

Supplementary: Overview of *M. tuberculosis* H37Rv proteins identified in this study

Accession#	Sanger ID	Gene Name	Description	MOWSE	pI	MW (Da)	GRAVY	TMHMM
gi 15607148	Rv0006	gyrA	DNA gyrase subunit A	141	5.41	92317.71	-0.303	0
gi 15607149	Rv0007		hypothetical protein Rv0007	218	8.98	31110.96	-0.131	2
gi 15607150	Rv0008c		hypothetical protein Rv0008c	274	11.41	15661.47	-0.284	1
gi 15607160	Rv0018c	pstP	possible serine/threonine phosphatase	83	5.05	54063.61	-0.109	1
gi 15607190	Rv0048c		hypothetical protein Rv0048c	228	5.70	30855.00	-0.121	1
gi 15607196	Rv0054	ssb	probable single-stranded DNA-binding protein	131	5.12	17447.58	-0.474	0
gi 15607198	Rv0056	rpII	Probable 50S ribosomal protein L9	133	8.93	16159.83	-0.021	0
gi 15607214	Rv0072		hypothetical protein Rv0072	283	10.24	36386.98	0.663	3
gi 15607249	Rv0107c	ctpl	probable cation-transporter ATPase I	87	5.87	169574.90	0.105	0
gi 15607273	Rv0131c	fadE1	probable acyl-CoA dehydrogenase	79	7.34	50362.77	-0.291	0
gi 15607276	Rv0134	ephF	possible epoxide hydrolase	145	5.87	33889.22	-0.196	0
gi 15607289	Rv0147		hypothetical protein Rv0147	2778	9.21	55114.80	-0.144	0
gi 15607290	Rv0148		hypothetical protein Rv0148	297	5.27	29874.22	0.111	0
gi 15607299	Rv0157	pntB	probable NAD(P) transhydrogenase (subunit beta)	185	6.05	48826.76	0.668	9
gi 15607313	Rv0172	mce1D	MCE-family protein	109	4.97	56498.40	-0.018	0
gi 15607314	Rv0173	lprK	possible mce-family lipoprotein	133	8.36	42384.33	-0.069	0
gi 15607316	Rv0175		hypothetical protein Rv0175	75	4.86	22513.15	-0.197	1
gi 15607319	Rv0178		hypothetical protein Rv0178	209	5.58	25896.04	-0.275	1
gi 15607321	Rv0180c		hypothetical protein Rv0180c	467	9.54	47563.39	0.482	6
gi 15607330	Rv0189c	ilvD	probable dihydroxy-acid dehydratase	135	5.06	59770.38	0.155	0
gi 15607340	Rv0199		probable conserved membrane protein	114	4.81	23520.30	-0.208	1
gi 15607347	Rv0206c	mmpL3	possible conserved transmembrane transport protein	336	9.48	101068.75	0.240	11
gi 15607352	Rv0211	pckA	probable iron-regulated phosphoenolpyruvate carboxykinase	138	4.92	67723.24	-0.321	0
gi 15607368	Rv0227c		hypothetical protein Rv0227c	818	4.82	45556.90	-0.410	1
gi 15607372	Rv0231	fadE4	probable acyl-CoA dehydrogenase	144	5.72	63682.95	-0.155	0
gi 15607378	Rv0237	lpqI	probable conserved lipoprotein	159	5.40	39665.59	0.123	0
gi 15607384	Rv0243	fadA2	probable acetyl-CoA acyltransferase	645	6.20	46306.72	-0.045	0
gi 15607385	Rv0244c	fadE5	probable acyl-CoA dehydrogenase	696	5.30	66061.64	-0.009	0
gi 15607389	Rv0248c		hypothetical protein Rv0248c	208	5.62	71092.39	-0.332	0
gi 15607407	Rv0266c		hypothetical protein Rv0266c	91	5.95	129968.97	-0.160	0
gi 15607411	Rv0270	fadD2	probable fatty-acid-CoA ligase	956	6.31	59855.65	-0.071	0
gi 15607423	Rv0282		hypothetical protein Rv0282	780	5.09	68292.90	-0.146	0
gi 15607424	Rv0283		hypothetical protein Rv0283	924	6.76	56022.24	0.039	1
gi 15607425	Rv0284		possible conserved membrane protein	1338	6.03	145253.10	-0.124	1
gi 15607431	Rv0290		hypothetical protein Rv0290	258	9.03	48027.77	1.002	11
gi 15607432	Rv0291	mycP3	probable membrane-anchored mycosin	137	5.30	46127.10	0.150	1
gi 15607433	Rv0292		hypothetical protein Rv0292	127	10.36	36081.10	-0.034	2
gi 15607479	Rv0338c		hypothetical protein Rv0338c	404	6.93	96394.35	-0.105	6
gi 15607498	Rv0357c	purA	probable adenylosuccinate synthetase (IMP--aspartate ligase)	534	6.28	47135.52	-0.137	0
gi 15607502	Rv0361		hypothetical protein Rv0361	200	4.90	30077.94	-0.477	1
gi 15607506	Rv0365c		hypothetical protein Rv0365c	173	9.77	41649.39	-0.260	0
gi 15607524	Rv0383c		hypothetical protein Rv0383c	300	10.13	31952.61	-0.445	0
gi 15607541	Rv0400c	fadE7	acyl-CoA dehydrogenase	158	6.21	42669.71	-0.007	0

