

**Table 1. Functional classification of *Mycobacterium tuberculosis* protein-coding genes**

I. Small-molecule metabolism					
<b>A. Degradation</b>					
1. Carbon compounds					
Rv0186	<i>bglS</i>	β-glucosidase	Rv3039c	<i>echA17</i>	enoyl-CoA hydratase/isomerase superfamily
Rv2202c	<i>cbhK</i>	carbohydrate kinase	Rv3373	<i>echA18</i>	enoyl-CoA hydratase/isomerase superfamily, N-term
Rv0727c	<i>fucA</i>	L-fucose phosphate aldolase	Rv3374	<i>echA18'</i>	enoyl-CoA hydratase/isomerase superfamily, C-term
Rv1731	<i>gabD1</i>	succinate-semialdehyde dehydrogenase	Rv3516	<i>echA19</i>	enoyl-CoA hydratase/isomerase superfamily
Rv0234c	<i>gabD2</i>	succinate-semialdehyde dehydrogenase	Rv3550	<i>echA20</i>	enoyl-CoA hydratase/isomerase superfamily
Rv0501	<i>galE1</i>	UDP-glucose 4-epimerase	Rv3774	<i>echA21</i>	enoyl-CoA hydratase/isomerase superfamily
Rv0536	<i>galE2</i>	UDP-glucose 4-epimerase	Rv0859	<i>fadA</i>	β oxidation complex, β subunit (acetyl-CoA C-acetyltransferase)
Rv0620	<i>galK</i>	galactokinase	Rv0243	<i>fadA2</i>	acetyl-CoA C-acetyltransferase
Rv0619	<i>galT</i>	galactose-1-phosphate uridylyltransferase C-term	Rv1074c	<i>fadA3</i>	acetyl-CoA C-acetyltransferase
Rv0618	<i>galT'</i>	galactose-1-phosphate uridylyltransferase N-term	Rv1323	<i>fadA4</i>	acetyl-CoA C-acetyltransferase (aka <i>thiL</i> )
Rv0993	<i>galU</i>	UTP-glucose-1-phosphate uridylyltransferase	Rv3546	<i>fadA5</i>	acetyl-CoA C-acetyltransferase
Rv3696c	<i>glpK</i>	ATP:glycerol 3-phosphotransferase	Rv3556c	<i>fadA6</i>	acetyl-CoA C-acetyltransferase
Rv3255c	<i>manA</i>	mannose-6-phosphate isomerase	Rv0860	<i>fadB</i>	β oxidation complex, α subunit (multiple activities)
Rv3441c	<i>mrsA</i>	phosphoglucosyltransferase or phosphomannomutase	Rv0468	<i>fadB2</i>	3-hydroxyacyl-CoA dehydrogenase
Rv0118c	<i>oxcA</i>	oxalyl-CoA decarboxylase	Rv1715	<i>fadB3</i>	3-hydroxyacyl-CoA dehydrogenase
Rv3068c	<i>pgmA</i>	phosphoglucosyltransferase	Rv3141	<i>fadB4</i>	3-hydroxyacyl-CoA dehydrogenase
Rv3257c	<i>pmmA</i>	phosphomannomutase	Rv1912c	<i>fadB5</i>	3-hydroxyacyl-CoA dehydrogenase
Rv3308	<i>pmmB</i>	phosphomannomutase	Rv1750c	<i>fadD1</i>	acyl-CoA synthase
Rv2702	<i>ppgK</i>	polyphosphate glucokinase	Rv0270	<i>fadD2</i>	acyl-CoA synthase
Rv0408	<i>pta</i>	phosphate acetyltransferase	Rv3561	<i>fadD3</i>	acyl-CoA synthase
Rv0729	<i>xyiB</i>	xylulose kinase	Rv0214	<i>fadD4</i>	acyl-CoA synthase
Rv1096	-	carbohydrate degrading enzyme	Rv1066	<i>fadD5</i>	acyl-CoA synthase
			Rv1206	<i>fadD6</i>	acyl-CoA synthase
			Rv0119	<i>fadD7</i>	acyl-CoA synthase
			Rv0551c	<i>fadD8</i>	acyl-CoA synthase
			Rv2590	<i>fadD9</i>	acyl-CoA synthase
			Rv0099	<i>fadD10</i>	acyl-CoA synthase
			Rv1550	<i>fadD11</i>	acyl-CoA synthase, N-term
			Rv1549	<i>fadD11'</i>	acyl-CoA synthase, C-term
			Rv1427c	<i>fadD12</i>	acyl-CoA synthase
			Rv3089	<i>fadD13</i>	acyl-CoA synthase
			Rv1058	<i>fadD14</i>	acyl-CoA synthase
			Rv2187	<i>fadD15</i>	acyl-CoA synthase
			Rv0852	<i>fadD16</i>	acyl-CoA synthase
			Rv3506	<i>fadD17</i>	acyl-CoA synthase
			Rv3513c	<i>fadD18</i>	acyl-CoA synthase
			Rv3515c	<i>fadD19</i>	acyl-CoA synthase
			Rv1185c	<i>fadD21</i>	acyl-CoA synthase
			Rv2948c	<i>fadD22</i>	acyl-CoA synthase
			Rv3826	<i>fadD23</i>	acyl-CoA synthase
			Rv1529	<i>fadD24</i>	acyl-CoA synthase
			Rv1521	<i>fadD25</i>	acyl-CoA synthase
			Rv2930	<i>fadD26</i>	acyl-CoA synthase
			Rv0275c	<i>fadD27</i>	acyl-CoA synthase
			Rv2941	<i>fadD28</i>	acyl-CoA synthase
			Rv2950c	<i>fadD29</i>	acyl-CoA synthase
			Rv0404	<i>fadD30</i>	acyl-CoA synthase
			Rv1925	<i>fadD31</i>	acyl-CoA synthase
			Rv3801c	<i>fadD32</i>	acyl-CoA synthase
			Rv1345	<i>fadD33</i>	acyl-CoA synthase
			Rv0035	<i>fadD34</i>	acyl-CoA synthase
			Rv2505c	<i>fadD35</i>	acyl-CoA synthase
			Rv1193	<i>fadD36</i>	acyl-CoA synthase
			Rv0131c	<i>fadE1</i>	acyl-CoA dehydrogenase
			Rv0154c	<i>fadE2</i>	acyl-CoA dehydrogenase
			Rv0215c	<i>fadE3</i>	acyl-CoA dehydrogenase
			Rv0231	<i>fadE4</i>	acyl-CoA dehydrogenase
			Rv0244c	<i>fadE5</i>	acyl-CoA dehydrogenase
			Rv0271c	<i>fadE6</i>	acyl-CoA dehydrogenase
			Rv0400c	<i>fadE7</i>	acyl-CoA dehydrogenase
			Rv0672	<i>fadE8</i>	acyl-CoA dehydrogenase (aka <i>aidB</i> )
			Rv0752c	<i>fadE9</i>	acyl-CoA dehydrogenase
			Rv0873	<i>fadE10</i>	acyl-CoA dehydrogenase
			Rv0972c	<i>fadE12</i>	acyl-CoA dehydrogenase
			Rv0975c	<i>fadE13</i>	acyl-CoA dehydrogenase
			Rv1346	<i>fadE14</i>	acyl-CoA dehydrogenase
			Rv1467c	<i>fadE15</i>	acyl-CoA dehydrogenase
			Rv1679	<i>fadE16</i>	acyl-CoA dehydrogenase
			Rv1934c	<i>fadE17</i>	acyl-CoA dehydrogenase
			Rv1933c	<i>fadE18</i>	acyl-CoA dehydrogenase
			Rv2500c	<i>fadE19</i>	acyl-CoA dehydrogenase (aka <i>mmgC</i> )
			Rv2724c	<i>fadE20</i>	acyl-CoA dehydrogenase
			Rv2789c	<i>fadE21</i>	acyl-CoA dehydrogenase
			Rv3061c	<i>fadE22</i>	acyl-CoA dehydrogenase
			Rv3140	<i>fadE23</i>	acyl-CoA dehydrogenase
			Rv3139	<i>fadE24</i>	acyl-CoA dehydrogenase
			Rv3274c	<i>fadE25</i>	acyl-CoA dehydrogenase
			Rv3504	<i>fadE26</i>	acyl-CoA dehydrogenase
			Rv3505	<i>fadE27</i>	acyl-CoA dehydrogenase
			Rv3544c	<i>fadE28</i>	acyl-CoA dehydrogenase
			Rv3543c	<i>fadE29</i>	acyl-CoA dehydrogenase
			Rv3560c	<i>fadE30</i>	acyl-CoA dehydrogenase
			Rv3562	<i>fadE31</i>	acyl-CoA dehydrogenase
			Rv3563	<i>fadE32</i>	acyl-CoA dehydrogenase
			Rv3564	<i>fadE33</i>	acyl-CoA dehydrogenase
			Rv3573c	<i>fadE34</i>	acyl-CoA dehydrogenase
			Rv3797	<i>fadE35</i>	acyl-CoA dehydrogenase
			Rv3761c	<i>fadE36</i>	acyl-CoA dehydrogenase
			Rv1175c	<i>fadH</i>	2,4-Dienoyl-CoA Reductase
			Rv0855	<i>far</i>	fatty acyl-CoA racemase
			Rv1143	<i>mcr</i>	α-methyl acyl-CoA racemase
			Rv1492	<i>mutA</i>	methylmalonyl-CoA mutase, β subunit
			Rv1493	<i>mutB</i>	methylmalonyl-CoA mutase, α subunit
			Rv2504c	<i>scoA</i>	3-oxo acid:CoA transferase, α subunit
			Rv2503c	<i>scoB</i>	3-oxo acid:CoA transferase, β subunit
			Rv1136	-	probable carnitine racemase
			Rv1683	-	possible acyl-CoA synthase
					4. Phosphorous compounds
			Rv2368c	<i>phoH</i>	ATP-binding <i>pho</i> regulon component
			Rv1095	<i>phoH2</i>	PhoH-like protein
			Rv3628	<i>ppa</i>	probable inorganic pyrophosphatase
			Rv2984	<i>ppk</i>	polyphosphate kinase
					B. Energy metabolism
					1. Glycolysis
			Rv1023	<i>eno</i>	enolase
			Rv0363c	<i>fba</i>	fructose bisphosphate aldolase
			Rv1436	<i>gap</i>	glyceraldehyde 3-phosphate dehydrogenase
			Rv0489	<i>gpm</i>	phosphoglycerate mutase I
			Rv3010c	<i>pfkA</i>	phosphofructokinase I
			Rv2029c	<i>pfkB</i>	phosphofructokinase II
			Rv0946c	<i>pgi</i>	glucose-6-phosphate isomerase
			Rv1437	<i>pgk</i>	phosphoglycerate kinase
			Rv1617	<i>pykA</i>	pyruvate kinase
			Rv1438	<i>tpi</i>	triosephosphate isomerase
			Rv2419c	-	putative phosphoglycerate mutase
			Rv3837c	-	putative phosphoglycerate mutase
					2. Pyruvate dehydrogenase
			Rv2241	<i>aceE</i>	pyruvate dehydrogenase E1 component
			Rv3303c	<i>lpdA</i>	dihydroliipoamide dehydrogenase
			Rv2497c	<i>pdhA</i>	pyruvate dehydrogenase E1 component α subunit
			Rv2496c	<i>pdhB</i>	pyruvate dehydrogenase E1 component β subunit
			Rv2495c	<i>pdhC</i>	dihydroliipoamide acetyltransferase
			Rv0462	-	probable dihydroliipoamide dehydrogenase
					3. TCA cycle
			Rv1475c	<i>acn</i>	aconitate hydratase
			Rv0889c	<i>citA</i>	citrate synthase 2
			Rv2498c	<i>citE</i>	citrate lyase β chain
			Rv1098c	<i>fum</i>	fumarase
			Rv1131	<i>glfA1</i>	citrate synthase 3
			Rv0896	<i>glfA2</i>	citrate synthase 1
			Rv3339c	<i>icd1</i>	isocitrate dehydrogenase
			Rv0066c	<i>icd2</i>	isocitrate dehydrogenase
			Rv0794c	<i>lpdB</i>	dihydroliipoamide dehydrogenase
			Rv1240	<i>mdh</i>	malate dehydrogenase
			Rv2967c	<i>pca</i>	pyruvate carboxylase
			Rv3318	<i>sdhA</i>	succinate dehydrogenase A
			Rv3319	<i>sdhB</i>	succinate dehydrogenase B
			Rv3316	<i>sdhC</i>	succinate dehydrogenase C subunit
			Rv3317	<i>sdhD</i>	succinate dehydrogenase D subunit
			Rv1248c	<i>sucA</i>	2-oxoglutarate dehydrogenase
			Rv2215	<i>sucB</i>	dihydroliipoamide succinyltransferase
			Rv0951	<i>sucC</i>	succinyl-CoA synthase β chain
			Rv0952	<i>sucD</i>	succinyl-CoA synthase α chain
					4. Glyoxylate bypass
			Rv0467	<i>aceA</i>	isocitrate lyase
			Rv1915	<i>aceAa</i>	isocitrate lyase, α module
			Rv1916	<i>aceAb</i>	isocitrate lyase, β module
			Rv1837c	<i>glcB</i>	malate synthase
			Rv3323c	<i>gphA</i>	phosphoglycolate phosphatase
					5. Pentose phosphate pathway
			Rv1445c	<i>devB</i>	glucose-6-phosphate 1-dehydrogenase
			Rv1844c	<i>gnd</i>	6-phosphogluconate dehydrogenase (Gram -)
			Rv1122	<i>gnd2</i>	6-phosphogluconate dehydrogenase (Gram +)
			Rv1446c	<i>opcA</i>	unknown function, may aid G6PDH

