA dehydrogenase FADE3	1	78	-	-	lipid metabolism
gi|31791408	acyl-CoA dehydrogenase FADE4	6	335	-	-	lipid metabolism
gi|31791422	acyl-CoA dehydrogenase fadE5	6	365	-	-	lipid metabolism

gi|31791576	acyl-CoA dehydrogenase FADE7	2	145	-	-	lipid metabolism
gi|224992213	acyl-CoA synthetase	5	237	+	-	lipid metabolism
gi|31793705	fatty acid synthase	4	248	-	-	lipid metabolism
gi|31792048	fatty oxidation protein fadB	5	298	-	-	lipid metabolism
gi|31793810	cytoplasmic protein, 35 kDa	2	236	-	-	unknown
gi|31791294	possible conserved membrane protein	1	66	+	-	unknown
gi|31791987	hypothetical protein Mb0822c	3	120	-	+	unknown
gi|31792157	hypothetical protein Mb0993	2	146	-	+	unknown
gi|31793706	hypothetical protein Mb2554c	1	125	-	+	unknown
gi|31794889	putative secreted protein	3	220	-	+	unknown
gi|31794904	hypothetical protein Mb3759	1	66	+	+	unknown
gi|224989193	29 kDa antigen	11	728	-	-	Virulence, detoxification, adaptation
gi|620092	catalase	3	150	-	-	Virulence, detoxification, adaptation
gi|31791618	chaperonin GroEL	5	305	-	+	Virulence, detoxification, adaptation
gi|31793477	heat shock protein 90	2	115	-	-	Virulence, detoxification, adaptation
gi|31792746	hypothetical protein Mb1587 similar to VapC 11 toxin	1	56	-	-	Virulence, detoxification, adaptation
gi|31791528	molecular chaperone DnaK	2	122	-	-	Virulence, detoxification, adaptation

a, Proteins identified with only one peptide were inspected manually

b, Cut-off values for Mascot scores of peptides and proteins were set to 45 ($p < 0.05$) and 51 ($p < 0.01$), respectively, for considering them as being accurate identifications

c, Prediction of Transmembrane domains with TMHMM v2.0 (http://www.cbs.dtu.dk/services/TMHMM)

d, Prediction of signal peptide with SignalP v3.0 (http://www.cbs.dtu.dk/services/SignalP)

e, Functional category as in Tuberculist v2.3 (http://tuberculist.epfl.ch)

Supporting table 2. *M. tuberculosis* H37Rv vesicles-associated proteins

Accesion number	Protein name	Mw (kDa)	unique peptides[a]	Score[b]	TMD[c]	SP[d]	Functional category[e]
gi|82408083	Putative Penicillin-Binding Protein Homolog	28.5	3	123	-	+	cell wall and cell processes
gi|15609121	cutinase precursor CFP21	22	1	104	-	+	cell wall and cell processes
gi|15842454	D-alanyl-D-alanine carboxypeptidase	30	3	164	-	+	cell wall and cell processes
gi|7476904	hypothetical protein Rv1792, putative ESAT-6 like protein EsxM	11	3	128	-	-	cell wall and cell processes
gi|15610173	hypothetical protein Rv3036c, probable secreted protein MPT64	24.6	3	133	-	+	cell wall and cell processes
gi|15610752	Esx-1 secretion-associated protein A, EspA	40	2	187	-	-	cell wall and cell processes
gi|15609063	immunogenic protein MPT63 (antigen MPT63/MPB63)	16.5	2	79	-	+	cell wall and cell processes
gi|15609117	immunogenic protein MPT64 (antigen MPT64/MPB64)	25.1	1	67	-	+	cell wall and cell processes
gi|15213986	iron-regulated heparin binding hemagglutinin hbhA (adhesin)	21.5	1	67	-	-	cell wall and cell processes
gi|15840357	phosphate ABC transporter, phosphate-binding protein	38.4	5	256	+	-	cell wall and cell processes
gi|15609483	putative ESAT-6 like protein ESXO (ESAT-6 like protein 6)	10	2	108	-	-	cell wall and cell processes
gi|15610015	soluble secreted antigen MPT53 precursor	18.5	1	81	-	+	cell wall and cell processes
gi|15611010	10 kDa culture filtrate antigen EsxB	10.8	4	306	-	-	cell wall and cell processes
gi|15610594	30S ribosomal protein S4	15.5	3	175	-	-	information pathways
gi|15607850	30S ribosomal protein S17	14.8	2	104	-	-	information pathways
gi|15607847	30S ribosomal protein S3	30.1	6	241	-	-	information pathways
gi|15607861	30S ribosomal protein S5	22.9	3	104	-	-	information pathways
gi|15607825	elongation factor Tu	44.4	3	203	-	-	information pathways
gi|15840782	alpha-amylase family protein 1	83.2	2	150	-	-	intermediary metabolism and respiration
gi|15609013	bacterioferritin	18.4	3	122	-	-	intermediary metabolism and respiration
gi|15610977	bacterioferritin BfrB	20.4	4	160	-	-	intermediary metabolism and respiration
gi|15841312	beta-1,3-glucanase precursor	32.3	1	58	-	+	intermediary metabolism and respiration
gi|15609357	glutamine synthetase GLNA1 (glutamine synthase) (GS-I)	53.7	14	677	-	-	intermediary metabolism and respiration
gi|15610807	membrane-associated serine protease	40.8	4	299	+	-	intermediary metabolism and respiration
gi|167967754	putative beta-glucanase	31	2	109	-	+	intermediary metabolism and respiration
gi|15841792	serine esterase	22.8	2	117	-	-	intermediary metabolism and respiration
gi|15607267	serine protease PepA	34.9	1	71	-	+	intermediary metabolism and respiration
gi|48828	antigen 85-C	36.8	2	166	-	-	lipid methabolism
gi|15610940	secreted antigen 85-A FBPA (Mycolyl transferase 85A)	35.8	3	171	-	+	lipid methabolism
gi|15842284	cytoplasmic protein, 35 kDa	29.2	1	54	-	-	unknown
gi|15607939	hypothetical protein Rv0799c	36.1	2	96	+	-	unknown
gi|15607971	hypothetical protein Rv0831c	30.2	4	213	-	-	unknown
gi|15609760	hypothetical protein Rv2623	31.7	1	69	-	-	unknown
gi|15610305	hypothetical protein Rv3169	41.9	1	95	-	-	unknown
gi|15610708	hypothetical protein Rv3572	19	2	60	-	+	unknown
gi|15610853	hypothetical protein Rv3717	24.9	2	96	-	+	unknown
gi|15841951	PPE family protein	39.4	1	75	-	+	unknown

gi|2190473	29 kDa antigen	28.9	4	233	-	-	virulence, detoxification, adaptation
gi|488436	catalase	80.7	6	365	-	-	virulence, detoxification, adaptation
gi|15607581	chaperonin GroEL	56.7	8	497	-	+	virulence, detoxification, adaptation
gi|44588	DnaK	65.7	1	75	-	-	virulence, detoxification, adaptation
gi|15609168	heat shock protein hspX	16.1	2	169	-	-	virulence, detoxification, adaptation
gi|15608535	hypothetical protein Rv1397c similar to VapC10 toxin	14.9	1	67	-	-	virulence, detoxification, adaptation

a, Proteins identified with only one peptide were inspected manually

b, Cut-off values for Mascot scores of peptides and proteins were set to 45 ($p < 0.05$) and 51 ($p < 0.01$), respectively, for considering them as being accurate identifications

c, Prediction of Transmembrane domains with TMHMM v2.0 (http://www.cbs.dtu.dk/services/TMHMM)

d, Prediction of signal peptide with SignalP v3.0 (http://www.cbs.dtu.dk/services/SignalP)

e, Functional category as in Tuberculist v2.3 (http://tuberculist.epfl.ch)

Supporting table 3. *M. smegmatis* vesicles-associated proteins

Accesion number	Protein name	Unique peptides[a]	Score[b]	TMD[c]	SP[d]	Functional category[e]
gi|118468477	ribosomal protein S9	1132	35	-	-	information pathways
gi|118472053	30S ribosomal protein S7	796	32	-	-	information pathways
gi|118473160	30S ribosomal protein S3	699	33	-	-	information pathways
gi|118468301	30S ribosomal protein S4	673	24	-	-	information pathways
gi|118472263	50S ribosomal protein L2	660	28	-	-	information pathways
gi|118473190	50S ribosomal protein L3	631	19	-	-	information pathways
gi|118467618	30S ribosomal protein S16	603	14	-	-	information pathways
gi|118469641	30S ribosomal protein S5	540	22	-	-	information pathways
gi|118468304	50S ribosomal protein L23	389	9	-	-	information pathways
gi|118470088	50S ribosomal protein L4	378	12	-	-	information pathways
gi|118470225	ribosomal protein L14	353	10	-	-	information pathways
gi|118471474	50S ribosomal protein L27	264	8	-	-	information pathways
gi|118469072	50S ribosomal protein L32	245	4	-	-	information pathways
gi|118471088	elongation factor Tu	154	4	-	-	information pathways
gi|118472813	30S ribosomal protein S1	95	2	-	-	information pathways
gi|118469435	single-strand DNA-binding protein	74	5	-	-	information pathways
gi|118471339	DNA-binding protein HU	69	2	-	-	information pathways
gi|118471079	transcriptional regulator, TetR family protein	36	5	-	-	information pathways
gi|118470803	extra cytoplasmic sigma factor	31	3	-	-	information pathways
gi|118469501	serine/threonine-protein kinase PknD	27	2	+	-	information pathways
gi|118470693	Formyl transferase	42	7	-	-	information pathways
gi|118473437	50S ribosomal protein L33	84	4	-	-	information pathways
gi|118467956	glutamine synthetase, type I	539	16	-	-	intermediary metabolism and respiration
gi|118472596	dihydrolipoamide dehydrogenase	463	9	-	-	intermediary metabolism and respiration
gi|118467799	glyceraldehyde-3-phosphate dehydrogenase, type I	311	10	-	-	intermediary metabolism and respiration
gi|118471656	alcohol dehydrogenase, iron-containing	235	8	-	-	intermediary metabolism and respiration
gi|118468145	bacterioferritin	170	9	-	-	intermediary metabolism and respiration
gi|118467432	isocitrate dehydrogenase, NADP-dependent	98	8	-	-	intermediary metabolism and respiration
gi|118468051	proteasome beta subunit	44	3	-	-	intermediary metabolism and respiration
gi|118469436	serine protease	43	4	-	+	intermediary metabolism and respiration
gi|118467514	isochorismate synthase DhbC	34	4	-	-	intermediary metabolism and respiration
gi|118471065	ribulokinase	31	3	-	-	intermediary metabolism and respiration
gi|118471101	glycosyltransferase	30	10	-	-	intermediary metabolism and respiration
gi|118471116	chitooligosaccharide deacetylase	29	4	-	-	intermediary metabolism and respiration
gi|118471831	short chain dehydrogenase	29	3	-	-	intermediary metabolism and respiration
gi|118468744	antigen 85-A	398	9	-	-	lipid metabolism
gi|118467737	antigen 85-C	278	7	-	-	lipid metabolism

gi|118469108	acetyl-/propionyl-coenzyme A carboxylase alpha chain	269	15	-	-	lipid metabolism
gi|118470265	29 kDa antigen Cfp29	630	19	-	+	Virulence, detoxification, adaptation
gi|118469216	chaperonin GroEL	293	19	-	+	Virulence, detoxification, adaptation
gi|118470273	low molecular weight antigen MTB12	111	4	-	+	Virulence, detoxification, adaptation
gi|118468785	virulence factor mce family protein	42	4	+	+	Virulence, detoxification, adaptation
gi|118471849	F0F1 ATP synthase subunit beta	88	5	+	-	cell wall and cell processes
gi|118471254	porin	73	3	+	-	cell wall and cell processes
gi|118471370	putative cell division protein FtsQ	28	7	+	-	cell wall and cell processes
gi|118473261	ABC-type transport system ATP-binding protein I	27	2	-	-	cell wall and cell processes
gi|118469684	ribose transport system permease protein RbsC	20	2	+	+	cell wall and cell processes
gi|118470974	hypothetical protein MSMEG_1629	170	10	-	-	unknown
gi|118473120	secreted protein	119	6	-	+	unknown
gi|118471597	hypothetical protein MSMEG_1076	82	4	-	-	unknown
gi|118469044	hypothetical protein MSMEG_1279	72	3	-	-	unknown
gi|118468070	hypothetical protein MSMEG_5309	40	2	-	-	unknown
gi|118467463	D-ribose-binding periplasmic protein RbsB	34	1	-	-	unknown
gi|118469415	hypothetical protein MSMEG_1475	34	2	-	-	unknown
gi|118473366	signal recognition particle-docking protein FtsY	32	4	-	+	unknown
gi|118468379	hypothetical protein MSMEG_0256	29	4	-	-	unknown
gi|118470619	hypothetical protein MSMEG_2634	29	3	-	+	unknown
gi|118470335	extracellular solute-binding protein, family protein 5	28	7	-	+	unknown
gi|118470876	hypothetical protein MSMEG_1891	28	2	-	-	unknown
gi|118467440	sensory box/response regulator	28	10	-	-	unknown
gi|118473828	hypothetical protein MSMEG_4456	27	2	-	-	unknown
gi|118471995	hypothetical protein MSMEG_0926	27	3	-	-	unknown
gi|118467409	hypothetical protein MSMEG_1384	27	2	-	-	unknown
gi|118468774	hypothetical protein MSMEG_4729	24	2	-	-	unknown

a, Proteins identified with only one peptide were inspected manually

b, Cut-off values for Mascot scores of peptides and proteins were set to 45 ($p < 0.05$) and 51 ($p < 0.01$), respectively, for considering them as being accurate identifications

c, Prediction of Transmembrane domains with TMHMM v2.0 (http://www.cbs.dtu.dk/services/TMHMM)

d, Prediction of signal peptide with SignalP v3.0 (http://www.cbs.dtu.dk/services/SignalP)

e, Functional category as in Smegmalist v1.0 (http://mycobrowser.epfl.ch/smegmalist.html)

Supporting Table 4. *M. bovis* BCG Pasteur cellular proteins

Accesion number	Protein name	Score	Unique peptides
gi|121636354	chaperonin GroEL [Mycobacterium bovis BCG str. Pasteur 1173P2]	11375	252
gi|121639343	co-chaperonin GroES [Mycobacterium bovis BCG str. Pasteur 1173P2]	3840	96
gi|121636264	molecular chaperone DnaK [Mycobacterium bovis BCG str. Pasteur 1173P2]	2962	106
gi|121636589	DNA-directed RNA polymerase subunit beta~ [Mycobacterium bovis BCG str. Pasteur 1173P2]	2550	85
gi|121636606	elongation factor Tu [Mycobacterium bovis BCG str. Pasteur 1173P2]	2197	71
gi|121639342	chaperonin GroEL [Mycobacterium bovis BCG str. Pasteur 1173P2]	2106	67
gi|121636588	DNA-directed RNA polymerase subunit beta [Mycobacterium bovis BCG str. Pasteur 1173P2]	1860	83
gi|121637814	catalase-peroxidase-peroxynitritase T katG [Mycobacterium bovis BCG str. Pasteur 1173P2]	1634	57
gi|121638822	putative multifunctional mycocerosic acid synthase membrane-associated mas [Mycobacterium bovis BCG str. Pasteur 1173P2]	1544	72
gi|121637065	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	1368	50
gi|121639162	putative transmembrane carbonic anhydrase [Mycobacterium bovis BCG str. Pasteur 1173P2]	1266	34
gi|121636597	putative transmembrane transport protein mmpL5 [Mycobacterium bovis BCG str. Pasteur 1173P2]	1108	34
gi|121636297	putative endopeptidase ATP binding protein (chain b) clpB [Mycobacterium bovis BCG str. Pasteur 1173P2]	1095	58
gi|121637406	aconitate hydratase [Mycobacterium bovis BCG str. Pasteur 1173P2]	1083	41
gi|121637239	F0F1 ATP synthase subunit beta [Mycobacterium bovis BCG str. Pasteur 1173P2]	992	36
gi|121637821	putative isocitrate lyase aceA [Mycobacterium bovis BCG str. Pasteur 1173P2]	967	45
gi|121639516	putative ATP-dependent Clp protease ATP-binding subunit clpC [Mycobacterium bovis BCG str. Pasteur 1173P2]	955	56
gi|121639137	S-adenosyl-L-homocysteine hydrolase [Mycobacterium bovis BCG str. Pasteur 1173P2]	950	39
gi|121638663	polynucleotide phosphorylase/polyadenylase [Mycobacterium bovis BCG str. Pasteur 1173P2]	875	32
gi|121636155	3-ketoacyl-(acyl-carrier-protein) reductase [Mycobacterium bovis BCG str. Pasteur 1173P2]	799	22
gi|121638126	acyl carrier protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	785	16
gi|121636605	elongation factor G [Mycobacterium bovis BCG str. Pasteur 1173P2]	780	31
gi|121638911	putative electron transfer flavoprotein (alpha-subunit) fixB [Mycobacterium bovis BCG str. Pasteur 1173P2]	760	15
gi|121637537	30S ribosomal protein S1 [Mycobacterium bovis BCG str. Pasteur 1173P2]	715	39
gi|121638344	ATP-dependent Clp protease proteolytic subunit [Mycobacterium bovis BCG str. Pasteur 1173P2]	712	12
gi|121638359	putative NAD-dependent glutamate dehydrogenase gdh [Mycobacterium bovis BCG str. Pasteur 1173P2]	711	47
gi|121636164	heat shock protein hsp [Mycobacterium bovis BCG str. Pasteur 1173P2]	706	21
gi|121638102	glutamine synthetase glnA1 [Mycobacterium bovis BCG str. Pasteur 1173P2]	702	19
gi|121636156	acetyl-CoA acetyltransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	689	15
gi|121637237	F0F1 ATP synthase subunit alpha [Mycobacterium bovis BCG str. Pasteur 1173P2]	675	37
gi|121636060	putative short-chain type dehydrogenase/reductase [Mycobacterium bovis BCG str. Pasteur 1173P2]	643	15
gi|121638622	hypothetical protein BCG_2760c [Mycobacterium bovis BCG str. Pasteur 1173P2]	632	17
gi|121636001	hypothetical protein BCG_0121 [Mycobacterium bovis BCG str. Pasteur 1173P2]	614	17
gi|121637543	hypothetical protein BCG_1674 [Mycobacterium bovis BCG str. Pasteur 1173P2]	583	20
gi|121636161	succinate dehydrogenase flavoprotein subunit [Mycobacterium bovis BCG str. Pasteur 1173P2]	569	30
gi|121636276	fructose-bisphosphate aldolase [Mycobacterium bovis BCG str. Pasteur 1173P2]	559	15
gi|121638077	putative ubiquinol-cytochrome C reductase QcrB (cytochrome B subunit) [Mycobacterium bovis BCG str. Pasteur 1173P2]	547	13

gi|121639112	short chain dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	514	14
gi|121637740	malate synthase G [Mycobacterium bovis BCG str. Pasteur 1173P2]	512	23
gi|121639129	preprotein translocase subunit SecA [Mycobacterium bovis BCG str. Pasteur 1173P2]	510	22
gi|121638912	putative electron transfer flavoprotein (beta-subunit) fixA [Mycobacterium bovis BCG str. Pasteur 1173P2]	509	16
gi|121639377	DNA-directed RNA polymerase subunit alpha [Mycobacterium bovis BCG str. Pasteur 1173P2]	498	21
gi|121636573	50S ribosomal protein L7/L12 [Mycobacterium bovis BCG str. Pasteur 1173P2]	493	21
gi|121639626	2-isopropylmalate synthase [Mycobacterium bovis BCG str. Pasteur 1173P2]	483	17
gi|121638407	putative fatty acid synthase fas [Mycobacterium bovis BCG str. Pasteur 1173P2]	475	58
gi|121638180	heat shock protein 90 [Mycobacterium bovis BCG str. Pasteur 1173P2]	463	18
gi|121638096	dihydrolipoamide acetyltransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	455	18
gi|121637177	alpha-ketoglutarate decarboxylase [Mycobacterium bovis BCG str. Pasteur 1173P2]	453	28
gi|121637779	putative bacterioferritin bfrA [Mycobacterium bovis BCG str. Pasteur 1173P2]	434	17
gi|121635892	putative iron-regulated peptidyl-prolyl cis-trans isomerase A ppiA [Mycobacterium bovis BCG str. Pasteur 1173P2]	422	12
gi|121638719	translation initiation factor IF-2 [Mycobacterium bovis BCG str. Pasteur 1173P2]	421	23
gi|121636391	Heparin binding hemagglutinin hbhA [Mycobacterium bovis BCG str. Pasteur 1173P2]	417	9
gi|121639075	hypothetical protein BCG_3215c [Mycobacterium bovis BCG str. Pasteur 1173P2]	415	21
gi|121636069	putative NAD(p) transhydrogenase (subunit beta) pntB [Mycobacterium bovis BCG str. Pasteur 1173P2]	406	16
gi|121635889	DNA gyrase subunit A [Mycobacterium bovis BCG str. Pasteur 1173P2]	399	31
gi|121639095	hypothetical protein BCG_3235c [Mycobacterium bovis BCG str. Pasteur 1173P2]	392	7
gi|121637730	hypothetical protein BCG_1862 [Mycobacterium bovis BCG str. Pasteur 1173P2]	388	16
gi|121637322	S-adenosylmethionine synthetase [Mycobacterium bovis BCG str. Pasteur 1173P2]	379	12
gi|121636572	50S ribosomal protein L10 [Mycobacterium bovis BCG str. Pasteur 1173P2]	375	10
gi|121638877	D-3-phosphoglycerate dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	373	18
gi|121639161	hypothetical protein BCG_3301 [Mycobacterium bovis BCG str. Pasteur 1173P2]	373	9
gi|121637169	malate dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	350	13
gi|121635964	single-stranded DNA-binding protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	350	10
gi|121638327	putative ribonuclease E rne [Mycobacterium bovis BCG str. Pasteur 1173P2]	340	22
gi|121639234	hypothetical protein BCG_3376 [Mycobacterium bovis BCG str. Pasteur 1173P2]	340	21
gi|121636738	hypothetical protein BCG_0866c [Mycobacterium bovis BCG str. Pasteur 1173P2]	323	6
gi|121639759	putative bacterioferritin bfrB [Mycobacterium bovis BCG str. Pasteur 1173P2]	320	16
gi|121636604	30S ribosomal protein S7 [Mycobacterium bovis BCG str. Pasteur 1173P2]	319	18
gi|121637003	acetyl-CoA acetyltransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	312	14
gi|121638022	hypothetical protein BCG_2157c [Mycobacterium bovis BCG str. Pasteur 1173P2]	312	8
gi|121638929	putative NADP-dependent alcohol dehydrogenase adhC [Mycobacterium bovis BCG str. Pasteur 1173P2]	312	20
gi|121639718	acyl-CoA synthetase [Mycobacterium bovis BCG str. Pasteur 1173P2]	309	22
gi|121636783	putative fatty oxidation protein fadB [Mycobacterium bovis BCG str. Pasteur 1173P2]	309	16
gi|121637318	putative integration host factor mihF [Mycobacterium bovis BCG str. Pasteur 1173P2]	302	16
gi|121638867	putative DNA-binding protein HU homolog hupB [Mycobacterium bovis BCG str. Pasteur 1173P2]	294	14
gi|121636755	hypothetical protein BCG_0884c [Mycobacterium bovis BCG str. Pasteur 1173P2]	288	15
gi|121638853	putative oxidoreductase [Mycobacterium bovis BCG str. Pasteur 1173P2]	282	7
gi|121639034	NADH dehydrogenase subunit G [Mycobacterium bovis BCG str. Pasteur 1173P2]	280	13