gi 15607548	Rv0407	fgd1	probable F420-dependent glucose-6-phosphate dehydrogenase	88	5.29	36956.80	-0.240	0
gi 15607553	Rv0412c		hypothetical protein Rv0412c	275	9.71	47086.88	-0.029	4
gi 15607559	Rv0418	lpqL	probable lipoprotein aminopeptidase	107	4.99	52181.21	-0.057	0
gi 15607572	Rv0431		putative tuberculin related peptide	93	4.55	16905.20	0.304	0
gi 15607573	Rv0432	sodC	probable periplasmic superoxide dismutase	741	5.60	24000.83	-0.061	0
gi 15607578	Rv0437c	psd	possible phosphatidylserine decarboxylase	247	9.48	24472.95	0.148	0
gi 15607581	Rv0440	groEL2	60 kDa chaperonin 2	462	4.85	56692.13	-0.091	0
gi 15607586	Rv0445c	sigK	probable alternative RNA polymerase sigma factor	110	7.68	21249.71	-0.390	0
gi 15607605	Rv0464c		hypothetical protein Rv0464c	375	9.74	21405.32	-0.145	0
gi 15607616	Rv0475		hypothetical protein Rv0475	392	9.18	21521.59	-0.593	0
gi 15607620	Rv0479c		hypothetical protein Rv0479c	571	9.32	37139.48	-0.190	1
gi 15607633	Rv0492c		probable oxidoreductase	87	9.53	66154.10	0.113	0
gi 15607641	Rv0500	proC	probable pyrroline-5-carboxylate reductase	144	4.73	30171.50	0.392	0
gi 15607646	Rv0505c	serB1	possible phosphoserine phosphatase	189	6.72	39711.61	-0.035	1
gi 15607652	Rv0511	cysG	possible multifunctional enzyme siroheme synthase	129	5.53	59141.66	-0.035	0
gi 15607663	Rv0523c		conserved hypothetical protein	155	11.27	14827.10	-0.298	0
gi 15607666	Rv0526		hypothetical protein Rv0526	130	7.74	23374.98	-0.135	0
gi 15607703	Rv0563	htpX	probable protease transmembrane protein heat shock protein	130	9.93	30681.90	0.304	3
gi 15607720	Rv0580c		hypothetical protein Rv0580c	4380	9.88	18023.61	-0.061	0
gi 15607723	Rv0583c	lpqN	probable conserved lipoprotein	127	4.57	23724.87	-0.158	0
gi 15607772	Rv0632c	echA3	probable enoyl-CoA hydratase	85	5.52	24453.51	0.206	0
gi 15607778	Rv0638	secE1	probable preprotein translocase	413	9.65	16945.89	-0.137	1
gi 15607787	Rv0647c		hypothetical protein Rv0647c	145	6.95	54789.59	-0.157	0
gi 15607807	Rv0667	rpoB	DNA-directed RNA polymerase (beta chain)	315	4.92	120987.32	-0.324	0
gi 15607808	Rv0668	rpoC	DNA-directed RNA polymerase (beta-chain)	4637	5.86	147362.11	-0.362	0
gi 15607809	Rv0669c		hypothetical protein	166	6.30	69731.98	-0.294	0
gi 15607816	Rv0676c	mmpL7	probable conserved transmembrane transport protein	119	5.67	104945.32	0.324	12
gi 15607823	Rv0683	rpsG	probable 30S ribosomal protein S7	639	10.56	17589.58	-0.606	0
gi 15607825	Rv0685	tuf	probable iron-regulated elongation factor Tu	190	5.28	44362.92	-0.283	0
gi 15607826	Rv0686		hypothetical protein Rv0686	333	8.68	28614.43	0.283	2
gi 15607834	Rv0694	lldD1	possible L-lactate dehydrogenase	110	8.81	42135.04	0.003	0
gi 15607841	Rv0701	rplC	Probable 50S ribosomal protein L3	164	10.30	23133.19	-0.308	0
gi 15607842	Rv0702	rplD	Probable 50S ribosomal protein L4	529	10.13	23728.55	-0.427	0
gi 15607843	Rv0703	rplW	probable 50S ribosomal protein L23	230	10.48	10951.08	-0.285	0
gi 15607844	Rv0704	rplB	probable 50S ribosomal protein L2	1587	11.39	30615.23	-0.851	0
gi 15607846	Rv0706	rplV	probable 50S ribosomal protein L22	799	11.74	20368.31	-0.494	0
gi 15607847	Rv0707	rpsC	probable 30S ribosomal protein S3	1050	10.14	30058.76	-0.612	0
gi 15607848	Rv0708	rplP	Probable 50S ribosomal protein L16	490	11.16	15682.55	-0.598	0
gi 15607850	Rv0710	rpsQ	probable ribosomal protein S17	158	10.57	14732.16	-0.648	0
gi 15607856	Rv0716	rplE	Probable 50S ribosomal protein L5	10596	10.09	21006.17	-0.344	0
gi 15607858	Rv0718	rpsH	probable 30S ribosomal protein S8	771	10.12	14411.50	-0.200	0
gi 15607859	Rv0719	rplF	Probable 50S ribosomal protein L6	432	10.21	19365.53	-0.367	0
gi 15607860	Rv0720	rplR	Probable 50S ribosomal protein L18	429	11.61	13176.19	-0.329	0