Rv2436	<i>rbsK</i>	ribokinase	Rv3250c	<i>rubB</i>	rubredoxin B	Rv1878	<i>glnA3</i>	probable glutamine synthase
Rv1408	<i>rpe</i>	ribulose-phosphate 3-epimerase				Rv2860c	<i>glnA4</i>	probable glutamine synthase
Rv2465c	<i>rpi</i>	phosphopentose isomerase	7. Miscellaneous oxidoreductases and oxygenases 171			Rv2918c	<i>glnD</i>	uridylyltransferase
Rv1448c	<i>tal</i>	transaldolase				Rv2221c	<i>glnE</i>	glutamate-ammonia-ligase
Rv1449c	<i>tkf</i>	transketolase						adenyltransferase
Rv1121	<i>zwf</i>	glucose-6-phosphate 1-dehydrogenase				Rv3859c	<i>glfB</i>	ferredoxin-dependent glutamate synthase
Rv1447c	<i>zwf2</i>	glucose-6-phosphate 1-dehydrogenase				Rv3858c	<i>glfD</i>	small subunit of NADH-dependent glutamate synthase
6. Respiration						Rv3704c	<i>gshA</i>	possible $\gamma$ -glutamylcysteine synthase
<i>a. aerobic</i>						Rv2427c	<i>proA</i>	$\gamma$ -glutamyl phosphate reductase
Rv0527	<i>ccsA</i>	cytochrome c-type biogenesis protein	C. Central intermediary metabolism			Rv2439c	<i>proB</i>	glutamate 5-kinase
			1. General			Rv0500	<i>proC</i>	pyrroline-5-carboxylate reductase
Rv0529	<i>ccsB</i>	cytochrome c-type biogenesis protein	Rv2589	<i>gabT</i>	4-aminobutyrate aminotransferase	2. Aspartate family		
Rv1451	<i>ctaB</i>	cytochrome c oxidase assembly factor	Rv3432c	<i>gabB</i>	glutamate decarboxylase	Rv3708c	<i>asd</i>	aspartate semialdehyde dehydrogenase
Rv2200c	<i>ctaC</i>	cytochrome c oxidase chain II	Rv1832	<i>gcvB</i>	glycine decarboxylase	Rv3709c	<i>ask</i>	aspartokinase
Rv3043c	<i>ctaD</i>	cytochrome c oxidase polypeptide I	Rv1826	<i>gcvH</i>	glycine cleavage system H protein	Rv2201	<i>asnB</i>	asparagine synthase B
			Rv2211c	<i>gcvT</i>	T protein of glycine cleavage system	Rv3565	<i>aspB</i>	aspartate aminotransferase
Rv2193	<i>ctaE</i>	cytochrome c oxidase polypeptide III	Rv1213	<i>glgC</i>	glucose-1-phosphate adenyltransferase	Rv0337c	<i>aspC</i>	aspartate aminotransferase
Rv1542c	<i>glbN</i>	hemoglobin-like, oxygen carrier	Rv3842c	<i>glpQ1</i>	glycerophosphoryl diester phosphodiesterase	Rv2753c	<i>dapA</i>	dihydrodipicolinate synthase
Rv2470	<i>glbO</i>	hemoglobin-like, oxygen carrier	Rv0317c	<i>glpQ2</i>	glycerophosphoryl diester phosphodiesterase	Rv2773c	<i>dapB</i>	dihydrodipicolinate reductase
Rv2249c	<i>glpD1</i>	glycerol-3-phosphate dehydrogenase	Rv3566c	<i>nhoA</i>	N-hydroxyarylamine <i>o</i> -acetyltransferase	Rv1202	<i>dapE</i>	succinyl-diaminopimelate desuccinylase
Rv3302c	<i>glpD2</i>	glycerol-3-phosphate dehydrogenase	Rv0155	<i>pntAA</i>	pyridine transhydrogenase subunit $\alpha$ 1	Rv2141c	<i>dapE2</i>	ArgE/DapE/Acy1/Cpg2/lycS family
Rv0694	<i>lldD1</i>	L-lactate dehydrogenase (cytochrome)	Rv0156	<i>pntAB</i>	pyridine transhydrogenase subunit $\alpha$ 2	Rv2726c	<i>dapF</i>	diaminopimelate epimerase
Rv1872c	<i>lldD2</i>	L-lactate dehydrogenase	Rv0157	<i>pntB</i>	pyridine transhydrogenase subunit $\beta$	Rv1293	<i>lysA</i>	diaminopimelate decarboxylase
Rv1854c	<i>ndh</i>	probable NADH dehydrogenase	Rv1127c	<i>ppdK</i>	similar to pyruvate, phosphate dikinase	Rv3341	<i>metA</i>	homoserine <i>o</i> -acetyltransferase
Rv3145	<i>nuoA</i>	NADH dehydrogenase chain A	2. Gluconeogenesis			Rv1079	<i>metB</i>	cystathionine $\gamma$ -synthase
Rv3146	<i>nuoB</i>	NADH dehydrogenase chain B	Rv0211	<i>pckA</i>	phosphoenolpyruvate carboxykinase	Rv3340	<i>metC</i>	cystathionine $\beta$ -lyase
Rv3147	<i>nuoC</i>	NADH dehydrogenase chain C	Rv0069c	<i>sdaA</i>	L-serine dehydratase 1	Rv1133c	<i>metE</i>	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase
Rv3148	<i>nuoD</i>	NADH dehydrogenase chain D	3. Sugar nucleotides			Rv2124c	<i>metH</i>	5-methyltetrahydrofolate-homocysteine methyltransferase
Rv3149	<i>nuoE</i>	NADH dehydrogenase chain E	Rv1512	<i>epiA</i>	nucleotide sugar epimerase	Rv1392	<i>metK</i>	S-adenosylmethionine synthase
Rv3150	<i>nuoF</i>	NADH dehydrogenase chain F	Rv3784	<i>epiB</i>	probable UDP-galactose 4-epimerase	Rv0391	<i>metZ</i>	<i>o</i> -succinylhomoserine sulfhydrylase
Rv3151	<i>nuoG</i>	NADH dehydrogenase chain G	Rv1511	<i>gmdA</i>	GDP-mannose 4,6 dehydratase	Rv1294	<i>thrA</i>	homoserine dehydrogenase
Rv3152	<i>nuoH</i>	NADH dehydrogenase chain H	Rv0334	<i>rmlA</i>	glucose-1-phosphate thymidyltransferase	Rv1296	<i>thrB</i>	homoserine kinase
Rv3153	<i>nuoI</i>	NADH dehydrogenase chain I	Rv3264c	<i>rmlA2</i>	glucose-1-phosphate thymidyltransferase	Rv1295	<i>thrC</i>	homoserine synthase
Rv3154	<i>nuoJ</i>	NADH dehydrogenase chain J	Rv3464	<i>rmlB</i>	dTDP-glucose 4,6-dehydratase	3. Serine family		
Rv3155	<i>nuoK</i>	NADH dehydrogenase chain K	Rv3634c	<i>rmlB2</i>	dTDP-glucose 4,6-dehydratase	Rv0815c	<i>cysA2</i>	thiosulfate sulfurtransferase
Rv3156	<i>nuoL</i>	NADH dehydrogenase chain L	Rv3468c	<i>rmlB3</i>	dTDP-glucose 4,6-dehydratase	Rv3117	<i>cysA3</i>	thiosulfate sulfurtransferase
Rv3157	<i>nuoM</i>	NADH dehydrogenase chain M	Rv3465	<i>rmlC</i>	dTDP-4-dehydrorhamnose 3,5-epimerase	Rv2335	<i>cysE</i>	serine acetyltransferase
Rv3158	<i>nuoN</i>	NADH dehydrogenase chain N	Rv3266c	<i>rmlD</i>	dTDP-4-dehydrorhamnose reductase	Rv0511	<i>cysG</i>	uroporphyrin-III C-methyltransferase
Rv2195	<i>qcrA</i>	Rieske iron-sulphur component of <i>ubiQ-cytB</i> reductase	Rv0322	<i>udgA</i>	UDP-glucose dehydrogenase/GDP-mannose 6-dehydrogenase	Rv2847c	<i>cysG2</i>	multifunctional enzyme, siroheme synthase
Rv2196	<i>qcrB</i>	cytochrome $\beta$ component of <i>ubiQ-cytB</i> reductase	Rv3265c	<i>wbbL</i>	dTDP-rhamnosyl transferase	Rv2334	<i>cysK</i>	cysteine synthase A
Rv2194	<i>qcrC</i>	cytochrome <i>b/c</i> component of <i>ubiQ-cytB</i> reductase	Rv1525	<i>wbb2</i>	dTDP-rhamnosyl transferase	Rv1336	<i>cysM</i>	cysteine synthase B
<i>b. anaerobic</i>			Rv3400	-	probable $\beta$ -phosphoglucomutase	Rv1077	<i>cysM2</i>	cystathionine $\beta$ -synthase
Rv2392	<i>cysH</i>	3'-phosphoadenylylsulfate (PAPS) reductase	4. Amino sugars			Rv0848	<i>cysM3</i>	putative cysteine synthase
Rv2899c	<i>fdhD</i>	affects formate dehydrogenase-N	Rv3436c	<i>glmS</i>	glucosamine-fructose-6-phosphate aminotransferase	Rv1093	<i>glyA</i>	serine hydroxymethyltransferase
Rv2900c	<i>fdhF</i>	molybdopterin-containing oxidoreductase	5. Sulphur metabolism			Rv0700c	<i>glyA2</i>	serine hydroxymethyltransferase
Rv1552	<i>frdA</i>	fumarate reductase flavoprotein subunit	Rv0711	<i>atsA</i>	arylsulfatase	Rv2996c	<i>serA</i>	D-3-phosphoglycerate dehydrogenase
Rv1553	<i>frdB</i>	fumarate reductase iron sulphur protein	Rv3299c	<i>atsB</i>	probable arylsulfatase	Rv0505c	<i>serB</i>	probable phosphoserine phosphatase
Rv1554	<i>frdC</i>	fumarate reductase 15kD anchor protein	Rv0663	<i>atsD</i>	probable arylsulfatase	Rv3042c	<i>serB2</i>	C-term similar to phosphoserine phosphatase
Rv1555	<i>frdD</i>	fumarate reductase 13kD anchor protein	Rv3077	<i>atsF</i>	probable arylsulfatase	Rv0884c	<i>serC</i>	phosphoserine aminotransferase
Rv1161	<i>narG</i>	nitrate reductase $\alpha$ subunit	Rv0296c	<i>atsG</i>	probable arylsulfatase	4. Aromatic amino acid family		
Rv1162	<i>narH</i>	nitrate reductase $\beta$ chain	Rv3796	<i>atsH</i>	probable arylsulfatase	Rv3227	<i>aroA</i>	3-phosphoshikimate
Rv1164	<i>narI</i>	nitrate reductase $\gamma$ chain	Rv1285	<i>cysD</i>	ATP:sulphurylase subunit 2	Rv2538c	<i>aroB</i>	1-carboxyvinyl transferase
Rv1163	<i>narJ</i>	nitrate reductase $\delta$ chain	Rv1286	<i>cysN</i>	ATP:sulphurylase subunit 1	Rv2537c	<i>aroD</i>	3-dehydroquininate synthase
Rv1736c	<i>narX</i>	fused nitrate reductase	Rv2131c	<i>cysQ</i>	homologue of <i>M.leprae cysQ</i>	Rv2552c	<i>aroE</i>	3-dehydroquininate dehydratase
Rv2391	<i>nirA</i>	probable nitrite reductase/sulphite reductase	Rv3248c	<i>sahH</i>	adenosylhomocysteinase	Rv2540c	<i>aroF</i>	shikimate 5-dehydrogenase
Rv0252	<i>nirB</i>	nitrite reductase flavoprotein	Rv3283	<i>sseA</i>	thiosulfate sulfurtransferase	Rv2540c	<i>aroG</i>	chorismate synthase
Rv0253	<i>nirD</i>	probable nitrite reductase small subunit	Rv2291	<i>sseB</i>	thiosulfate sulfurtransferase	Rv2178c	<i>aroG</i>	DAHPh synthase
<i>c. Electron transport</i>			Rv3118	<i>sseC</i>	thiosulfate sulfurtransferase	Rv2539c	<i>aroK</i>	shikimate kinase I
Rv0409	<i>ackA</i>	acetate kinase	Rv0814c	<i>sseC2</i>	thiosulfate sulfurtransferase	Rv3838c	<i>pheA</i>	prephenate dehydratase
Rv1623c	<i>appC</i>	cytochrome <i>bd-II</i> oxidase subunit I	Rv3762c	-	probable alkyl sulfatase	Rv1613	<i>trpA</i>	tryptophan synthase $\alpha$ chain
Rv1622c	<i>cydB</i>	cytochrome <i>d</i> ubiquinol oxidase subunit II	D. Amino acid biosynthesis			Rv1612	<i>trpB</i>	tryptophan synthase $\beta$ chain
Rv1620c	<i>cydC</i>	ABC transporter	1. Glutamate family			Rv1611	<i>trpC</i>	indole-3-glycerol phosphate synthase
Rv1621c	<i>cydD</i>	ABC transporter	Rv1654	<i>argB</i>	acetylglutamate kinase	Rv2192c	<i>trpD</i>	anthranilate phosphoribosyltransferase
Rv2007c	<i>fdxA</i>	ferredoxin	Rv1652	<i>argC</i>	N-acetyl- $\gamma$ -glutamyl-phosphate reductase	Rv1609	<i>trpE</i>	anthranilate synthase component I
Rv3554	<i>fdxB</i>	ferredoxin	Rv1655	<i>argD</i>	acetylornithine aminotransferase	Rv2386c	<i>trpE2</i>	anthranilate synthase component I
Rv1177	<i>fdxC</i>	probable ferredoxin	Rv1656	<i>argF</i>	acetylornithine aminotransferase	Rv3754	<i>tyrA</i>	prephenate dehydrogenase
Rv3503c	<i>fdxD</i>	electron transfer flavoprotein $\beta$ subunit	Rv1658	<i>argG</i>	arginosuccinate synthase	5. Histidine		
Rv3029c	<i>fixA</i>	electron transfer flavoprotein $\alpha$ subunit	Rv1659	<i>argH</i>	arginosuccinate lyase	Rv1603	<i>hisA</i>	phosphoribosylformimino-5-aminimidazole carboxamide ribonucleotide isomerase
Rv3028c	<i>fixB</i>	electron transfer flavoprotein $\alpha$ subunit	Rv1653	<i>argJ</i>	glutamate N-acetyltransferase	Rv1601	<i>hisB</i>	imidazole glycerol-phosphate dehydratase
Rv3106	<i>fprA</i>	adrenodoxin and NADPH ferredoxin reductase	Rv2220	<i>glnA1</i>	glutamine synthase class I	Rv1600	<i>hisC</i>	histidinol-phosphate aminotransferase
Rv0886	<i>fprB</i>	ferredoxin, ferredoxin-NADP reductase	Rv2222c	<i>glnA2</i>	glutamine synthase class II	Rv3772	<i>hisC2</i>	histidinol-phosphate aminotransferase
Rv3251c	<i>rubA</i>	rubredoxin A				Rv1599	<i>hisD</i>	histidinol dehydrogenase