gi|121639363	30S ribosomal protein S9 [Mycobacterium bovis BCG str. Pasteur 1173P2]	275	10
gi|121639677	**19 kDa lipoprotein antigen precursor lpqH [Mycobacterium bovis BCG str. Pasteur 1173P2]**	275	4
gi|121638123	pyruvate dehydrogenase subunit E1 [Mycobacterium bovis BCG str. Pasteur 1173P2]	273	29
gi|121635963	30S ribosomal protein S6 [Mycobacterium bovis BCG str. Pasteur 1173P2]	265	9
gi|121637448	putative polyketide synthase pks5 [Mycobacterium bovis BCG str. Pasteur 1173P2]	262	33
gi|121635988	putative oxidoreductase [Mycobacterium bovis BCG str. Pasteur 1173P2]	260	14
gi|121638790	30S ribosomal protein S16 [Mycobacterium bovis BCG str. Pasteur 1173P2]	257	6
gi|121639022	putative acyl-CoA dehydrogenase fadE24 [Mycobacterium bovis BCG str. Pasteur 1173P2]	256	10
gi|121637410	putative transcriptional regulatory protein moxR1 [Mycobacterium bovis BCG str. Pasteur 1173P2]	256	11
gi|121637394	putative cysteine desulfurase csd [Mycobacterium bovis BCG str. Pasteur 1173P2]	254	10
gi|121639777	putative ferredoxin-dependent glutamate synthase [NADPH] large subunit gltB [Mycobacterium bovis BCG str. Pasteur 1173P2]	253	25
gi|121636630	50S ribosomal protein L16 [Mycobacterium bovis BCG str. Pasteur 1173P2]	253	8
gi|121638027	hypothetical protein BCG_2162c [Mycobacterium bovis BCG str. Pasteur 1173P2]	250	15
gi|121636265	putative grpE protein (hsp-70 cofactor) [Mycobacterium bovis BCG str. Pasteur 1173P2]	250	9
gi|121638771	30S ribosomal protein S2 [Mycobacterium bovis BCG str. Pasteur 1173P2]	250	14
gi|121636067	putative NAD(p) transhydrogenase (subunit alpha) pntAa [Mycobacterium bovis BCG str. Pasteur 1173P2]	248	6
gi|121638817	phenolpthiocerol synthesis type-I polyketide synthase ppsE [Mycobacterium bovis BCG str. Pasteur 1173P2]	245	23
gi|121637479	hypothetical protein BCG_1610 [Mycobacterium bovis BCG str. Pasteur 1173P2]	243	4
gi|121636641	50S ribosomal protein L6 [Mycobacterium bovis BCG str. Pasteur 1173P2]	239	10
gi|121639697	hypothetical protein BCG_3842 [Mycobacterium bovis BCG str. Pasteur 1173P2]	239	9
gi|121637396	hypothetical protein BCG_1527 [Mycobacterium bovis BCG str. Pasteur 1173P2]	237	5
gi|121637029	fumarate hydratase [Mycobacterium bovis BCG str. Pasteur 1173P2]	235	15
gi|121636638	50S ribosomal protein L5 [Mycobacterium bovis BCG str. Pasteur 1173P2]	230	14
gi|121636640	30S ribosomal protein S8 [Mycobacterium bovis BCG str. Pasteur 1173P2]	227	7
gi|121637366	putative glyceraldehyde 3-phosphate dehydrogenase gap [Mycobacterium bovis BCG str. Pasteur 1173P2]	226	8
gi|121637024	serine hydroxymethyltransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	226	19
gi|121637590	acyl-CoA synthetase [Mycobacterium bovis BCG str. Pasteur 1173P2]	225	19
gi|121637419	hypothetical protein BCG_1550 [Mycobacterium bovis BCG str. Pasteur 1173P2]	224	21
gi|121636627	30S ribosomal protein S19 [Mycobacterium bovis BCG str. Pasteur 1173P2]	219	11
gi|121638065	hypothetical protein BCG_2200c [Mycobacterium bovis BCG str. Pasteur 1173P2]	217	8
gi|121639379	30S ribosomal protein S11 [Mycobacterium bovis BCG str. Pasteur 1173P2]	216	6
gi|121636796	putative acyl-CoA dehydrogenase fadE10 [Mycobacterium bovis BCG str. Pasteur 1173P2]	216	19
gi|121638360	putative ABC transporter ATP-binding protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	214	15
gi|121637393	putative ATP-binding protein ABC transporter [Mycobacterium bovis BCG str. Pasteur 1173P2]	213	7
gi|121639376	50S ribosomal protein L17 [Mycobacterium bovis BCG str. Pasteur 1173P2]	212	14
gi|121638345	trigger factor [Mycobacterium bovis BCG str. Pasteur 1173P2]	211	10
gi|121639503	putative transcription factor [Mycobacterium bovis BCG str. Pasteur 1173P2]	202	9
gi|121636498	hypothetical protein BCG_0625c [Mycobacterium bovis BCG str. Pasteur 1173P2]	197	6
gi|121637236	F0F1 ATP synthase subunit delta [Mycobacterium bovis BCG str. Pasteur 1173P2]	196	13
gi|121635900	thioredoxin trxC (TRX) (MPT46) [Mycobacterium bovis BCG str. Pasteur 1173P2]	196	4
gi|121639634	hypothetical protein BCG_3778c [Mycobacterium bovis BCG str. Pasteur 1173P2]	194	8

gi|121639708	short chain dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	194	7
gi|121636624	50S ribosomal protein L4 [Mycobacterium bovis BCG str. Pasteur 1173P2]	192	10
gi|121639541	inorganic pyrophosphatase ppa [Mycobacterium bovis BCG str. Pasteur 1173P2]	192	9
gi|121637818	putative oxidoreductase fadB5 [Mycobacterium bovis BCG str. Pasteur 1173P2]	189	11
gi|121636782	acetyl-CoA acetyltransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	187	10
gi|121639085	putative transmembrane cation transporter [Mycobacterium bovis BCG str. Pasteur 1173P2]	187	9
gi|121638134	putative flavoprotein [Mycobacterium bovis BCG str. Pasteur 1173P2]	184	10
gi|121638447	putative glutamine-transport transmembrane protein ABC transporter [Mycobacterium bovis BCG str. Pasteur 1173P2]	179	6
gi|121638750	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase [Mycobacterium bovis BCG str. Pasteur 1173P2]	179	10
gi|121636556	(3R)-hydroxyacyl-ACP dehydratase subunit HadA [Mycobacterium bovis BCG str. Pasteur 1173P2]	176	2
gi|121636199	hypothetical protein BCG_0324 [Mycobacterium bovis BCG str. Pasteur 1173P2]	176	25
gi|121638104	putative glutamine synthetase glnA2 [Mycobacterium bovis BCG str. Pasteur 1173P2]	175	16
gi|121639364	50S ribosomal protein L13 [Mycobacterium bovis BCG str. Pasteur 1173P2]	174	11
gi|121635930	hypothetical protein BCG_0050c [Mycobacterium bovis BCG str. Pasteur 1173P2]	174	10
gi|121636676	putative methylmalonate-semialdehyde dehydrogenase mmsA [Mycobacterium bovis BCG str. Pasteur 1173P2]	173	12
gi|121637009	transcription elongation factor GreA [Mycobacterium bovis BCG str. Pasteur 1173P2]	173	10
gi|121637724	preprotein translocase subunit SecA [Mycobacterium bovis BCG str. Pasteur 1173P2]	172	29
gi|121636484	putative nucleotide-binding protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	170	7
gi|121638511	putative methyltransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	170	11
gi|121638128	3-oxoacyl-(acyl carrier protein) synthase II [Mycobacterium bovis BCG str. Pasteur 1173P2]	169	11
gi|121636558	(3R)-hydroxyacyl-ACP dehydratase subunit HadC [Mycobacterium bovis BCG str. Pasteur 1173P2]	169	8
gi|121638828	putative polyketide synthase pks1 [Mycobacterium bovis BCG str. Pasteur 1173P2]	169	31
gi|121637524	pyruvate kinase [Mycobacterium bovis BCG str. Pasteur 1173P2]	169	13
gi|121637775	putative L-lactate dehydrogenase (cytochrome) lldD2 [Mycobacterium bovis BCG str. Pasteur 1173P2]	169	12
gi|121638472	preprotein translocase subunit SecD [Mycobacterium bovis BCG str. Pasteur 1173P2]	169	9
gi|121638325	50S ribosomal protein L21 [Mycobacterium bovis BCG str. Pasteur 1173P2]	169	8
gi|121639111	RNA polymerase sigma factor RpoE [Mycobacterium bovis BCG str. Pasteur 1173P2]	168	3
gi|121638404	putative bacterioferritin comigratory protein bcp [Mycobacterium bovis BCG str. Pasteur 1173P2]	167	7
gi|121635966	50S ribosomal protein L9 [Mycobacterium bovis BCG str. Pasteur 1173P2]	166	3
gi|121639710	integral membrane indolylacetylinositol arabinosyltransferase embC [Mycobacterium bovis BCG str. Pasteur 1173P2]	166	18
gi|121636632	30S ribosomal protein S17 [Mycobacterium bovis BCG str. Pasteur 1173P2]	165	10
gi|121636623	50S ribosomal protein L3 [Mycobacterium bovis BCG str. Pasteur 1173P2]	164	6
gi|121636855	transmembrane serine/threonine-protein kinase D pknDa [Mycobacterium bovis BCG str. Pasteur 1173P2]	162	10
gi|121638770	elongation factor Ts [Mycobacterium bovis BCG str. Pasteur 1173P2]	162	10
gi|121639242	succinate dehydrogenase flavoprotein subunit [Mycobacterium bovis BCG str. Pasteur 1173P2]	162	19
gi|121636877	succinyl-CoA synthetase subunit alpha [Mycobacterium bovis BCG str. Pasteur 1173P2]	161	14
gi|121638350	putative aminopeptidase N pepN [Mycobacterium bovis BCG str. Pasteur 1173P2]	161	10
gi|121639632	hypothetical protein BCG_3776c [Mycobacterium bovis BCG str. Pasteur 1173P2]	160	2
gi|121639045	putative dioxygenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	160	10
gi|121639041	NADH dehydrogenase subunit N [Mycobacterium bovis BCG str. Pasteur 1173P2]	159	2
gi|121639561	putative cold shock protein A cspA [Mycobacterium bovis BCG str. Pasteur 1173P2]	157	5

gi|121639380	30S ribosomal protein S13 [Mycobacterium bovis BCG str. Pasteur 1173P2]	156	7
gi|121639504	**putative lipoprotein lpqE [Mycobacterium bovis BCG str. Pasteur 1173P2]**	155	5
gi|121635885	DNA polymerase III subunit beta [Mycobacterium bovis BCG str. Pasteur 1173P2]	155	12
gi|121636562	50S ribosomal protein L1 [Mycobacterium bovis BCG str. Pasteur 1173P2]	155	12
gi|121638343	ATP-dependent Clp protease proteolytic subunit [Mycobacterium bovis BCG str. Pasteur 1173P2]	154	12
gi|121638785	50S ribosomal protein L19 [Mycobacterium bovis BCG str. Pasteur 1173P2]	153	8
gi|121639135	two component sensory transduction transcriptional regulatory protein mtrA [Mycobacterium bovis BCG str. Pasteur 1173P2]	152	8
gi|121639466	hypothetical protein BCG_3611 [Mycobacterium bovis BCG str. Pasteur 1173P2]	151	7
gi|121639023	putative acyl-CoA dehydrogenase fadE23 [Mycobacterium bovis BCG str. Pasteur 1173P2]	151	9
gi|121639227	hypothetical protein BCG_3369 [Mycobacterium bovis BCG str. Pasteur 1173P2]	149	5
gi|121636685	putative zinc-containing alcohol dehydrogenase NAD dependant adhB [Mycobacterium bovis BCG str. Pasteur 1173P2]	148	7
gi|121636118	transmembrane transport protein mmpL3 [Mycobacterium bovis BCG str. Pasteur 1173P2]	148	9
gi|121636557	(3R)-hydroxyacyl-ACP dehydratase subunit HadB [Mycobacterium bovis BCG str. Pasteur 1173P2]	147	4
gi|121636642	50S ribosomal protein L18 [Mycobacterium bovis BCG str. Pasteur 1173P2]	147	9
gi|121637384	putative quinone reductase qor [Mycobacterium bovis BCG str. Pasteur 1173P2]	146	11
gi|121639182	putative piperideine-6-carboxilic acid dehydrogenase pcd [Mycobacterium bovis BCG str. Pasteur 1173P2]	145	14
gi|121638083	adenosine kinase [Mycobacterium bovis BCG str. Pasteur 1173P2]	144	6
gi|121636622	30S ribosomal protein S10 [Mycobacterium bovis BCG str. Pasteur 1173P2]	143	8
gi|121636379	hypothetical protein BCG_0504c [Mycobacterium bovis BCG str. Pasteur 1173P2]	143	6
gi|121636042	secreted antigen 85-c fbpC (85C) [Mycobacterium bovis BCG str. Pasteur 1173P2]	140	8
gi|121638328	nucleoside diphosphate kinase [Mycobacterium bovis BCG str. Pasteur 1173P2]	137	5
gi|121636681	putative two component system response transcriptional positive regulator phoP [Mycobacterium bovis BCG str. Pasteur 1173P2]	137	4
gi|121636603	30S ribosomal protein S12 [Mycobacterium bovis BCG str. Pasteur 1173P2]	135	6
gi|121637787	hypothetical protein BCG_1920c [Mycobacterium bovis BCG str. Pasteur 1173P2]	134	3
gi|121639517	putative lsr2 protein precursor [Mycobacterium bovis BCG str. Pasteur 1173P2]	133	6
gi|121639428	hypothetical protein BCG_3573c [Mycobacterium bovis BCG str. Pasteur 1173P2]	133	11
gi|121636559	preprotein translocase subunit SecE [Mycobacterium bovis BCG str. Pasteur 1173P2]	133	1
gi|121639313	putative dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	133	3
gi|121636252	putative iron-sulfur-binding reductase [Mycobacterium bovis BCG str. Pasteur 1173P2]	133	23
gi|121639174	putative bifunctional protein acetyl-/propionyl-coenzyme A carboxylase (alpha chain) accA3: biotin carboxylase + biotin carboxyl carrier p	130	22
gi|121636059	putative aldehyde dehydrogenase (NAD+) dependant [Mycobacterium bovis BCG str. Pasteur 1173P2]	130	8
gi|121636040	hypothetical protein BCG_0161 [Mycobacterium bovis BCG str. Pasteur 1173P2]	129	11
gi|121639404	short chain dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	128	6
gi|121636739	putative thiosulfate sulfurtransferase cysA2 [Mycobacterium bovis BCG str. Pasteur 1173P2]	127	12
gi|121639661	hypothetical protein BCG_3806 [Mycobacterium bovis BCG str. Pasteur 1173P2]	127	3
gi|121636228	hypothetical protein BCG_0353 [Mycobacterium bovis BCG str. Pasteur 1173P2]	127	4
gi|121637379	transketolase [Mycobacterium bovis BCG str. Pasteur 1173P2]	126	16
gi|121636066	putative acyl-CoA dehydrogenase fadE2 [Mycobacterium bovis BCG str. Pasteur 1173P2]	126	13
gi|121637334	putative transcriptional regulatory protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	125	10
gi|121636154	hypothetical protein BCG_0279c [Mycobacterium bovis BCG str. Pasteur 1173P2]	124	10
gi|121636626	50S ribosomal protein L2 [Mycobacterium bovis BCG str. Pasteur 1173P2]	124	8

gi|121638440	alanyl-tRNA synthetase [Mycobacterium bovis BCG str. Pasteur 1173P2]	124	22
gi|121636911	putative pterin-4-alpha-carbinolamine dehydratase moaB2 [Mycobacterium bovis BCG str. Pasteur 1173P2]	123	4
gi|121636551	enoyl-CoA hydratase [Mycobacterium bovis BCG str. Pasteur 1173P2]	123	9
gi|121639158	hypothetical protein BCG_3298 [Mycobacterium bovis BCG str. Pasteur 1173P2]	121	6
gi|121637976	hypothetical protein BCG_2111c [Mycobacterium bovis BCG str. Pasteur 1173P2]	120	3
gi|121637238	F0F1 ATP synthase subunit gamma [Mycobacterium bovis BCG str. Pasteur 1173P2]	118	15
gi|121637415	enoyl-(acyl carrier protein) reductase [Mycobacterium bovis BCG str. Pasteur 1173P2]	118	5
gi|121636807	phosphoserine aminotransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	117	5
gi|121636859	**periplasmic phosphate-binding lipoprotein pstS1 [Mycobacterium bovis BCG str. Pasteur 1173P2]**	115	2
gi|121639591	hypothetical protein BCG_3736c [Mycobacterium bovis BCG str. Pasteur 1173P2]	115	2
gi|121639326	hypothetical protein BCG_3471 [Mycobacterium bovis BCG str. Pasteur 1173P2]	114	8
gi|121636205	putative transmembrane protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	114	5
gi|121636163	hypothetical protein BCG_0288c [Mycobacterium bovis BCG str. Pasteur 1173P2]	113	5
gi|121637189	hypothetical protein BCG_1320c [Mycobacterium bovis BCG str. Pasteur 1173P2]	112	7
gi|121636819	type II citrate synthase [Mycobacterium bovis BCG str. Pasteur 1173P2]	111	4
gi|121638932	ribonucleotide-diphosphate reductase subunit beta [Mycobacterium bovis BCG str. Pasteur 1173P2]	111	20
gi|121636292	putative protein transport protein secE2 [Mycobacterium bovis BCG str. Pasteur 1173P2]	111	4
gi|121638869	isopropylmalate isomerase large subunit [Mycobacterium bovis BCG str. Pasteur 1173P2]	110	20
gi|121637378	transaldolase [Mycobacterium bovis BCG str. Pasteur 1173P2]	110	16
gi|121636645	50S ribosomal protein L15 [Mycobacterium bovis BCG str. Pasteur 1173P2]	110	6
gi|121639163	putative acyl-CoA dehydrogenase fadE25 [Mycobacterium bovis BCG str. Pasteur 1173P2]	109	12
gi|121636160	fumarate reductase iron-sulfur subunit [Mycobacterium bovis BCG str. Pasteur 1173P2]	109	11
gi|121639083	putative glutaredoxin protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	107	1
gi|121638935	ribonucleotide-diphosphate reductase subunit alpha [Mycobacterium bovis BCG str. Pasteur 1173P2]	106	11
gi|121638139	hypothetical protein BCG_2274c [Mycobacterium bovis BCG str. Pasteur 1173P2]	105	2
gi|121638616	epoxide hydrolase [Mycobacterium bovis BCG str. Pasteur 1173P2]	105	3
gi|121637551	50S ribosomal protein L20 [Mycobacterium bovis BCG str. Pasteur 1173P2]	105	4
gi|121636629	30S ribosomal protein S3 [Mycobacterium bovis BCG str. Pasteur 1173P2]	105	17
gi|121639473	putative electron transfer protein fdxB [Mycobacterium bovis BCG str. Pasteur 1173P2]	103	9
gi|121636383	3-hydroxybutyryl-CoA dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	102	10
gi|121635977	putative isocitrate dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	102	21
gi|121636643	30S ribosomal protein S5 [Mycobacterium bovis BCG str. Pasteur 1173P2]	102	8
gi|121636179	putative 5-oxoprolinase oplA [Mycobacterium bovis BCG str. Pasteur 1173P2]	101	29
gi|121637824	hypothetical protein BCG_1958c [Mycobacterium bovis BCG str. Pasteur 1173P2]	100	3
gi|121638596	putative transmembrane alanine and glycine rich protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	99	9
gi|121636999	enoyl-CoA hydratase [Mycobacterium bovis BCG str. Pasteur 1173P2]	99	5
gi|121639691	enoyl-CoA hydratase [Mycobacterium bovis BCG str. Pasteur 1173P2]	97	11
gi|121639191	putative glycerol-3-phosphate dehydrogenase glpD2 [Mycobacterium bovis BCG str. Pasteur 1173P2]	97	15
gi|121639764	superoxide dismutase [Fe] sodA [Mycobacterium bovis BCG str. Pasteur 1173P2]	96	3
gi|121639164	putative phosphoribosylaminoimidazole carboxylase catalytic subunit purE [Mycobacterium bovis BCG str. Pasteur 1173P2]	96	4
gi|121636377	dihydrolipoamide dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	96	14

gi|121639091	hypothetical protein BCG_3231c [Mycobacterium bovis BCG str. Pasteur 1173P2]	95	7
gi|121636828	enoyl-CoA hydratase [Mycobacterium bovis BCG str. Pasteur 1173P2]	95	5
gi|121638108	hypothetical protein BCG_2243 [Mycobacterium bovis BCG str. Pasteur 1173P2]	94	8
gi|121638179	hypothetical protein BCG_2314 [Mycobacterium bovis BCG str. Pasteur 1173P2]	93	3
gi|121636092	putative transmembrane protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	93	7
gi|121636882	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Mycobacterium bovis BCG str. Pasteur 1	93	5
gi|121637837	thiol peroxidase [Mycobacterium bovis BCG str. Pasteur 1173P2]	92	6
gi|121636532	hypothetical protein BCG_0660c [Mycobacterium bovis BCG str. Pasteur 1173P2]	91	12
gi|121636952	phosphopyruvate hydratase [Mycobacterium bovis BCG str. Pasteur 1173P2]	91	11
gi|121637240	F0F1 ATP synthase subunit epsilon [Mycobacterium bovis BCG str. Pasteur 1173P2]	91	4
gi|121639790	hypothetical protein BCG_3935c [Mycobacterium bovis BCG str. Pasteur 1173P2]	90	2
gi|121636554	hypothetical protein BCG_0682 [Mycobacterium bovis BCG str. Pasteur 1173P2]	90	4
gi|121639029	NADH dehydrogenase subunit B [Mycobacterium bovis BCG str. Pasteur 1173P2]	89	10
gi|121639321	GMP synthase [Mycobacterium bovis BCG str. Pasteur 1173P2]	88	12
gi|121638665	30S ribosomal protein S15 [Mycobacterium bovis BCG str. Pasteur 1173P2]	87	11
gi|121638870	putative transcriptional regulatory protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	87	4
gi|121638095	short chain dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	86	17
gi|121638823	acyl-CoA synthetase [Mycobacterium bovis BCG str. Pasteur 1173P2]	86	6
gi|121636856	**periplasmic phosphate-binding lipoprotein pstS2 [Mycobacterium bovis BCG str. Pasteur 1173P2]**	85	4
gi|121639770	putative histone-like protein hns [Mycobacterium bovis BCG str. Pasteur 1173P2]	85	4
gi|121636599	hypothetical protein BCG_0727 [Mycobacterium bovis BCG str. Pasteur 1173P2]	85	4
gi|121638471	preprotein translocase subunit SecF [Mycobacterium bovis BCG str. Pasteur 1173P2]	84	7
gi|121638293	30S ribosomal protein S20 [Mycobacterium bovis BCG str. Pasteur 1173P2]	84	7
gi|121638892	6-phosphofructokinase [Mycobacterium bovis BCG str. Pasteur 1173P2]	84	8
gi|121638348	ribose-5-phosphate isomerase B [Mycobacterium bovis BCG str. Pasteur 1173P2]	84	4
gi|121638574	hypothetical protein BCG_2712c [Mycobacterium bovis BCG str. Pasteur 1173P2]	84	2
gi|121637254	acetyl-CoA acetyltransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	83	3
gi|121636967	putative ESAT-6 like protein 1 [Mycobacterium bovis BCG str. Pasteur 1173P2]	83	1
gi|121638548	putative transmembrane protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	83	14
gi|121638865	polyphosphate kinase [Mycobacterium bovis BCG str. Pasteur 1173P2]	82	15
gi|121636561	50S ribosomal protein L11 [Mycobacterium bovis BCG str. Pasteur 1173P2]	82	3
gi|121637367	phosphoglycerate kinase [Mycobacterium bovis BCG str. Pasteur 1173P2]	82	8
gi|121638048	cell division protein MraZ [Mycobacterium bovis BCG str. Pasteur 1173P2]	81	2
gi|121637695	hypothetical protein BCG_1826 [Mycobacterium bovis BCG str. Pasteur 1173P2]	81	4
gi|121639589	CRP/FNR family transcriptional regulator [Mycobacterium bovis BCG str. Pasteur 1173P2]	81	6
gi|121636353	short chain dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	81	5
gi|121637735	glycine dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	81	10
gi|121638097	hypothetical protein BCG_2232 [Mycobacterium bovis BCG str. Pasteur 1173P2]	80	2
gi|121638883	ketol-acid reductoisomerase [Mycobacterium bovis BCG str. Pasteur 1173P2]	80	8
gi|121638644	putative alanine rich hydrolase [Mycobacterium bovis BCG str. Pasteur 1173P2]	80	5
gi|121638850	putative membrane or secreted protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	80	4