gi 15607861	Rv0721	rpsE	probable 30S ribosomal protein S5	607	10.17	22931.30	-0.171	0
gi 15607862	Rv0722	rpmD	probable 50S ribosomal protein L30	186	11.83	7342.11	-0.440	0
gi 15607863	Rv0723	rplO	Probable 50S ribosomal protein L15	1774	11.34	15523.54	-0.412	0

gi 15607864	Rv0724	sppA	possible protease IV	156	5.75	66123.08	-0.018	0
gi 15607897	Rv0757	phoP	possible two component system response transcriptional positive regulator	179	6.02	27496.55	-0.191	0
gi 15607938	Rv0798c		hypothetical protein Rv0798c	7497	4.90	28869.87	-0.141	0
gi 15607939	Rv0799c		hypothetical protein Rv0799c	456	5.09	36139.29	-0.072	0
gi 15607964	Rv0824c	desA1	probable Acyl-[Acyl-carrier protein] desaturase	279	6.21	38859.68	-0.461	0
gi 15608000	Rv0860	fadB	probable fatty oxidation protein	96	5.42	76170.44	-0.055	0
gi 15608013	Rv0873	fadE10	probable acyl-CoA dehydrogenase	555	5.68	70985.71	-0.147	0
gi 15608036	Rv0896	gltA2	probable citrate synthase I	3450	5.36	48062.43	-0.196	0
gi 15608039	Rv0899	ompA	outer membrane protein A	153	7.01	33667.62	0.042	1
gi 15608042	Rv0902c		hypothetical protein Rv0902c	110	5.72	47914.26	-0.021	2
gi 15608043	Rv0903c		hypothetical protein Rv0903c	331	4.97	25295.36	0.182	0
gi 15608045	Rv0905	echA6	probable enoyl-CoA hydratase	116	5.97	26126.52	-0.031	0
gi 15608046	Rv0906		hypothetical protein Rv0906	184	6.07	40729.85	-0.034	0
gi 15608047	Rv0907		hypothetical protein Rv0907	82	5.43	56815.38	-0.187	0
gi 15608067	Rv0927c		hypothetical protein Rv0927c	129	5.49	26786.09	0.410	0
gi 15608068	Rv0928	phoS3	periplasmic phosphate-binding lipoprotein	328	5.77	38214.88	-0.140	0
gi 15608071	Rv0931c	pknD	transmembrane serine/threonine-protein kinase D	694	5.53	69616.53	-0.051	1
gi 15608072	Rv0932c	pstS2	periplasmic phosphate-binding lipoprotein	591	4.76	38125.64	-0.132	0
gi 15608073	Rv0933	pstB	phosphate-transport ATP-binding protein ABC transporter	144	9.35	30091.65	-0.127	0
gi 15608074	Rv0934	phoS1	periplasmic phosphate-binding lipoprotein	6206	4.82	38390.35	0.072	0
gi 15608086	Rv0946c	pgi	probable glucose-6-phosphate isomerase	95	5.40	59937.38	-0.082	0
gi 15608094	Rv0954		hypothetical protein Rv0954	80	6.24	30184.93	-0.015	4
gi 15608108	Rv0968		hypothetical protein Rv0968	2171	5.88	10257.34	0.132	0
gi 15608109	Rv0969	ctpV	probable metal cation transporter p-type ATPase	16616	9.19	82557.14	0.303	6
gi 15840404	Rv0979A		hypothetical protein	270	12.18	19899.61	-0.789	0
gi 15608125	Rv0985c	mscL	possible large-conductance ion mechanosensitive channel	152	6.56	11619.50	0.283	2
gi 15608139	Rv0999		hypothetical protein Rv0999	157	9.00	26181.62	0.146	0
gi 15608146	Rv1006		hypothetical protein Rv1006	1200	5.38	61601.72	-0.304	0
gi 15608153	Rv1013	pks16	putative polyketide synthase	96	5.13	58449.20	0.102	0
gi 15608156	Rv1016c	lpqT	probable conserved lipoprotein	396	6.57	24179.32	0.017	0
gi 15608200	Rv1060		hypothetical protein	137	8.89	16866.50	0.178	0
gi 15608209	Rv1069c		hypothetical protein Rv1069c	129	6.47	64357.91	0.029	5
gi 15608232	Rv1092c	coaA	probable pantothenate kinase	79	7.21	35691.70	-0.193	0
gi 15608234	Rv1094	desA2	probable Acyl-[Acyl-carrier protein] desaturase	186	4.82	31567.91	-0.189	0
gi 15608237	Rv1097c		probable membrane glycine and proline rich protein	79	4.75	29873.60	-0.088	1
gi 15608238	Rv1098c	fum	probable fumarase	113	5.31	50281.08	0.021	0
gi 15608241	Rv1101c		hypothetical protein Rv1101c	118	9.65	41803.92	0.847	7
gi 15608246	Rv1106c		hypothetical protein Rv1106c	315	6.51	40943.85	-0.054	0
gi 15608301	Rv1161	narG	probable respiratory nitrate reductase	77	6.22	137383.21	-0.362	0
gi 15608334	Rv1194c		hypothetical protein Rv1194c	775	6.20	46183.94	-0.195	0
gi 15608341	Rv1201c		probable transferase	114	5.60	32609.80	0.175	0