Rv1605	<i>hisF</i>	imidazole glycerol-phosphate synthase	Rv3048c	<i>nrdG</i>	subunit ribonucleoside-diphosphate small subunit	Rv3119	<i>moaE</i>	subunit 1 molybdopterin-converting factor
Rv2121c	<i>hisG</i>	ATP phosphoribosyltransferase	Rv3053c	<i>nrdH</i>	glutaredoxin electron transport component of NrdEF system	Rv0866	<i>moaE2</i>	subunit 2 molybdopterin-converting factor
Rv1602	<i>hisH</i>	amidotransferase	Rv3052c	<i>nrdI</i>	NrdI/YgaO/YmaA family	Rv3322c	<i>moaE3</i>	subunit 2 molybdopterin-converting factor
Rv2122c	<i>hisI</i>	phosphoribosyl-AMP cyclohydro-lase	Rv3247c	<i>tmk</i>	thymidylate kinase	Rv0994	<i>moaE</i>	subunit 2 molybdopterin biosynthesis
Rv1606	<i>hisI2</i>	probable phosphoribosyl-AMP 1,6 cyclohydrolyase	Rv2764c	<i>thyA</i>	thymidylate synthase	Rv3116	<i>moaB</i>	molybdopterin biosynthesis
Rv0114	-	similar to HisB	Rv0570	<i>nrdZ</i>	ribonucleotide reductase, class II	Rv2338c	<i>moaW</i>	molybdopterin biosynthesis
6. Pyruvate family			Rv3752c	-	probable cytidine/deoxycytidylate deaminase	Rv1681	<i>moaX</i>	weak similarity to <i>E. coli</i> MoaA
Rv3423c	<i>alr</i>	alanine racemase	4. Salvage of nucleosides and nucleotides			Rv1355c	<i>moaY</i>	weak similarity to <i>E. coli</i> MoeB
7. Branched amino acid family			Rv3313c	<i>add</i>	probable adenosine deaminase	Rv3206c	<i>moaZ</i>	probably involved in molybdopterin biosynthesis
Rv1559	<i>ilvA</i>	threonine deaminase	Rv2584c	<i>apt</i>	adenine phosphoribosyltransferases	Rv0865	<i>mog</i>	molybdopterin biosynthesis
Rv3003c	<i>ilvB</i>	acetolactate synthase I large sub-unit	Rv3315c	<i>cdd</i>	probable cytidine deaminase	5. Pantothenate		
Rv3470c	<i>ilvB2</i>	acetolactate synthase large sub-unit	Rv3314c	<i>deoA</i>	thymidine phosphorylase	Rv1092c	<i>coaA</i>	pantothenate kinase
Rv3001c	<i>ilvC</i>	ketol-acid reductoisomerase	Rv0478	<i>deoC</i>	deoxyribose-phosphate aldolase	Rv2225	<i>panB</i>	3-methyl-2-oxobutanoate hydroxymethyltransferase
Rv0189c	<i>ilvD</i>	dihydroxy-acid dehydratase	Rv3307	<i>deoD</i>	probable purine nucleoside phosphorylase	Rv3602c	<i>panC</i>	pantoate-β-alanine ligase
Rv2210c	<i>ilvE</i>	branched-chain-amino-acid transaminase	Rv3624c	<i>hpt</i>	probable hypoxanthine-guanine phosphoribosyltransferase	Rv3601c	<i>panD</i>	aspartate 1-decarboxylase
Rv1820	<i>ilvG</i>	acetolactate synthase II	Rv3393	<i>iunH</i>	probable inosine-uridine preferring nucleoside hydrolase	6. Pyridoxine		
Rv3002c	<i>ilvN</i>	acetolactate synthase I small sub-unit	Rv0535	<i>pnp</i>	phosphorylase from Pnp/MtaP family 2	Rv2607	<i>pxdH</i>	pyridoxamine 5'-phosphate oxidase
Rv3509c	<i>ilvX</i>	probable acetohydroxyacid synthase I large subunit	Rv3309c	<i>upp</i>	uracil phosphoribosyltransferase	7. Pyridine nucleotide		
Rv3710	<i>leuA</i>	α-isopropyl malate synthase	5. Miscellaneous nucleoside/nucleotide reactions			Rv1594	<i>nadA</i>	quinolinate synthase
Rv2995c	<i>leuB</i>	3-isopropylmalate dehydrogenase	Rv0733	<i>adk</i>	probable adenylate kinase	Rv1595	<i>nadB</i>	L-aspartate oxidase
Rv2988c	<i>leuC</i>	3-isopropylmalate dehydratase large subunit	Rv2364c	<i>bex</i>	GTP-binding protein of Era/ThdF family	Rv1596	<i>nadC</i>	nicotinate-nucleotide pyrophosphatase
Rv2987c	<i>leuD</i>	3-isopropylmalate dehydratase small subunit	Rv1712	<i>cmk</i>	cytidylate kinase	Rv0423c	<i>thiC</i>	thiamine synthesis, pyrimidine moiety
Rv2344c	<i>dgt</i>		Rv2344c	<i>dgt</i>	probable deoxyguanosine triphosphate hydrolase	8. Thiamine		
<i>E. Polyamine synthesis</i>			Rv2404c	<i>lepA</i>	GTP-binding protein LepA	Rv0422c	<i>thiD</i>	phosphomethylpyrimidine kinase
Rv2601	<i>speE</i>	spermidine synthase	Rv2727c	<i>miaA</i>	tRNA δ(2)-isopentenylpyrophosphate transferase	Rv0414c	<i>thiE</i>	thiamine synthesis, thiazole moiety
<i>F. Purines, pyrimidines, nucleosides and nucleotides</i>			Rv2445c	<i>ndkA</i>	nucleoside diphosphate kinase	Rv0417	<i>thiG</i>	thiamine synthesis, thiazole moiety
1. Purine ribonucleotide biosynthesis			Rv2440c	<i>obg</i>	Obg GTP-binding protein	Rv2977c	<i>thiL</i>	probable thiamine-monophosphate kinase
Rv1389	<i>gmK</i>	putative guanylate kinase	Rv2583c	<i>relA</i>	(p)ppGpp synthase I	9. Riboflavin		
Rv3396c	<i>guaA</i>	GMP synthase	<i>G. Biosynthesis of cofactors, prosthetic groups and carriers</i>			Rv1940	<i>ribA</i>	GTP cyclohydrolyase II
Rv1843c	<i>guaB1</i>	inosine-5'-monophosphate dehydrogenase	1. Biotin			Rv1415	<i>ribA2</i>	probable GTP cyclohydrolyase II
Rv3411c	<i>guaB2</i>	inosine-5'-monophosphate dehydrogenase	Rv1568	<i>bioA</i>	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	Rv1412	<i>ribC</i>	riboflavin synthase α chain
Rv3410c	<i>guaB3</i>	inosine-5'-monophosphate dehydrogenase	Rv1589	<i>bioB</i>	biotin synthase	Rv2671	<i>ribD</i>	probable riboflavin deaminase
Rv1017c	<i>prsA</i>	ribose-phosphate pyrophosphokinase	Rv1570	<i>bioD</i>	dethiobiotin synthase	Rv2786c	<i>ribF</i>	riboflavin kinase
Rv0357c	<i>purA</i>	adenylosuccinate synthase	Rv1569	<i>bioF</i>	8-amino-7-oxononanoate synthase	Rv1409	<i>ribG</i>	riboflavin biosynthesis
Rv0777	<i>purB</i>	adenylosuccinate lyase	Rv0032	<i>bioF2</i>	C-terminal similar to <i>B. subtilis</i> BioF	Rv1416	<i>ribH</i>	riboflavin synthase β chain
Rv0780	<i>purC</i>	phosphoribosylaminoimidazole-succinocarboxamide synthase	Rv3279c	<i>birA</i>	biotin apo-protein ligase	Rv3300c	-	probable deaminase, riboflavin synthesis
Rv0772	<i>purD</i>	phosphoribosylamine-glycine ligase	Rv1442	<i>bisC</i>	biotin sulfoxide reductase	10. Thioredoxin, glutaredoxin and mycothiol		
Rv3275c	<i>purE</i>	phosphoribosylaminoimidazole carboxylase	Rv0089	-	possible <i>bioC</i> biotin synthesis gene	Rv0773c	<i>ggtA</i>	putative γ-glutamyl transpeptidase
Rv0808	<i>purF</i>	amidophosphoribosyltransferase	2. Folic acid			Rv2394	<i>ggtB</i>	γ-glutamyl transpeptidase precursor
Rv0957	<i>purH</i>	phosphoribosylaminoimidazole-carboxamide formyltransferase	Rv2763c	<i>dfra</i>	dihydrofolate reductase	Rv2855	<i>gorA</i>	glutathione reductase homologue
Rv3276c	<i>purK</i>	phosphoribosylaminoimidazole-carboxylase ATPase subunit	Rv2447c	<i>folC</i>	folypolyglutamate synthase	Rv0816c	<i>thiX</i>	equivalent to <i>M. leprae</i> ThiX
Rv0803	<i>purL</i>	phosphoribosylformylglycinamide synthase II	Rv3356c	<i>folD</i>	methylenetetrahydrofolate dehydrogenase	Rv1470	<i>trxA</i>	thioredoxin
Rv0809	<i>purM</i>	5'-phosphoribosyl-5-aminoimidazole synthase	Rv3609c	<i>folE</i>	GTP cyclohydrolyase I	Rv1471	<i>trxB</i>	thioredoxin reductase
Rv0956	<i>purN</i>	phosphoribosylglycinamide formyltransferase I	Rv3606c	<i>folK</i>	7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase	Rv3913	<i>trxB2</i>	thioredoxin reductase
Rv0788	<i>purQ</i>	phosphoribosylformylglycinamide synthase I	Rv3608c	<i>folP</i>	dihydropterolate synthase	Rv3914	<i>trxC</i>	thioredoxin
Rv0389	<i>purT</i>	phosphoribosylglycinamide formyltransferase II	Rv1207	<i>folP2</i>	dihydropterolate synthase	11. Menaquinone, PQQ, ubiquinone and other terpenoids		
Rv2964	<i>purU</i>	formyltetrahydrofolate deformylase	Rv3607c	<i>folX</i>	may be involved in folate biosynthesis	Rv2682c	<i>dxs</i>	1-deoxy-D-xylulose 5-phosphate synthase
2. Pyrimidine ribonucleotide biosynthesis			Rv0013	<i>pabA</i>	p-aminobenzoate synthase glutamine amidotransferase	Rv0562	<i>grcC1</i>	heptaprenyl diphosphate synthase II
Rv1383	<i>carA</i>	carbamoyl-phosphate synthase subunit	Rv1005c	<i>pabB</i>	p-aminobenzoate synthase	Rv0989c	<i>grcC2</i>	heptaprenyl diphosphate synthase II
Rv1384	<i>carB</i>	carbamoyl-phosphate synthase subunit	Rv0812	<i>pabC</i>	aminodeoxychorismate lyase	Rv3398c	<i>idsA</i>	geranylgeranyl pyrophosphate synthase
Rv1380	<i>pyrB</i>	aspartate carbamoyltransferase	3. Lipoate			Rv2173	<i>idsA2</i>	geranylgeranyl pyrophosphate synthase
Rv1381	<i>pyrC</i>	dihydroorotate	Rv2218	<i>lipA</i>	lipoate biosynthesis protein A	Rv3383c	<i>idsB</i>	transfergeranyl, similar geranyl pyrophosphate synthase
Rv2139	<i>pyrD</i>	dihydroorotate dehydrogenase	Rv2217	<i>lipB</i>	lipoate biosynthesis protein B	Rv0534c	<i>menA</i>	pyrophosphate synthase
Rv1385	<i>pyrF</i>	orotidine 5'-phosphate decarboxylase	4. Molybdopterin			Rv0548c	<i>menB</i>	4-dihydroxy-2-naphthoate octaprenyltransferase
Rv1699	<i>pyrG</i>	CTP synthase	Rv3109	<i>moaA</i>	molybdenum cofactor biosynthesis, protein A	Rv0553	<i>menC</i>	naphthoate synthase
Rv2883c	<i>pyrH</i>	uridylate kinase	Rv0869c	<i>moaA2</i>	molybdenum cofactor biosynthesis, protein A	Rv0555	<i>menD</i>	o-succinylbenzoate-CoA synthase
Rv0382c	<i>umpA</i>	probable uridine 5'-monophosphate synthase	Rv0438c	<i>moaA3</i>	molybdenum cofactor biosynthesis, protein A	Rv0542c	<i>menE</i>	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase
3. 2'-deoxyribonucleotide metabolism			Rv3110	<i>moaB</i>	molybdenum cofactor biosynthesis, protein B	Rv3853	<i>menG</i>	o-succinylbenzoic acid-CoA ligase
Rv0321	<i>dcd</i>	deoxycytidine triphosphate deaminase	Rv0984	<i>moaB2</i>	molybdenum cofactor biosynthesis, protein B	Rv3397c	<i>phyA</i>	S-adenosylmethionine: 2-demethylmenaquinone phytoene synthase
Rv2697c	<i>dut</i>	deoxyuridine triphosphatase	Rv3111	<i>moaC</i>	molybdenum cofactor biosynthesis, protein C	Rv0693	<i>pqqE</i>	coenzyme PQQ synthesis protein E
Rv0233	<i>nrdB</i>	ribonucleoside-diphosphate reductase B2 (eukaryotic-like)	Rv0864	<i>moaC2</i>	molybdenum cofactor biosynthesis, protein C	Rv0558	<i>ubiE</i>	ubiquinone/menaquinone biosynthesis methyltransferase
Rv3051c	<i>nrdE</i>	ribonucleoside diphosphate reductase α chain	Rv3324c	<i>moaC3</i>	molybdenum cofactor biosynthesis, protein C	12. Heme and porphyrin		
Rv1981c	<i>nrdF</i>	ribonucleotide reductase small	Rv3112	<i>moaD</i>	molybdopterin converting factor subunit 1	Rv0509	<i>hemA</i>	glutamyl-tRNA reductase
			Rv0868c	<i>moaD2</i>	molybdopterin converting factor	Rv0512	<i>hemB</i>	δ-aminolevulinic acid dehydratase
						Rv0510	<i>hemC</i>	porphobilinogen deaminase
						Rv2678c	<i>hemE</i>	uroporphyrinogen decarboxylase