gi|121636563	methoxy mycolic acid synthase [Mycobacterium bovis BCG str. Pasteur 1173P2]	80	10
gi|121635907	putative inner membrane protein translocase component YidC [Mycobacterium bovis BCG str. Pasteur 1173P2]	80	8
gi|121638589	hypothetical protein BCG_2727 [Mycobacterium bovis BCG str. Pasteur 1173P2]	79	6
gi|121636576	putative ribonucleotide-transport ATP-binding protein ABC transporter mkl [Mycobacterium bovis BCG str. Pasteur 1173P2]	79	7
gi|121635956	myo-inositol-1-phosphate synthase INO1 [Mycobacterium bovis BCG str. Pasteur 1173P2]	79	8
gi|121636230	putative beta-1,3-glucanase precursor [Mycobacterium bovis BCG str. Pasteur 1173P2]	79	10
gi|121636653	hypothetical protein BCG_0781c [Mycobacterium bovis BCG str. Pasteur 1173P2]	78	6
gi|121639717	polyketide synthase pks13 [Mycobacterium bovis BCG str. Pasteur 1173P2]	78	23
gi|121638960	hypothetical protein BCG_3100c [Mycobacterium bovis BCG str. Pasteur 1173P2]	77	8
gi|121637373	hypothetical protein BCG_1504c [Mycobacterium bovis BCG str. Pasteur 1173P2]	76	4
gi|121636777	hypothetical protein BCG_0906 [Mycobacterium bovis BCG str. Pasteur 1173P2]	76	3
gi|121639467	short chain dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	76	6
gi|121638085	hypothetical protein BCG_2220c [Mycobacterium bovis BCG str. Pasteur 1173P2]	76	4
gi|121636384	putative mycolic acid synthase umaA1 [Mycobacterium bovis BCG str. Pasteur 1173P2]	75	10
gi|121639695	putative aminotransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	74	4
gi|121637212	Beta-carbonic anhydrase [Mycobacterium bovis BCG str. Pasteur 1173P2]	74	8
gi|121638420	putative transmembrane protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	73	7
gi|121636202	hypothetical protein BCG_0327 [Mycobacterium bovis BCG str. Pasteur 1173P2]	73	1
gi|121639625	aspartate kinase [Mycobacterium bovis BCG str. Pasteur 1173P2]	73	6
gi|121636968	putative ESAT-6 like protein 2 [Mycobacterium bovis BCG str. Pasteur 1173P2]	72	6
gi|121639026	putative response regulator [Mycobacterium bovis BCG str. Pasteur 1173P2]	72	4
gi|121636876	succinyl-CoA synthetase subunit beta [Mycobacterium bovis BCG str. Pasteur 1173P2]	72	7
gi|121636946	ribose-phosphate pyrophosphokinase [Mycobacterium bovis BCG str. Pasteur 1173P2]	72	14
gi|121637509	imidazole glycerol phosphate synthase subunit HisH [Mycobacterium bovis BCG str. Pasteur 1173P2]	70	2
gi|121636400	putative short-chain type oxidoreductase [Mycobacterium bovis BCG str. Pasteur 1173P2]	70	3
gi|121637560	N-acetyl-gamma-glutamyl-phosphate reductase [Mycobacterium bovis BCG str. Pasteur 1173P2]	70	8
gi|121639032	NADH dehydrogenase subunit E [Mycobacterium bovis BCG str. Pasteur 1173P2]	70	2
gi|121637112	putative polyketide beta-ketoacyl synthase pks3 [Mycobacterium bovis BCG str. Pasteur 1173P2]	70	12
gi|121637259	putative glycogen phosphorylase glgP [Mycobacterium bovis BCG str. Pasteur 1173P2]	69	22
gi|121636598	putative membrane protein mmpS5 [Mycobacterium bovis BCG str. Pasteur 1173P2]	69	2
gi|121638177	haloalkane dehalogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	68	9
gi|121637320	DNA-directed RNA polymerase subunit omega [Mycobacterium bovis BCG str. Pasteur 1173P2]	67	2
gi|121638094	leucyl aminopeptidase [Mycobacterium bovis BCG str. Pasteur 1173P2]	67	2
gi|121638843	putative glycosyl transferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	67	11
gi|121637135	acyl-CoA synthetase [Mycobacterium bovis BCG str. Pasteur 1173P2]	67	10
gi|121638927	putative cytochrome C oxidase polypeptide I ctaD [Mycobacterium bovis BCG str. Pasteur 1173P2]	67	8
gi|121638309	gamma-glutamyl phosphate reductase [Mycobacterium bovis BCG str. Pasteur 1173P2]	67	12
gi|121636306	putative secreted protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	66	2
gi|121636628	50S ribosomal protein L22 [Mycobacterium bovis BCG str. Pasteur 1173P2]	66	7
gi|121637520	tryptophan synthase subunit alpha [Mycobacterium bovis BCG str. Pasteur 1173P2]	66	4
gi|121639733	putative acyltransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	66	16

gi|121635925	transmembrane serine/threonine-protein kinase A pknA [Mycobacterium bovis BCG str. Pasteur 1173P2]	66	3
gi|121636422	hypothetical protein BCG_0547c [Mycobacterium bovis BCG str. Pasteur 1173P2]	66	2
gi|121639243	succinate dehydrogenase iron-sulfur subunit [Mycobacterium bovis BCG str. Pasteur 1173P2]	66	5
gi|121639650	hypothetical protein BCG_3794c [Mycobacterium bovis BCG str. Pasteur 1173P2]	66	7
gi|121637991	proteasome subunit alpha PrcA [Mycobacterium bovis BCG str. Pasteur 1173P2]	65	3
gi|121636477	putative secreted protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	65	1
gi|121637341	**putative lipoprotein lprG [Mycobacterium bovis BCG str. Pasteur 1173P2]**	65	1
gi|121639181	hypothetical protein BCG_3321 [Mycobacterium bovis BCG str. Pasteur 1173P2]	65	7
gi|121637610	putative catechol-o-methyltransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	65	8
gi|121637346	6,7-dimethyl-8-ribityllumazine synthase [Mycobacterium bovis BCG str. Pasteur 1173P2]	64	9
gi|121639582	putative transmembrane protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	64	4
gi|121638324	50S ribosomal protein L27 [Mycobacterium bovis BCG str. Pasteur 1173P2]	63	7
gi|121637563	acetylornithine aminotransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	63	7
gi|121638183	hypothetical protein BCG_2318 [Mycobacterium bovis BCG str. Pasteur 1173P2]	63	2
gi|121638058	putative 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase AroG [Mycobacterium bovis BCG str. Pasteur 1173P2]	62	7
gi|121639705	nucleoside diphosphate kinase regulator [Mycobacterium bovis BCG str. Pasteur 1173P2]	62	4
gi|121637226	transcription termination factor Rho [Mycobacterium bovis BCG str. Pasteur 1173P2]	62	19
gi|121636095	putative lysophospholipase [Mycobacterium bovis BCG str. Pasteur 1173P2]	62	2
gi|121637680	hypothetical protein BCG_1811c [Mycobacterium bovis BCG str. Pasteur 1173P2]	62	6
gi|121639035	NADH dehydrogenase subunit H [Mycobacterium bovis BCG str. Pasteur 1173P2]	61	11
gi|121638381	putative oxidase regulatory-related protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	61	2
gi|121638245	putative transmembrane protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	61	6
gi|121637054	6-phosphogluconate dehydrogenase-like protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	61	8
gi|121638757	major secreted immunogenic protein mpb70 precursor [Mycobacterium bovis BCG str. Pasteur 1173P2]	59	1
gi|121636364	putative transmembrane transport protein mmpL4 [Mycobacterium bovis BCG str. Pasteur 1173P2]	59	9
gi|121639232	uracil phosphoribosyltransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	59	7
gi|121636448	hypothetical protein BCG_0573 [Mycobacterium bovis BCG str. Pasteur 1173P2]	59	6
gi|121635951	leucyl-tRNA synthetase [Mycobacterium bovis BCG str. Pasteur 1173P2]	59	11
gi|121636084	MCE-family protein mce1D [Mycobacterium bovis BCG str. Pasteur 1173P2]	58	12
gi|121636639	30S ribosomal protein S14 [Mycobacterium bovis BCG str. Pasteur 1173P2]	58	4
gi|121636183	acyl-CoA synthetase [Mycobacterium bovis BCG str. Pasteur 1173P2]	58	7
gi|121637934	putative polyketide synthase pks12 [Mycobacterium bovis BCG str. Pasteur 1173P2]	58	33
gi|121636076	hypothetical protein BCG_0200 [Mycobacterium bovis BCG str. Pasteur 1173P2]	58	6
gi|121638763	ribosome recycling factor [Mycobacterium bovis BCG str. Pasteur 1173P2]	58	12
gi|121637685	hypothetical protein BCG_1816 [Mycobacterium bovis BCG str. Pasteur 1173P2]	57	22
gi|121636101	dihydroxy-acid dehydratase [Mycobacterium bovis BCG str. Pasteur 1173P2]	57	8
gi|121638509	putative transmembrane protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	57	3
gi|121637784	putative cytochrome p450 140 CYP140 [Mycobacterium bovis BCG str. Pasteur 1173P2]	57	16
gi|121636088	putative mce associated transmembrane protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	56	4
gi|121638743	methionine aminopeptidase [Mycobacterium bovis BCG str. Pasteur 1173P2]	56	1
gi|121637732	hypothetical protein BCG_1864 [Mycobacterium bovis BCG str. Pasteur 1173P2]	56	1

gi|121637466	putative ketoacyl reductase [Mycobacterium bovis BCG str. Pasteur 1173P2]	55	5
gi|121639169	putative propionyl-CoA carboxylase beta chain 5 accD5 [Mycobacterium bovis BCG str. Pasteur 1173P2]	55	10
gi|121639512	hypothetical protein BCG_3657 [Mycobacterium bovis BCG str. Pasteur 1173P2]	55	4
gi|121638933	putative monooxygenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	55	11
gi|121638986	putative cell division protein ftsX [Mycobacterium bovis BCG str. Pasteur 1173P2]	54	6
gi|121636267	heat shock protein transcriptional regulator HspR [Mycobacterium bovis BCG str. Pasteur 1173P2]	54	3
gi|121637407	hypothetical protein BCG_1538 [Mycobacterium bovis BCG str. Pasteur 1173P2]	54	2
gi|121638351	hypothetical protein BCG_2488c [Mycobacterium bovis BCG str. Pasteur 1173P2]	54	2
gi|121636128	hypothetical protein BCG_0253 [Mycobacterium bovis BCG str. Pasteur 1173P2]	54	1
gi|121635965	30S ribosomal protein S18 [Mycobacterium bovis BCG str. Pasteur 1173P2]	54	2
gi|121638939	hypothetical protein BCG_3079c [Mycobacterium bovis BCG str. Pasteur 1173P2]	53	1
gi|121637040	hypothetical protein BCG_1169c [Mycobacterium bovis BCG str. Pasteur 1173P2]	53	2
gi|121639180	AsnC family transcriptional regulator [Mycobacterium bovis BCG str. Pasteur 1173P2]	53	8
gi|121636247	hypothetical protein BCG_0372 [Mycobacterium bovis BCG str. Pasteur 1173P2]	53	2
gi|121636895	putative metal cation transporter P-type atpase ctpV [Mycobacterium bovis BCG str. Pasteur 1173P2]	53	9
gi|121638467	putative peptidyl-prolyl cis-trans isomerase B ppiB [Mycobacterium bovis BCG str. Pasteur 1173P2]	52	4
gi|121639053	hypothetical protein BCG_3193 [Mycobacterium bovis BCG str. Pasteur 1173P2]	52	5
gi|121638076	putative Rieske iron-sulfur protein QcrA [Mycobacterium bovis BCG str. Pasteur 1173P2]	52	10
gi|121637091	pterin-4-alpha-carbinolamine dehydratase [Mycobacterium bovis BCG str. Pasteur 1173P2]	52	2
gi|121638490	hypothetical protein BCG_2628c [Mycobacterium bovis BCG str. Pasteur 1173P2]	51	5
gi|121636365	putative membrane protein mmpS4 [Mycobacterium bovis BCG str. Pasteur 1173P2]	51	2
gi|121638776	putative mycobactin utilization protein viuB [Mycobacterium bovis BCG str. Pasteur 1173P2]	51	2
gi|121636385	mycolic acid synthase pcaA [Mycobacterium bovis BCG str. Pasteur 1173P2]	51	7
gi|121638987	putative cell division ATP-binding protein ftsE [Mycobacterium bovis BCG str. Pasteur 1173P2]	50	5
gi|121638782	hypothetical protein BCG_2922c [Mycobacterium bovis BCG str. Pasteur 1173P2]	50	2
gi|121638493	pyridoxal biosynthesis lyase PdxS [Mycobacterium bovis BCG str. Pasteur 1173P2]	50	5
gi|121638135	diacylglycerol kinase [Mycobacterium bovis BCG str. Pasteur 1173P2]	50	1
gi|121639723	phosphoribose diphosphate:decaprenyl-phosphate phosphoribosyltransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	50	1
gi|121639378	30S ribosomal protein S4 [Mycobacterium bovis BCG str. Pasteur 1173P2]	49	7
gi|121638585	RNA polymerase sigma factor SigB [Mycobacterium bovis BCG str. Pasteur 1173P2]	49	13
gi|121639501	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Mycobacterium bovis BCG str. Pasteur 1173P2]	49	4
gi|121636912	large-conductance mechanosensitive channel [Mycobacterium bovis BCG str. Pasteur 1173P2]	49	3
gi|121639724	putative transmembrane protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	48	1
gi|121639523	putative transmembrane protein rich in alanine and arginine and proline [Mycobacterium bovis BCG str. Pasteur 1173P2]	48	7
gi|121636222	hypothetical protein BCG_0347c [Mycobacterium bovis BCG str. Pasteur 1173P2]	48	3
gi|121639614	hypothetical protein BCG_3758 [Mycobacterium bovis BCG str. Pasteur 1173P2]	47	1
gi|121636223	putative integral membrane protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	47	6
gi|121638926	putative phosphoserine phosphatase serB2 [Mycobacterium bovis BCG str. Pasteur 1173P2]	47	4
gi|121639535	hypothetical protein BCG_3680c [Mycobacterium bovis BCG str. Pasteur 1173P2]	47	2
gi|121638252	putative chaperone protein dnaJ2 [Mycobacterium bovis BCG str. Pasteur 1173P2]	47	5
gi|121638160	putative dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	47	3

gi|121637639	succinic semialdehyde dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	46	6
gi|121636637	50S ribosomal protein L24 [Mycobacterium bovis BCG str. Pasteur 1173P2]	46	4
gi|121637377	glucose-6-phosphate 1-dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	46	2
gi|121638417	transcription antitermination protein NusB [Mycobacterium bovis BCG str. Pasteur 1173P2]	45	6
gi|121638868	isopropylmalate isomerase small subunit [Mycobacterium bovis BCG str. Pasteur 1173P2]	45	2
gi|121637992	proteasome subunit beta PrcB [Mycobacterium bovis BCG str. Pasteur 1173P2]	45	5
gi|121636944	50S ribosomal protein L25/general stress protein Ctc [Mycobacterium bovis BCG str. Pasteur 1173P2]	45	5
gi|121638092	glycine cleavage system aminomethyltransferase T [Mycobacterium bovis BCG str. Pasteur 1173P2]	44	1
gi|121636652	hypothetical protein BCG_0780 [Mycobacterium bovis BCG str. Pasteur 1173P2]	44	8
gi|121638893	aspartyl/glutamyl-tRNA amidotransferase subunit A [Mycobacterium bovis BCG str. Pasteur 1173P2]	43	5
gi|121638041	hypothetical protein BCG_2176c [Mycobacterium bovis BCG str. Pasteur 1173P2]	43	7
gi|121638331	valyl-tRNA synthetase [Mycobacterium bovis BCG str. Pasteur 1173P2]	43	16
gi|121635888	DNA gyrase subunit B [Mycobacterium bovis BCG str. Pasteur 1173P2]	42	15
gi|121637518	indole-3-glycerol-phosphate synthase [Mycobacterium bovis BCG str. Pasteur 1173P2]	42	8
gi|121639786	hypothetical protein BCG_3931 [Mycobacterium bovis BCG str. Pasteur 1173P2]	41	16
gi|121639559	DNA topoisomerase I [Mycobacterium bovis BCG str. Pasteur 1173P2]	41	20
gi|121636198	hypothetical protein BCG_0323 [Mycobacterium bovis BCG str. Pasteur 1173P2]	41	5
gi|121636776	putative pyruvate or indole-3-pyruvate decarboxylase pdc [Mycobacterium bovis BCG str. Pasteur 1173P2]	40	2
gi|121639190	putative phosphate-transport system transcriptional regulatory protein phoU homolog 1 phoY1 [Mycobacterium bovis BCG str. Pasteur 11	40	11
gi|121638120	peroxiredoxin AhpE [Mycobacterium bovis BCG str. Pasteur 1173P2]	40	2
gi|121638415	putative amino acid decarboxylase [Mycobacterium bovis BCG str. Pasteur 1173P2]	40	8
gi|121638576	putative extragenic suppressor protein suhB [Mycobacterium bovis BCG str. Pasteur 1173P2]	39	6
gi|121639030	NADH dehydrogenase subunit C [Mycobacterium bovis BCG str. Pasteur 1173P2]	39	3
gi|121637420	hypothetical protein BCG_1551 [Mycobacterium bovis BCG str. Pasteur 1173P2]	39	1
gi|121636631	50S ribosomal protein L29 [Mycobacterium bovis BCG str. Pasteur 1173P2]	39	5
gi|121638885	acetolactate synthase 1 catalytic subunit [Mycobacterium bovis BCG str. Pasteur 1173P2]	39	5
gi|121638052	hypothetical protein BCG_2187c [Mycobacterium bovis BCG str. Pasteur 1173P2]	39	9
gi|121636444	putative thioredoxin protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	39	3
gi|121639348	alanine racemase [Mycobacterium bovis BCG str. Pasteur 1173P2]	39	7
gi|121639037	NADH dehydrogenase subunit J [Mycobacterium bovis BCG str. Pasteur 1173P2]	39	2
gi|121639098	putative ATP-dependent RNA helicase rhlE [Mycobacterium bovis BCG str. Pasteur 1173P2]	38	7
gi|121637037	putative cholesterol dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	38	7
gi|121639716	putative propionyl-CoA carboxylase beta chain 4 accD4 [Mycobacterium bovis BCG str. Pasteur 1173P2]	38	6
gi|121637763	alanine and proline rich secreted protein apa [Mycobacterium bovis BCG str. Pasteur 1173P2]	38	1
gi|121637778	hypothetical protein BCG_1911 [Mycobacterium bovis BCG str. Pasteur 1173P2]	37	3
gi|121637657	putative integral membrane protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	37	6
gi|121637729	glycine cleavage system protein H [Mycobacterium bovis BCG str. Pasteur 1173P2]	37	3
gi|121637946	hypothetical protein BCG_2080c [Mycobacterium bovis BCG str. Pasteur 1173P2]	37	2
gi|121636301	phosphoribosylglycinamide formyltransferase 2 [Mycobacterium bovis BCG str. Pasteur 1173P2]	36	7
gi|121639721	secreted antigen 85-A fbpA [Mycobacterium bovis BCG str. Pasteur 1173P2]	36	4
gi|121638848	pyruvate carboxylase [Mycobacterium bovis BCG str. Pasteur 1173P2]	36	9

gi|121636184	putative acyl-CoA dehydrogenase fadE6 [Mycobacterium bovis BCG str. Pasteur 1173P2]	36	7
gi|121637646	hypothetical protein BCG_1777 [Mycobacterium bovis BCG str. Pasteur 1173P2]	36	2
gi|121639533	hypothetical protein BCG_3678c [Mycobacterium bovis BCG str. Pasteur 1173P2]	35	3
gi|121636417	pyrroline-5-carboxylate reductase [Mycobacterium bovis BCG str. Pasteur 1173P2]	35	10
gi|121637015	Short (C15) chain Z-isoprenyl diphosphate synthase [Mycobacterium bovis BCG str. Pasteur 1173P2]	35	3
gi|121639283	putative bifunctional protein folD: methylenetetrahydrofolate dehydrogenase + methenyltetrahydrofolate cyclohydrolase [Mycobacterium b	34	3
gi|121636466	naphthoate synthase [Mycobacterium bovis BCG str. Pasteur 1173P2]	34	5
gi|121639146	phosphomannomutase/phosphoglucomutase [Mycobacterium bovis BCG str. Pasteur 1173P2]	34	10
gi|121637913	histidine kinase response regulator [Mycobacterium bovis BCG str. Pasteur 1173P2]	33	12
gi|121637391	hypothetical protein BCG_1522 [Mycobacterium bovis BCG str. Pasteur 1173P2]	33	12
gi|121636073	putative oxidoreductase [Mycobacterium bovis BCG str. Pasteur 1173P2]	33	6
gi|121637910	hypothetical protein BCG_2043c [Mycobacterium bovis BCG str. Pasteur 1173P2]	33	21
gi|121639800	hypothetical protein BCG_3945c [Mycobacterium bovis BCG str. Pasteur 1173P2]	33	9
gi|121638547	putative secreted protease [Mycobacterium bovis BCG str. Pasteur 1173P2]	32	10
gi|121639019	PPE family protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	32	12
gi|121637536	DNA polymerase I [Mycobacterium bovis BCG str. Pasteur 1173P2]	32	18
gi|121636150	**putative lipoprotein lpqI [Mycobacterium bovis BCG str. Pasteur 1173P2]**	32	9
gi|121639637	DNA polymerase III subunits gamma and tau [Mycobacterium bovis BCG str. Pasteur 1173P2]	32	6
gi|121636921	putative molybdopterin biosynthesis protein moeA1 [Mycobacterium bovis BCG str. Pasteur 1173P2]	32	8
gi|121638378	putative pyruvate dehydrogenase E1 component subunit beta pdhB [Mycobacterium bovis BCG str. Pasteur 1173P2]	31	3
gi|121636296	putative secreted protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	31	9
gi|121639493	putative acyl-CoA dehydrogenase fadE34 [Mycobacterium bovis BCG str. Pasteur 1173P2]	31	8
gi|121638768	putative transcriptional regulatory protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	31	11
gi|121638819	putative daunorubicin-DIM-transport integral membrane protein ABC transporter drrB [Mycobacterium bovis BCG str. Pasteur 1173P2]	31	2
gi|121637723	hypothetical protein BCG_1855 [Mycobacterium bovis BCG str. Pasteur 1173P2]	31	3
gi|121638839	putative glycosyl transferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	31	3
gi|121637464	putative fatty acyl-CoA reductase [Mycobacterium bovis BCG str. Pasteur 1173P2]	31	7
gi|121639495	LacI family transcriptional regulator [Mycobacterium bovis BCG str. Pasteur 1173P2]	31	7
gi|121638320	NAD synthetase [Mycobacterium bovis BCG str. Pasteur 1173P2]	30	17
gi|121638175	putative aminotransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	30	5
gi|121638455	hypothetical protein BCG_2593 [Mycobacterium bovis BCG str. Pasteur 1173P2]	30	4
gi|121636061	putative quinone oxidoreductase [Mycobacterium bovis BCG str. Pasteur 1173P2]	30	3
gi|121637771	hypothetical protein BCG_1904 [Mycobacterium bovis BCG str. Pasteur 1173P2]	30	7
gi|121638827	**putative lipoprotein lppX [Mycobacterium bovis BCG str. Pasteur 1173P2]**	30	4
gi|121637655	putative transmembrane ATP-binding protein ABC transporter [Mycobacterium bovis BCG str. Pasteur 1173P2]	29	12
gi|121636312	putative acyl-CoA dehydrogenase fadE7 [Mycobacterium bovis BCG str. Pasteur 1173P2]	29	8
gi|121638836	hypothetical protein BCG_2976c [Mycobacterium bovis BCG str. Pasteur 1173P2]	29	4
gi|121637056	putative epoxide hydrolase ephC [Mycobacterium bovis BCG str. Pasteur 1173P2]	29	6
gi|121636397	hypothetical protein BCG_0522c [Mycobacterium bovis BCG str. Pasteur 1173P2]	29	2
gi|121636369	hypothetical protein BCG_0494c [Mycobacterium bovis BCG str. Pasteur 1173P2]	29	1
gi|121636102	hypothetical protein BCG_0227 [Mycobacterium bovis BCG str. Pasteur 1173P2]	29	7

gi|121636372	putative peptidase [Mycobacterium bovis BCG str. Pasteur 1173P2]	29	16
gi|121636014	putative peptide synthetase nrp [Mycobacterium bovis BCG str. Pasteur 1173P2]	29	16
gi|121636568	hypothetical protein BCG_0696c [Mycobacterium bovis BCG str. Pasteur 1173P2]	29	13
gi|121638111	bifunctional RNase H/acid phosphatase [Mycobacterium bovis BCG str. Pasteur 1173P2]	29	6
gi|121638218	hypothetical protein BCG_2353 [Mycobacterium bovis BCG str. Pasteur 1173P2]	29	6
gi|121636636	50S ribosomal protein L14 [Mycobacterium bovis BCG str. Pasteur 1173P2]	28	5
gi|121637506	histidinol dehydrogenase [Mycobacterium bovis BCG str. Pasteur 1173P2]	28	4
gi|121639771	ribonuclease activity regulator protein RraA [Mycobacterium bovis BCG str. Pasteur 1173P2]	28	2
gi|121636920	putative UTP--glucose-1-phosphate uridylyltransferase galU [Mycobacterium bovis BCG str. Pasteur 1173P2]	28	5
gi|121639357	glucosamine--fructose-6-phosphate aminotransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	28	3
gi|121638032	cell division protein FtsZ [Mycobacterium bovis BCG str. Pasteur 1173P2]	28	5
gi|121638802	putative cell division protein ftsY [Mycobacterium bovis BCG str. Pasteur 1173P2]	28	8
gi|121639179	L-lysine aminotransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	28	7
gi|121636874	putative ATP dependent DNA helicase uvrD1 [Mycobacterium bovis BCG str. Pasteur 1173P2]	28	12
gi|121637357	acyl-CoA synthetase [Mycobacterium bovis BCG str. Pasteur 1173P2]	28	6
gi|121636415	hypothetical protein BCG_0540 [Mycobacterium bovis BCG str. Pasteur 1173P2]	28	2
gi|121635970	hypothetical protein BCG_0091 [Mycobacterium bovis BCG str. Pasteur 1173P2]	27	6
gi|121638340	ATP-dependent protease ATP-binding subunit ClpX [Mycobacterium bovis BCG str. Pasteur 1173P2]	27	5
gi|121636495	hypothetical protein BCG_0622 [Mycobacterium bovis BCG str. Pasteur 1173P2]	27	1
gi|121636812	citrate synthase 2 [Mycobacterium bovis BCG str. Pasteur 1173P2]	27	7
gi|121638462	hypothetical protein BCG_2600 [Mycobacterium bovis BCG str. Pasteur 1173P2]	27	8
gi|121636655	adenylate kinase [Mycobacterium bovis BCG str. Pasteur 1173P2]	27	6
gi|121637093	putative respiratory nitrate reductase (alpha chain) narG [Mycobacterium bovis BCG str. Pasteur 1173P2]	27	13
gi|121637450	acyl-CoA synthetase [Mycobacterium bovis BCG str. Pasteur 1173P2]	27	7
gi|121637566	argininosuccinate synthase [Mycobacterium bovis BCG str. Pasteur 1173P2]	27	3
gi|121636747	putative transcriptional regulatory protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	27	5
gi|121639474	hypothetical protein BCG_3619c [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	2
gi|121639086	putative ATP-dependent DNA helicase [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	24
gi|121636075	hypothetical protein BCG_0199 [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	2
gi|121638210	AsnC family transcriptional regulator [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	6
gi|121636960	potassium-transporting ATPase subunit B [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	7
gi|121637372	putative biotin sulfoxide reductase bisC [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	12
gi|121638553	uroporphyrinogen decarboxylase [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	3
gi|121638212	putative transmembrane ATP-binding protein ABC transporter [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	11
gi|121638816	phenolpthiocerol synthesis type-I polyketide synthase ppsD [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	27
gi|121639628	putative ligase [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	8
gi|121636389	putative transmembrane protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	26
gi|121636266	putative chaperone protein dnaJ1 [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	11
gi|121639153	putative mannose-1-phosphate guanyltransferase manC [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	6
gi|121639261	hypothetical protein BCG_3403c [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	7
gi|121636705	putative protease II ptrB (oligopeptidase B) [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	8