gi 15608346	Rv1206	fadD6	probable fatty-acid-CoA ligase	163	8.07	64752.86	-0.042	0
gi 15608355	Rv1215c		hypothetical protein Rv1215c	194	9.52	62914.09	-0.414	0
gi 15608363	Rv1223	HtrA	probable serine protease	521	4.95	54156.92	-0.112	1
gi 15608372	Rv1232c		hypothetical protein Rv1232c	107	5.20	47516.01	-0.027	0
gi 15608374	Rv1234		hypothetical protein Rv1234	90	9.57	18649.76	0.202	2

gi 15608379	Rv1239c	corA	possible magnesium cobalt transport transmembrane protein	226	5.46	41702.21	-0.082	2
gi 15608385	Rv1245c		hypothetical protein Rv1245c	239	7.08	29197.44	0.101	0
gi 15608388	Rv1248c	sucA	probable 2-oxoglutarate dehydrogenase	1087	5.95	134227.94	-0.280	0
gi 15608403	Rv1263	amiB2	probable amidase	113	6.74	49278.56	0.006	0
gi 15608410	Rv1270c	lprA	possible lipoprotein	4629	5.26	24972.68	0.014	0
gi 15608419	Rv1279		hypothetical protein Rv1279	528	6.88	57694.42	-0.143	0
gi 15608420	Rv1280c	oppA	probable periplasmic oligopeptide-binding lipoprotein	571	6.62	63551.47	-0.142	1
gi 15608444	Rv1304	atpB	probable ATP synthase A chain	174	6.11	27505.89	0.818	5
gi 15608446	Rv1306	atpF	probable ATP synthase B chain	255	5.11	18313.58	0.040	1
gi 15608447	Rv1307	atpH	probable ATP synthase delta chain	1237	5.40	48833.06	0.027	1
gi 15608448	Rv1308	atpA	probable ATP synthase alpha chain	724	5.03	59479.79	-0.207	0
gi 15608449	Rv1309	atpG	probable ATP synthase gamma chain	223	5.39	33926.37	-0.267	0
gi 15608450	Rv1310	atpD	probable ATP synthase beta chain	198	4.86	53175.20	-0.168	0
gi 15608468	Rv1328	glgP	probable glycogen phosphorylase	211	5.19	95627.12	-0.198	0
gi 15608482	Rv1342c	pks14	conserved membrane protein	138	9.46	13430.41	0.584	3
gi 15608508	Rv1368	lprF	probable conserved lipoprotein	276	6.93	26949.11	-0.032	0
gi 15608535	Rv1397c		hypothetical protein Rv1397c	101	10.95	14943.00	-0.008	0
gi 15608548	Rv1410c		hypothetical protein Rv1410c	120	6.90	54710.50	0.757	13
gi 15608549	Rv1411c	lprG	probable conserved lipoprotein	1005	5.07	24646.73	-0.127	0
gi 15608574	Rv1436	gap	probable glyceraldehyde 3-phosphate dehydrogenase	110	5.19	36104.85	0.031	0
gi 15608581	Rv1443c		hypothetical protein Rv1443c	144	10.88	18304.61	-0.289	0
gi 15608605	Rv1467c	fadE15	probable acyl-CoA dehydrogenase	169	5.09	66053.59	-0.013	0
gi 15608617	Rv1479	moxR1	probable transcriptional regulatory protein	475	5.96	40737.51	0.051	0
gi 15608619	Rv1481		hypothetical protein Rv1481	104	9.48	36007.13	0.207	3
gi 15608622	Rv1484	inhA	NADH-dependent enoyl-[acyl-carrier-protein] reductase	204	5.73	28405.71	0.152	0
gi 15608626	Rv1488		hypothetical protein Rv1488	973	6.12	41256.81	-0.089	0
gi 15840950	Rv1489		hypothetical protein	292	10.16	12354.91	0.814	2
gi 15608651	Rv1513		hypothetical protein Rv1513	120	7.78	26838.74	-0.170	0
gi 15608681	Rv1543		hypothetical protein Rv1543	130	9.07	36912.02	-0.084	0
gi 15608682	Rv1544		hypothetical protein Rv1544	76	8.55	28352.94	0.184	0
gi 15608729	Rv1591		hypothetical protein Rv1591	119	6.40	23168.21	0.441	4
gi 15608734	Rv1596	nadC	probable nicotinate-nucleotide pyrophosphatase	87	5.09	29989.79	0.100	0
gi 15608736	Rv1598c		hypothetical protein Rv1598c	90	10.59	14883.13	-0.105	0
gi 15608752	Rv1614	lgt	possible prolipoprotein diacylglycerol transferases	339	4.71	50645.89	0.040	6
gi 15608781	Rv1643	rplT	probable 50S ribosomal protein L20	4873	11.10	14517.97	-0.611	0
gi 15608785	Rv1647		hypothetical protein Rv1647	82	9.24	33992.82	-0.145	0
gi 15608869	Rv1731	gabD1	probable succinate-semialdehyde dehydrogenase [NADP+] dependent	319	8.00	55745.76	0.000	0
gi 15608876	Rv1738		hypothetical protein Rv1738	104	6.18	10656.53	-0.439	0
gi 15608908	Rv1770		hypothetical protein	365	6.09	46162.97	-0.025	0