Rv1300	<i>hemK</i>	protoporphyrinogen oxidase	Rv0470c	<i>umaA2</i>	unknown mycolic acid methyltransferase	Rv2931	<i>ppsA</i>	phenolphthiocerol synthesis ( <i>pkkB</i> )
Rv0524	<i>hemL</i>	glutamate-1-semialdehyde aminotransferase				Rv2932	<i>ppsB</i>	phenolphthiocerol synthesis ( <i>pkbC</i> )
Rv2388c	<i>hemN</i>	oxygen-independent coproporphyrinogen III oxidase		3. Acyltransferases, mycoloyltransferases and phospholipid synthesis		Rv2933	<i>ppsC</i>	phenolphthiocerol synthesis ( <i>pkbD</i> )
Rv2677c	<i>hemY</i>	protoporphyrinogen oxidase	Rv2289	<i>cdh</i>	CDP-diacylglycerol phosphatidylhydrolase	Rv2934	<i>ppsD</i>	phenolphthiocerol synthesis ( <i>pkbE</i> )
Rv1485	<i>hemZ</i>	ferrochelatase				Rv2935	<i>ppsE</i>	phenolphthiocerol synthesis ( <i>pkbF</i> )
						Rv2928	<i>tesA</i>	thioesterase
						Rv1544	-	probable ketoacyl reductase
13. Cobalamin			Rv2881c	<i>cdsA</i>	phosphatidate cytidyltransferase		<b>J. Broad regulatory functions</b>	
Rv2849c	<i>cobA</i>	cob(I)alamin adenosyltransferase	Rv3804c	<i>fbpA</i>	antigen 85A, mycolyltransferase		<b>1. Repressors/activators</b>	
Rv2848c	<i>cobB</i>	cobyrinic acid a,c-diamide synthase	Rv1886c	<i>fbpB</i>	antigen 85B, mycolyltransferase	Rv1657	<i>argR</i>	arginine repressor
Rv2231c	<i>cobC</i>	aminotransferase	Rv3803c	<i>fbpC1</i>	antigen 85C, mycolyltransferase	Rv1267c	<i>embR</i>	regulator of <i>embAB</i> genes (AfsR/DndI/RedD family)
Rv2236c	<i>cobD</i>	cobinamide synthase	Rv0129c	<i>fbpC2</i>	antigen 85C', mycolyltransferase			
Rv2064	<i>cobG</i>	percorrin reductase	Rv0564c	<i>gpdA1</i>	glycerol-3-phosphate dehydrogenase	Rv1909c	<i>furA</i>	ferric uptake regulatory protein
Rv2065	<i>cobH</i>	percorrin isomerase				Rv2359	<i>furB</i>	ferric uptake regulatory protein
Rv2066	<i>cobI</i>	CobI-CobJ fusion protein	Rv2982c	<i>gpdA2</i>	glycerol-3-phosphate dehydrogenase	Rv2919c	<i>glnB</i>	ferric uptake regulatory protein
Rv2070c	<i>cobK</i>	percorrin reductase	Rv2612c	<i>pgsA</i>	CDP-diacylglycerol-glycerol-3-phosphate phosphatidyltransferase	Rv2711c	<i>ideR</i>	iron dependent repressor, IdeR
Rv2072c	<i>cobL</i>	probable methyltransferase				Rv2720	<i>lexA</i>	SOS repressor protein
Rv2071c	<i>cobM</i>	percorrin-3 methylase	Rv1822	<i>pgsA2</i>	CDP-diacylglycerol-glycerol-3-phosphate phosphatidyltransferase	Rv1479	<i>moxR</i>	transcriptional regulator, MoxR homologue
Rv2062c	<i>cobN</i>	cobalt insertion				Rv3692	<i>moxR2</i>	transcriptional regulator, MoxR homologue
Rv2208	<i>cobS</i>	cobalamin (5'-phosphate) synthase	Rv2746c	<i>pgsA3</i>	CDP-diacylglycerol-glycerol-3-phosphate phosphatidyltransferase	Rv3164c	<i>moxR3</i>	transcriptional regulator, MoxR homologue
Rv2207	<i>cobT</i>	nicotinate-nucleotide-dimethylbenzimidazole transferase	Rv1551	<i>plsB1</i>	glycerol-3-phosphate acyltransferase	Rv0212c	<i>nadR</i>	similar to <i>E. coli</i> NadR
Rv0254c	<i>cobU</i>	cobinamide kinase	Rv2482c	<i>plsB2</i>	glycerol-3-phosphate acyltransferase	Rv0117	<i>oxyS</i>	transcriptional regulator (LysR family)
Rv0255c	<i>cobQ</i>	cobyrinic acid synthase				Rv1379	<i>pyrR</i>	regulatory protein pyrimidine biosynthesis
Rv3713	<i>cobQ2</i>	possible cobyrinic acid synthase	Rv0437c	<i>psd</i>	putative phosphatidylserine decarboxylase	Rv2788	<i>sirR</i>	iron-dependent transcriptional repressor
Rv0306	-	similar to BluB cobalamin synthesis protein <i>R. capsulatus</i>	Rv0436c	<i>pssA</i>	CDP-diacylglycerol-serine o-phosphatidyltransferase	Rv3082c	<i>virS</i>	putative virulence regulating protein (AraC/XylS family)
14. Iron utilization			Rv0045c	-	possible dihydroloipoamide acetyltransferase	Rv3219	<i>whiB1</i>	WhiB transcriptional activator homologue
Rv1876	<i>bfrA</i>	bacterioferritin	Rv0914c	-	lipid transfer protein	Rv3260c	<i>whiB2</i>	WhiB transcriptional activator homologue
Rv3841	<i>bfrB</i>	bacterioferritin	Rv1543	-	probable fatty-acyl CoA reductase			
Rv3215	<i>entC</i>	probable isochorismate synthase	Rv1627c	-	lipid carrier protein	Rv3416	<i>whiB3</i>	WhiB transcriptional activator homologue
Rv3214	<i>entD</i>	weak similarity to many phosphoglycerate mutases	Rv1814	-	possible C-5 sterol desaturase	Rv3681c	<i>whiB4</i>	WhiB transcriptional activator homologue
Rv2895c	<i>viuB</i>	similar to proteins involved in vibriobactin uptake	Rv1867	-	similar to acetyl CoA synthase/lipid carriers			
Rv3525c	-	similar to ferripyochelin binding protein	Rv2261c	-	apolipoprotein N-acyltransferase-a	Rv0023	-	putative transcriptional regulator
						Rv0043c	-	transcriptional regulator (GntR family)
			Rv2262c	-	apolipoprotein N-acyltransferase-b	Rv0067c	-	transcriptional regulator (TetR/AcrR family)
			Rv3523	-	lipid carrier protein	Rv0078	-	transcriptional regulator (TetR/AcrR family)
			Rv3720	-	C-term similar to cyclopropane fatty acid synthases	Rv0081	-	transcriptional regulator (ArsR family)
<b>H. Lipid biosynthesis</b>								
1. Synthesis of fatty and mycolic acids					<b>I. Polyketide and non-ribosomal peptide synthesis</b>			
Rv3285	<i>accA3</i>	acetyl/propionyl CoA carboxylase $\alpha$ subunit	Rv2940c	<i>mas</i>	mycocerosic acid synthase	Rv0135c	-	putative transcriptional regulator
Rv0904c	<i>accD3</i>	acetyl/propionyl CoA carboxylase $\beta$ subunit	Rv2384	<i>mbtA</i>	mycobactin/exochelin synthesis (salicylate-AMP ligase)	Rv0144	-	putative transcriptional regulator
Rv3799c	<i>accD4</i>	acetyl/propionyl CoA carboxylase $\beta$ subunit	Rv2383c	<i>mbtB</i>	mycobactin/exochelin synthesis (serine/threonine ligation)	Rv0158	-	transcriptional regulator (TetR/AcrR family)
Rv3280	<i>accD5</i>	acetyl/propionyl CoA carboxylase $\beta$ subunit	Rv2382c	<i>mbtC</i>	mycobactin/exochelin synthesis	Rv0165c	-	transcriptional regulator (GntR family)
Rv2247	<i>accD6</i>	acetyl/propionyl CoA carboxylase $\beta$ subunit	Rv2381c	<i>mbtD</i>	mycobactin/exochelin synthesis (polyketide synthase)	Rv0195	-	transcriptional regulator (LuxR/UhpA family)
Rv2244	<i>acpM</i>	acyl carrier protein (meromycolate extension)	Rv2380c	<i>mbtE</i>	mycobactin/exochelin synthesis (lysine ligation)	Rv0196	-	transcriptional regulator (TetR/AcrR family)
Rv2523c	<i>acpS</i>	CoA:apo-[ACP] pantethienophosphotransferase	Rv2379c	<i>mbtF</i>	mycobactin/exochelin synthesis (lysine ligation)	Rv0232	-	transcriptional regulator (TetR/AcrR family)
Rv2243	<i>fabD</i>	malonyl CoA-[ACP] transacylase	Rv2378c	<i>mbtG</i>	mycobactin/exochelin synthesis (lysine hydroxylation)	Rv0238	-	transcriptional regulator (TetR/AcrR family)
Rv0649	<i>fabD2</i>	malonyl CoA-[ACP] transacylase	Rv2377c	<i>mbtH</i>	mycobactin/exochelin synthesis	Rv0273c	-	putative transcriptional regulator
Rv1483	<i>fabG1</i>	3-oxoacyl-[ACP] reductase (aka MabA)	Rv0101	<i>nrp</i>	unknown non-ribosomal peptide synthase	Rv0302	-	transcriptional regulator (TetR/AcrR family)
Rv1350	<i>fabG2</i>	3-oxoacyl-[ACP] reductase	Rv1153c	<i>omt</i>	PKS $\alpha$ -methyltransferase	Rv0324	-	putative transcriptional regulator
Rv2002	<i>fabG3</i>	3-oxoacyl-[ACP] reductase	Rv3824c	<i>papA1</i>	PKS-associated protein, unknown function	Rv0328	-	transcriptional regulator (TetR/AcrR family)
Rv0242c	<i>fabG4</i>	3-oxoacyl-[ACP] reductase	Rv3820c	<i>papA2</i>	PKS-associated protein, unknown function	Rv0348	-	putative transcriptional regulator
Rv2766c	<i>fabG5</i>	3-oxoacyl-[ACP] reductase	Rv1182	<i>papA3</i>	PKS-associated protein, unknown function	Rv0377	-	transcriptional regulator (LysR family)
Rv0533c	<i>fabH</i>	$\beta$ -ketoacyl-ACP synthase III	Rv1528c	<i>papA4</i>	PKS-associated protein, unknown function	Rv0386	-	transcriptional regulator (LuxR/UhpA family)
Rv2524c	<i>fas</i>	fatty acid synthase	Rv2939	<i>papA5</i>	PKS-associated protein, unknown function	Rv0452	-	putative transcriptional regulator
Rv1484	<i>inhA</i>	enoyl-[ACP] reductase	Rv2946c	<i>pkb1</i>	polyketide synthase	Rv0465c	-	transcriptional regulator (PbsX/Xre family)
Rv2245	<i>kasA</i>	$\beta$ -ketoacyl-ACP synthase (meromycolate extension)	Rv1660	<i>pkb10</i>	polyketide synthase (chalcone synthase-like)	Rv0472c	-	transcriptional regulator (TetR/AcrR family)
Rv2246	<i>kasB</i>	$\beta$ -ketoacyl-ACP synthase (meromycolate extension)	Rv1665	<i>pkb11</i>	polyketide synthase (chalcone synthase-like)	Rv0474	-	transcriptional regulator (PbsX/Xre family)
Rv1618	<i>tesB1</i>	thioesterase II	Rv2048c	<i>pkb12</i>	polyketide synthase (erythronolide synthase-like)	Rv0485	-	transcriptional regulator (ROK family)
Rv2605c	<i>tesB2</i>	thioesterase II	Rv3800c	<i>pkb13</i>	polyketide synthase	Rv0494	-	transcriptional regulator (GntR family)
Rv0033	-	possible acyl carrier protein	Rv1342c	<i>pkb14</i>	polyketide synthase (chalcone synthase-like)	Rv0552	-	putative transcriptional regulator
Rv1344	-	possible acyl carrier protein	Rv2947c	<i>pkb15</i>	polyketide synthase	Rv0576	-	putative transcriptional regulator
Rv1722	-	possible biotin carboxylase	Rv1013	<i>pkb16</i>	polyketide synthase	Rv0586	-	transcriptional regulator (GntR family)
Rv3221c	-	resembles biotin carboxyl carrier	Rv1663	<i>pkb17</i>	polyketide synthase			
Rv3472	-	possible acyl carrier protein	Rv1372	<i>pkb18</i>	polyketide synthase	Rv0650	-	transcriptional regulator (ROK family)
2. Modification of fatty and mycolic acids			Rv3825c	<i>pkb2</i>	polyketide synthase	Rv0653c	-	putative transcriptional regulator
Rv3391	<i>acrA1</i>	fatty acyl-CoA reductase	Rv1180	<i>pkb3</i>	polyketide synthase	Rv0681	-	transcriptional regulator (TetR/AcrR family)
Rv3392c	<i>cmaA1</i>	cyclopropane mycolic acid synthase 1	Rv1181	<i>pkb4</i>	polyketide synthase	Rv0691c	-	transcriptional regulator (TetR/AcrR family)
Rv0503c	<i>cmaA2</i>	cyclopropane mycolic acid synthase 2	Rv1527c	<i>pkb5</i>	polyketide synthase			
Rv0824c	<i>desA1</i>	acyl-[ACP] desaturase	Rv0405	<i>pkb6</i>	polyketide synthase	Rv0737	-	putative transcriptional regulator
Rv1094	<i>desA2</i>	acyl-[ACP] desaturase	Rv1661	<i>pkb7</i>	polyketide synthase	Rv0744c	-	putative transcriptional regulator
Rv3229c	<i>desA3</i>	acyl-[ACP] desaturase	Rv1662	<i>pkb8</i>	polyketide synthase	Rv0792c	-	transcriptional regulator (GntR family)
Rv0645c	<i>mmaA1</i>	methoxymycolic acid synthase 1	Rv1664	<i>pkb9</i>	polyketide synthase			
Rv0644c	<i>mmaA2</i>	methoxymycolic acid synthase 2						
Rv0643c	<i>mmaA3</i>	methoxymycolic acid synthase 3						
Rv0642c	<i>mmaA4</i>	methoxymycolic acid synthase 4						
Rv0447c	<i>ufaA1</i>	unknown fatty acid methyltransferase						
Rv3538	<i>ufaA2</i>	unknown fatty acid methyltransferase						
Rv0469	<i>umaA1</i>	unknown mycolic acid methyltransferase						