gi|121636743	hypothetical protein BCG_0871 [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	4
gi|121636596	enoyl-CoA hydratase [Mycobacterium bovis BCG str. Pasteur 1173P2]	26	18
gi|121637515	putative peroxidoxin bcpB [Mycobacterium bovis BCG str. Pasteur 1173P2]	25	5
gi|121637521	**prolipoprotein diacylglyceryl transferase [Mycobacterium bovis BCG str. Pasteur 1173P2]**	25	6
gi|121637937	polyprenol-monophosphomannose synthase Ppm1 [Mycobacterium bovis BCG str. Pasteur 1173P2]	25	12
gi|121639077	hypothetical protein BCG_3217 [Mycobacterium bovis BCG str. Pasteur 1173P2]	25	3
gi|121637802	hypothetical protein BCG_1935c [Mycobacterium bovis BCG str. Pasteur 1173P2]	25	12
gi|121639421	3-ketoacyl-(acyl-carrier-protein) reductase [Mycobacterium bovis BCG str. Pasteur 1173P2]	25	9
gi|121636742	transcriptional regulatory protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	25	2
gi|121637709	PPE family protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	25	8
gi|121637507	histidinol-phosphate aminotransferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	25	6
gi|121638473	preprotein translocase subunit YajC [Mycobacterium bovis BCG str. Pasteur 1173P2]	25	1
gi|121639159	putative metal cation-transporting P-type atpase C ctpC [Mycobacterium bovis BCG str. Pasteur 1173P2]	25	10
gi|121638628	3-ketoacyl-(acyl-carrier-protein) reductase [Mycobacterium bovis BCG str. Pasteur 1173P2]	25	3
gi|121637681	hypothetical protein BCG_1812c [Mycobacterium bovis BCG str. Pasteur 1173P2]	25	8
gi|121636930	arginine deiminase [Mycobacterium bovis BCG str. Pasteur 1173P2]	24	10
gi|121636792	molybdenum cofactor biosynthesis protein A [Mycobacterium bovis BCG str. Pasteur 1173P2]	24	10
gi|121636345	putative tuberculin related peptide [Mycobacterium bovis BCG str. Pasteur 1173P2]	23	4
gi|121636100	putative transmembrane protein [Mycobacterium bovis BCG str. Pasteur 1173P2]	23	1
gi|121639756	prephenate dehydratase [Mycobacterium bovis BCG str. Pasteur 1173P2]	22	4
gi|121639725	galactofuranosyl transferase [Mycobacterium bovis BCG str. Pasteur 1173P2]	22	5
gi|121639712	integral membrane indolylacetylinositol arabinosyltransferase embB [Mycobacterium bovis BCG str. Pasteur 1173P2]	22	8
gi|121639521	pantoate--beta-alanine ligase [Mycobacterium bovis BCG str. Pasteur 1173P2]	21	6
gi|121637235	F0F1 ATP synthase subunit B [Mycobacterium bovis BCG str. Pasteur 1173P2]	18	8
gi|121636485	putative methyltransferase/methylase [Mycobacterium bovis BCG str. Pasteur 1173P2]	18	11

Supporting Table 5. ***M. tuberculosis*** **H37Rv cellular proteins**

Accesion number	Protein name	Score	Unique peptides
gi|1806151	PROBABLE IRON-REGULATED ELONGATION FACTOR TU TUF (EF-TU) [Mycobacterium tuberculosis H37Rv]	2181	78
gi|2104319	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	2047	66
gi|2094829	PROBABLE CHAPERONE PROTEIN DNAK (HEAT SHOCK PROTEIN 70) (HEAT SHOCK 70 KDA PROTEIN) (HSP70) [Mycobac	1921	77
gi|3261680	POSSIBLE L-LACTATE DEHYDROGENASE (CYTOCHROME) LLDD2 [Mycobacterium tuberculosis H37Rv]	1611	64
gi|2117227	PROBABLE 5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE METE (methioni	1460	55
gi|1449370	60 KDA CHAPERONIN 1 GROEL1 (PROTEIN CPN60-1) (GROEL PROTEIN 1) [Mycobacterium tuberculosis H37Rv]	1445	47
gi|3261568	GLUTAMINE SYNTHETASE GLNA1 (GLUTAMINE SYNTHASE) (GS-I) [Mycobacterium tuberculosis H37Rv]	1277	34
gi|2143292	DNA-DIRECTED RNA POLYMERASE (BETA~ CHAIN) RPOC (TRANSCRIPTASE BETA~ CHAIN) (RNA POLYMERASE BETA~	1133	40
gi|1877273	PROBABLE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE [Mycobacterium tuberculosis H37Rv]	1027	18
gi|41353447	CONSERVED 35 KDA ALANINE RICH PROTEIN [Mycobacterium tuberculosis H37Rv]	975	26
gi|1322432	PROBABLE ATP SYNTHASE ALPHA CHAIN ATPA [Mycobacterium tuberculosis H37Rv]	958	42
gi|1322434	PROBABLE ATP SYNTHASE BETA CHAIN ATPD [Mycobacterium tuberculosis H37Rv]	878	36
gi|2225952	CATALASE-PEROXIDASE-PEROXYNITRITASE T KATG [Mycobacterium tuberculosis H37Rv]	867	36
gi|2224820	PROBABLE POLYKETIDE SYNTHASE PKS2 [Mycobacterium tuberculosis H37Rv]	849	44
gi|1261947	3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE 1 KASA (BETA-KETOACYL-ACP SYNTHASE) (KAS I) [Mycobacterium tu	842	19
gi|2909473	POSSIBLE CONSERVED MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	830	41
gi|2950419	POLYKETIDE SYNTHASE PKS13 [Mycobacterium tuberculosis H37Rv]	787	58
gi|3261686	PROBABLE FATTY ACID SYNTHASE FAS (FATTY ACID SYNTHETASE) [Mycobacterium tuberculosis H37Rv]	769	47
gi|2791626	PROBABLE ELECTRON TRANSFER FLAVOPROTEIN (ALPHA-SUBUNIT) FIXB (ALPHA-ETF) (ELECTRON TRANSFER FLAV	760	24
gi|1781116	POSSIBLE BACTERIOFERRITIN BFRB [Mycobacterium tuberculosis H37Rv]	754	25
gi|2104333	CONSERVED HYPOTHETICAL PROTEIN WAG31 [Mycobacterium tuberculosis H37Rv]	740	25
gi|2695965	PROBABLE POLYKETIDE BETA-KETOACYL SYNTHASE PKS4 [Mycobacterium tuberculosis H37Rv]	730	35
gi|2104380	PROBABLE DNA-DIRECTED RNA POLYMERASE (ALPHA CHAIN) RPOA (TRANSCRIPTASE ALPHA CHAIN) (RNA POLYMER	698	17
gi|2950420	PROBABLE FATTY-ACID-CoA LIGASE FADD32 (FATTY-ACID-CoA SYNTHETASE) (FATTY-ACID-CoA SYNTHASE [Mycobacte	689	30
gi|1877340	PROBABLE BIFUNCTIONAL PROTEIN ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE (ALPHA CHAIN) ACCA3: BIOTI	641	21
gi|2791409	PROBABLE IRON-REGULATED ACONITATE HYDRATASE ACN (Citrate hydro-lyase) (Aconitase) [Mycobacterium tuberculosis	637	20
gi|2131060	PROBABLE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE GAP (GAPDH) [Mycobacterium tuberculosis H37Rv]	632	16
gi|2916889	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	616	18
gi|1694845	PROBABLE DNA-BINDING PROTEIN HU HOMOLOG HUPB (HISTONE-LIKE PROTEIN) (HLP) (21-KDA LAMININ-2-BINDING P	610	24
gi|2909446	PROBABLE 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE FABG4 (3-KETOACYL-ACYL CARRIER PROTEIN REDUC	608	21
gi|1552563	PROBABLE IRON-REGULATED PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A PPIA (PPIase A) (ROTAMASE A) [Mycobacter	599	12
gi|1449273	IRON-REGULATED HEPARIN BINDING HEMAGGLUTININ HBHA (ADHESIN) [Mycobacterium tuberculosis H37Rv]	597	15
gi|41353623	**PERIPLASMIC PHOSPHATE-BINDING LIPOPROTEIN PSTS1 (PBP-1) (PSTS1) [Mycobacterium tuberculosis H37Rv]**	595	14
gi|2094844	PROBABLE FRUCTOSE-BISPHOSPHATE ALDOLASE FBA [Mycobacterium tuberculosis H37Rv]	589	17
gi|2791627	PROBABLE ELECTRON TRANSFER FLAVOPROTEIN (BETA-SUBUNIT) FIXA (BETA-ETF) (ELECTRON TRANSFER FLAVOP	582	13
gi|2916918	POSSIBLE ACYL-CoA THIOLASE FADA [Mycobacterium tuberculosis H37Rv]	555	15

gi|2960187	**19 KDA LIPOPROTEIN ANTIGEN PRECURSOR LPQH [Mycobacterium tuberculosis H37Rv]**	545	9
gi|38490389	6 KDA EARLY SECRETORY ANTIGENIC TARGET ESXA (ESAT-6) [Mycobacterium tuberculosis H37Rv]	542	7
gi|1449302	CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE 2 CMAA2 (CYCLOPROPANE FATTY ACID SYNTHASE) (CFA SY	541	19
gi|1314035	PROBABLE CITRATE SYNTHASE I GLTA2 [Mycobacterium tuberculosis H37Rv]	532	16
gi|2960100	PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN (PROBABLY CRP/FNR-FAMILY) [Mycobacterium tuberculosis H37R	525	17
gi|2909481	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	504	20
gi|2143293	DNA-DIRECTED RNA POLYMERASE (BETA CHAIN) RPOB (TRANSCRIPTASE BETA CHAIN) (RNA POLYMERASE BETA SUB	482	39
gi|2225974	SECRETED ANTIGEN 85-B FBPB (85B) (ANTIGEN 85 COMPLEX B) (MYCOLYL TRANSFERASE 85B) (FIBRONECTIN-BINDIN	458	14
gi|2072715	PROBABLE ADENOSYLHOMOCYSTEINASE SAHH (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) [Mycoba	450	17
gi|2104288	CONSERVED HYPOTHETICAL PROTEIN TB31.7 [Mycobacterium tuberculosis H37Rv]	434	17
gi|3261676	PROBABLE MULTIFUNCTIONAL MYCOCEROSIC ACID SYNTHASE MEMBRANE-ASSOCIATED MAS [Mycobacterium tubercul	430	39
gi|1524210	PROBABLE SUCCINYL-CoA SYNTHETASE (ALPHA CHAIN) SUCD (SCS-ALPHA) [Mycobacterium tuberculosis H37Rv]	427	16
gi|1403402	RIBOSOME RECYCLING FACTOR FRR (RIBOSOME RELEASING FACTOR) (RRF) [Mycobacterium tuberculosis H37Rv]	416	18
gi|1552559	DNA GYRASE (SUBUNIT A) GYRA (DNA TOPOISOMERASE (ATP-HYDROLYSING)) (DNA TOPOISOMERASE II) (TYPE II DNA	413	15
gi|38490278	PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN MOXR1 [Mycobacterium tuberculosis H37Rv]	409	12
gi|1648889	PROBABLE ENOYL-CoA HYDRATASE ECHA16 (ENOYL HYDRASE) (UNSATURATED ACYL-CoA HYDRATASE) (CROTONAS	388	12
gi|2113914	PROBABLE RIBOSOMAL PROTEIN S1 RPSA [Mycobacterium tuberculosis H37Rv]	381	26
gi|2896731	POSSIBLE ACYL-[ACYL-CARRIER PROTEIN] DESATURASE DESA2 (ACYL-[ACP] DESATURASE) (STEAROYL-ACP DESATU	380	14
gi|2909472	POSSIBLE CONSERVED MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	379	16
gi|1449324	Probable haloalkane dehalogenase [Mycobacterium tuberculosis H37Rv]	379	17
gi|41353706	PROBABLE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1 CLPP1 (ENDOPEPTIDASE CLP) [Mycobacterium t	375	14
gi|2695834	PROBABLE 2-OXOGLUTARATE DEHYDROGENASE SUCA (Alpha-ketoglutarate dehydrogenase) [Mycobacterium tuberculosis H	375	24
gi|2896711	PROBABLE BETA-KETOACYL CoA THIOLASE FADA3 [Mycobacterium tuberculosis H37Rv]	374	17
gi|3256013	PROBABLE S-ADENOSYLMETHIONINE SYNTHETASE METK (MAT) (AdoMet synthetase) (Methionine adenosyltransferase) [My	372	14
gi|41352771	PROBABLE D-3-PHOSPHOGLYCERATE DEHYDROGENASE SERA1 (PGDH) [Mycobacterium tuberculosis H37Rv]	362	16
gi|1870005	PROBABLE ENOLASE ENO [Mycobacterium tuberculosis H37Rv]	359	15
gi|2911007	PROBABLE ADENYLATE KINASE ADK (ATP-AMP TRANSPHOSPHORYLASE) [Mycobacterium tuberculosis H37Rv]	358	13
gi|1781110	SUPEROXIDE DISMUTASE [FE] SODA [Mycobacterium tuberculosis H37Rv]	356	18
gi|2909471	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	355	24
gi|3261551	PROBABLE ACYL-CoA DEHYDROGENASE FADE10 [Mycobacterium tuberculosis H37Rv]	349	18
gi|1850115	PROBABLE FATTY-ACID-CoA LIGASE FADD2 (FATTY-ACID-CoA SYNTHETASE) (FATTY-ACID-CoA SYNTHASE) [Mycobacter	339	19
gi|2695826	PROBABLE MALATE DEHYDROGENASE MDH [Mycobacterium tuberculosis H37Rv]	330	14
gi|1403410	PROBABLE ELONGATION FACTOR TSF (EF-TS) [Mycobacterium tuberculosis H37Rv]	318	13
gi|1524234	POSSIBLE EXPORTED CONSERVED PROTEIN [Mycobacterium tuberculosis H37Rv]	316	24
gi|2076692	PROBABLE THIOSULFATE SULFURTRANSFERASE CYSA3 (RHODANESE-LIKE PROTEIN) (THIOSULFATE CYANIDE TRANS	311	16
gi|1524230	NADH-DEPENDENT ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE INHA (NADH-DEPENDENT ENOYL-ACP REDUCTASE	308	11
gi|2896715	Probable Proline-rich antigen homolog pra [Mycobacterium tuberculosis H37Rv]	307	10
gi|2909636	CONSERVED HYPOTHETICAL PROTEIN TB27.3 [Mycobacterium tuberculosis H37Rv]	307	5
gi|2791516	PROBABLE NAD-DEPENDENT GLUTAMATE DEHYDROGENASE GDH (NAD-GDH) (NAD-DEPENDENT GLUTAMIC DEHYDR	304	29
gi|2924475	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	294	7
gi|2909447	PROBABLE ACETYL-CoA ACYLTRANSFERASE FADA2 (3-KETOACYL-CoA THIOLASE) (BETA-KETOTHIOLASE) [Mycobacteri	291	6

gi|2078052	TRANSMEMBRANE SERINE/THREONINE-PROTEIN KINASE D PKND (PROTEIN KINASE D) (STPK D) [Mycobacterium tubercu	291	12
gi|1694860	PROBABLE OXIDOREDUCTASE [Mycobacterium tuberculosis H37Rv]	290	9
gi|2916919	PROBABLE FATTY OXIDATION PROTEIN FADB [Mycobacterium tuberculosis H37Rv]	289	14
gi|1449369	10 KDA CHAPERONIN GROES (PROTEIN CPN10) (PROTEIN GROES) (BCG-A HEAT SHOCK PROTEIN) (10 KDA ANTIGEN) [	287	14
gi|1877369	PROBABLE ENOYL-CoA HYDRATASE ECHA3 (ENOYL HYDRASE) (UNSATURATED ACYL-CoA HYDRATASE) (CROTONASE	285	15
gi|1877272	PROBABLE ALDEHYDE DEHYDROGENASE (NAD+) DEPENDENT [Mycobacterium tuberculosis H37Rv]	280	13
gi|1261943	Probable pyruvate dehydrogenase E1 component aceE (PYRUVATE DECARBOXYLASE) (PYRUVATE DEHYDROGENASE) (PY	273	12
gi|2072661	POSSIBLE IRON-REGULATED SHORT-CHAIN DEHYDROGENASE/REDUCTASE [Mycobacterium tuberculosis H37Rv]	267	15
gi|1877382	METHOXY MYCOLIC ACID SYNTHASE 2 MMAA2 (METHYL MYCOLIC ACID SYNTHASE 2) (MMA2) (HYDROXY MYCOLIC AC	267	7
gi|2911107	Probable long-chain-fatty-acid-CoA ligase fadD15 (FATTY-ACID-CoA SYNTHETASE) (FATTY-ACID-CoA SYNTHASE) [Mycobact	252	11
gi|38490383	SECRETED MPT51/MPB51 ANTIGEN PROTEIN FBPD (MPT51/MPB51 ANTIGEN 85 COMPLEX C) (AG58C) (MYCOLYL TRAN	252	6
gi|1877389	PROBABLE 50S RIBOSOMAL PROTEIN L10 RPLJ [Mycobacterium tuberculosis H37Rv]	251	7
gi|2131048	PROBABLE TRANSALDOLASE TAL [Mycobacterium tuberculosis H37Rv]	248	14
gi|2076674	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	248	5
gi|41352812	PROBABLE ATP-DEPENDENT PROTEASE ATP-BINDING SUBUNIT CLPC1 [Mycobacterium tuberculosis H37Rv]	248	27
gi|1449340	Probable dehydrogenase [Mycobacterium tuberculosis H37Rv]	247	5
gi|1322433	PROBABLE ATP SYNTHASE GAMMA CHAIN ATPG [Mycobacterium tuberculosis H37Rv]	246	12
gi|3256016	**PROBABLE CONSERVED LIPOPROTEIN LPRG [Mycobacterium tuberculosis H37Rv]**	246	6
gi|2094830	PROBABLE GRPE PROTEIN (HSP-70 COFACTOR) [Mycobacterium tuberculosis H37Rv]	244	9
gi|2104379	PROBABLE 50S RIBOSOMAL PROTEIN L17 RPLQ [Mycobacterium tuberculosis H37Rv]	239	8
gi|2896735	PROBABLE FUMARASE FUM (Fumarate hydratase) [Mycobacterium tuberculosis H37Rv]	238	14
gi|2695964	PROBABLE POLYKETIDE BETA-KETOACYL SYNTHASE PKS3 [Mycobacterium tuberculosis H37Rv]	238	12
gi|2104381	PROBABLE 30S RIBOSOMAL PROTEIN S4 RPSD [Mycobacterium tuberculosis H37Rv]	236	13
gi|1871605	PROBABLE ACYL-CoA DEHYDROGENASE FADE4 [Mycobacterium tuberculosis H37Rv]	233	11
gi|2791584	PROBABLE 3-ISOPROPYLMALATE DEHYDRATASE (SMALL SUBUNIT) LEUD (ISOPROPYLMALATE ISOMERASE) (ALPHA-I	232	7
gi|1877329	PROBABLE ACYL-CoA DEHYDROGENASE FADE25 [Mycobacterium tuberculosis H37Rv]	230	14
gi|1877380	METHOXY MYCOLIC ACID SYNTHASE 4 MMAA4 (METHYL MYCOLIC ACID SYNTHASE 4) (MMA4) (HYDROXY MYCOLIC AC	230	13
gi|2253068	Probable oxidoreductase [Mycobacterium tuberculosis H37Rv]	230	11
gi|1806169	PROBABLE 50S RIBOSOMAL PROTEIN L3 RPLC [Mycobacterium tuberculosis H37Rv]	228	7
gi|1524211	PROBABLE SUCCINYL-CoA SYNTHETASE (BETA CHAIN) SUCC (SCS-BETA) [Mycobacterium tuberculosis H37Rv]	228	13
gi|1261948	3-OXOACYL-[ACYL-CARRIER PROTEIN] SYNTHASE 2 KASB (BETA-KETOACYL-ACP SYNTHASE) (KAS I) [Mycobacterium tu	228	13
gi|2960116	PROBABLE METHANOL DEHYDROGENASE TRANSCRIPTIONAL REGULATORY PROTEIN MOXR2 [Mycobacterium tuberculo	224	6
gi|1237053	PROBABLE TRANSMEMBRANE CYTOCHROME C OXIDASE (SUBUNIT II) CTAC [Mycobacterium tuberculosis H37Rv]	222	8
gi|2916913	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	222	7
gi|3261597	**POSSIBLE LIPOPROTEIN LPRA [Mycobacterium tuberculosis H37Rv]**	222	6
gi|1403448	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	222	12
gi|1261924	PROBABLE GLUTAMINE SYNTHETASE GLNA2 (GLUTAMINE SYNTHASE) (GS-II) [Mycobacterium tuberculosis H37Rv]	219	13
gi|38490238	PROBABLE ACYL-[ACYL-CARRIER PROTEIN] DESATURASE DESA1 (ACYL-[ACP] DESATURASE) (STEAROYL-ACP DESAT	219	13
gi|1483534	PROBABLE MALATE SYNTHASE G GLCB [Mycobacterium tuberculosis H37Rv]	213	20
gi|2143306	POSSIBLE RIBONUCLEOTIDE-TRANSPORT ATP-BINDING PROTEIN ABC TRANSPORTER MKL [Mycobacterium tuberculosis	209	15
gi|2117241	Probable nicotinate-nucleotide pyrophosphatase nadC [Mycobacterium tuberculosis H37Rv]	207	3