gi 15608909	Rv1771		hypothetical protein Rv1771	885	7.14	48243.37	-0.373	0
gi 15608956	Rv1819c		hypothetical protein Rv1819c	111	8.75	71500.59	0.143	6
gi 15608962	Rv1825		hypothetical protein Rv1825	125	6.34	30683.25	-0.036	1
gi 15608973	Rv1836c		hypothetical protein Rv1836c	101	4.74	69747.96	-0.087	1
gi 15608991	Rv1854c	ndh	probable NADH dehydrogenase	75	9.30	49619.00	0.030	1
gi 15609009	Rv1872c	lldD2	possible L-lactate dehydrogenase	12309	9.76	45541.12	0.058	0
gi 15609013	Rv1876	bfrA	probable bacterioferritin	3804	4.50	18443.18	-0.455	0

gi 15609045	Rv1908c	katG	catalase-peroxidase-peroxynitritase T	776	5.09	80709.28	-0.322	0
gi 15609056	Rv1919c		hypothetical protein Rv1919c	142	10.48	16792.71	-0.281	0
gi 15609061	Rv1924c		hypothetical protein	87	11.03	14165.90	0.802	3
gi 15609062	Rv1925	fadD31	probable acyl-CoA ligase	1625	5.42	66629.13	-0.013	0
gi 15609115	Rv1978		hypothetical protein Rv1978	281	6.80	30679.11	-0.055	0
gi 15609129	Rv1992c	ctpG	probable metal cation-transporting p-type ATPase G	91	5.55	79602.50	0.405	5
gi 15609134	Rv1997	ctpF	probable metal cation-transporting p-type ATPase A	113	5.37	95315.02	0.352	10
gi 15609167	Rv2030c		hypothetical protein Rv2030c	348	5.56	75169.21	-0.212	0
gi 15609168	Rv2031c	hspX	heat shock protein	170	5.00	16217.20	-0.520	0
gi 15609191	Rv2054		hypothetical protein Rv2054	106	9.50	25395.22	0.010	0
gi 15609195	Rv2058c	rpmB2	probable 50S ribosomal protein L28	132	12.01	9146.95	-0.938	0
gi 15609198	Rv2061c		hypothetical protein Rv2061c	232	9.84	14861.95	-0.249	0
gi 15609205	Rv2068c	blaC	class A beta-lactamase	188	5.26	32775.67	-0.091	0
gi 15609228	Rv2091c		probable membrane protein	322	5.76	26019.70	-0.685	1
gi 15609250	Rv2113		probable integral membrane protein	82	8.69	42394.10	0.732	8
gi 15609253	Rv2116	lppK	probable conserved lipoprotein	81	5.10	19772.99	-0.094	0
gi 15609266	Rv2129c		hypothetical protein Rv2129c	254	9.59	31425.63	0.180	0
gi 15609276	Rv2139	pyrD	probable dihydroorotate dehydrogenase	98	9.96	37975.35	-0.005	0
gi 15609288	Rv2151c	ftsQ	possible cell division protein	94	6.18	33970.03	-0.276	1
gi 15609296	Rv2159c		hypothetical protein Rv2159c	696	7.20	36467.91	-0.050	0
gi 15609319	Rv2182c		hypothetical protein Rv2182c	251	9.66	26938.04	-0.008	0
gi 15609331	Rv2194	qcrC	probable Ubiquinol-cytochrome C reductase	184	9.76	29348.12	-0.038	1
gi 15609332	Rv2195	qcrA	probable Rieske iron-sulfur protein	606	5.83	47178.14	-0.164	3
gi 15609333	Rv2196	qcrB	probable Ubiquinol-cytochrome C reductase	1108	8.49	61032.02	0.324	9
gi 15609335	Rv2198c	mmpS3	probable conserved transmembrane transport protein	376	4.35	31050.19	-0.482	1
gi 15609337	Rv2200c	ctaC	probable transmembrane cytochrome C oxidase subunit II	687	5.62	40681.97	-0.088	2
gi 15609338	Rv2201	asnB	probable asparagine synthetase	103	6.31	72117.50	-0.029	0
gi 15609351	Rv2214c	ephD	possible short-chain dehydrogenase	119	8.71	64218.11	-0.061	1
gi 15609356	Rv2219		hypothetical protein Rv2219	195	11.60	26846.83	-0.039	2
gi 15609357	Rv2220	glnA1	glutamine synthetase	792	5.04	53707.41	-0.416	0
gi 15609359	Rv2222c	glnA2	probable glutamine synthetase	105	5.29	49804.55	-0.255	0
gi 15609361	Rv2224c		probable exported protease	370	5.38	54945.57	-0.210	0
gi 15609378	Rv2241	aceE	probable pyruvate dehydrogenase E1 component	130	5.63	100184.70	-0.380	0
gi 15609381	Rv2244	acpM	meromycolate extension Acyl carrier protein	151	4.00	12516.32	-0.229	0
gi 15609383	Rv2246	kasB	3-oxoacyl-[acyl-carrier protein] synthase 2	84	5.29	46388.70	0.004	0
gi 15609421	Rv2284	lipM	probable esterase	168	9.34	46709.27	-0.016	2
gi 15609426	Rv2289	cdh	probable CDP-diacylglycerol pyrophosphatase	123	6.12	28818.85	-0.152	0
gi 15609433	Rv2296		hypothetical protein Rv2296	616	6.45	33337.10	-0.228	0