Rv0823c	-	family) transcriptional regulator (NifR3/Smm1 family)	Rv3160c	-	putative transcriptional regulator	Rv0018c	<i>ppp</i>	truncated putative phosphoprotein phosphatase
Rv0827c	-	transcriptional regulator (ArsR family)	Rv3167c	-	putative transcriptional regulator	Rv2234	<i>ptpA</i>	low molecular weight protein-tyrosine-phosphatase
Rv0890c	-	transcriptional regulator (LuxR/UhpA family)	Rv3173c	-	transcriptional regulator (TetR/AcrR family)	Rv0153c	-	putative protein-tyrosine-phosphatase
Rv0891c	-	putative transcriptional regulator	Rv3183	-	putative transcriptional regulator	<b>II. Macromolecule metabolism</b>		
Rv0894	-	putative transcriptional regulator	Rv3208	-	transcriptional regulator (TetR/AcrR family)	<b>A. Synthesis and modification of macromolecules</b>		
Rv1019	-	transcriptional regulator (TetR/AcrR family)	Rv3249c	-	transcriptional regulator (TetR/AcrR family)	<b>1. Ribosomal protein synthesis and modification</b>		
Rv1049	-	transcriptional regulator (MarR family)	Rv3291c	-	transcriptional regulator (Lrp/AsnC family)	Rv3420c	<i>rimI</i>	ribosomal protein S18 acetyltransferase
Rv1129c	-	transcriptional regulator (PbsX/Xre family)	Rv3295	-	transcriptional regulator (TetR/AcrR family)	Rv0995	<i>rimJ</i>	acetylation of 30S S5 subunit
Rv1151c	-	putative transcriptional regulator	Rv3334	-	transcriptional regulator (MerR family)	Rv0641	<i>rplA</i>	50S ribosomal protein L1
Rv1152	-	transcriptional regulator (GntR family)	Rv3405c	-	putative transcriptional regulator	Rv0704	<i>rplB</i>	50S ribosomal protein L2
Rv1167c	-	putative transcriptional regulator	Rv3522	-	putative transcriptional regulator	Rv0701	<i>rplC</i>	50S ribosomal protein L3
Rv1219c	-	putative transcriptional regulator	Rv3557c	-	transcriptional regulator (TetR/AcrR family)	Rv0702	<i>rplD</i>	50S ribosomal protein L4
Rv1255c	-	transcriptional regulator (TetR/AcrR family)	Rv3574	-	transcriptional regulator (TetR/AcrR family)	Rv0716	<i>rplE</i>	50S ribosomal protein L5
Rv1332	-	putative transcriptional regulator	Rv3575c	-	transcriptional regulator (LacI family)	Rv0719	<i>rplF</i>	50S ribosomal protein L6
Rv1353c	-	transcriptional regulator (TetR/AcrR family)	Rv3583c	-	putative transcriptional regulator	Rv0056	<i>rplI</i>	50S ribosomal protein L9
Rv1358	-	transcriptional regulator (LuxR/UhpA family)	Rv3676	-	transcriptional regulator (Crp/Fnr family)	Rv0651	<i>rplJ</i>	50S ribosomal protein L10
Rv1359	-	putative transcriptional regulator	Rv3678c	-	transcriptional regulator (LysR family)	Rv0640	<i>rplK</i>	50S ribosomal protein L11
Rv1395	-	transcriptional regulator (AraC/XylS family)	Rv3736	-	transcriptional regulator (AraC/XylS family)	Rv0652	<i>rplL</i>	50S ribosomal protein L7/L12
Rv1404	-	transcriptional regulator (MarR family)	Rv3744	-	transcriptional regulator (ArsR family)	Rv3443c	<i>rplM</i>	50S ribosomal protein L13
Rv1423	-	putative transcriptional regulator	Rv3830c	-	transcriptional regulator (TetR/AcrR family)	Rv0714	<i>rplN</i>	50S ribosomal protein L14
Rv1460	-	putative transcriptional regulator	Rv3833	-	transcriptional regulator (AraC/XylS family)	Rv0723	<i>rplO</i>	50S ribosomal protein L15
Rv1474c	-	transcriptional regulator (TetR/AcrR family)	Rv3840	-	putative transcriptional regulator	Rv0708	<i>rplP</i>	50S ribosomal protein L16
Rv1534	-	transcriptional regulator (TetR/AcrR family)	Rv3855	-	putative transcriptional regulator	Rv3456c	<i>rplQ</i>	50S ribosomal protein L17
Rv1556	-	putative transcriptional regulator	<b>2. Two component systems</b>			Rv0720	<i>rplR</i>	50S ribosomal protein L18
Rv1674c	-	putative transcriptional regulator	Rv1028c	<i>kdpD</i>	sensor histidine kinase	Rv2904c	<i>rplS</i>	50S ribosomal protein L19
Rv1675c	-	putative transcriptional regulator	Rv1027c	<i>kdpE</i>	two-component response regulator	Rv1643	<i>rplT</i>	50S ribosomal protein L20
Rv1719	-	transcriptional regulator (IclR family)	Rv3246c	<i>mtrA</i>	two-component response regulator	Rv2442c	<i>rplU</i>	50S ribosomal protein L21
Rv1773c	-	transcriptional regulator (IclR family)	Rv3245c	<i>mtrB</i>	sensor histidine kinase	Rv0706	<i>rplV</i>	50S ribosomal protein L22
Rv1776c	-	putative transcriptional regulator	Rv0844c	<i>narL</i>	two-component response regulator	Rv0703	<i>rplW</i>	50S ribosomal protein L23
Rv1816	-	putative transcriptional regulator	Rv0757	<i>phoP</i>	two-component response regulator	Rv0715	<i>rplX</i>	50S ribosomal protein L24
Rv1846c	-	putative transcriptional regulator	Rv0758	<i>phoR</i>	sensor histidine kinase	Rv1015c	<i>rplY</i>	50S ribosomal protein L25
Rv1931c	-	transcriptional regulator (AraC/XylS family)	Rv0491	<i>regX3</i>	two-component response regulator	Rv2441c	<i>rpmA</i>	50S ribosomal protein L27
Rv1956	-	putative transcriptional regulator	Rv0490	<i>senX3</i>	sensor histidine kinase	Rv0105c	<i>rpmB</i>	50S ribosomal protein L28
Rv1963c	-	putative transcriptional regulator	Rv0602c	<i>tcra</i>	two-component response regulator	Rv2058c	<i>rpmB2</i>	50S ribosomal protein L28
Rv1985c	-	transcriptional regulator (LysR family)	Rv0260c	-	two-component response regulator	Rv0709	<i>rpmC</i>	50S ribosomal protein L29
Rv1990c	-	putative transcriptional regulator	Rv0600c	-	sensor histidine kinase	Rv0722	<i>rpmD</i>	50S ribosomal protein L30
Rv1994c	-	transcriptional regulator (MerR family)	Rv0601c	-	sensor histidine kinase	Rv1298	<i>rpmE</i>	50S ribosomal protein L31
Rv2017	-	putative transcriptional regulator (PbsX/Xre family)	Rv0818	-	two-component response regulator	Rv2057c	<i>rpmG</i>	50S ribosomal protein L33
Rv2021c	-	putative transcriptional regulator	Rv0845	-	sensor histidine kinase	Rv3924c	<i>rpmH</i>	50S ribosomal protein L34
Rv2034	-	transcriptional regulator (ArsR family)	Rv0902c	-	sensor histidine kinase	Rv1642	<i>rpmI</i>	50S ribosomal protein L35
Rv2175c	-	putative transcriptional regulator	Rv0903c	-	two-component response regulator	Rv3461c	<i>rpmJ</i>	50S ribosomal protein L36
Rv2250c	-	putative transcriptional regulator	Rv0981	-	two-component response regulator	Rv1630	<i>rpsA</i>	30S ribosomal protein S1
Rv2258c	-	putative transcriptional regulator	Rv0982	-	sensor histidine kinase	Rv2890c	<i>rpsB</i>	30S ribosomal protein S2
Rv2282c	-	transcriptional regulator (LysR family)	Rv1032c	-	sensor histidine kinase	Rv0707	<i>rpsC</i>	30S ribosomal protein S3
Rv2308	-	putative transcriptional regulator	Rv1033c	-	two-component response regulator	Rv3458c	<i>rpsD</i>	30S ribosomal protein S4
Rv2324	-	transcriptional regulator (Lrp/AsnC family)	Rv1626	-	two-component response regulator	Rv0721	<i>rpsE</i>	30S ribosomal protein S5
Rv2358	-	transcriptional regulator (ArsR family)	Rv2027c	-	sensor histidine kinase	Rv0053	<i>rpsF</i>	30S ribosomal protein S6
Rv2488c	-	transcriptional regulator (LuxR/UhpA family)	Rv2884	-	two-component response regulator	Rv0683	<i>rpsG</i>	30S ribosomal protein S7
Rv2506	-	transcriptional regulator (TetR/AcrR family)	Rv3132c	-	sensor histidine kinase	Rv0718	<i>rpsH</i>	30S ribosomal protein S8
Rv2621c	-	putative transcriptional regulator	Rv3133c	-	two-component response regulator	Rv3442c	<i>rpsI</i>	30S ribosomal protein S9
Rv2640c	-	transcriptional regulator (ArsR family)	Rv3143	-	putative sensory transduction protein	Rv0700	<i>rpsJ</i>	30S ribosomal protein S10
Rv2642	-	transcriptional regulator (ArsR family)	Rv3220c	-	sensor histidine kinase	Rv3459c	<i>rpsK</i>	30S ribosomal protein S11
Rv2669	-	putative transcriptional regulator	Rv3764c	-	sensor histidine kinase	Rv0682	<i>rpsL</i>	30S ribosomal protein S12
Rv2745c	-	putative transcriptional regulator	Rv3765c	-	two-component response regulator	Rv3460c	<i>rpsM</i>	30S ribosomal protein S13
Rv2779c	-	transcriptional regulator (Lrp/AsnC family)	<b>3. Serine-threonine protein kinases and phosphoprotein phosphatases</b>			Rv0717	<i>rpsN</i>	30S ribosomal protein S14
Rv2887	-	transcriptional regulator (MarR family)	Rv0015c	<i>pknA</i>	serine-threonine protein kinase	Rv2056c	<i>rpsN2</i>	30S ribosomal protein S14
Rv2912c	-	transcriptional regulator (TetR/AcrR family)	Rv0014c	<i>pknB</i>	serine-threonine protein kinase	Rv2785c	<i>rpsO</i>	30S ribosomal protein S15
Rv2989	-	transcriptional regulator (IclR family)	Rv0931c	<i>pknD</i>	serine-threonine protein kinase	Rv2909c	<i>rpsP</i>	30S ribosomal protein S16
Rv3050c	-	putative transcriptional regulator	Rv1743	<i>pknE</i>	serine-threonine protein kinase	Rv0710	<i>rpsQ</i>	30S ribosomal protein S17
Rv3055	-	putative transcriptional regulator	Rv1746	<i>pknF</i>	serine-threonine protein kinase	Rv0055	<i>rpsR</i>	30S ribosomal protein S18
Rv3058c	-	putative transcriptional regulator	Rv0410c	<i>pknG</i>	serine-threonine protein kinase	Rv2055c	<i>rpsR2</i>	30S ribosomal protein S18
Rv3060c	-	transcriptional regulator (GntR family)	Rv2914c	<i>pknH</i>	serine-threonine protein kinase	Rv0705	<i>rpsS</i>	30S ribosomal protein S19
Rv3066	-	putative transcriptional regulator	Rv2088	<i>pknJ</i>	serine-threonine protein kinase	Rv2412	<i>rpsT</i>	30S ribosomal protein S20
Rv3095	-	putative transcriptional regulator	Rv3080c	<i>pknK</i>	serine-threonine protein kinase	Rv3241c	-	member of S30AE ribosomal protein family
Rv3124	-	transcriptional regulator (AfsR/DndI/RedD family)	Rv2176	<i>pknL</i>	serine-threonine protein kinase,	<b>2. Ribosome modification and maturation</b>		
						Rv1010	<i>ksgA</i>	16S rRNA dimethyltransferase
						Rv2838c	<i>rbfA</i>	ribosome-binding factor A
						Rv2907c	<i>rimM</i>	16S rRNA processing protein
						<b>3. Aminoacyl tRNA synthases and their modification</b>		
						Rv2555c	<i>alaS</i>	alanyl-tRNA synthase
						Rv1292	<i>argS</i>	arginyl-tRNA synthase
						Rv2572c	<i>aspS</i>	aspartyl-tRNA synthase
						Rv3580c	<i>cysS</i>	cysteinyl-tRNA synthase
						Rv2130c	<i>cysS2</i>	cysteinyl-tRNA synthase
						Rv1406	<i>fmt</i>	methionyl-tRNA formyltransferase
						Rv3011c	<i>gatA</i>	glu-tRNA-gln amidotransferase, subunit B
						Rv3009c	<i>gatB</i>	glu-tRNA-gln amidotransferase, subunit A
						Rv3012c	<i>gatC</i>	glu-tRNA-gln amidotransferase, subunit C
						Rv2992c	<i>gltS</i>	glutamyl-tRNA synthase
						Rv2357c	<i>glyS</i>	glycyl-tRNA synthase
						Rv2580c	<i>hisS</i>	histidyl-tRNA synthase
						Rv1536	<i>ileS</i>	isoleucyl-tRNA synthase
						Rv0041	<i>leuS</i>	leucyl-tRNA synthase
						Rv3598c	<i>lysS</i>	lysyl-tRNA synthase
						Rv1640c	<i>lysX</i>	C-term lysyl-tRNA synthase
						Rv1007c	<i>metS</i>	methionyl-tRNA synthase
						Rv1649	<i>pheS</i>	phenylalanyl-tRNA synthase $\alpha$ subunit