gi|1483544	CONSERVED HYPOTHETICAL PROTEIN CFP17 [Mycobacterium tuberculosis H37Rv]	205	6
gi|2911027	PROBABLE METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE MMSA (METHYLMALONIC ACID SEMIALDEHYDE DE	205	12
gi|1877379	PROBABLE 50S RIBOSOMAL PROTEIN L1 RPLA [Mycobacterium tuberculosis H37Rv]	204	15
gi|2909544	PROBABLE 3-HYDROXYBUTYRYL-CoA DEHYDROGENASE FADB2 (BETA-HYDROXYBUTYRYL-CoA DEHYDROGENASE) (B	202	9
gi|38490231	POSSIBLE ZINC-CONTAINING ALCOHOL DEHYDROGENASE NAD DEPENDENT ADHB [Mycobacterium tuberculosis H37Rv]	201	7
gi|2909479	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	198	10
gi|2113992	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	197	15
gi|1806172	PROBABLE 50S ribosomal protein L2 RPLB [Mycobacterium tuberculosis H37Rv]	196	11
gi|3242248	PROBABLE OXIDOREDUCTASE [Mycobacterium tuberculosis H37Rv]	196	14
gi|1806170	PROBABLE 50S RIBOSOMAL PROTEIN L4 RPLD [Mycobacterium tuberculosis H37Rv]	194	8
gi|1403498	Possible ketoacyl reductase [Mycobacterium tuberculosis H37Rv]	194	6
gi|2225984	PROBABLE BACTERIOFERRITIN BFRA [Mycobacterium tuberculosis H37Rv]	193	10
gi|2113960	CONSERVED HYPOTHETICAL ALANINE AND GLYCINE RICH PROTEIN [Mycobacterium tuberculosis H37Rv]	189	4
gi|2661668	POSSIBLE DEHYDROGENASE [Mycobacterium tuberculosis H37Rv]	188	11
gi|1870013	PROBABLE 50S RIBOSOMAL PROTEIN L25 RPLY [Mycobacterium tuberculosis H37Rv]	187	7
gi|2113962	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	185	7
gi|2909534	PROBABLE ALDEHYDE DEHYDROGENASE [Mycobacterium tuberculosis H37Rv]	184	7
gi|2808723	PROBABLE ISOCITRATE DEHYDROGENASE [NADP] ICD2 (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+-SPECIFIC	183	15
gi|3261618	PROBABLE GLUTAMINE-TRANSPORT TRANSMEMBRANE PROTEIN ABC TRANSPORTER [Mycobacterium tuberculosis H37R	182	7
gi|38490291	ALANINE AND PROLINE RICH SECRETED PROTEIN APA (FIBRONECTIN ATTACHMENT PROTEIN) (Immunogenic protein MP	182	5
gi|2213511	MCE-FAMILY PROTEIN MCE1F [Mycobacterium tuberculosis H37Rv]	181	6
gi|1877335	PROBABLE PROPIONYL-CoA CARBOXYLASE BETA CHAIN 5 ACCD5 (PCCASE) (PROPANOYL-COA:CARBON DIOXIDE LIGA	180	9
gi|1781234	TWO COMPONENT TRANSCRIPTIONAL REGULATORY PROTEIN DEVR (PROBABLY LUXR/UHPA-FAMILY) [Mycobacterium t	179	13
gi|2104363	PROBABLE 30S RIBOSOMAL PROTEIN S9 RPSI [Mycobacterium tuberculosis H37Rv]	177	5
gi|1314045	POSSIBLE ENOYL-CoA HYDRATASE ECHA6 (ENOYL HYDRASE) (UNSATURATED ACYL-CoA HYDRATASE) (CROTONASE)	177	8
gi|2213507	MCE-FAMILY PROTEIN MCE1B [Mycobacterium tuberculosis H37Rv]	176	13
gi|2791500	PROBABLE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 2 CLPP2 (ENDOPEPTIDASE CLP 2) [Mycobacterium	175	8
gi|2213524	PROBABLE O-METHYLTRANSFERASE [Mycobacterium tuberculosis H37Rv]	174	4
gi|1806237	PROBABLE ACYL-CoA LIGASE FADD31 (ACYL-COA SYNTHETASE) (ACYL-CoA SYNTHASE) [Mycobacterium tuberculosis H37	173	12
gi|2911004	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	173	12
gi|3242284	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	172	6
gi|1806184	PROBABLE 50S RIBOSOMAL PROTEIN L5 RPLE [Mycobacterium tuberculosis H37Rv]	169	7
gi|1666140	POSSIBLE RIBONUCLEASE E RNE [Mycobacterium tuberculosis H37Rv]	169	13
gi|38684052	POSSIBLE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE [NADP+] DEPENDENT (SSDH) GABD2 [Mycobacterium tubercul	167	8
gi|38490217	PROBABLE PREPROTEIN TRANSLOCASE SECE1 [Mycobacterium tuberculosis H37Rv]	167	2
gi|38490186	POSSIBLE MYCOLIC ACID SYNTHASE UMAA [Mycobacterium tuberculosis H37Rv]	165	7
gi|1403431	PROBABLE 30S RIBOSOMAL PROTEIN S16 RPSP [Mycobacterium tuberculosis H37Rv]	159	10
gi|1237072	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	159	6
gi|2909625	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	156	5
gi|1449322	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	155	7
gi|1403475	IMMUNOGENIC PROTEIN MPT64 (ANTIGEN MPT64/MPB64) [Mycobacterium tuberculosis H37Rv]	153	5

gi|2695831	PROBABLE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE [Mycobacterium tuberculosis H37Rv]	152	6
gi|2225961	**POSSIBLE LIPOPROTEIN LPPD [Mycobacterium tuberculosis H37Rv]**	151	3
gi|2924446	PROBABLE ACETOHYDROXYACID SYNTHASE ILVX (ACETOLACTATE SYNTHASE) [Mycobacterium tuberculosis H37Rv]	151	13
gi|41353449	PROBABLE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE [Mycobacterium tuberculosis H37Rv]	150	5
gi|1877269	PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN (POSSIBLY TETR-FAMILY) [Mycobacterium tuberculosis H37Rv]	150	9
gi|2827603	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	149	15
gi|41352734	SECRETED ANTIGEN 85-C FBPC (85C) (ANTIGEN 85 COMPLEX C) (AG58C) (MYCOLYL TRANSFERASE 85C) (FIBRONECTI	149	7
gi|1405777	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	148	11
gi|1841458	**PROBABLE CONSERVED LIPOPROTEIN LPPX [Mycobacterium tuberculosis H37Rv]**	146	5
gi|1478225	PROBABLE PROTEIN-EXPORT MEMBRANE PROTEIN SECD [Mycobacterium tuberculosis H37Rv]	144	13
gi|2909538	DIHYDROLIPOAMIDE DEHYDROGENASE LPD (LIPOAMIDE REDUCTASE (NADH)) (LIPOYL DEHYDROGENASE) (DIHYDROL	144	9
gi|2213509	MCE-FAMILY PROTEIN MCE1D [Mycobacterium tuberculosis H37Rv]	142	18
gi|1817697	PUTATIVE TUBERCULIN RELATED PEPTIDE [Mycobacterium tuberculosis H37Rv]	142	3
gi|3261612	Probable CDP-diacylglycerol pyrophosphatase Cdh (CDP-diacylglycerol diphosphatase) (CDP-diacylglycerol phosphatidylhydrolas	141	9
gi|3261796	POSSIBLE CONSERVED TRANSMEMBRANE ALANINE AND GLYCINE RICH PROTEIN [Mycobacterium tuberculosis H37Rv]	134	7
gi|2193936	POSSIBLE BETA-1,3-GLUCANASE PRECURSOR [Mycobacterium tuberculosis H37Rv]	134	6
gi|1877377	PROBABLE TRANSCRIPTION ANTITERMINATION PROTEIN NUSG [Mycobacterium tuberculosis H37Rv]	133	4
gi|1621250	**PROBABLE CONSERVED LIPOPROTEIN LPRF [Mycobacterium tuberculosis H37Rv]**	133	8
gi|2181967	PROBABLE SERINE PROTEASE PEPA (SERINE PROTEINASE) (MTB32A) [Mycobacterium tuberculosis H37Rv]	131	4
gi|1568593	PROBABLE SINGLE-STRAND BINDING PROTEIN SSB (HELIX-DESTABILIZING PROTEIN) [Mycobacterium tuberculosis H37Rv	129	2
gi|3261523	POSSIBLE CONSERVED TRANSMEMBRANE TRANSPORT PROTEIN MMPL3 [Mycobacterium tuberculosis H37Rv]	129	9
gi|1370258	Probable membrane protein [Mycobacterium tuberculosis H37Rv]	125	3
gi|2791598	PROBABLE KETOL-ACID REDUCTOISOMERASE ILVC (Acetohydroxy-acid isomeroreductase) (Alpha-keto-beta-hydroxylacil redu	125	9
gi|1877338	PROBABLE THIOSULFATE SULFURTRANSFERASE SSEA (RHODANESE) (THIOSULFATE CYANIDE TRANSSULFURASE) (T	124	9
gi|2213510	**POSSIBLE MCE-FAMILY LIPOPROTEIN LPRK (MCE-FAMILY LIPOPROTEIN MCE1E) [Mycobacterium tuberculosis H37Rv]**	123	12
gi|2896707	PROBABLE ENOYL-CoA HYDRATASE ECHA8 (ENOYL HYDRASE) (UNSATURATED ACYL-CoA HYDRATASE) (CROTONASE	122	7
gi|2950423	SECRETED ANTIGEN 85-A FBPA (MYCOLYL TRANSFERASE 85A) (FIBRONECTIN-BINDING PROTEIN A) (ANTIGEN 85 COM	121	6
gi|1781097	PROBABLE FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE [NADPH] (LARGE SUBUNIT) GLTB (L-GLUTAMATE SYNTH	121	25
gi|2131047	PROBABLE TRANSKETOLASE TKT (TK) [Mycobacterium tuberculosis H37Rv]	120	5
gi|1237068	Probable pyruvate dehydrogenase (E2 component) SucB [Mycobacterium tuberculosis H37Rv]	120	5
gi|2916903	POSSIBLE NITRATE/NITRITE RESPONSE TRANSCRIPTIONAL REGULATORY PROTEIN NARL [Mycobacterium tuberculosis H	119	6
gi|2104317	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	117	8
gi|2105066	INORGANIC PYROPHOSPHATASE PPA (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) (INORGANIC DIPHOSPHAT	117	4
gi|2113910	Probable two-component system transcriptional regulator [Mycobacterium tuberculosis H37Rv]	117	6
gi|2326746	Probable catechol-o-methyltransferase [Mycobacterium tuberculosis H37Rv]	117	7
gi|1237049	Probable Ubiquinol-cytochrome C reductase QcrB (cytochrome B subunit) [Mycobacterium tuberculosis H37Rv]	116	6
gi|1877328	PROBABLE TRANSMEMBRANE CARBONIC ANHYDRASE (CARBONATE DEHYDRATASE) (CARBONIC DEHYDRATASE) [My	116	4
gi|1781220	PROBABLE NADH DEHYDROGENASE I (CHAIN D) NUOD (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN D) [Mycobacteriu	116	4
gi|1870011	PROBABLE RIBOSE-PHOSPHATE PYROPHOSPHOKINASE PRSA (Phosphoribosyl pyrophosphate synthetase) (PRPP syntheta	115	8
gi|2924466	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	115	13
gi|2113936	PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE (BETA SUBUNIT) SCOB (3-OXO-ACID:COA TRANS	114	9

gi|2791643	PROBABLE NADP-DEPENDENT ALCOHOL DEHYDROGENASE ADHC [Mycobacterium tuberculosis H37Rv]	113	7
gi|2960112	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	113	2
gi|1237048	Probable Rieske iron-sulfur protein QcrA [Mycobacterium tuberculosis H37Rv]	111	12
gi|41353622	**PERIPLASMIC PHOSPHATE-BINDING LIPOPROTEIN PSTS2 (PBP-2) (PSTS2) [Mycobacterium tuberculosis H37Rv]**	110	3
gi|2909480	PROBABLE MEMBRANE-ANCHORED MYCOSIN MYCP3 (SERINE PROTEASE) (SUBTILISIN-LIKE PROTEASE) (SUBTILASE-I	110	5
gi|1480321	HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	108	7
gi|2791592	PROBABLE 3-ISOPROPYLMALATE DEHYDROGENASE LEUB (BETA-IPM DEHYDROGENASE) (IMDH) (3-IPM-DH) [Mycobacte	108	8
gi|2960129	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	107	2
gi|2190473	29 KDa ANTIGEN CFP29 [Mycobacterium tuberculosis H37Rv]	107	6
gi|1322431	PROBABLE ATP SYNTHASE DELTA CHAIN ATPH [Mycobacterium tuberculosis H37Rv]	105	13
gi|1806189	PROBABLE 30S RIBOSOMAL PROTEIN S5 RPSE [Mycobacterium tuberculosis H37Rv]	104	7
gi|1314023	POSSIBLE PHOSPHOSERINE AMINOTRANSFERASE SERC (PSAT) [Mycobacterium tuberculosis H37Rv]	104	2
gi|2960114	PROBABLE CONSERVED MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	104	5
gi|1237047	Probable Ubiquinol-cytochrome C reductase QcrC(cytochrome C subunit) [Mycobacterium tuberculosis H37Rv]	104	5
gi|2791388	PROBABLE QUINONE REDUCTASE QOR (NADPH:quinone reductase) (Zeta-crystallin homolog protein) [Mycobacterium tubercu	103	7
gi|1929075	PROBABLE TRANSFERASE [Mycobacterium tuberculosis H37Rv]	102	4
gi|1542918	AMINOGLYCOSIDES/TETRACYCLINE-TRANSPORT INTEGRAL MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	102	1
gi|1806175	PROBABLE 30S RIBOSOMAL PROTEIN S3 RPSC [Mycobacterium tuberculosis H37Rv]	102	23
gi|1781106	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	101	2
gi|1552861	POSSIBLE AMINOTRANSFERASE [Mycobacterium tuberculosis H37Rv]	101	9
gi|2326726	Possible long-chain acyl-CoA synthase [Mycobacterium tuberculosis H37Rv]	100	8
gi|1403416	POSSIBLE MYCOBACTIN UTILIZATION PROTEIN VIUB [Mycobacterium tuberculosis H37Rv]	98	5
gi|1403499	POSSIBLE FATTY ACYL-CoA REDUCTASE [Mycobacterium tuberculosis H37Rv]	98	9
gi|2131049	PROBABLE GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE ZWF2 (G6PD) [Mycobacterium tuberculosis H37Rv]	98	6
gi|2105071	**PROBABLE CONSERVED LIPOPROTEIN LPQG [Mycobacterium tuberculosis H37Rv]**	98	1
gi|2182002	IRON-DEPENDENT REPRESSOR AND ACTIVATOR IDER [Mycobacterium tuberculosis H37Rv]	97	5
gi|2909639	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	96	3
gi|1552575	CONSERVED HYPOTHETICAL PROTEIN TB39.8 [Mycobacterium tuberculosis H37Rv]	96	10
gi|2909597	PROBABLE CONSERVED MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	95	7
gi|1552560	POSSIBLE CONSERVED MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	95	6
gi|2117199	PROBABLE RESPIRATORY NITRATE REDUCTASE (ALPHA CHAIN) NARG [Mycobacterium tuberculosis H37Rv]	94	12
gi|2052143	HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	93	4
gi|1552857	POSSIBLE ENOYL-CoA HYDRATASE ECHA21 (ENOYL HYDRASE) (UNSATURATED ACYL-CoA HYDRATASE) (CROTONASE	92	5
gi|2896708	POSSIBLE ENOYL-CoA HYDRATASE ECHA9 (ENOYL HYDRASE) (UNSATURATED ACYL-CoA HYDRATASE) (CROTONASE)	92	3
gi|2909540	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	91	1
gi|2661671	CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE 1 CMAA1 (CYCLOPROPANE FATTY ACID SYNTHASE) (CFA SY	91	2
gi|2072713	TWO COMPONENT SENSORY TRANSDUCTION TRANSCRIPTIONAL REGULATORY PROTEIN MTRA [Mycobacterium tubercu	91	4
gi|2924462	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	90	4
gi|1314041	POSSIBLE CONSERVED EXPORTED OR MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	90	2
gi|41352743	POSSIBLE LYSOPHOSPHOLIPASE [Mycobacterium tuberculosis H37Rv]	88	4
gi|1806174	PROBABLE 50S RIBOSOMAL PROTEIN L22 RPLV [Mycobacterium tuberculosis H37Rv]	87	5

gi|2827610	POSSIBLE TRANSMEMBRANE CATION TRANSPORTER [Mycobacterium tuberculosis H37Rv]	87	5
gi|2661669	**PROBABLE CONSERVED LIPOPROTEIN LPQD [Mycobacterium tuberculosis H37Rv]**	86	6
gi|41353626	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	86	4
gi|1403459	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	84	6
gi|2253049	proteasome (alpha subunit) PrcA [Mycobacterium tuberculosis H37Rv]	84	3
gi|1694862	POSSIBLE CONSERVED MEMBRANE OR SECRETED PROTEIN [Mycobacterium tuberculosis H37Rv]	83	5
gi|1405964	PROBABLE THIOESTERASE TESA [Mycobacterium tuberculosis H37Rv]	83	5
gi|2104408	PROBABLE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE [Mycobacterium tuberculosis H37Rv]	82	7
gi|2276335	PROBABLE IRON-SULFUR-BINDING REDUCTASE [Mycobacterium tuberculosis H37Rv]	82	11
gi|2117243	Probable quinolinate synthetase nadA [Mycobacterium tuberculosis H37Rv]	82	7
gi|1871584	PROBABLE IRON-REGULATED PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP] PCKA (PHOSPHOENOLPYRUVATE C	82	6
gi|2076700	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	82	7
gi|2181990	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	82	3
gi|2911005	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	82	2
gi|2909452	PROBABLE SUCCINATE DEHYDROGENASE [IRON-SULFUR SUBUNIT] (SUCCINIC DEHYDROGENASE) [Mycobacterium tube	82	9
gi|3261657	PROBABLE GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR GGTB (GAMMA-GLUTAMYLTRANSFERASE) (GLUTAMYL	81	7
gi|1806187	PROBABLE 50S RIBOSOMAL PROTEIN L6 RPLF [Mycobacterium tuberculosis H37Rv]	81	4
gi|1261946	MEROMYCOLATE EXTENSION ACYL CARRIER PROTEIN ACPM [Mycobacterium tuberculosis H37Rv]	81	2
gi|3261563	Possible short-chain dehydrogenase EphD [Mycobacterium tuberculosis H37Rv]	80	21
gi|3261513	DNA POLYMERASE III (BETA CHAIN) DNAN (DNA NUCLEOTIDYLTRANSFERASE) [Mycobacterium tuberculosis H37Rv]	78	10
gi|2896743	PROBABLE CHOLESTEROL DEHYDROGENASE [Mycobacterium tuberculosis H37Rv]	78	6
gi|2808706	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	78	3
gi|1552572	PROBABLE CELL DIVISION PROTEIN RODA [Mycobacterium tuberculosis H37Rv]	78	1
gi|2131058	PROBABLE TRIOSEPHOSPHATE ISOMERASE TPI (TIM) [Mycobacterium tuberculosis H37Rv]	77	9
gi|2624287	PROBABLE ALANINE RICH HYDROLASE [Mycobacterium tuberculosis H37Rv]	77	3
gi|1781067	PROBABLE CYTOPLASMIC PEPTIDASE PEPQ [Mycobacterium tuberculosis H37Rv]	77	11
gi|2695961	PROBABLE FERREDOXIN FDXC [Mycobacterium tuberculosis H37Rv]	76	2
gi|1314043	TWO COMPONENT RESPONSE TRANSCRIPTIONAL REGULATORY PROTEIN PRRA [Mycobacterium tuberculosis H37Rv]	76	3
gi|1449386	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	75	4
gi|2078074	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	74	6
gi|2909445	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	74	8
gi|3261571	ACETYL/PROPIONYL-CoA CARBOXYLASE (BETA SUBUNIT) ACCD6 [Mycobacterium tuberculosis H37Rv]	74	7
gi|1478226	PROBABLE PROTEIN-EXPORT MEMBRANE PROTEIN SECF [Mycobacterium tuberculosis H37Rv]	73	3
gi|1552863	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	73	12
gi|2909519	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	73	3
gi|38490198	PROBABLE UROPORPHYRIN-III C-METHYLTRANSFERASE HEMD (UROPORPHYRINOGEN III METHYLASE) (UROGEN III M	73	4
gi|1648881	PROBABLE TRANSLATION INITIATION FACTOR IF-2 INFB [Mycobacterium tuberculosis H37Rv]	73	11
gi|1322438	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	72	2
gi|2076677	PUTATIVE CELL DIVISION ATP-BINDING PROTEIN FTSE (SEPTATION COMPONENT-TRANSPORT ATP-BINDING PROTEIN	72	7
gi|1817698	PROBABLE PERIPLASMIC SUPEROXIDE DISMUTASE [CU-ZN] SODC [Mycobacterium tuberculosis H37Rv]	72	4
gi|1552570	TRANSMEMBRANE SERINE/THREONINE-PROTEIN KINASE A PKNA (PROTEIN KINASE A) (STPK A) [Mycobacterium tubercu	72	8

gi|1483550	POSSIBLE PREPROTEIN TRANSLOCASE ATPase SECA2 [Mycobacterium tuberculosis H37Rv]	72	10
gi|1781172	FATTY-ACID-CoA LIGASE FADD28 (FATTY-ACID-CoA SYNTHETASE) (FATTY-ACID-CoA SYNTHASE) [Mycobacterium tubercu	72	12
gi|2131012	PROBABLE CONSERVED TRANSMEMBRANE ATP-BINDING PROTEIN ABC TRANSPORTER [Mycobacterium tuberculosis H3	71	9
gi|1478228	ADENINE PHOSPHORIBOSYLTRANSFERASE APT (APRT) (AMP DIPHOSPHORYLASE) (AMP PYROPHOSPHORYLASE) (TR	71	6
gi|1877262	PROBABLE PEPTIDE METHIONINE SULFOXIDE REDUCTASE MSRA (PROTEIN-METHIONINE-S-OXIDE REDUCTASE) (PEP	71	4
gi|2896706	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	71	4
gi|2916911	POSSIBLE FATTY-ACID-CoA LIGASE FADD16 (FATTY-ACID-CoA SYNTHETASE) (FATTY-ACID-CoA SYNTHASE) [Mycobacte	71	2
gi|1621261	PROBABLE PYRIMIDINE OPERON REGULATORY PROTEIN PYRR [Mycobacterium tuberculosis H37Rv]	69	4
gi|2624295	DIHYDRODIPICOLINATE REDUCTASE DAPB (DHPR) [Mycobacterium tuberculosis H37Rv]	69	6
gi|3261562	Probable aminopeptidase PepB [Mycobacterium tuberculosis H37Rv]	69	8
gi|1806238	HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	68	1
gi|3261627	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	68	4
gi|1694883	POSSIBLE OXIDOREDUCTASE [Mycobacterium tuberculosis H37Rv]	68	5
gi|1552591	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	68	6
gi|2960132	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE ASD (ASA DEHYDROGENASE) (ASADH) (ASPARTIC SEMIALDEHYDE DE	67	5
gi|1449282	PROBABLE SHORT-CHAIN TYPE OXIDOREDUCTASE [Mycobacterium tuberculosis H37Rv]	67	3
gi|2131030	HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	67	2
gi|38490179	PROBABLE OROTATE PHOSPHORIBOSYLTRANSFERASE PYRE (OPRT) (OPRTASE) [Mycobacterium tuberculosis H37Rv]	66	2
gi|2808729	PROBABLE GLUTAMINE-TRANSPORT TRANSMEMBRANE PROTEIN ABC TRANSPORTER [Mycobacterium tuberculosis H37	66	2
gi|41352742	MCE-FAMILY PROTEIN MCE1A [Mycobacterium tuberculosis H37Rv]	66	6
gi|1877381	METHOXY MYCOLIC ACID SYNTHASE 3 MMAA3 (METHYL MYCOLIC ACID SYNTHASE 3) (MMA3) (HYDROXY MYCOLIC AC	66	5
gi|1460076	PROBABLE GLUTAMINE-TRANSPORT ATP-BINDING PROTEIN ABC TRANSPORTER GLNQ [Mycobacterium tuberculosis H37	65	4
gi|2909656	PROBABLE 30S RIBOSOMAL PROTEIN S7 RPSG [Mycobacterium tuberculosis H37Rv]	65	4
gi|2253054	HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	65	5
gi|1877280	PROBABLE NAD(P) TRANSHYDROGENASE (SUBUNIT ALPHA) PNTAA [FIRST PART; CATALYTIC PART] (PYRIDINE NUCLE	65	6
gi|2225980	Probable cytochrome p450 140 CYP140 [Mycobacterium tuberculosis H37Rv]	65	3
gi|41353649	Probable Serine hydroxymethyltransferase 1 glyA1 [Mycobacterium tuberculosis H37Rv]	64	6
gi|2113898	**Possible prolipoprotein diacylglyceryl transferases Lgt [Mycobacterium tuberculosis H37Rv]**	64	5
gi|1666132	HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	64	5
gi|41352792	PE FAMILY PROTEIN [Mycobacterium tuberculosis H37Rv]	64	3
gi|1838991	Possible lysyl-tRNA synthetase 2 lysX [Mycobacterium tuberculosis H37Rv]	62	13
gi|1781219	PROBABLE NADH DEHYDROGENASE I (CHAIN E) NUOE (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN E) [Mycobacteriu	62	1
gi|1781178	Probable reductase [Mycobacterium tuberculosis H37Rv]	62	3
gi|2791502	PROBABLE TRIGGER FACTOR (TF) PROTEIN TIG [Mycobacterium tuberculosis H37Rv]	62	4
gi|41353632	PROBABLE MOLYBDOPTERIN BIOSYNTHESIS PROTEIN MOEA1 [Mycobacterium tuberculosis H37Rv]	61	7
gi|2113895	Probable indole-3-glycerol phosphate synthase trpC [Mycobacterium tuberculosis H37Rv]	61	5
gi|2791513	POSSIBLE ALANINE AND PROLINE RICH MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	61	3
gi|2052127	PROBABLE UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE GALU (UDP-GLUCOSE PYROPHOSPHORYLASE) (U	61	6
gi|3261542	Probable polyketide synthase pks5 [Mycobacterium tuberculosis H37Rv]	61	21
gi|1781066	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	60	5
gi|1483541	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	60	4