gi 15609442	Rv2305		hypothetical protein	83	5.67	46123.90	0.118	0
gi 15609463	Rv2326c		hypothetical protein Rv2326c	202	6.64	73188.52	0.307	4
gi 15609482	Rv2345		hypothetical protein Rv2345	1404	8.01	69987.57	-0.130	2
gi 15609498	Rv2361c		hypothetical protein Rv2361c	117	9.34	33998.28	-0.553	0
gi 15609531	Rv2394	ggtB	probable gamma-glutamyltranspeptidase precursor	371	5.66	66803.34	-0.108	0
gi 15609537	Rv2400c	subI	probable sulfate-binding lipoprotein	166	6.31	37566.37	-0.011	0
gi 15609547	Rv2410c		hypothetical protein Rv2410c	85	5.26	36112.36	-0.167	0
gi 15609555	Rv2418c		hypothetical protein	98	9.13	27225.10	-0.140	0

gi 15609575	Rv2438c		hypothetical protein Rv2438c	404	5.45	80782.97	-0.139	0
gi 15609586	Rv2449c		hypothetical protein Rv2449c	318	9.40	44578.81	-0.039	0
gi 15609592	Rv2455c		hypothetical protein Rv2455c	233	5.29	69310.79	-0.087	0
gi 15609597	Rv2460c	clpP2	probable ATP-dependent CLP protease proteolytic subunit 2	233	4.99	23582.01	-0.138	0
gi 15609613	Rv2476c		hypothetical protein Rv2476c	2208	5.55	177189.62	-0.056	0
gi 15609614	Rv2477c		probable macrolide-transport ATP-binding protein ABC transporter	92	5.17	61893.00	-0.412	0
gi 15609657	Rv2520c		hypothetical protein Rv2520c	144	10.37	8368.69	-0.033	1
gi 15609673	Rv2536		hypothetical protein Rv2536	159	4.91	24610.83	0.253	3
gi 15609692	Rv2555c	alaS	probable ananyl-tRNA synthetase	191	5.41	97467.86	-0.156	0
gi 15609700	Rv2563		hypothetical protein Rv2563	302	8.09	36002.89	0.714	3
gi 15609711	Rv2574		hypothetical protein Rv2574	145	9.29	19160.77	-0.105	0
gi 15609719	Rv2582	ppiB	probable peptidyl-prolyl cis-trans isomerase B	661	9.45	32635.73	-0.256	1
gi 15609723	Rv2586c	secF	probable protein-export membrane protein	174	9.54	46984.79	0.098	6
gi 15609724	Rv2587c	secD	probable protein-export membrane protein	222	8.87	60343.73	0.098	6
gi 15609734	Rv2597		hypothetical protein Rv2597	135	4.68	21986.07	0.042	0
gi 15609746	Rv2609c		hypothetical protein Rv2609c	125	6.27	38187.07	-0.035	0
gi 15609760	Rv2623		hypothetical protein Rv2623	424	5.45	31746.53	0.104	0
gi 15609762	Rv2625c		hypothetical protein Rv2625c	263	9.94	41454.40	0.514	5
gi 15609764	Rv2627c		hypothetical protein	750	9.70	46295.16	-0.245	0
gi 15609809	Rv2672		possible secreted protease	129	4.88	54015.70	0.043	0
gi 15609816	Rv2679	echA15	probable enoyl-CoA hydratase	138	5.50	29844.36	0.009	0
gi 15609837	Rv2700		hypothetical protein	167	5.25	22930.52	-0.052	0
gi 15609840	Rv2703	sigA	RNA polymerase sigma factor	202	4.72	51529.38	-0.635	0
gi 15609858	Rv2721c		hypothetical protein Rv2721c	179	4.47	72326.89	-0.094	1
gi 15609881	Rv2744c	35kd_ag	conserved 35 kDa alanine rich protein	15059	5.71	29239.94	-0.464	0
gi 15609888	Rv2751		hypothetical protein Rv2751	196	9.32	33703.67	-0.287	0
gi 15609922	Rv2785c	rpsO	probable 30S ribosomal protein S15	373	10.45	10468.86	-0.571	0
gi 15609968	Rv2831	echA16	probable enoyl-CoA hydratase	324	5.82	26785.05	0.077	0
gi 15609979	Rv2842c		hypothetical protein Rv2842c	155	5.37	19610.41	-0.048	0
gi 15609982	Rv2845c	proS	probable prolyl-tRNA synthetase (proline-tRNA ligase)	115	5.07	63319.69	-0.134	0
gi 15609989	Rv2852c		hypothetical protein Rv2852c	180	9.08	53789.91	-0.066	0
gi 15610010	Rv2873	mpt83	cell surface lipoprotein	696	4.67	24412.29	0.188	0
gi 15610020	Rv2883c	pyrH	probable uridylyate kinase	100	5.17	27429.50	0.192	0
gi 15610025	Rv2888c	amiC	probable amidase	381	6.62	50941.65	0.018	0
gi 15610027	Rv2890c	rpsB	probable 30S ribosomal protein S2	1301	6.03	31127.06	-0.284	0
gi 15610040	Rv2903c	lepB	probable signal peptidase I	76	5.64	32202.13	-0.222	1
gi 15610041	Rv2904c	rplS	probable 50S ribosomal protein L19	87	10.22	13005.13	-0.620	0