Rv1650	<i>pheT</i>	phenylalanyl-tRNA synthase $\beta$ subunit	Rv2090	-	partially similar to DNA polymerase I	2. DNA	<i>end</i>	endonuclease IV (apurinase)
Rv2845c	<i>proS</i>	prolyl-tRNA synthase	Rv2191	-	similar to both PolC and UvrC proteins	Rv0670	<i>xseA</i>	exonuclease VII large subunit
Rv3834c	<i>serS</i>	seryl-tRNA synthase	Rv2464c	-	probable DNA glycosylase, endonuclease VIII	Rv1108c	<i>xseB</i>	exonuclease VII small subunit
Rv2614c	<i>thrS</i>	threonyl-tRNA synthase	Rv3201c	-	probable ATP-dependent DNA helicase	3. Proteins, peptides and glycopeptides		
Rv2906c	<i>trmD</i>	tRNA (guanine-N1)-methyltransferase	Rv3202c	-	similar to UvrD proteins	Rv3305c	<i>amiA</i>	probable aminohydrolase
Rv3336c	<i>trpS</i>	tryptophanyl tRNA synthase	Rv3263	-	probable DNA methylase	Rv3306c	<i>amiB</i>	probable aminohydrolase
Rv1689	<i>tyrS</i>	tyrosyl-tRNA synthase	Rv3644c	-	similar in N-term to DNA polymerase III	Rv3596c	<i>clpC</i>	ATP-dependent Clp protease
Rv2448c	<i>valS</i>	valyl-tRNA synthase				Rv2461c	<i>clpP</i>	ATP-dependent Clp protease proteolytic subunit
4. Nucleoproteins						Rv2460c	<i>clpP2</i>	ATP-dependent Clp protease proteolytic subunit
Rv1407	<i>imu</i>	similar to Fmu protein				Rv2457c	<i>clpX</i>	ATP-dependent Clp protease
Rv3852	<i>hns</i>	HU-histone protein	6. Protein translation and modification			Rv2667	<i>clpX'</i>	ATP-binding subunit ClpX similar to ClpC from <i>M. leprae</i> but shorter
Rv2986c	<i>hupB</i>	DNA-binding protein II	Rv0429c	<i>def</i>	polypeptide deformylase	Rv3419c	<i>gcp</i>	glycoprotease
Rv1388	<i>mlHF</i>	integration host factor	Rv2534c	<i>efp</i>	elongation factor P	Rv2725c	<i>hflX</i>	GTP-binding protein
5. DNA replication, repair, recombination and restriction/modification			Rv2882c	<i>frr</i>	ribosome recycling factor	Rv1223	<i>htrA</i>	serine protease
Rv1317c	<i>alkA</i>	DNA-3-methyladenine glycosidase II	Rv0684	<i>fusA</i>	elongation factor G	Rv2861c	<i>map</i>	methionine aminopeptidase
Rv2836c	<i>dinF</i>	DNA-damage-inducible protein F	Rv0120c	<i>fusA2</i>	elongation factor G	Rv0734	<i>map'</i>	probable methionine aminopeptidase
Rv1329c	<i>dinG</i>	probable ATP-dependent helicase	Rv1080c	<i>greA</i>	transcription elongation factor G	Rv0319	<i>pcp</i>	pyrrolidone-carboxylate peptidase
Rv3056	<i>dinP</i>	DNA-damage-inducible protein	Rv3462c	<i>infA</i>	initiation factor IF-1	Rv0125	<i>pepA</i>	probable serine protease
Rv1537	<i>dinX</i>	probable DNA-damage-inducible protein	Rv2839c	<i>infB</i>	initiation factor IF-2	Rv2213	<i>pepB</i>	aminopeptidase A/I
Rv0001	<i>dnaA</i>	chromosomal replication initiator protein	Rv1641	<i>infC</i>	initiation factor IF-3	Rv0800	<i>pepC</i>	aminopeptidase I
Rv0058	<i>dnaB</i>	DNA helicase (contains intein)	Rv0009	<i>ppiA</i>	peptidyl-prolyl <i>cis-trans</i> isomerase	Rv2467	<i>pepD</i>	probable aminopeptidase
Rv1547	<i>dnaE1</i>	DNA polymerase III, $\alpha$ subunit	Rv2582	<i>ppiB</i>	peptidyl-prolyl <i>cis-trans</i> isomerase	Rv2089c	<i>pepE</i>	cytoplasmic peptidase
Rv3370c	<i>dnaE2</i>	DNA polymerase III $\alpha$ chain	Rv1299	<i>prfA</i>	peptide chain release factor 1	Rv2535c	<i>pepQ</i>	cytoplasmic peptidase
Rv2343c	<i>dnaG</i>	DNA primase	Rv3105c	<i>prfB</i>	peptide chain release factor 2	Rv2782c	<i>pepR</i>	protease II, M16 family (insulinase)
Rv0002	<i>dnaN</i>	DNA polymerase III, $\beta$ subunit	Rv2889c	<i>tsf</i>	elongation factor EF-Ts	Rv2109c	<i>prcA</i>	proteasome $\alpha$ -type subunit 1
Rv3711c	<i>dnaQ</i>	DNA polymerase III $\epsilon$ chain	Rv0685	<i>tuf</i>	elongation factor EF-Tu	Rv2110c	<i>prcB</i>	proteasome $\beta$ -type subunit 2
Rv3721c	<i>dnaZX</i>	DNA polymerase III, $\gamma$ (dnaZ) and $\tau$ (dnaX)	7. RNA synthesis, RNA modification and DNA transcription			Rv0782	<i>ptrBa</i>	protease II, $\alpha$ subunit
Rv2924c	<i>fpg</i>	formamidopyrimidine-DNA glycosylase	Rv1253	<i>deaD</i>	ATP-dependent DNA/RNA helicase	Rv0781	<i>ptrBb</i>	protease II, $\beta$ subunit
Rv0006	<i>gyrA</i>	DNA gyrase subunit A	Rv2783c	<i>gpsI</i>	pppGpp synthase and polyribonucleotide phosphorylase	Rv0724	<i>sppA</i>	protease IV, signal peptide peptidase
Rv0005	<i>gyrB</i>	DNA gyrase subunit B	Rv2841c	<i>nusA</i>	transcription termination factor	Rv0198c	-	probable zinc metalloprotease
Rv2092c	<i>helY</i>	probable helicase, Ski2 subfamily	Rv2533c	<i>nusB</i>	N-utilization substance protein B	Rv0457c	-	probable peptidase
Rv2101	<i>helZ</i>	probable helicase, Snf2/Rad54 family	Rv0639	<i>nusG</i>	transcription antitermination protein	Rv0840c	-	probable proline iminopeptidase
Rv2756c	<i>hsdM</i>	type I restriction/modification system DNA methylase	Rv3907c	<i>pcnA</i>	polynucleotide polymerase	Rv0983	-	probable serine protease
Rv2755c	<i>hsdS'</i>	type I restriction/modification system specificity determinant	Rv3232c	<i>pvdS</i>	alternative sigma factor for siderophore production	Rv1977	-	probable zinc metallopeptidase
Rv3296	<i>lhr</i>	ATP-dependent helicase	Rv3211	<i>rhlE</i>	RNA helicase	Rv3668c	-	probable alkaline serine protease
Rv3014c	<i>ligA</i>	DNA ligase	Rv1297	<i>rho</i>	transcription termination factor rho	Rv3671c	-	probable serine protease
Rv3062	<i>ligB</i>	DNA ligase	Rv3457c	<i>rpoA</i>	$\alpha$ subunit of RNA polymerase	Rv3883c	-	probable serine protease
Rv3731	<i>ligC</i>	probable DNA ligase	Rv0667	<i>rpoB</i>	$\beta$ subunit of RNA polymerase	Rv3886c	-	probable protease
Rv1020	<i>mid</i>	restriction-repair coupling factor	Rv0668	<i>rpoC</i>	$\beta'$ subunit of RNA polymerase	4. Polysaccharides, lipopolysaccharides and phospholipids		
Rv2528c	<i>mrr</i>	restriction system protein	Rv1364c	<i>rsbU</i>	SigB regulation protein	Rv0062	<i>celA</i>	cellulase/endoglucanase
Rv2985	<i>mutT1</i>	MutT homologue	Rv3287c	<i>rsbW</i>	anti-sigma B factor	Rv3915	<i>cwlM</i>	hydrolase
Rv1160	<i>mutT2</i>	MutT homologue	Rv2703	<i>sigA</i>	RNA polymerase sigma factor (aka MysA, RpoV)	Rv0315	-	probable $\beta$ -1,3-glucanase
Rv0413	<i>mutT3</i>	MutT homologue	Rv2710	<i>sigB</i>	RNA polymerase sigma factor (aka MysB)	Rv1090	-	probable inactivated cellulase/endoglucanase
Rv3589	<i>mutY</i>	probable DNA glycosylase	Rv2069	<i>sigC</i>	ECF subfamily sigma factor	Rv1327c	-	probable glycosyl hydrolase, $\alpha$ -amylase family
Rv3297	<i>nei</i>	probable endonuclease VIII	Rv3414c	<i>sigD</i>	ECF subfamily sigma subunit	Rv1333	-	probable hydrolase
Rv3674c	<i>nth</i>	probable endonuclease III	Rv1221	<i>sigE</i>	ECF subfamily sigma subunit	Rv3463	-	probable neuraminidase
Rv1316c	<i>ogt</i>	methylated-DNA-protein-cysteine methyltransferase	Rv3286c	<i>sigF</i>	ECF subfamily sigma subunit	Rv3717	-	possible N-acetylmuramoyl-L-alanine amidase
Rv1629	<i>polA</i>	DNA polymerase I	Rv0182c	<i>sigG</i>	sigma-70 factors ECF subfamily	5. Esterases and lipases		
Rv1402	<i>priA</i>	putative primosomal protein n' (replication factor Y)	Rv3223c	<i>sigH</i>	ECF subfamily sigma subunit	Rv0220	<i>lipC</i>	probable esterase
Rv3585	<i>radA</i>	probable DNA repair RadA homologue	Rv1189	<i>sigI</i>	ECF family sigma factor	Rv1923	<i>lipD</i>	probable esterase
Rv2737c	<i>recA</i>	recombinase (contains intein)	Rv3328c	<i>sigJ</i>	similar to SigI, ECF family	Rv3775	<i>lipE</i>	probable hydrolase
Rv0630c	<i>recB</i>	exodeoxyribonuclease V	Rv0445c	<i>sigK</i>	ECF-type sigma factor	Rv3487c	<i>lipF</i>	probable esterase
Rv0631c	<i>recC</i>	exodeoxyribonuclease V	Rv0735	<i>sigL</i>	sigma-70 factors ECF subfamily	Rv0646c	<i>lipG</i>	probable hydrolase
Rv0629c	<i>recD</i>	exodeoxyribonuclease V	Rv3911	<i>sigM</i>	probable sigma factor, similar to SigE	Rv1399c	<i>lipH</i>	probable lipase
Rv0003	<i>recF</i>	DNA replication and SOS induction	Rv3366	<i>spoU</i>	probable rRNA methylase	Rv1400c	<i>lipI</i>	probable lipase
Rv2973c	<i>recG</i>	ATP-dependent DNA helicase	Rv3455c	<i>truA</i>	probable pseudouridylylase synthase	Rv1900c	<i>lipJ</i>	probable esterase
Rv1696	<i>recN</i>	recombination and DNA repair	Rv2793c	<i>truB</i>	tRNA pseudouridine 55 synthase	Rv2385	<i>lipK</i>	probable acetyl-hydrolase
Rv3715c	<i>recR</i>	RecBC-Independent process of DNA repair	Rv1644	<i>tsnR</i>	putative 23S rRNA methyltransferase	Rv1497	<i>lipL</i>	esterase
Rv2736c	<i>recX</i>	regulatory protein for RecA	Rv3649	-	ATP-dependent DNA/RNA helicase	Rv2284	<i>lipM</i>	probable esterase
Rv2593c	<i>ruvA</i>	Holliday junction binding protein, DNA helicase	8. Polysaccharides (cytoplasmic)			Rv2970c	<i>lipN</i>	probable lipase/esterase
Rv2592c	<i>ruvB</i>	Holliday junction binding protein	Rv1326c	<i>glgB</i>	1,4- $\alpha$ -glucan branching enzyme	Rv1426c	<i>lipO</i>	probable esterase
Rv2594c	<i>ruvC</i>	Holliday junction resolvase, endodeoxyribonuclease	Rv1328	<i>glgP</i>	probable glycogen phosphorylase	Rv2463	<i>lipP</i>	probable esterase
Rv0054	<i>ssb</i>	single strand binding protein	Rv1564c	<i>glgX</i>	probable glycogen debranching enzyme	Rv2485c	<i>lipQ</i>	probable carboxylesterase
Rv1210	<i>tagA</i>	DNA-3-methyladenine glycosidase I	Rv1563c	<i>glgY</i>	putative $\alpha$ -amylase	Rv3084	<i>lipR</i>	probable acetyl-hydrolase
Rv3646c	<i>topA</i>	DNA topoisomerase	Rv1562c	<i>glgZ</i>	maltooligosyltrehalose trehalohydrolase	Rv3176c	<i>lipS</i>	probable esterase/lipase
Rv2976c	<i>ung</i>	uracil-DNA glycosylase	Rv0126	-	probable glycosyl hydrolase	Rv2045c	<i>lipT</i>	probable carboxylesterase
Rv1638	<i>uvrA</i>	excinuclease ABC subunit A	Rv1781c	-	probable 4- $\alpha$ -glucanotransferase	Rv1076	<i>lipU</i>	probable esterase
Rv1633	<i>uvrB</i>	excinuclease ABC subunit B	Rv2471	-	probable maltase $\alpha$ -glucosidase	Rv3203	<i>lipV</i>	probable lipase
Rv1420	<i>uvrC</i>	excinuclease ABC subunit C	B. Degradation of macromolecules			Rv0217c	<i>lipW</i>	probable esterase
Rv0949	<i>uvrD</i>	DNA-dependent ATPase I and helicase II	1. RNA			Rv2351c	<i>plcA</i>	phospholipase C precursor
Rv3198c	<i>uvrD2</i>	putative UvrD	Rv1014c	<i>pth</i>	peptidyl-tRNA hydrolase	Rv2350c	<i>plcB</i>	phospholipase C precursor
Rv0427c	<i>xthA</i>	exodeoxyribonuclease III	Rv2925c	<i>rnc</i>	RNAse III	Rv2349c	<i>plcC</i>	phospholipase C precursor
Rv0071	-	group II intron maturase	Rv2444c	<i>rne</i>	similar at C-term to ribonuclease E	Rv1755c	<i>plcD</i>	partial CDS for phospholipase C
Rv0861c	-	probable DNA helicase	Rv2902c	<i>rnhB</i>	ribonuclease HII	Rv1104	-	probable esterase pseudogene
Rv0944	-	possible formamidopyrimidine-DNA glycosylase	Rv3923c	<i>rnpA</i>	ribonuclease P protein component	Rv1105	-	probable esterase pseudogene
Rv1688	-	probable 3-methylpurine DNA glycosylase	Rv1340	<i>rphA</i>	ribonuclease PH	6. Aromatic hydrocarbons		
						Rv3469c	<i>mhpE</i>	probable 4-hydroxy-2-oxovalerate aldolase
						Rv0316	-	probable muconolactone isomerase
						Rv0771	-	probable 4-carboxymuconolactone decarboxylase
						Rv0939	-	probable dehydrase
						Rv1723	-	6-aminohexanoate-dimer hydro-