gi|2791517	PROBABLE MACROLIDE-TRANSPORT ATP-BINDING PROTEIN ABC TRANSPORTER [Mycobacterium tuberculosis H37Rv]	60	11
gi|2791397	PROBABLE CONSERVED ATP-BINDING PROTEIN ABC TRANSPORTER [Mycobacterium tuberculosis H37Rv]	59	4
gi|1552593	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	59	6
gi|2224829	POSSIBLE ACYLTRANSFERASE [Mycobacterium tuberculosis H37Rv]	58	7
gi|2624275	PROBABLE DIHYDRODIPICOLINATE SYNTHASE DAPA (DHDPS) (DIHYDRODIPICOLINATE SYNTHETASE) [Mycobacterium t	58	3
gi|38490187	MYCOLIC ACID SYNTHASE PCAA (CYCLOPROPANE SYNTHASE) [Mycobacterium tuberculosis H37Rv]	58	6
gi|2911105	CONSERVED HYPOTHETICAL PROTEIN TB16.3 [Mycobacterium tuberculosis H37Rv]	58	3
gi|1694881	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	57	4
gi|1524229	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE FABG1 (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE) (MYC	57	2
gi|2791493	PROBABLE MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN A MOBA [Mycobacterium tuberculosis H3	56	5
gi|2827579	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	56	5
gi|1524193	PROBABLE METAL CATION TRANSPORTER P-TYPE ATPASE CTPV [Mycobacterium tuberculosis H37Rv]	56	5
gi|1552877	INTEGRAL MEMBRANE INDOLYLACETYLINOSITOL ARABINOSYLTRANSFERASE EMBA (ARABINOSYLINDOLYLACETYLIN	56	11
gi|1781192	POSSIBLE OXIDOREDUCTASE [Mycobacterium tuberculosis H37Rv]	55	5
gi|2896709	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	55	3
gi|38490339	POSSIBLE PHOSPHOGLYCERATE MUTASE GPM2 (PHOSPHOGLYCEROMUTASE) (PGAM) (BPG-DEPENDENT PGAM) [Myc	55	1
gi|2104307	Possible pyridoxine biosynthesis protein [Mycobacterium tuberculosis H37Rv]	55	5
gi|1877282	PROBABLE NAD(P) TRANSHYDROGENASE (SUBUNIT BETA) PNTB [INTEGRAL MEMBRANE PROTEIN] (PYRIDINE NUCLE	55	5
gi|1781138	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	54	1
gi|3261509	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE (ALPHA CHAIN) NRDE (RIBONUCLEOTIDE REDUCTASE SMALL SUBUNIT	54	8
gi|2072680	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	53	3
gi|2104300	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	53	6
gi|2131038	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	53	3
gi|2924476	CONSERVED HYPOTHETICAL MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	53	2
gi|2253050	proteasome (beta subunit) PrcB [Mycobacterium tuberculosis H37Rv]	52	5
gi|2076667	PROBABLE CONSERVED INTEGRAL MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	52	6
gi|2909514	PROBABLE DEHYDROGENASE/REDUCTASE [Mycobacterium tuberculosis H37Rv]	51	2
gi|2911012	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	50	3
gi|1449321	PROBABLE CHAPERONE PROTEIN HTPG (HEAT SHOCK PROTEIN) (HSP90 FAMILY PROTEIN) (HIGH TEMPERATURE PR	50	11
gi|2916974	HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	50	4
gi|1781230	PROBABLE MONOPHOSPHATASE [Mycobacterium tuberculosis H37Rv]	50	4
gi|2113999	PROBABLE INTEGRAL MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	50	6
gi|38490190	PROBABLE PHOSPHOGLYCERATE MUTASE 1 GPM1 (PHOSPHOGLYCEROMUTASE) (PGAM) (BPG-DEPENDENT PGAM) [	50	7
gi|2909542	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	50	4
gi|1552876	INTEGRAL MEMBRANE INDOLYLACETYLINOSITOL ARABINOSYLTRANSFERASE EMBC (ARABINOSYLINDOLYLACETYLIN	49	21
gi|2896693	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	49	2
gi|2909520	PROBABLE ALTERNATIVE RNA POLYMERASE SIGMA FACTOR SIGK [Mycobacterium tuberculosis H37Rv]	49	2
gi|2896785	Probable polyketide synthase pks12 [Mycobacterium tuberculosis H37Rv]	49	18
gi|38490219	PROBABLE ENOYL-CoA HYDRATASE ECHA5 (ENOYL HYDRASE) (UNSATURATED ACYL-CoA HYDRATASE) (CROTONASE	48	14
gi|38490345	PROBABLE PREPROTEIN TRANSLOCASE SECA1 1 SUBUNIT [Mycobacterium tuberculosis H37Rv]	48	6
gi|1449377	PROBABLE INOSINE-5~-MONOPHOSPHATE DEHYDROGENASE GUAB3 (IMP DEHYDROGENASE) (INOSINIC ACID DEHYD	47	5

gi|1781222	PROBABLE NADH DEHYDROGENASE I (CHAIN B) NUOB (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN B) [Mycobacteriu	47	5
gi|2104364	PROBABLE 50S RIBOSOMAL PROTEIN L13 RPLM [Mycobacterium tuberculosis H37Rv]	47	3
gi|2117218	PROBABLE EPOXIDE HYDROLASE EPHC (EPOXIDE HYDRATASE) [Mycobacterium tuberculosis H37Rv]	47	3
gi|2916883	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	47	6
gi|2661634	PROBABLE BIFUNCTIONAL PROTEIN FOLD: METHYLENETETRAHYDROFOLATE DEHYDROGENASE + METHENYLTETRAH	46	12
gi|2916879	PROBABLE PHOSPHATE-TRANSPORT SYSTEM TRANSCRIPTIONAL REGULATORY PROTEIN PHOY2 [Mycobacterium tuber	46	1
gi|2193929	PROBABLE CONSERVED INTEGRAL MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	46	4
gi|2909463	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	45	1
gi|2661647	POSSIBLE OXIDOREDUCTASE [Mycobacterium tuberculosis H37Rv]	45	6
gi|2052133	HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	45	1
gi|2924456	HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	45	6
gi|2612804	POSSIBLE AMIDOTRANSFERASE [Mycobacterium tuberculosis H37Rv]	45	2
gi|2181958	PROBABLE PHOSPHATE-TRANSPORT SYSTEM TRANSCRIPTIONAL REGULATORY PROTEIN PHOU HOMOLOG 1 PHOY1	45	9
gi|1877373	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	45	2
gi|2104320	Probable UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelat e ligase MurE [Mycobacterium tuberculosis H37Rv]	45	10
gi|1850117	HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	45	7
gi|2909470	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	44	3
gi|3261719	PROBABLE INITIATION FACTOR IF-3 INFC [Mycobacterium tuberculosis H37Rv]	44	4
gi|2950448	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	44	4
gi|1237055	Probable carbohydrate kinase CbhK [Mycobacterium tuberculosis H37Rv]	44	6
gi|1550635	POSSIBLE TWO COMPONENT SYSTEM RESPONSE TRANSCRIPTIONAL POSITIVE REGULATOR PHOP [Mycobacterium tub	44	4
gi|1340098	PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN [Mycobacterium tuberculosis H37Rv]	43	6
gi|1781253	PUTATIVE ESAT-6 LIKE PROTEIN ESXO (ESAT-6 LIKE PROTEIN 6) [Mycobacterium tuberculosis H37Rv]	43	1
gi|1261945	MALONYL CoA-ACYL CARRIER PROTEIN TRANSACYLASE FABD (Malonyl CoA:AcpM acyltransferase) (MCT) [Mycobacterium	43	4
gi|2224821	PROBABLE CONSERVED POLYKETIDE SYNTHASE ASSOCIATED PROTEIN PAPA1 [Mycobacterium tuberculosis H37Rv]	43	7
gi|2131059	PROBABLE PHOSPHOGLYCERATE KINASE PGK [Mycobacterium tuberculosis H37Rv]	43	3
gi|2896723	SHORT (C15) CHAIN Z-ISOPRENYL DIPHOSPHATE SYNTHASE (Z-FPP SYNTHASE) (Z-FARNESYL DIPHOSPHATE SYNTHA	42	2
gi|2791590	POSSIBLE 2-HYDROXYHEPTA-2,4-DIENE-1,7-DIOATE ISOMERASE (HHDD ISOMERASE) [Mycobacterium tuberculosis H37Rv	42	1
gi|41353675	PROBABLE CUTINASE CUT2 [Mycobacterium tuberculosis H37Rv]	42	1
gi|2894220	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	42	5
gi|1478222	PROBABLE FATTY-ACID-CoA LIGASE FADD9 (FATTY-ACID-CoA SYNTHETASE) (FATTY-ACID-CoA SYNTHASE) [Mycobacter	42	8
gi|1781156	PROBABLE SHORT CHAIN ALCOHOL DEHYDROGENASE/REDUCTASE [Mycobacterium tuberculosis H37Rv]	42	6
gi|2960233	CONSERVED HYPOTHETICAL ALANINE AND GLYCINE RICH PROTEIN [Mycobacterium tuberculosis H37Rv]	42	4
gi|2225986	HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	41	2
gi|1403411	PROBABLE 30S RIBOSOMAL PROTEIN S2 RPSB [Mycobacterium tuberculosis H37Rv]	41	13
gi|1449376	PROBABLE INOSINE-5~-MONOPHOSPHATE DEHYDROGENASE GUAB2 (IMP DEHYDROGENASE) (INOSINIC ACID DEHYDI	41	6
gi|2916912	PROBABLE PYRUVATE OR INDOLE-3-PYRUVATE DECARBOXYLASE PDC [Mycobacterium tuberculosis H37Rv]	41	3
gi|2113916	HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	41	2
gi|2117182	PROBABLE SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE [Mycobacterium tuberculosis H37Rv]	41	4
gi|3261674	PROBABLE POLYPHOSPHATE KINASE PPK (POLYPHOSPHORIC ACID KINASE) (ATP-POLYPHOSPHATE PHOSPHOTRANS	41	8
gi|2909600	PROBABLE CONSERVED TRANSMEMBRANE TRANSPORT PROTEIN MMPL11 [Mycobacterium tuberculosis H37Rv]	41	7

gi|2896737	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	40	1
gi|1850116	PROBABLE ACYL-CoA DEHYDROGENASE FADE6 [Mycobacterium tuberculosis H37Rv]	40	8
gi|2213526	PROBABLE DIHYDROXY-ACID DEHYDRATASE ILVD (DAD) [Mycobacterium tuberculosis H37Rv]	40	6
gi|1524255	Probable membrane protein [Mycobacterium tuberculosis H37Rv]	39	4
gi|2072704	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	39	3
gi|2911092	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	39	4
gi|1550658	PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE PURC (SAICAR SYNTHETASE) [Mycobacterium	39	5
gi|41352745	SMALL SECRETED PROTEIN [Mycobacterium tuberculosis H37Rv]	38	1
gi|1524258	GDP-D-mannose dehydratase gmdA (GDP-mannose 4,6 dehydratase) (GMD) [Mycobacterium tuberculosis H37Rv]	38	3
gi|1877350	PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN (PROBABLY TETR-FAMILY) [Mycobacterium tuberculosis H37Rv]	38	3
gi|1666158	PROBABLE GAMMA-GLUTAMYL PHOSPHATE REDUCTASE PROTEIN PROA (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHY	38	6
gi|1781257	PROBABLE MEMBRANE-ASSOCIATED PHOSPHOLIPASE C 2 PLCB [Mycobacterium tuberculosis H37Rv]	38	2
gi|2114023	POSSIBLE OXIDOREDUCTASE [Mycobacterium tuberculosis H37Rv]	38	7
gi|1261932	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	38	4
gi|1781233	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	37	2
gi|2960156	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	37	2
gi|3261677	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	37	2
gi|2104338	CONSERVED HYPOTHETICAL PROTEIN TB18.6 [Mycobacterium tuberculosis H37Rv]	37	1
gi|2909642	**PROBABLE CONSERVED LIPOPROTEIN LPQN [Mycobacterium tuberculosis H37Rv]**	36	1
gi|1781137	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	36	7
gi|2916954	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	36	4
gi|2695824	PROBABLE SUGAR-TRANSPORT ATP-BINDING PROTEIN ABC TRANSPORTER SUGC [Mycobacterium tuberculosis H37Rv]	36	4
gi|2114010	PROBABLE NAPHTHOATE SYNTHASE MENB (DIHYDROXYNAPHTHOIC ACID SYNTHETASE) (DHNA SYNTHETASE) [Mycob	36	3
gi|1806181	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	36	2
gi|1322430	PROBABLE ATP SYNTHASE B CHAIN ATPF [Mycobacterium tuberculosis H37Rv]	36	3
gi|2960158	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	35	10
gi|2253053	Probable integral membrane protein [Mycobacterium tuberculosis H37Rv]	35	2
gi|2896738	CONSERVED MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	35	2
gi|2791641	PROBABLE CYTOCHROME C OXIDASE POLYPEPTIDE I CTAD (CYTOCHROME AA3 SUBUNIT 1) [Mycobacterium tuberculosis	35	2
gi|3261795	PROBABLE CONSERVED INTEGRAL MEMBRANE ALANINE AND VALINE AND LEUCINE RICH PROTEIN [Mycobacterium tube	35	11
gi|38490371	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	34	5
gi|2909451	PROBABLE SUCCINATE DEHYDROGENASE [IRON-SULFUR SUBUNIT] (SUCCINIC DEHYDROGENASE) [Mycobacterium tube	34	5
gi|1781236	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	34	6
gi|1568585	MYO-INOSITOL-1-PHOSPHATE SYNTHASE INO1 (Inositol 1-phosphate synthetase) (D-glucose 6-phosphate cycloaldolase) (Glu	34	5
gi|1929068	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	34	3
gi|2213500	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	33	4
gi|2909627	POSSIBLE CYTOCHROME P450 135B1 CYP135B1 [Mycobacterium tuberculosis H37Rv]	33	11
gi|2960093	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	33	6
gi|2916871	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	33	4
gi|2916867	PROBABLE PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE PURM (AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZ	32	1
gi|3261779	PROBABLE DIHYDROLIPOAMIDE S-ACETYLTRANSFERASE E2 COMPONENT PDHC (LIPOATE ACETYLTRANSFERASE) (T	32	5

gi|2960095	POSSIBLE MEMBRANE-ASSOCIATED SERINE PROTEASE [Mycobacterium tuberculosis H37Rv]	32	2
gi|2916869	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	32	3
gi|1524254	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	31	1
gi|1871596	PROBABLE ALDEHYDE DEHYDROGENASE [Mycobacterium tuberculosis H37Rv]	31	5
gi|2213513	PROBABLE CONSERVED MCE ASSOCIATED TRANSMEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	31	5
gi|2791514	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	31	2
gi|2078021	LYSINE-N-OXYGENASE MBTG (L-LYSINE 6-MONOOXYGENASE) (LYSINE N6-HYDROXYLASE) [Mycobacterium tuberculosis H	31	4
gi|2117226	CONSERVED MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	31	5
gi|2113901	Probable pyruvate kinase pykA [Mycobacterium tuberculosis H37Rv]	30	7
gi|41353684	HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	30	4
gi|2105048	DNA TOPOISOMERASE I TOPA (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE) (TYPE I D	30	10
gi|2960220	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	30	5
gi|1542920	PROBABLE RIBOFLAVIN SYNTHASE ALPHA CHAIN RIBC (RIBE) [Mycobacterium tuberculosis H37Rv]	30	6
gi|1478230	PROBABLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE B PPIB (CYCLOPHILIN) (PPIASE) (ROTAMASE) (PEPTIDYLPROLY	30	3
gi|2113913	PROBABLE DNA POLYMERASE I POLA [Mycobacterium tuberculosis H37Rv]	30	12
gi|2213515	PROBABLE CONSERVED MCE ASSOCIATED MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	30	3
gi|1781221	PROBABLE NADH DEHYDROGENASE I (CHAIN C) NUOC (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN C) [Mycobacteriu	30	3
gi|1261930	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	30	8
gi|2924455	PROBABLE CYTOCHROME P450 MONOOXYGENASE 142 CYP142 [Mycobacterium tuberculosis H37Rv]	30	4
gi|1781115	PROBABLE GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE GLPQ1 (GLYCEROPHOSPHODIESTER PHOSPHOD	30	5
gi|1370234	CLASS A BETA-LACTAMASE BLAC [Mycobacterium tuberculosis H37Rv]	29	7
gi|3261780	OLIGORIBONUCLEASE ORN [Mycobacterium tuberculosis H37Rv]	29	2
gi|2193940	PROBABLE PYRROLIDONE-CARBOXYLATE PEPTIDASE PCP (5-OXOPROLYL-PEPTIDASE) (PYROGLUTAMYL-PEPTIDASE	29	3
gi|1542917	PROBABLE BIFUNCTIONAL riboflavin biosynthesis protein RIBG : Diaminohydroxyphosphoribosylaminopyrimidine deaminase (Ri	29	7
gi|1524222	POSSIBLE OXIDOREDUCTASE [Mycobacterium tuberculosis H37Rv]	29	2
gi|1449298	PROBABLE PYRROLINE-5-CARBOXYLATE REDUCTASE PROC (P5CR) (P5C REDUCTASE) [Mycobacterium tuberculosis H37	28	3
gi|3242256	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	28	7
gi|1817673	PROBABLE F420-DEPENDENT GLUCOSE-6-PHOSPHATE DEHYDROGENASE FGD1 [Mycobacterium tuberculosis H37Rv]	28	4
gi|2695823	PROBABLE SUGAR-TRANSPORT INTEGRAL MEMBRANE PROTEIN ABC TRANSPORTER SUGB [Mycobacterium tuberculosis	28	2
gi|2193935	POSSIBLE CONSERVED MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	28	2
gi|2266715	PROBABLE DELTA-AMINOLEVULINIC ACID DEHYDRATASE HEMB (PORPHOBILINOGEN SYNTHASE) (ALAD) (ALADH) [Myc	28	4
gi|2182004	PROBABLE SOLUBLE PYRIDINE NUCLEOTIDE TRANSHYDROGENASE STHA (STH) (NAD(P)(+) TRANSHYDROGENASE [B-	28	4
gi|41353429	POSSIBLE HALOALKANE DEHALOGENASE DHAA (1-CHLOROHEXANE HALIDOHYDROLASE) [Mycobacterium tuberculosis H	28	2
gi|1314028	PROBABLE CITRATE SYNTHASE II CITA [Mycobacterium tuberculosis H37Rv]	28	3
gi|2224831	POSSIBLE ACYLTRANSFERASE [Mycobacterium tuberculosis H37Rv]	27	5
gi|41352773	PROBABLE ACETOLACTATE SYNTHASE (LARGE SUBUNIT) ILVB1 (ACETOHYDROXY-ACID SYNTHASE) [Mycobacterium tub	27	2
gi|2924494	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	27	5
gi|2896764	Probable histidine kinase response regulator [Mycobacterium tuberculosis H37Rv]	27	7
gi|1817674	PROBABLE PHOSPHATE ACETYLTRANSFERASE PTA (PHOSPHOTRANSACETYLASE) [Mycobacterium tuberculosis H37Rv]	27	2
gi|1817689	PROBABLE THIAMINE BIOSYNTHESIS PROTEIN THIC [Mycobacterium tuberculosis H37Rv]	27	3
gi|1781145	PROBABLE PHOSPHOGLUCOMUTASE PGMA (GLUCOSE PHOSPHOMUTASE) (PGM) [Mycobacterium tuberculosis H37Rv]	27	1

gi|1550666	PROBABLE PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE I PURG (FGAM SYNTHASE I) [Mycobacterium tubercul	27	1
gi|1817678	POSSIBLE CONSERVED MEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	26	7
gi|41352759	NADPH-DEPENDENT MYCOTHIOL REDUCTASE MTR [Mycobacterium tuberculosis H37Rv]	26	3
gi|1806191	PROBABLE 50S RIBOSOMAL PROTEIN L15 RPLO [Mycobacterium tuberculosis H37Rv]	24	4
gi|2924437	CONSERVED HYPOTHETICAL INTEGRAL MEMBRANE PROTEIN YRBE4B [Mycobacterium tuberculosis H37Rv]	24	5
gi|1781214	PROBABLE NADH DEHYDROGENASE I (CHAIN J) NUOJ (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN J) [Mycobacterium	24	2
gi|2909598	POSSIBLE CONSERVED TRANSMEMBRANE PROTEIN [Mycobacterium tuberculosis H37Rv]	22	2
gi|38490223	PROBABLE METHIONINE AMINOPEPTIDASE MAPA (MAP) (PEPTIDASE M) (MetAP) [Mycobacterium tuberculosis H37Rv]	21	5
gi|2909518	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	20	1
gi|41352784	POSSIBLE MULTIFUNCTIONAL ENZYME SIROHEME SYNTHASE CYSG: UROPORPHYRIN-III C-METHYLTRANSFERASE (U	18	4
gi|2896765	CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]	17	6

Supporting Table 6. *M. smegmatis* cellular proteins

Accesion number	Protein name	Score	Unique peptides
gi|118469510	chaperonin GroEL [Mycobacterium smegmatis str. MC2 155]	3302	83
gi|118471088	elongation factor Tu [Mycobacterium smegmatis str. MC2 155]	3171	105
gi|118469921	glycerol kinase [Mycobacterium smegmatis str. MC2 155]	3039	89
gi|118467920	fatty acid synthase [Mycobacterium smegmatis str. MC2 155]	2078	82
gi|118473120	secreted protein [Mycobacterium smegmatis str. MC2 155]	1946	57
gi|118469856	alcohol dehydrogenase [Mycobacterium smegmatis str. MC2 155]	1891	54
gi|118467956	glutamine synthetase, type I [Mycobacterium smegmatis str. MC2 155]	1763	59
gi|118469216	chaperonin GroEL [Mycobacterium smegmatis str. MC2 155]	1732	49
gi|118467799	glyceraldehyde-3-phosphate dehydrogenase, type I [Mycobacterium smegmatis str. MC2 155]	1702	38
gi|118469768	DNA-directed RNA polymerase subunit beta~ [Mycobacterium smegmatis str. MC2 155]	1598	80
gi|118472509	negative regulator of genetic competence ClpC/mecB [Mycobacterium smegmatis str. MC2 155]	1545	49
gi|118473102	transketolase [Mycobacterium smegmatis str. MC2 155]	1485	47
gi|118467432	isocitrate dehydrogenase, NADP-dependent [Mycobacterium smegmatis str. MC2 155]	1481	49
gi|118471656	alcohol dehydrogenase, iron-containing [Mycobacterium smegmatis str. MC2 155]	1402	42
gi|118468193	elongation factor Ts [Mycobacterium smegmatis str. MC2 155]	1281	35
gi|118468129	DNA-directed RNA polymerase subunit beta [Mycobacterium smegmatis str. MC2 155]	1185	52
gi|118472813	30S ribosomal protein S1 [Mycobacterium smegmatis str. MC2 155]	1029	40
gi|118471676	aconitate hydratase 1 [Mycobacterium smegmatis str. MC2 155]	996	39
gi|118471177	fructose-1,6-bisphosphate aldolase [Mycobacterium smegmatis str. MC2 155]	939	23
gi|118471849	F0F1 ATP synthase subunit beta [Mycobacterium smegmatis str. MC2 155]	909	28
gi|118470966	alcohol dehydrogenase, class IV [Mycobacterium smegmatis str. MC2 155]	868	34
gi|118469852	succinyl-CoA synthetase subunit alpha [Mycobacterium smegmatis str. MC2 155]	826	21
gi|118469254	electron transfer flavoprotein, beta subunit [Mycobacterium smegmatis str. MC2 155]	802	23
gi|118472263	50S ribosomal protein L2 [Mycobacterium smegmatis str. MC2 155]	802	30
gi|118472182	ketol-acid reductoisomerase [Mycobacterium smegmatis str. MC2 155]	800	25
gi|118471525	ABC-type amino acid transport system, secreted component [Mycobacterium smegmatis str. MC2 155]	799	15
gi|118469108	acetyl-/propionyl-coenzyme A carboxylase alpha chain [Mycobacterium smegmatis str. MC2 155]	790	30
gi|118468850	sulfate-binding protein [Mycobacterium smegmatis str. MC2 155]	775	23
gi|118471339	DNA-binding protein HU [Mycobacterium smegmatis str. MC2 155]	773	30
gi|118472055	alpha-ketoglutarate decarboxylase [Mycobacterium smegmatis str. MC2 155]	766	33
gi|118473196	50S ribosomal protein L1 [Mycobacterium smegmatis str. MC2 155]	758	24
gi|118471055	dihydrolipoamide acetyltransferase [Mycobacterium smegmatis str. MC2 155]	742	22
gi|118471172	3-oxoacyl-(acyl carrier protein) synthase II [Mycobacterium smegmatis str. MC2 155]	729	19
gi|118469915	30S ribosomal protein S2 [Mycobacterium smegmatis str. MC2 155]	712	29
gi|118470425	methoxy mycolic acid synthase 1 [Mycobacterium smegmatis str. MC2 155]	678	23
gi|118469023	transcriptional regulator, Crp/Fnr family protein [Mycobacterium smegmatis str. MC2 155]	664	24
gi|118471409	electron transfer flavoprotein, alpha subunit [Mycobacterium smegmatis str. MC2 155]	643	16