gi 15610053	Rv2916c	ffh	probable signal recognition particle protein	85	7.91	54969.40	-0.038	0
gi 15610058	Rv2921c	ftsY	possible cell division protein	133	5.18	44004.58	0.108	0
gi 15610072	Rv2935	ppsE	phenolphthiocerol synthesis type-1 polyketide synthase	148	5.42	159615.89	-0.052	0
gi 15610077	Rv2940c	mas	probable multifunctional mycocerosic acid synthase membrane-associated	98	5.05	225494.94	-0.053	0
gi 15610079	Rv2942	mmpL7	conserved transmembrane transport protein	115	9.03	95404.52	0.392	12
gi 15610082	Rv2945c	lppX	probable conserved lipoprotein	581	4.89	24296.50	0.013	0
gi 15610088	Rv2951c		possible oxidoreductase	189	9.10	41315.50	-0.007	0
gi 15610096	Rv2959c		hypothetical protein Rv2959c	235	5.40	27883.97	-0.295	0
gi 15610106	Rv2969c		hypothetical protein Rv2969c	427	5.69	27072.89	0.106	0

gi 15610132	Rv2995c	leuB	probable 3-isopropylmalate dehydrogenase	554	5.44	35398.44	0.121	0
gi 15610133	Rv2996c	serA1	probable D-3-phosphoglycerate dehydrogenase	109	4.80	54635.19	0.338	0
gi 15610136	Rv2999	lppY	probable conserved lipoprotein	113	6.45	33949.60	-0.110	0
gi 15610138	Rv3001c	ilvC	probable ketol-acid reductoisomerase	85	5.03	36181.53	-0.144	0
gi 15610143	Rv3006	lppZ	probable conserved lipoprotein	568	4.85	39069.88	-0.065	0
gi 15610175	Rv3038c		hypothetical protein Rv3038c	100	5.61	36198.33	-0.185	0
gi 15610180	Rv3043c	ctaD	probable cytochrome C oxidase polypeptide I	94	6.50	63858.75	0.585	12
gi 15610181	Rv3044	fecB	probable FeIII-dicitrate-binding periplasmic lipoprotein	434	5.20	37115.76	0.039	0
gi 15610198	Rv3061c	fadE22	probable acyl-CoA dehydrogenase	119	5.34	76921.96	0.020	0
gi 15610227	Rv3090		hypothetical protein Rv3090	383	8.37	32478.80	-0.006	1
gi 15610228	Rv3091		hypothetical protein Rv3091	733	6.26	61834.92	-0.117	0
gi 15610238	Rv3101c	ftsX	putative cell division protein	91	8.83	32787.30	0.394	3
gi 15610266	Rv3130c		hypothetical protein Rv3130c	313	10.11	50859.93	-0.039	0
gi 15610269	Rv3133c		hypothetical protein Rv3133c	114	5.62	23393.37	-0.006	0
gi 15610290	Rv3154	nuoJ	probable NADH dehydrogenase I (chain J)	103	8.09	27571.65	0.661	5
gi 15610294	Rv3158	nuoN	probable NADH dehydrogenase I (chain N)	92	8.83	55342.20	0.846	13
gi 15610329	Rv3193c		hypothetical protein Rv3193c	309	9.05	107549.18	0.063	6
gi 15610330	Rv3194c		hypothetical protein Rv3194c	184	5.28	35564.46	0.123	0
gi 15610336	Rv3200c		hypothetical protein Rv3200c	149	8.02	38165.71	0.222	3
gi 15610348	Rv3212		conserved hypothetical alanine valine rich protein	82	8.89	42506.10	-0.009	0
gi 15610354	Rv3218		hypothetical protein Rv3218	163	9.23	34681.00	0.015	0
gi 15610380	Rv3244c	lpqB	probable conserved lipoprotein	139	5.19	61170.53	-0.030	0
gi 15610406	Rv3270	ctpC	probable metal cation-transporting p-type ATPase C	370	6.98	76676.11	0.204	0
gi 15610409	Rv3273		hypothetical protein Rv3273	416	6.19	80914.23	0.479	10
gi 15610410	Rv3274c	fadE25	probable acyl-CoA dehydrogenase	125	5.21	41924.99	-0.127	0
gi 15610434	Rv3298c	lpqC	possible esterase lipoprotein	93	5.45	31690.62	0.126	0
gi 15610437	Rv3301c	phoY1	probable phosphate-transport system transcriptional regulatory protein	257	5.73	24924.93	-0.073	0
gi 15610438	Rv3302c	glpD2	probable glycerol-3-phosphate dehydrogenase	634	6.26	62909.90	0.080	0
gi 15610520	Rv3384c		conserved hypothetical protein	80	10.18	14316.70	-0.045	0
gi 15610526	Rv3390	lpqD	probable conserved lipoprotein	300	6.90	25154.73	-0.087	0
gi 15610537	Rv3401		hypothetical protein Rv3401	411	5.50	87660.30	-0.266	0
gi 15610545	Rv3409c	choD	probable cholesterol oxidase precursor	279	9.39	63326.41	-0.300	0
gi 15610553	Rv3417c	groEL1	60 kDa chaperonin 1	171	4.98	55843.49	0.110	0
gi 15610578	Rv3442c	rpsI	probable 30S ribosomal protein S9	162	10.67	16426.02	-0.460	0