Rv2715 - lase  
2-hydroxyruconic semialdehyde  
hydrolase  
Rv3530c - probable *cis*-diol dehydrogenase  
Rv3534c - 4-hydroxy-2-oxovalerate aldolase  
Rv3536c - aromatic hydrocarbon degradation

### C. Cell envelope

#### 1. Lipoproteins (*lppA-lppO*) 65

#### 2. Surface polysaccharides, lipopolysaccharides, proteins and antigens

Rv0806c *cpsY* probable UDP-glucose-4-epimerase  
secreted protein  
Rv3811 *csp* highly similar to C-term Mpt53  
Rv1677 *dsbF* involved in arabinogalactan synthesis  
Rv3794 *embA* involved in arabinogalactan synthesis  
Rv3795 *embB* involved in arabinogalactan synthesis  
Rv3793 *embC* involved in arabinogalactan synthesis  
Rv3875 *esat6* early secretory antigen target  
Rv0112 *gca* probable GDP-mannose dehydratase  
Rv0113 *gmhA* phosphoheptose isomerase  
Rv2965c *kdtB* lipopolysaccharide core biosynthesis protein  
secreted protein Mpt53  
Rv2878c *mpt53* secreted immunogenic protein  
Rv1980c *mpt64* Mpb64/Mpt64  
Rv2875 *mpt70* major secreted immunogenic protein Mpt70 precursor  
Rv2873 *mpt83* surface lipoprotein Mpt83  
Rv0899 *ompA* member of OmpA family  
Rv3810 *pirG* cell surface protein precursor (Erp protein)  
Rv3782 *rfbE* similar to rhamnosyl transferase  
Rv1302 *rfe* undecaprenyl-phosphate  $\alpha$ -N-acetylglucosaminyltransferase  
antigen 84 (aka wag31)  
Rv2145c *wag31* tuberculin related peptide (AT103)  
Rv0431 - cell envelope antigen  
Rv0954 - involved in polysaccharide synthesis  
Rv1514c - involved in exopolysaccharide synthesis  
Rv1758 - partial cutinase  
Rv1910c - probable secreted protein  
Rv1919c - weak similarity to pollen antigens  
Rv1984c - probable secreted protein  
Rv1987 - probable secreted protein  
Rv2223c - probable exported protease  
Rv2224c - probable exported protease  
Rv2301 - probable cutinase  
Rv2345 - precursor of probable membrane protein  
Rv2672 - putative exported protease  
Rv3019c - similar to Esat6  
Rv3036c - probable secreted protein  
Rv3449 - probable precursor of serine protease  
Rv3451 - probable cutinase  
Rv3452 - probable cutinase precursor  
Rv3724 - probable cutinase precursor

#### 3. Murein sacculus and peptidoglycan

Rv2911 *dacB* penicillin binding protein  
Rv2981c *ddlA* D-alanine-D-alanine ligase A  
Rv3809c *glf* UDP-galactopyranose mutase  
Rv1018c *glmU* UDP-N-acetylglucosamine pyrophosphorylase  
Rv3382c *lytB* LytB protein homologue  
Rv1110 *lytB'* very similar to LytB  
Rv1315 *murA* UDP-N-acetylglucosamine-1-carboxyvinyltransferase  
Rv0482 *murB* UDP-N-acetylenolpyruvoylglucosamine reductase  
Rv2152c *murC* UDP-N-acetyl-muramate-alanine ligase  
Rv2155c *murD* UDP-N-acetylmuramoylalanine-D-glutamate ligase  
Rv2158c *murE* *meso*-diaminopimelate-adding enzyme  
Rv2157c *murF* D-alanine:D-alanine-adding enzyme  
Rv2153c *murG* transferase in peptidoglycan synthesis  
Rv1338 *murl* glutamate racemase  
Rv2156c *murX* phospho-N-acetylmuramoyl-petapeptide transferase  
Rv3332 *nagA* N-acetylglucosamine-6-P-deacetylase  
Rv0016c *pbpA* penicillin-binding protein  
Rv2163c *pbpB* penicillin-binding protein 2  
Rv0050 *ponA* penicillin-binding protein  
Rv3682 *ponA'* class A penicillin binding protein  
Rv0017c *rodA* FtsW/RodA/SpovE family  
Rv0907 - probable penicillin binding protein

Rv1367c - probable penicillin binding protein  
Rv1730c - probable penicillin binding protein  
Rv1922 - probable penicillin binding protein  
Rv2864c - probable penicillin binding protein  
Rv3330 - probable penicillin binding protein  
Rv3627c - probable penicillin binding protein

#### 4. Conserved membrane proteins

Rv0402c *mmpL1* conserved large membrane protein  
Rv0507 *mmpL2* conserved large membrane protein  
Rv0206c *mmpL3* conserved large membrane protein  
Rv0450c *mmpL4* conserved large membrane protein  
Rv0676c *mmpL5* conserved large membrane protein  
Rv1557 *mmpL6* conserved large membrane protein  
Rv2942 *mmpL7* conserved large membrane protein  
Rv3823c *mmpL8* conserved large membrane protein  
Rv2339 *mmpL9* conserved large membrane protein  
Rv1183 *mmpL10* conserved large membrane protein  
Rv0202c *mmpL11* conserved large membrane protein  
Rv1522c *mmpL12* conserved large membrane protein  
Rv0403c *mmpS1* conserved small membrane protein  
Rv0506 *mmpS2* conserved small membrane protein  
Rv2198c *mmpS3* conserved small membrane protein  
Rv0451c *mmpS4* conserved small membrane protein  
Rv0677c *mmpS5* conserved small membrane protein