gi|118469725	malate synthase G [Mycobacterium smegmatis str. MC2 155]	635	23
gi|118470564	branched-chain amino acid ABC transporter substrate-binding protein [Mycobacterium smegmatis str. MC2 155]	634	16
gi|118472423	molecular chaperone DnaK [Mycobacterium smegmatis str. MC2 155]	630	28
gi|118472444	glycerol-3-phosphate dehydrogenase 2 [Mycobacterium smegmatis str. MC2 155]	629	27
gi|118471714	trigger factor [Mycobacterium smegmatis str. MC2 155]	620	15
gi|118472788	putative thiosulfate sulfurtransferase [Mycobacterium smegmatis str. MC2 155]	606	31
gi|118468422	peptidyl-prolyl cis-trans isomerase B [Mycobacterium smegmatis str. MC2 155]	585	16
gi|118470200	transaldolase [Mycobacterium smegmatis str. MC2 155]	584	22
gi|118470248	glutamate binding protein [Mycobacterium smegmatis str. MC2 155]	583	14
gi|118471749	phosphopyruvate hydratase [Mycobacterium smegmatis str. MC2 155]	570	19
gi|118471281	polynucleotide phosphorylase/polyadenylase [Mycobacterium smegmatis str. MC2 155]	561	22
gi|118469786	succinyl-CoA synthetase subunit beta [Mycobacterium smegmatis str. MC2 155]	559	16
gi|118471400	50S ribosomal protein L17 [Mycobacterium smegmatis str. MC2 155]	549	15
gi|118471197	transcription termination factor Rho [Mycobacterium smegmatis str. MC2 155]	545	17
gi|118473144	adenylate kinase [Mycobacterium smegmatis str. MC2 155]	544	16
gi|118467390	sulfonate binding protein [Mycobacterium smegmatis str. MC2 155]	525	10
gi|118471486	alkylhydroperoxide reductase [Mycobacterium smegmatis str. MC2 155]	519	20
gi|118468007	S-adenosylmethionine synthetase [Mycobacterium smegmatis str. MC2 155]	510	15
gi|118471051	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [Mycobacterium smegmatis str. MC2 155]	506	23
gi|118470491	type II citrate synthase [Mycobacterium smegmatis str. MC2 155]	491	22
gi|118467594	eptc-inducible aldehyde dehydrogenase [Mycobacterium smegmatis str. MC2 155]	488	16
gi|118469481	acetyl-CoA acetyltransferase [Mycobacterium smegmatis str. MC2 155]	487	14
gi|118470335	extracellular solute-binding protein, family protein 5, putative [Mycobacterium smegmatis str. MC2 155]	480	10
gi|118470637	DivIVA protein [Mycobacterium smegmatis str. MC2 155]	477	14
gi|118469591	polyketide synthase [Mycobacterium smegmatis str. MC2 155]	476	28
gi|118469556	DNA-directed RNA polymerase subunit alpha [Mycobacterium smegmatis str. MC2 155]	472	15
gi|118473128	50S ribosomal protein L10 [Mycobacterium smegmatis str. MC2 155]	466	16
gi|118468923	35 kDa protein [Mycobacterium smegmatis str. MC2 155]	458	16
gi|118471041	50S ribosomal protein L6 [Mycobacterium smegmatis str. MC2 155]	458	13
gi|118470856	pyruvate kinase [Mycobacterium smegmatis str. MC2 155]	451	16
gi|118473190	50S ribosomal protein L3 [Mycobacterium smegmatis str. MC2 155]	442	16
gi|118473447	putative periplasmic binding protein [Mycobacterium smegmatis str. MC2 155]	442	11
gi|118468301	30S ribosomal protein S4 [Mycobacterium smegmatis str. MC2 155]	432	24
gi|118471064	enoyl-(acyl carrier protein) reductase [Mycobacterium smegmatis str. MC2 155]	427	16
gi|118473252	starvation-induced DNA protecting protein [Mycobacterium smegmatis str. MC2 155]	425	18
gi|118472900	50S ribosomal protein L5 [Mycobacterium smegmatis str. MC2 155]	418	17
gi|118468034	ribonucleotide-diphosphate reductase subunit alpha [Mycobacterium smegmatis str. MC2 155]	411	16
gi|118467381	leucyl aminopeptidase [Mycobacterium smegmatis str. MC2 155]	392	13
gi|118470249	eptc-inducible aldehyde dehydrogenase [Mycobacterium smegmatis str. MC2 155]	392	20
gi|118468744	antigen 85-A [Mycobacterium smegmatis str. MC2 155]	392	12
gi|118470088	50S ribosomal protein L4 [Mycobacterium smegmatis str. MC2 155]	391	18

gi|118467618	30S ribosomal protein S16 [Mycobacterium smegmatis str. MC2 155]	384	9
gi|118467392	aminopeptidase N [Mycobacterium smegmatis str. MC2 155]	382	15
gi|118468477	ribosomal protein S9 [Mycobacterium smegmatis str. MC2 155]	380	17
gi|118471723	2,5-diketo-D-gluconic acid reductase A [Mycobacterium smegmatis str. MC2 155]	378	10
gi|118469641	30S ribosomal protein S5 [Mycobacterium smegmatis str. MC2 155]	378	16
gi|118473160	30S ribosomal protein S3 [Mycobacterium smegmatis str. MC2 155]	371	25
gi|118469528	carbamoyl phosphate synthase large subunit [Mycobacterium smegmatis str. MC2 155]	368	20
gi|118470644	myo-inositol-1-phosphate synthase [Mycobacterium smegmatis str. MC2 155]	362	19
gi|118469699	phosphoglycerate kinase [Mycobacterium smegmatis str. MC2 155]	362	10
gi|118471917	propionyl-CoA carboxylase beta chain [Mycobacterium smegmatis str. MC2 155]	360	9
gi|118472596	dihydrolipoamide dehydrogenase [Mycobacterium smegmatis str. MC2 155]	359	15
gi|118467508	geranylgeranyl reductase [Mycobacterium smegmatis str. MC2 155]	357	10
gi|118469548	universal stress protein family protein [Mycobacterium smegmatis str. MC2 155]	354	9
gi|118473759	ubiquinol-cytochrome c reductase iron-sulfur subunit [Mycobacterium smegmatis str. MC2 155]	352	15
gi|118472552	hypothetical protein MSMEG_5246 [Mycobacterium smegmatis str. MC2 155]	346	16
gi|118471482	ATP-dependent Clp protease proteolytic subunit [Mycobacterium smegmatis str. MC2 155]	342	9
gi|118469532	FeS assembly ATPase SufC [Mycobacterium smegmatis str. MC2 155]	340	9
gi|118473057	50S ribosomal protein L25/general stress protein Ctc [Mycobacterium smegmatis str. MC2 155]	328	15
gi|118470567	DNA gyrase subunit B [Mycobacterium smegmatis str. MC2 155]	328	23
gi|118473766	hypothetical protein MSMEG_2450 [Mycobacterium smegmatis str. MC2 155]	319	12
gi|118467515	acetyl-CoA acetyltransferase [Mycobacterium smegmatis str. MC2 155]	312	14
gi|118472968	fumarate hydratase [Mycobacterium smegmatis str. MC2 155]	308	20
gi|118467355	acetyl-coenzyme A synthetase [Mycobacterium smegmatis str. MC2 155]	308	17
gi|118471852	acyl-CoA synthetase [Mycobacterium smegmatis str. MC2 155]	305	15
gi|118473588	phosphoribosylformylglycinamidine synthase II [Mycobacterium smegmatis str. MC2 155]	300	11
gi|118471761	catalase/peroxidase HPI [Mycobacterium smegmatis str. MC2 155]	300	11
gi|118473709	antigen 85-C [Mycobacterium smegmatis str. MC2 155]	295	8
gi|118471745	universal stress protein family protein [Mycobacterium smegmatis str. MC2 155]	294	13
gi|118470627	F0F1 ATP synthase subunit alpha [Mycobacterium smegmatis str. MC2 155]	290	12
gi|118469118	translation initiation factor IF-2 [Mycobacterium smegmatis str. MC2 155]	287	9
gi|118468008	linear gramicidin synthetase subunit D [Mycobacterium smegmatis str. MC2 155]	287	18
gi|118469767	[Mn] superoxide dismutase [Mycobacterium smegmatis str. MC2 155]	277	12
gi|118467417	glycerol kinase [Mycobacterium smegmatis str. MC2 155]	277	20
gi|118471642	iron-sulfur cluster-binding protein [Mycobacterium smegmatis str. MC2 155]	268	10
gi|118473731	short chain dehydrogenase [Mycobacterium smegmatis str. MC2 155]	264	9
gi|118472731	cytochrome c oxidase subunit 2 [Mycobacterium smegmatis str. MC2 155]	249	5
gi|118469115	50S ribosomal protein L22 [Mycobacterium smegmatis str. MC2 155]	246	11
gi|118469821	succinate dehydrogenase iron-sulfur subunit [Mycobacterium smegmatis str. MC2 155]	242	10
gi|118469926	O-acetylhomoserine aminocarboxypropyltransferase [Mycobacterium smegmatis str. MC2 155]	241	9
gi|118467781	hypothetical protein MSMEG_5792 [Mycobacterium smegmatis str. MC2 155]	236	7
gi|118472895	hypothetical protein MSMEG_1680 [Mycobacterium smegmatis str. MC2 155]	231	6

gi|118471043	nucleoside-diphosphate-sugar epimerase [Mycobacterium smegmatis str. MC2 155]	230	7
gi|118469836	methylmalonate-semialdehyde dehydrogenase [Mycobacterium smegmatis str. MC2 155]	229	10
gi|118472963	hypothetical protein MSMEG_3620 [Mycobacterium smegmatis str. MC2 155]	221	5
gi|118472072	immunogenic protein MPT63 [Mycobacterium smegmatis str. MC2 155]	220	5
gi|118467449	inositol-5-monophosphate dehydrogenase [Mycobacterium smegmatis str. MC2 155]	220	14
gi|118473013	acyl-[ACP] desaturase [Mycobacterium smegmatis str. MC2 155]	218	7
gi|118467666	dihydroxyacetone kinase, L subunit [Mycobacterium smegmatis str. MC2 155]	218	6
gi|118472629	ribosome recycling factor [Mycobacterium smegmatis str. MC2 155]	218	14
gi|118473568	copper/zinc superoxide dismutase [Mycobacterium smegmatis str. MC2 155]	216	7
gi|118470886	integral membrane protein [Mycobacterium smegmatis str. MC2 155]	210	9
gi|118471699	triosephosphate isomerase [Mycobacterium smegmatis str. MC2 155]	210	18
gi|118470078	monooxygenase [Mycobacterium smegmatis str. MC2 155]	205	11
gi|118472344	hypothetical protein MSMEG_0948 [Mycobacterium smegmatis str. MC2 155]	196	5
gi|118473859	isochorismatase hydrolase [Mycobacterium smegmatis str. MC2 155]	192	9
gi|118470552	hypothetical protein MSMEG_2739 [Mycobacterium smegmatis str. MC2 155]	191	5
gi|118468811	LprG protein [Mycobacterium smegmatis str. MC2 155]	191	12
gi|118472424	hypothetical protein MSMEG_6365 [Mycobacterium smegmatis str. MC2 155]	187	6
gi|118472853	putative non-ribosomal peptide synthase [Mycobacterium smegmatis str. MC2 155]	186	13
gi|118472151	protein RecA [Mycobacterium smegmatis str. MC2 155]	185	3
gi|118467737	antigen 85-C [Mycobacterium smegmatis str. MC2 155]	184	5
gi|118468959	ferritin family protein [Mycobacterium smegmatis str. MC2 155]	182	9
gi|118472339	transcriptional accessory protein [Mycobacterium smegmatis str. MC2 155]	182	14
gi|118469999	phosphonoacetaldehyde hydrolase [Mycobacterium smegmatis str. MC2 155]	180	6
gi|118467664	ATP:cob(I)alamin adenosyltransferase [Mycobacterium smegmatis str. MC2 155]	177	6
gi|118471822	peptide synthetase [Mycobacterium smegmatis str. MC2 155]	176	14
gi|118467503	hypothetical protein MSMEG_1959 [Mycobacterium smegmatis str. MC2 155]	175	12
gi|118473140	universal stress protein family protein [Mycobacterium smegmatis str. MC2 155]	174	4
gi|118471352	R3H domain-containing protein [Mycobacterium smegmatis str. MC2 155]	174	5
gi|118471786	FHA domain-containing protein [Mycobacterium smegmatis str. MC2 155]	172	3
gi|118468078	succinate dehydrogenase flavoprotein subunit [Mycobacterium smegmatis str. MC2 155]	172	11
gi|118467606	propanediol utilization: dehydratase, medium subunit [Mycobacterium smegmatis str. MC2 155]	170	6
gi|118473255	F0F1 ATP synthase subunit gamma [Mycobacterium smegmatis str. MC2 155]	165	7
gi|118473442	morphine 6-dehydrogenase [Mycobacterium smegmatis str. MC2 155]	165	10
gi|118473678	ATP-dependent Clp protease proteolytic subunit [Mycobacterium smegmatis str. MC2 155]	165	9
gi|118472168	indole-3-glycerol-phosphate synthase [Mycobacterium smegmatis str. MC2 155]	164	4
gi|118467701	universal stress protein family protein [Mycobacterium smegmatis str. MC2 155]	162	12
gi|118472545	[Mn] superoxide dismutase [Mycobacterium smegmatis str. MC2 155]	162	5
gi|118469232	ribonucleotide-diphosphate reductase subunit beta [Mycobacterium smegmatis str. MC2 155]	160	8
gi|118470522	isopropylmalate isomerase small subunit [Mycobacterium smegmatis str. MC2 155]	159	4
gi|118470577	pyruvate dehydrogenase subunit E1 [Mycobacterium smegmatis str. MC2 155]	158	17
gi|118471814	forkhead-associated protein [Mycobacterium smegmatis str. MC2 155]	157	4

gi|118467544	tetrahydrofolate dehydrogenase/cyclohydrolase FolD [Mycobacterium smegmatis str. MC2 155]	156	8
gi|118467655	3-oxoacyl-(acyl carrier protein) synthase II [Mycobacterium smegmatis str. MC2 155]	155	9
gi|118470882	immunogenic protein MPB64/MPT64 [Mycobacterium smegmatis str. MC2 155]	154	4
gi|118471239	D-3-phosphoglycerate dehydrogenase [Mycobacterium smegmatis str. MC2 155]	150	8
gi|118473243	propionyl-CoA carboxylase beta chain [Mycobacterium smegmatis str. MC2 155]	150	13
gi|118467540	Sua5/YciO/YrdC/YwlC family protein [Mycobacterium smegmatis str. MC2 155]	148	2
gi|118468168	acetyl-CoA acetyltransferase [Mycobacterium smegmatis str. MC2 155]	148	6
gi|118472894	F420-dependent glucose-6-phosphate dehydrogenase [Mycobacterium smegmatis str. MC2 155]	147	11
gi|118473192	3-hydroxyacyl-CoA dehydrogenase [Mycobacterium smegmatis str. MC2 155]	146	8
gi|118473027	aspartate-semialdehyde dehydrogenase [Mycobacterium smegmatis str. MC2 155]	141	4
gi|118473695	[NADP+] succinate-semialdehyde dehydrogenase [Mycobacterium smegmatis str. MC2 155]	138	4
gi|118467925	ABC-type molybdenum transport system, ATPase component [Mycobacterium smegmatis str. MC2 155]	138	6
gi|118468997	sodium:solute symporter [Mycobacterium smegmatis str. MC2 155]	137	9
gi|118472532	NAD/mycothiol-dependent formaldehyde dehydrogenase [Mycobacterium smegmatis str. MC2 155]	136	5
gi|118468060	ferredoxin-dependent glutamate synthase 1 [Mycobacterium smegmatis str. MC2 155]	136	16
gi|118468373	cation ABC transporter, periplasmic cation-binding protein, putative [Mycobacterium smegmatis str. MC2 155]	134	3
gi|118470740	hypothetical protein MSMEG_1244 [Mycobacterium smegmatis str. MC2 155]	131	15
gi|118468465	heparin-binding hemagglutinin [Mycobacterium smegmatis str. MC2 155]	131	6
gi|118468145	bacterioferritin [Mycobacterium smegmatis str. MC2 155]	130	6
gi|118470193	phosphomethylpyrimidine kinase [Mycobacterium smegmatis str. MC2 155]	127	2
gi|118470308	alpha-glucan phosphorylase family protein [Mycobacterium smegmatis str. MC2 155]	125	13
gi|118468878	hypothetical protein MSMEG_2782 [Mycobacterium smegmatis str. MC2 155]	123	9
gi|118469046	hypothetical protein MSMEG_5715 [Mycobacterium smegmatis str. MC2 155]	118	7
gi|118469602	3-hydroxybutyryl-CoA dehydrogenase [Mycobacterium smegmatis str. MC2 155]	118	2
gi|118468818	serine hydroxymethyltransferase [Mycobacterium smegmatis str. MC2 155]	117	5
gi|118469194	F0F1 ATP synthase subunit delta [Mycobacterium smegmatis str. MC2 155]	117	5
gi|118471928	malonyl CoA-acyl carrier protein transacylase [Mycobacterium smegmatis str. MC2 155]	117	7
gi|118469543	ferredoxin [Mycobacterium smegmatis str. MC2 155]	116	3
gi|118467811	DNA gyrase subunit A [Mycobacterium smegmatis str. MC2 155]	115	13
gi|118469171	translation initiation factor IF-3 [Mycobacterium smegmatis str. MC2 155]	114	3
gi|118467842	hypothetical protein MSMEG_4631 [Mycobacterium smegmatis str. MC2 155]	113	3
gi|118468786	cobalamin synthesis protein/P47K [Mycobacterium smegmatis str. MC2 155]	113	3
gi|118473119	**lipoprotein, nlpa family protein [Mycobacterium smegmatis str. MC2 155]**	112	5
gi|118467795	hypothetical protein MSMEG_2940 [Mycobacterium smegmatis str. MC2 155]	112	4
gi|118468649	tuberculin related peptide [Mycobacterium smegmatis str. MC2 155]	111	2
gi|118472021	ATPase associated with various cellular activities, AAA-5 [Mycobacterium smegmatis str. MC2 155]	111	4
gi|118471302	30S ribosomal protein S12 [Mycobacterium smegmatis str. MC2 155]	111	6
gi|118469435	single-strand DNA-binding protein [Mycobacterium smegmatis str. MC2 155]	110	5
gi|118472299	PTS system, glucose-specific IIBC component [Mycobacterium smegmatis str. MC2 155]	110	5
gi|118469884	FMN-dependent dehydrogenase [Mycobacterium smegmatis str. MC2 155]	110	7
gi|118471565	fructose 1,6-bisphosphatase II [Mycobacterium smegmatis str. MC2 155]	108	10

gi|118470801	ATPase, AAA family protein [Mycobacterium smegmatis str. MC2 155]	107	9
gi|118471646	type I modular polyketide synthase [Mycobacterium smegmatis str. MC2 155]	106	22
gi|118472891	ubiquinol-cytochrome c reductase cytochrome c subunit [Mycobacterium smegmatis str. MC2 155]	105	1
gi|118473106	cell division protein [Mycobacterium smegmatis str. MC2 155]	105	9
gi|118470244	bifunctional udp-galactofuranosyl transferase glft [Mycobacterium smegmatis str. MC2 155]	105	5
gi|118472776	NAD(P) transhydrogenase subunit alpha [Mycobacterium smegmatis str. MC2 155]	105	9
gi|118473594	orotate phosphoribosyltransferase [Mycobacterium smegmatis str. MC2 155]	104	6
gi|118468522	co-chaperone GrpE [Mycobacterium smegmatis str. MC2 155]	103	5
gi|118471944	ferredoxin sulfite reductase [Mycobacterium smegmatis str. MC2 155]	101	16
gi|118471316	short chain dehydrogenase [Mycobacterium smegmatis str. MC2 155]	101	5
gi|118470670	peptide deformylase [Mycobacterium smegmatis str. MC2 155]	100	1
gi|118472437	hypothetical protein MSMEG_5225 [Mycobacterium smegmatis str. MC2 155]	100	3
gi|118471300	binding-protein-dependent transport systems inner membrane component [Mycobacterium smegmatis str. MC2 155]	100	4
gi|118473956	pyruvate synthase [Mycobacterium smegmatis str. MC2 155]	99	12
gi|118472079	hypothetical protein MSMEG_3489 [Mycobacterium smegmatis str. MC2 155]	99	7
gi|118471625	enoyl-CoA hydratase [Mycobacterium smegmatis str. MC2 155]	97	6
gi|118473206	glycine cleavage system aminomethyltransferase T [Mycobacterium smegmatis str. MC2 155]	97	3
gi|118471509	isocitrate lyase [Mycobacterium smegmatis str. MC2 155]	97	4
gi|118472457	putative thiosulfate sulfurtransferase [Mycobacterium smegmatis str. MC2 155]	96	6
gi|118470103	ATPase involved in DNA repair [Mycobacterium smegmatis str. MC2 155]	96	10
gi|118472513	phosphoribosylformylglycinamidine synthase subunit I [Mycobacterium smegmatis str. MC2 155]	96	3
gi|118473288	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase [Mycobacterium smegmatis str. MC2 155	96	3
gi|118471368	threonyl-tRNA synthetase [Mycobacterium smegmatis str. MC2 155]	95	8
gi|118472220	pyrroline-5-carboxylate reductase [Mycobacterium smegmatis str. MC2 155]	95	10
gi|118471103	propionyl-CoA carboxylase beta chain [Mycobacterium smegmatis str. MC2 155]	95	4
gi|118471254	porin [Mycobacterium smegmatis str. MC2 155]	95	4
gi|118472131	hypothetical protein MSMEG_6329 [Mycobacterium smegmatis str. MC2 155]	94	5
gi|118469201	leucyl-tRNA synthetase [Mycobacterium smegmatis str. MC2 155]	93	8
gi|118469785	deoxycytidine triphosphate deaminase [Mycobacterium smegmatis str. MC2 155]	92	5
gi|118473366	signal recognition particle-docking protein FtsY [Mycobacterium smegmatis str. MC2 155]	91	3
gi|118473826	secreted protein [Mycobacterium smegmatis str. MC2 155]	91	3
gi|118472725	adenylosuccinate synthetase [Mycobacterium smegmatis str. MC2 155]	90	7
gi|118470287	glycine dehydrogenase [Mycobacterium smegmatis str. MC2 155]	90	3
gi|118468031	hydrolase [Mycobacterium smegmatis str. MC2 155]	89	2
gi|118468739	forkhead-associated protein [Mycobacterium smegmatis str. MC2 155]	89	4
gi|118467446	phosphoserine aminotransferase [Mycobacterium smegmatis str. MC2 155]	88	2
gi|118471957	macrocin-O-methyltransferase [Mycobacterium smegmatis str. MC2 155]	87	5
gi|118471438	ubiquinol-cytochrome c reductase cytochrome b subunit [Mycobacterium smegmatis str. MC2 155]	87	4
gi|118470647	nucleotide-binding protein [Mycobacterium smegmatis str. MC2 155]	87	2
gi|118469633	3-oxoacyl-(acyl-carrier-protein) reductase [Mycobacterium smegmatis str. MC2 155]	86	5
gi|118469973	acetyl-CoA acetyltransferase [Mycobacterium smegmatis str. MC2 155]	86	2