gi 15610592	Rv3456c	rplQ	Probable 50S ribosomal protein L17	184	9.52	19463.33	-0.672	0
gi 15610594	Rv3458c	rpsD	probable 30S ribosomal protein S4	447	10.02	23461.46	-0.722	0
gi 15610595	Rv3459c	rpsK	probable 30S ribosomal protein S11	210	11.69	14775.98	-0.709	0
gi 15610596	Rv3460c	rpsM	probable 30S ribosomal protein S13	490	11.02	14455.73	-0.823	0
gi 15610615	Rv3479		hypothetical protein Rv3479	95	6.92	115177.42	0.017	3
gi 15610618	Rv3482c		hypothetical protein Rv3482c	158	9.55	28597.62	-0.495	1
gi 15610619	Rv3483c		possible exported protein	106	4.32	22950.50	-0.115	1
gi 15610629	Rv3493c		hypothetical protein Rv3493c	95	10.10	25595.22	-0.352	1
gi 15610633	Rv3497c		hypothetical protein Rv3497c	109	9.10	38184.24	0.024	0
gi 15610655	Rv3519		hypothetical protein Rv3519	80	9.66	26000.46	-0.076	0
gi 15610683	Rv3547		hypothetical protein Rv3547	403	9.52	17416.94	-0.544	0
gi 15610720	Rv3584	lpqE	possible conserved lipoprotein	1337	8.11	18920.96	0.222	0

gi 15610733	Rv3597c	lsr2	probable iron-regulated LSR2 protein precursor	137	10.74	12091.23	-0.659	0
gi 15610752	Rv3616c		hypothetical protein Rv3616c	274	5.19	39920.68	0.240	0
gi 15610759	Rv3623	lpqG	probable conserved lipoprotein	722	5.52	24878.83	-0.055	0
gi 15610763	Rv3627c		hypothetical protein Rv3627c	135	6.92	46976.56	0.147	0
gi 15610805	Rv3669		hypothetical protein Rv3669	182	9.81	18907.22	0.291	2
gi 15610807	Rv3671c		hypothetical protein Rv3671c	303	6.33	40810.14	0.528	4
gi 15610812	Rv3676		hypothetical protein Rv3676	622	9.57	24776.19	-0.260	0
gi 15610815	Rv3679		hypothetical protein Rv3679	237	5.27	35834.32	0.177	0
gi 15610816	Rv3680		hypothetical protein Rv3680	321	5.78	41549.48	0.049	0
gi 15610828	Rv3692	moxR2	probable methanol dehydrogenase transcriptional regulatory protein	631	5.47	37969.98	-0.023	0
gi 15610855	Rv3719		conserved hypothetical protein	82	7.12	53006.90	-0.313	0
gi 15610856	Rv3720		possible fatty acid synthase	181	6.22	46852.80	-0.362	0
gi 15610859	Rv3723		probable conserved transmembrane protein	107	9.15	27367.40	-0.178	4
gi 15610862	Rv3726		possible dehydrogenase	82	7.18	42035.70	0.183	0
gi 15610868	Rv3732		hypothetical protein Rv3732	116	6.10	37737.43	0.150	1
gi 15610870	Rv3734c		hypothetical protein Rv3734c	199	6.36	49500.62	-0.018	0
gi 15610899	Rv3763	lpqH	19 kDa lipoprotein antigen precursor	965	5.12	15308.58	0.126	0
gi 15610927	Rv3791		hypothetical protein Rv3791	241	7.78	27565.48	0.157	0
gi 15610930	Rv3794	embA	integral membrane indolylacetylinoitol arabinosyltransferase	80	9.61	115692.00	0.338	12
gi 15610935	Rv3799c	accD4	probable propionyl-CoA carboxylase beta chain 4	118	5.33	56506.79	-0.041	0
gi 15610937	Rv3801c	fadD32	probable fatty-acid-CoA ligase	500	5.79	69417.43	-0.185	0
gi 15610938	Rv3802c		hypothetical protein Rv3802c	370	6.50	35653.99	-0.152	0
gi 15610942	Rv3806c		hypothetical protein Rv3806c	122	8.69	32804.49	0.705	7
gi 15610977	Rv3841	bfrB	possible bacterioferritin	387	4.73	20429.21	-0.277	0
gi 15610982	Rv3846	sodA	superoxide dismutase	368	5.96	23019.59	-0.195	0
gi 15610986	Rv3850		hypothetical protein Rv3850	603	11.64	23796.37	-0.386	0
gi 15610988	Rv3852	hns	possible histone-like protein	80	10.59	13823.00	-0.535	1
gi 15611022	Rv3886c	mycP2	probable alanine and proline rich membrane-anchored mycosin	114	5.66	55594.30	0.015	1
gi 15611046	Rv3910		hypothetical protein Rv3910	256	6.91	123544.35	0.323	15
gi 15611057	Rv3921c		probable conserved transmembrane protein	304	10.11	40947.32	-0.090	5

Note:

Accession #, from NCBI. Novel protein identifications are shown in bold fonts;

MOWSE, score reported by Mascot;

GRAVY, grand average of hydrophobicity;

TMHMM, predicted number of transmembrane helices returned by TMHMM.