gi|118474029	antigen MTB48 [Mycobacterium smegmatis str. MC2 155]	86	3
gi|118471914	aspartyl-tRNA synthetase [Mycobacterium smegmatis str. MC2 155]	85	5
gi|118469318	transcriptional regulatory protein [Mycobacterium smegmatis str. MC2 155]	85	5
gi|118473752	phosphoribosylamine--glycine ligase [Mycobacterium smegmatis str. MC2 155]	85	4
gi|118470192	arabinosyltransferase A [Mycobacterium smegmatis str. MC2 155]	84	10
gi|118474021	glutamine synthetase, type I [Mycobacterium smegmatis str. MC2 155]	82	5
gi|118470446	hypothetical protein MSMEG_1931 [Mycobacterium smegmatis str. MC2 155]	82	1
gi|118472063	serine esterase, cutinase family protein [Mycobacterium smegmatis str. MC2 155]	82	3
gi|118467493	MmpL4 protein [Mycobacterium smegmatis str. MC2 155]	81	10
gi|118467934	MmpL4 protein [Mycobacterium smegmatis str. MC2 155]	81	6
gi|118470186	uracil phosphoribosyltransferase [Mycobacterium smegmatis str. MC2 155]	79	5
gi|118469816	response regulator [Mycobacterium smegmatis str. MC2 155]	79	3
gi|118468368	pyridine nucleotide-disulphide oxidoreductase [Mycobacterium smegmatis str. MC2 155]	78	7
gi|118472342	hypothetical protein MSMEG_0067 [Mycobacterium smegmatis str. MC2 155]	78	6
gi|118473047	ABC transporter, ATP-binding protein SugC [Mycobacterium smegmatis str. MC2 155]	77	5
gi|118471284	cyclase/dehydrase [Mycobacterium smegmatis str. MC2 155]	77	4
gi|118470848	**polyamine-binding lipoprotein [Mycobacterium smegmatis str. MC2 155]**	77	5
gi|118468148	carbonic anhydrase [Mycobacterium smegmatis str. MC2 155]	77	2
gi|118468481	preprotein translocase subunit SecE [Mycobacterium smegmatis str. MC2 155]	76	3
gi|118471837	preprotein translocase subunit SecA [Mycobacterium smegmatis str. MC2 155]	76	9
gi|118470710	ribose-phosphate pyrophosphokinase [Mycobacterium smegmatis str. MC2 155]	75	2
gi|118472454	nitroreductase family protein [Mycobacterium smegmatis str. MC2 155]	75	5
gi|118468533	DNA-damage-inducible protein [Mycobacterium smegmatis str. MC2 155]	75	10
gi|118472042	SAM-dependent methyltransferase [Mycobacterium smegmatis str. MC2 155]	75	2
gi|118469404	NADH dehydrogenase [Mycobacterium smegmatis str. MC2 155]	74	6
gi|118473087	pyruvate carboxylase [Mycobacterium smegmatis str. MC2 155]	73	12
gi|118472561	short chain dehydrogenase [Mycobacterium smegmatis str. MC2 155]	73	4
gi|118472266	phosphoenolpyruvate carboxykinase [Mycobacterium smegmatis str. MC2 155]	73	5
gi|118467769	methyltransferase, UbiE/COQ5 family protein [Mycobacterium smegmatis str. MC2 155]	73	4
gi|118468207	serine 3-dehydrogenase [Mycobacterium smegmatis str. MC2 155]	73	2
gi|118472812	methylmalonyl-CoA mutase [Mycobacterium smegmatis str. MC2 155]	72	5
gi|118469826	hypothetical protein MSMEG_4199 [Mycobacterium smegmatis str. MC2 155]	72	4
gi|118473142	inositol-5-monophosphate dehydrogenase [Mycobacterium smegmatis str. MC2 155]	72	4
gi|118468125	urease accessory protein UreG [Mycobacterium smegmatis str. MC2 155]	72	3
gi|118472260	6-phosphogluconate dehydrogenase [Mycobacterium smegmatis str. MC2 155]	72	2
gi|118471574	glucose-6-phosphate isomerase [Mycobacterium smegmatis str. MC2 155]	71	10
gi|118471372	tyramine oxidase [Mycobacterium smegmatis str. MC2 155]	71	2
gi|118472218	5-carboxymethyl-2-hydroxymuconate delta-isomerase [Mycobacterium smegmatis str. MC2 155]	71	1
gi|118470532	hypothetical protein MSMEG_2261 [Mycobacterium smegmatis str. MC2 155]	70	1
gi|118467566	NAD-dependent malic enzyme [Mycobacterium smegmatis str. MC2 155]	70	1
gi|118471926	ABC transporter, ATP-binding protein [Mycobacterium smegmatis str. MC2 155]	70	9

gi|118468194	quinone oxidoreductase [Mycobacterium smegmatis str. MC2 155]	70	6
gi|118468158	NAD(P) transhydrogenase subunit alpha [Mycobacterium smegmatis str. MC2 155]	70	9
gi|118472687	phenylalanyl-tRNA synthetase subunit alpha [Mycobacterium smegmatis str. MC2 155]	69	6
gi|118472463	aspartyl/glutamyl-tRNA amidotransferase subunit A [Mycobacterium smegmatis str. MC2 155]	69	6
gi|118469316	beta-lactamase [Mycobacterium smegmatis str. MC2 155]	69	7
gi|118467561	antigen 85-C [Mycobacterium smegmatis str. MC2 155]	69	3
gi|118473957	uricase [Mycobacterium smegmatis str. MC2 155]	68	4
gi|118471082	NAD(P) transhydrogenase, beta subunit [Mycobacterium smegmatis str. MC2 155]	68	3
gi|118472999	ribonuclease, Rne/Rng family protein [Mycobacterium smegmatis str. MC2 155]	67	7
gi|118467931	methylmalonyl-CoA mutase, small subunit [Mycobacterium smegmatis str. MC2 155]	67	1
gi|118471890	CobW/P47K domain-containing protein [Mycobacterium smegmatis str. MC2 155]	66	6
gi|118470626	preprotein translocase subunit SecF [Mycobacterium smegmatis str. MC2 155]	66	4
gi|118473730	hypothetical protein MSMEG_3144 [Mycobacterium smegmatis str. MC2 155]	65	2
gi|118469198	isopropylmalate isomerase large subunit [Mycobacterium smegmatis str. MC2 155]	65	7
gi|118469498	phosphate transport system regulatory protein PhoU [Mycobacterium smegmatis str. MC2 155]	65	2
gi|118468277	putative beta-1,3-glucanase [Mycobacterium smegmatis str. MC2 155]	65	3
gi|118471931	alpha-methylacyl-CoA racemase [Mycobacterium smegmatis str. MC2 155]	64	3
gi|118469253	membrane protein [Mycobacterium smegmatis str. MC2 155]	64	2
gi|118473461	hypothetical protein MSMEG_6434 [Mycobacterium smegmatis str. MC2 155]	63	2
gi|118473166	elongation factor P [Mycobacterium smegmatis str. MC2 155]	63	3
gi|118471954	6-phosphogluconate dehydrogenase-like protein [Mycobacterium smegmatis str. MC2 155]	62	4
gi|118469646	ribonuclease activity regulator protein RraA [Mycobacterium smegmatis str. MC2 155]	62	4
gi|118468049	alcohol dehydrogenase, zinc-containing [Mycobacterium smegmatis str. MC2 155]	62	4
gi|118468890	threonine synthase [Mycobacterium smegmatis str. MC2 155]	62	8
gi|118473876	(3R)-hydroxyacyl-ACP dehydratase subunit HadA [Mycobacterium smegmatis str. MC2 155]	62	3
gi|118470171	siderophore binding protein [Mycobacterium smegmatis str. MC2 155]	61	1
gi|118470603	ammonium transporter [Mycobacterium smegmatis str. MC2 155]	61	1
gi|118468999	short-chain dehydrogenase [Mycobacterium smegmatis str. MC2 155]	61	3
gi|118473158	peptide chain release factor 2 [Mycobacterium smegmatis str. MC2 155]	61	6
gi|118469997	ATPase, MoxR family protein [Mycobacterium smegmatis str. MC2 155]	60	6
gi|118470151	hypothetical protein MSMEG_1601 [Mycobacterium smegmatis str. MC2 155]	60	1
gi|118470472	protease 2 [Mycobacterium smegmatis str. MC2 155]	59	1
gi|118467403	DNA topoisomerase I [Mycobacterium smegmatis str. MC2 155]	59	13
gi|118472100	glutamate transport ATP-binding protein GluA [Mycobacterium smegmatis str. MC2 155]	59	1
gi|118467521	putative acyl-CoA dehydrogenase [Mycobacterium smegmatis str. MC2 155]	58	3
gi|118468808	hypothetical protein MSMEG_3645 [Mycobacterium smegmatis str. MC2 155]	58	7
gi|118472088	binding protein [Mycobacterium smegmatis str. MC2 155]	58	3
gi|118472003	glutamyl-tRNA synthetase [Mycobacterium smegmatis str. MC2 155]	57	6
gi|118471012	methionine sulfoxide reductase A [Mycobacterium smegmatis str. MC2 155]	57	1
gi|118467379	riboflavin synthase subunit alpha [Mycobacterium smegmatis str. MC2 155]	57	3
gi|118471450	50S ribosomal protein L13 [Mycobacterium smegmatis str. MC2 155]	57	2

gi|118468280	hypothetical protein MSMEG_3935 [Mycobacterium smegmatis str. MC2 155]	56	8
gi|118472528	CAIB/BAIF family protein [Mycobacterium smegmatis str. MC2 155]	56	4
gi|118473994	CTP synthetase [Mycobacterium smegmatis str. MC2 155]	56	4
gi|118469122	RNA polymerase sigma factor [Mycobacterium smegmatis str. MC2 155]	55	3
gi|118469694	hypothetical protein MSMEG_3081 [Mycobacterium smegmatis str. MC2 155]	55	6
gi|118469496	fatty acid desaturase [Mycobacterium smegmatis str. MC2 155]	54	7
gi|118467831	putative ABC transporter ATP-binding protein [Mycobacterium smegmatis str. MC2 155]	54	13
gi|118469773	transaldolase [Mycobacterium smegmatis str. MC2 155]	53	5
gi|118472491	DoxX subfamily protein, putative [Mycobacterium smegmatis str. MC2 155]	53	9
gi|118470807	bifunctional GMP synthase/glutamine amidotransferase protein [Mycobacterium smegmatis str. MC2 155]	53	14
gi|118473018	integral membrane protein [Mycobacterium smegmatis str. MC2 155]	53	2
gi|118467601	hypothetical protein MSMEG_1513 [Mycobacterium smegmatis str. MC2 155]	52	3
gi|118471877	hypothetical protein MSMEG_1733 [Mycobacterium smegmatis str. MC2 155]	52	5
gi|118470811	thioesterase family protein [Mycobacterium smegmatis str. MC2 155]	52	3
gi|118472053	30S ribosomal protein S7 [Mycobacterium smegmatis str. MC2 155]	52	6
gi|118468458	precorrin-8X methylmutase [Mycobacterium smegmatis str. MC2 155]	52	4
gi|118469642	short chain dehydrogenase [Mycobacterium smegmatis str. MC2 155]	51	4
gi|118467631	cell division protein FtsZ [Mycobacterium smegmatis str. MC2 155]	51	6
gi|118473000	tena/thi-4 family protein [Mycobacterium smegmatis str. MC2 155]	51	3
gi|118469940	putative integral membrane protein [Mycobacterium smegmatis str. MC2 155]	50	2
gi|118472270	prolyl-tRNA synthetase [Mycobacterium smegmatis str. MC2 155]	50	1
gi|118467578	deoxyuridine 5~-triphosphate nucleotidohydrolase [Mycobacterium smegmatis str. MC2 155]	50	2
gi|118473939	TetR-family protein transcriptional regulator [Mycobacterium smegmatis str. MC2 155]	50	1
gi|118472779	phosphoribose diphosphate:decaprenyl-phosphate phosphoribosyltransferase [Mycobacterium smegmatis str. MC2 155]	50	2
gi|118471448	**solute-binding lipoprotein [Mycobacterium smegmatis str. MC2 155]**	50	6
gi|118468351	hypothetical protein MSMEG_0824 [Mycobacterium smegmatis str. MC2 155]	50	3
gi|118467542	transcription antitermination protein NusG [Mycobacterium smegmatis str. MC2 155]	50	3
gi|118467916	ferredoxin-dependent glutamate synthase 1 [Mycobacterium smegmatis str. MC2 155]	49	8
gi|118469964	DNA polymerase III subunits gamma and tau [Mycobacterium smegmatis str. MC2 155]	49	5
gi|118470482	RNA polymerase sigma factor SigF [Mycobacterium smegmatis str. MC2 155]	49	4
gi|118473627	phosphatidylserine decarboxylase [Mycobacterium smegmatis str. MC2 155]	49	1
gi|118471491	ParB-like partition proteins [Mycobacterium smegmatis str. MC2 155]	49	4
gi|118469073	16S rRNA-processing protein [Mycobacterium smegmatis str. MC2 155]	47	3
gi|118469044	hypothetical protein MSMEG_1279 [Mycobacterium smegmatis str. MC2 155]	47	6
gi|118471351	phosphoribosylaminoimidazole-succinocarboxamide synthase [Mycobacterium smegmatis str. MC2 155]	47	4
gi|118473653	hydrogenase-2, small subunit [Mycobacterium smegmatis str. MC2 155]	47	3
gi|118472473	membrane protein, MmpL family protein [Mycobacterium smegmatis str. MC2 155]	46	9
gi|118469590	NHL repeat-containing protein [Mycobacterium smegmatis str. MC2 155]	46	9
gi|118469252	carnitinyl-CoA dehydratase [Mycobacterium smegmatis str. MC2 155]	46	3
gi|118470342	integral membrane protein [Mycobacterium smegmatis str. MC2 155]	46	3
gi|118473811	cell division ATP-binding protein FtsE [Mycobacterium smegmatis str. MC2 155]	46	7

gi|118472583	cytochrome c oxidase, subunit I [Mycobacterium smegmatis str. MC2 155]	46	3
gi|118473307	hypothetical protein MSMEG_4909 [Mycobacterium smegmatis str. MC2 155]	45	3
gi|118470672	acyl-CoA synthetase [Mycobacterium smegmatis str. MC2 155]	45	4
gi|118471289	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Mycobacterium smegmatis	45	3
gi|118471527	acyl carrier protein [Mycobacterium smegmatis str. MC2 155]	45	4
gi|118472995	isoleucyl-tRNA synthetase [Mycobacterium smegmatis str. MC2 155]	44	4
gi|118468679	mannose-binding lectin [Mycobacterium smegmatis str. MC2 155]	44	1
gi|118472921	acetolactate synthase 1 catalytic subunit [Mycobacterium smegmatis str. MC2 155]	44	4
gi|118472450	extracellular solute-binding protein, family protein 3 [Mycobacterium smegmatis str. MC2 155]	44	3
gi|118467584	cystathionine gamma-synthase [Mycobacterium smegmatis str. MC2 155]	43	5
gi|118467923	thiopurine S-methyltransferase (tpmt) superfamily protein [Mycobacterium smegmatis str. MC2 155]	43	1
gi|118471704	catalase/peroxidase HPI [Mycobacterium smegmatis str. MC2 155]	43	3
gi|118469222	glycerate kinase [Mycobacterium smegmatis str. MC2 155]	42	4
gi|118470303	hypothetical protein MSMEG_1951 [Mycobacterium smegmatis str. MC2 155]	42	8
gi|118470039	chaperone ClpB [Mycobacterium smegmatis str. MC2 155]	42	8
gi|118469355	dihydroxyacetone kinase, DhaK subunit [Mycobacterium smegmatis str. MC2 155]	42	4
gi|118470653	adenosine kinase [Mycobacterium smegmatis str. MC2 155]	42	4
gi|118467576	para-aminobenzoate synthase component II [Mycobacterium smegmatis str. MC2 155]	41	1
gi|118472922	oligopeptide transport ATP-binding protein OppD [Mycobacterium smegmatis str. MC2 155]	41	2
gi|118470965	UDP-galactopyranose mutase [Mycobacterium smegmatis str. MC2 155]	41	5
gi|118468117	DNA polymerase III subunit beta [Mycobacterium smegmatis str. MC2 155]	40	5
gi|118469719	alanine and proline-rich secreted protein apa [Mycobacterium smegmatis str. MC2 155]	40	6
gi|118467614	alcohol dehydrogenase [Mycobacterium smegmatis str. MC2 155]	40	1
gi|118468825	short chain dehydrogenase [Mycobacterium smegmatis str. MC2 155]	40	3
gi|118467529	1-aminocyclopropane-1-carboxylate deaminase [Mycobacterium smegmatis str. MC2 155]	40	3
gi|118468205	O-succinylhomoserine sulfhydrylase [Mycobacterium smegmatis str. MC2 155]	40	5
gi|118472323	ATPase, AAA family protein [Mycobacterium smegmatis str. MC2 155]	39	12
gi|118472145	intracellular protease, PfpI family protein [Mycobacterium smegmatis str. MC2 155]	39	4
gi|118470195	hypothetical protein MSMEG_0905 [Mycobacterium smegmatis str. MC2 155]	39	5
gi|118470981	6-phosphogluconolactonase [Mycobacterium smegmatis str. MC2 155]	39	2
gi|118472006	regulatory protein, TetR [Mycobacterium smegmatis str. MC2 155]	39	2
gi|118471653	carbon-nitrogen hydrolase family protein [Mycobacterium smegmatis str. MC2 155]	39	1
gi|118471755	isochorismatase hydrolase [Mycobacterium smegmatis str. MC2 155]	39	3
gi|118470420	MmpL4 protein [Mycobacterium smegmatis str. MC2 155]	38	4
gi|118472114	hypothetical protein MSMEG_2458 [Mycobacterium smegmatis str. MC2 155]	37	1
gi|118472346	ABC transporter, permease/ATP-binding protein [Mycobacterium smegmatis str. MC2 155]	37	6
gi|118471443	aspartate kinase [Mycobacterium smegmatis str. MC2 155]	37	7
gi|118469839	DNA polymerase III subunit alpha [Mycobacterium smegmatis str. MC2 155]	37	12
gi|118469707	ABC transporter, permease/ATP-binding protein [Mycobacterium smegmatis str. MC2 155]	37	4
gi|118467505	hypothetical protein MSMEG_5452 [Mycobacterium smegmatis str. MC2 155]	37	3
gi|118473361	hypothetical protein MSMEG_6415 [Mycobacterium smegmatis str. MC2 155]	36	2

gi|118472166	two component transcriptional regulatory protein devr [Mycobacterium smegmatis str. MC2 155]	36	7
gi|118471546	signal transduction histidine kinase [Mycobacterium smegmatis str. MC2 155]	35	3
gi|118468268	enoyl-CoA hydratase [Mycobacterium smegmatis str. MC2 155]	35	2
gi|118468799	MmcI protein [Mycobacterium smegmatis str. MC2 155]	35	4
gi|118470350	ABC transporter, ATP-binding protein [Mycobacterium smegmatis str. MC2 155]	35	2
gi|118468647	inv protein [Mycobacterium smegmatis str. MC2 155]	35	1
gi|118469291	LysR-family protein trancsriptional regulator [Mycobacterium smegmatis str. MC2 155]	35	10
gi|118468485	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein [Mycobacterium smegmatis str. MC2 155]	35	3
gi|118468754	3-hydroxyacyl-CoA dehydrogenase type-2 [Mycobacterium smegmatis str. MC2 155]	35	6
gi|118471479	acetaldehyde dehydrogenase [Mycobacterium smegmatis str. MC2 155]	34	3
gi|118472374	hypothetical protein MSMEG_3909 [Mycobacterium smegmatis str. MC2 155]	34	5
gi|118473156	allophanate hydrolase subunit 2 [Mycobacterium smegmatis str. MC2 155]	34	1
gi|118468354	cyclopropane-fatty-acyl-phospholipid synthase 1 [Mycobacterium smegmatis str. MC2 155]	34	2
gi|118468484	thymidylate kinase [Mycobacterium smegmatis str. MC2 155]	34	4
gi|118473504	RNA pseudouridine synthase family protein [Mycobacterium smegmatis str. MC2 155]	34	5
gi|118473981	tRNA-dihydrouridine synthase, putative [Mycobacterium smegmatis str. MC2 155]	33	2
gi|118471722	3-ketoacyl-(acyl-carrier-protein) reductase [Mycobacterium smegmatis str. MC2 155]	33	3
gi|118467725	adenosine deaminase [Mycobacterium smegmatis str. MC2 155]	33	9
gi|118473962	enoyl-CoA hydratase [Mycobacterium smegmatis str. MC2 155]	32	3
gi|118470915	[NADP+] succinate-semialdehyde dehydrogenase [Mycobacterium smegmatis str. MC2 155]	32	6
gi|118473304	GTP-binding protein TypA/BipA [Mycobacterium smegmatis str. MC2 155]	32	3
gi|118473851	**lipoprotein Lpps [Mycobacterium smegmatis str. MC2 155]**	32	5
gi|118472696	valyl-tRNA synthetase [Mycobacterium smegmatis str. MC2 155]	32	12
gi|118469451	hypothetical protein MSMEG_2198 [Mycobacterium smegmatis str. MC2 155]	32	5
gi|118470693	Formyl transferase [Mycobacterium smegmatis str. MC2 155]	32	3
gi|118473949	transcriptional regulatory protein [Mycobacterium smegmatis str. MC2 155]	32	5
gi|118468070	hypothetical protein MSMEG_5309 [Mycobacterium smegmatis str. MC2 155]	32	1
gi|118468685	**lipoprotein [Mycobacterium smegmatis str. MC2 155]**	32	5
gi|118473586	transcriptional regulator, GntR family protein [Mycobacterium smegmatis str. MC2 155]	32	6
gi|118473076	2-oxoglutarate ferredoxin oxidoreductase subunit beta [Mycobacterium smegmatis str. MC2 155]	31	2
gi|118472760	inorganic pyrophosphatase [Mycobacterium smegmatis str. MC2 155]	31	2
gi|118473813	ABC transporter, permease protein SugB [Mycobacterium smegmatis str. MC2 155]	31	4
gi|118469041	enoyl-CoA hydratase [Mycobacterium smegmatis str. MC2 155]	31	7
gi|118473031	diguanylate cyclase [Mycobacterium smegmatis str. MC2 155]	31	2
gi|118471079	transcriptional regulator, TetR family protein [Mycobacterium smegmatis str. MC2 155]	31	3
gi|118473179	homoserine dehydrogenase [Mycobacterium smegmatis str. MC2 155]	30	5
gi|118470332	glyoxalase family protein [Mycobacterium smegmatis str. MC2 155]	30	2
gi|118468884	transcriptional regulator, TetR family protein [Mycobacterium smegmatis str. MC2 155]	30	3
gi|118470254	glutamine-binding periplasmic protein/glutamine transport system permease protein [Mycobacterium smegmatis str. MC2 1	30	5
gi|118467865	ribonuclease PH [Mycobacterium smegmatis str. MC2 155]	30	1
gi|118473375	hypothetical protein MSMEG_0317 [Mycobacterium smegmatis str. MC2 155]	30	3

gi|118469867	4-hydroxy-2-ketovalerate aldolase [Mycobacterium smegmatis str. MC2 155]	30	2
gi|118474039	maleylacetate reductase [Mycobacterium smegmatis str. MC2 155]	29	10
gi|118470931	metallo-beta-lactamase family protein [Mycobacterium smegmatis str. MC2 155]	29	2
gi|118472981	extracellular solute-binding protein, family protein 5 [Mycobacterium smegmatis str. MC2 155]	29	7
gi|118470031	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase [Mycobacterium s	29	5
gi|118470803	extra cytoplasmic sigma factor [Mycobacterium smegmatis str. MC2 155]	29	2
gi|118468236	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase [Mycobacterium smegmatis str. MC2 155]	29	9
gi|118467974	FeS assembly protein SufD [Mycobacterium smegmatis str. MC2 155]	29	4
gi|118468834	acyl-CoA synthetase [Mycobacterium smegmatis str. MC2 155]	29	3
gi|118472496	branched-chain amino acid aminotransferase [Mycobacterium smegmatis str. MC2 155]	29	1
gi|118467579	amino acid carrier protein [Mycobacterium smegmatis str. MC2 155]	29	3
gi|118470718	hypothetical protein MSMEG_6447 [Mycobacterium smegmatis str. MC2 155]	29	2
gi|118468925	hypothetical protein MSMEG_3682 [Mycobacterium smegmatis str. MC2 155]	29	1
gi|118471246	respiratory nitrate reductase, gamma subunit [Mycobacterium smegmatis str. MC2 155]	29	3
gi|118471350	ferrochelatase [Mycobacterium smegmatis str. MC2 155]	28	7
gi|118473515	amylo-alpha-1,6-glucosidase [Mycobacterium smegmatis str. MC2 155]	28	6
gi|118471817	hypothetical protein MSMEG_4820 [Mycobacterium smegmatis str. MC2 155]	28	2
gi|118470314	NAD-dependent DNA ligase LigA [Mycobacterium smegmatis str. MC2 155]	28	6
gi|118468633	carbon starvation protein A [Mycobacterium smegmatis str. MC2 155]	28	9
gi|118471548	amino-acid acetyltransferase [Mycobacterium smegmatis str. MC2 155]	28	3
gi|118473677	rhamnulokinase [Mycobacterium smegmatis str. MC2 155]	28	2
gi|118467440	sensory box/response regulator [Mycobacterium smegmatis str. MC2 155]	28	5
gi|118470602	linear gramicidin synthetase subunit B [Mycobacterium smegmatis str. MC2 155]	28	21
gi|118469030	penicillin binding protein transpeptidase domain-containing protein [Mycobacterium smegmatis str. MC2 155]	27	3
gi|118468182	extracellular solute-binding protein, family protein 5 [Mycobacterium smegmatis str. MC2 155]	27	5
gi|118473807	putative 3-hydroxyacyl-CoA dehydrogenase [Mycobacterium smegmatis str. MC2 155]	26	6
gi|118468051	proteasome beta subunit [Mycobacterium smegmatis str. MC2 155]	26	2
gi|118471631	alkanesulfonate monooxygenase family protein [Mycobacterium smegmatis str. MC2 155]	26	1
gi|118470922	hypothetical protein MSMEG_0222 [Mycobacterium smegmatis str. MC2 155]	26	3
gi|118468699	SseC protein [Mycobacterium smegmatis str. MC2 155]	26	3
gi|118473601	dihydroorotase [Mycobacterium smegmatis str. MC2 155]	26	5
gi|118473505	preprotein translocase subunit SecY [Mycobacterium smegmatis str. MC2 155]	25	1
gi|118469828	DEAD/DEAH box helicase [Mycobacterium smegmatis str. MC2 155]	25	12
gi|118472188	hypothetical protein MSMEG_3278 [Mycobacterium smegmatis str. MC2 155]	25	3
gi|118473814	hydrolase [Mycobacterium smegmatis str. MC2 155]	25	4