#### 5. Other membrane proteins 211

### III. Cell processes

#### A. Transport/binding proteins

##### 1. Amino acids

Rv2127 *ansP* L-asparagine permease  
Rv0346c *aroP2* probable aromatic amino acid permease  
Rv0917 *betP* glycine betaine transport  
Rv1704c *cycA* transport of D-alanine, D-serine and glycine  
Rv3666c *dppA* probable peptide transport system permease  
Rv3665c *dppB* probable peptide transport system permease  
Rv3664c *dppC* probable peptide transport system permease  
Rv3663c *dppD* probable ABC-transporter  
Rv0522 *gabP* probable 4-amino butyrate transporter  
Rv0411c *glnH* putative glutamine binding protein  
Rv2564 *glnQ* probable ATP-binding transport protein  
Rv1280c *oppA* probable oligopeptide transport protein  
Rv1283c *oppB* oligopeptide transport protein  
Rv1282c *oppC* oligopeptide transport system permease  
Rv1281c *oppD* probable peptide transport protein  
Rv2320c *rocE* arginine/ornithine transporter  
Rv3253c - probable cationic amino acid transport  
Rv3454 - possible proline permease

##### 2. Cations

Rv2920c *amt* putative ammonium transporter  
Rv1607 *chaA* putative calcium/proton antiporter  
Rv1239c *corA* probable magnesium and cobalt transport protein  
Rv0092 *ctpA* cation-transporting ATPase  
Rv0103c *ctpB* cation transport ATPase  
Rv3270 *ctpC* cation transport ATPase  
Rv1469 *ctpD* probable cadmium-transporting ATPase  
Rv0908 *ctpE* probable cation transport ATPase  
Rv1997 *ctpF* probable cation transport ATPase  
Rv1992c *ctpG* probable cation transport ATPase  
Rv0425c *ctpH* C-terminal region putative cation-transporting ATPase  
Rv0107c *ctpl* probable magnesium transport ATPase  
Rv0969 *ctpV* cation transport ATPase  
Rv3044 *fecB* putative FeIII-dicitrate transporter  
Rv0265c *fecB2* iron transport protein FeIII dicitrate transporter  
Rv1029 *kdpA* potassium-transporting ATPase A chain

Rv1030 *kdpB* potassium-transporting ATPase B chain  
Rv1031 *kdpC* potassium-transporting ATPase C chain  
Rv3236c *kefB* probable glutathione-regulated potassium-efflux protein  
Rv2877c *merT* possible mercury resistance transport system  
Rv1811 *mgtC* probable magnesium transport ATPase protein C  
Rv0362 *mgtE* putative magnesium ion transporter  
Rv2856 *nicT* probable nickel transport protein  
Rv0924c *nramp* transmembrane protein belonging to Nramp family  
Rv2691 *trkA* probable potassium uptake protein  
Rv2692 *trkB* probable potassium uptake protein  
Rv2287 *yjcE* probable Na<sup>+</sup>/H<sup>+</sup> exchanger  
Rv2723 - probable membrane protein, tellurium resistance  
Rv3162c - probable membrane protein  
Rv3237c - possible potassium channel protein  
Rv3743c - probable cation-transporting ATPase

#### 3. Carbohydrates, organic acids and alcohols

Rv2443 *dctA* C4-dicarboxylate transport protein  
Rv3476c *kgtP* sugar transport protein  
Rv1902c *nanT* probable sialic acid transporter  
Rv1236c *sugA* membrane protein probably involved in sugar transport  
Rv1237 *sugB* sugar transport protein  
Rv1238 *sugC* ABC transporter component of sugar uptake system  
Rv3331 *sugI* probable sugar transport protein  
Rv2835c *ugpA* sn-glycerol-3-phosphate permease  
Rv2833c *ugpB* sn-glycerol-3-phosphate-binding periplasmic lipoprotein  
Rv2832c *ugpC* sn-glycerol-3-phosphate transport ATP-binding protein  
Rv2834c *ugpE* sn-glycerol-3-phosphate transport system protein  
Rv2316 *uspA* sugar transport protein  
Rv2318 *uspC* sugar transport protein  
Rv2317 *uspE* sugar transport protein  
Rv1200 - probable sugar transporter  
Rv2038c - probable ABC sugar transporter  
Rv2039c - probable sugar transporter  
Rv2040c - probable sugar transporter  
Rv2041c - probable sugar transporter

#### 4. Anions

Rv2684 *arsA* probable arsenical pump  
Rv2685 *arsB* probable arsenical pump  
Rv3578 *arsB2* probable arsenical pump  
Rv2643 *arsC* probable arsenical pump  
Rv2397c *cysA* sulphate transport ATP-binding protein  
Rv2399c *cysT* sulphate transport system permease protein  
Rv2398c *cysW* sulphate transport system permease protein  
Rv1857 *modA* molybdate binding protein  
Rv1858 *modB* transport system permease, molybdate uptake  
Rv1859 *modC* molybdate uptake ABC-transporter  
Rv1860 *modD* precursor of Apa (45/47 kD secreted protein)  
Rv2329c *narK1* probable nitrite extrusion protein  
Rv1737c *narK2* nitrite extrusion protein  
Rv0261c *narK3* nitrite extrusion protein1  
Rv0267 *narU* similar to nitrite extrusion protein 2  
Rv0934 *phoS1* PstS component of phosphate uptake  
Rv0928 *phoS2* PstS component of phosphate uptake  
Rv0820 *phoT* phosphate transport system ABC transporter  
Rv3301c *phoY1* phosphate transport system regulator  
Rv0821c *phoY2* phosphate transport system regulator  
Rv0545c *pitA* low-affinity inorganic phosphate transporter  
Rv2281 *pitB* phosphate permease  
Rv0930 *pstA1* PstA component of phosphate uptake  
Rv0936 *pstA2* PstA component of phosphate uptake  
Rv0933 *pstB* ABC transport component of phosphate uptake  
Rv0935 *pstC* PstC component of phosphate uptake  
Rv0929 *pstC2* membrane-bound component of

Rv0932c	<i>pstS</i>	phosphate transport system PstS component of phosphate uptake	Rv1821	<i>secA2</i>	unit SecA, preprotein translocase sub-unit	Rv3500c	-	part of <i>mce4</i> operon
Rv2400c	<i>subI</i>	sulphate binding precursor	Rv2587c	<i>secD</i>	protein-export membrane protein	Rv3501c	-	part of <i>mce4</i> operon
Rv0143c	-	probable chloride channel	Rv0638	<i>secE</i>	SecE preprotein translocase	Rv3896c	-	putative p60 homologue
Rv1707	-	probable sulphate permease	Rv2586c	<i>secF</i>	protein-export membrane protein	Rv3922c	-	possible hemolysin
Rv1739c	-	possible sulphate transporter	Rv1440	<i>secG</i>	protein-export membrane protein	<i>B. IS elements, Repeated sequences, and Phase 1. IS elements</i>		
Rv3679	-	possible anion transporter	Rv0732	<i>secY</i>	SecY subunit of preprotein translocase	IS6110	-	16 copies
Rv3680	-	probable anion transporter	Rv2462c	<i>tig</i>	chaperone protein, similar to trigger factor	IS1081	-	6 copies
5. Fatty acid transport			Rv2813	-	probable general secretion pathway protein	Others	-	37 copies
Rv2790c	<i>ltp1</i>	non-specific lipid transport protein				2. REP13E12 family 7 copies		
Rv3540c	<i>ltp2</i>	non-specific lipid transport protein				3. Phage-related functions		
6. Efflux proteins			<i>E. Adaptations and atypical conditions</i>			Rv2894c	<i>xerC</i>	integrase/recombinase
Rv2936	<i>drvA</i>	similar daunorubicin resistance ABC-transporter	Rv1901	<i>cinA</i>	competence damage protein	Rv1701	<i>xerD</i>	integrase/recombinase
Rv2937	<i>drvB</i>	similar daunorubicin resistance transmembrane protein	Rv3648c	<i>cspA</i>	cold shock protein, transcriptional regulator	Rv1054	-	integrase-a
Rv2938	<i>drvC</i>	similar daunorubicin resistance transmembrane protein	Rv0871	<i>cspB</i>	probable cold shock protein	Rv1055	-	integrase-b
Rv2846c	<i>efpA</i>	putative efflux protein	Rv3063	<i>cstA</i>	starvation-induced stress response protein	Rv1573	-	phiRV1 phage related protein
Rv3065	<i>emrE</i>	resistance to ethidium bromide	Rv3490	<i>otsA</i>	probable $\alpha,\alpha$ -trehalose-phosphate synthase	Rv1574	-	phiRV1 phage related protein
Rv0783c	-	multidrug resistance protein	Rv2006	<i>otsB</i>	trehalose-6-phosphate phosphatase	Rv1575	-	phiRV1 phage related protein
Rv0849	-	possible quinolone efflux pump	Rv3372	<i>otsB2</i>	trehalose-6-phosphate phosphatase	Rv1576c	-	phiRV1 phage related protein
Rv1145	-	probable drug transporter	Rv3758c	<i>proV</i>	osmoprotection ABC transporter	Rv1577c	-	phiRV1 phage related protein
Rv1146	-	probable drug transporter	Rv3757c	<i>proW</i>	transport system permease	Rv1578c	-	phiRV1 phage related protein
Rv1250	-	probable drug efflux protein	Rv3759c	<i>proX</i>	similar to osmoprotection proteins	Rv1579c	-	phiRV1 phage related protein
Rv1258c	-	probable multidrug resistance pump	Rv3756c	<i>proZ</i>	transport system permease	Rv1580c	-	phiRV1 phage related protein
Rv1410c	-	probable drug efflux protein	Rv1026	-	probable pppGpp-5'phosphohydrolyase	Rv1581c	-	phiRV1 phage related protein
Rv1634	-	probable drug efflux protein	<i>F. Detoxification</i>			Rv1582c	-	phiRV1 phage related protein
Rv1819c	-	probable multidrug resistance pump	Rv2428	<i>ahpC</i>	alkyl hydroperoxide reductase	Rv1583c	-	phiRV1 phage related protein
Rv2136c	-	putative bacitracin resistance protein	Rv2429	<i>ahpD</i>	member of AhpC/TSA family	Rv1584c	-	phiRV1 phage related protein
Rv2209	-	probable drug efflux protein	Rv2238c	<i>ahpE</i>	member of AhpC/TSA family	Rv1585c	-	phiRV1 phage related protein
Rv2333c	-	probable tetracycline C resistance protein	Rv2521	<i>bcp</i>	bacterioferritin comigratory protein	Rv1586c	-	phiRV1 phage related protein
Rv2994	-	probable fluoroquinolone efflux protein	Rv1608c	<i>bcpB</i>	probable bacterioferritin comigratory protein	Rv2309c	-	integrase
Rv1877	-	probable drug efflux protein	Rv3473c	<i>bpoA</i>	probable non-heme bromoperoxidase	Rv2310	-	excisionase
Rv2459	-	probable drug efflux protein	Rv1123c	<i>bpoB</i>	probable non-heme bromoperoxidase	Rv2646	-	phiRV2 integrase
<i>B. Chaperones/Heat shock</i>			Rv0554	<i>bpoC</i>	probable non-heme bromoperoxidase	Rv2647	-	phiRV2 phage related protein
Rv0384c	<i>clpB</i>	heat shock protein	Rv3617	<i>ephA</i>	probable epoxide hydrolase	Rv2650c	-	phiRV2 phage related protein
Rv0352	<i>dnaJ</i>	acts with GrpE to stimulate DnaK ATPase	Rv1938	<i>ephB</i>	probable epoxide hydrolase	Rv2651c	-	phiRV2 prohead protease
Rv2373c	<i>dnaJ2</i>	DnaJ homologue	Rv1124	<i>ephC</i>	probable epoxide hydrolase	Rv2652c	-	phiRV2 phage related protein
Rv0350	<i>dnaK</i>	70 kD heat shock protein, chromosome replication	Rv2214c	<i>ephD</i>	probable epoxide hydrolase	Rv2653c	-	phiRV2 phage related protein
Rv3417c	<i>groEL1</i>	60 kD chaperonin 1	Rv3670	<i>ephE</i>	probable epoxide hydrolase	Rv2654c	-	phiRV2 phage related protein
Rv0440	<i>groEL2</i>	60 kD chaperonin 2	Rv0134	<i>ephF</i>	probable non-heme haloperoxidase	Rv2655c	-	phiRV2 phage related protein
Rv3418c	<i>groES</i>	10 kD chaperone	Rv3171c	<i>hpx</i>	catalase-peroxidase	Rv2656c	-	phiRV2 phage related protein
Rv0351	<i>grpE</i>	stimulates DnaK ATPase activity	Rv1908c	<i>katG</i>	catalase-peroxidase	Rv2657c	-	phiRV2 phage related protein similar to gp36 of mycobacteriophage L5
Rv2374c	<i>hrcA</i>	heat-inducible transcription repressor	Rv3846	<i>sodA</i>	superoxide dismutase	Rv2658c	-	phiRV2 phage related protein
Rv0251c	<i>hsp</i>	possible heat shock protein	Rv0432	<i>sodC</i>	superoxide dismutase precursor - (Cu-Zn)	Rv2659c	-	phiRV2 integrase
Rv0353	<i>hspR</i>	heat shock regulator	Rv1932	<i>tpx</i>	thiol peroxidase	Rv2830c	-	similar to phase P1 <i>phd</i> gene
Rv2031c	<i>hspX</i>	14kD antigen, heat shock protein Hsp20 family	Rv0634c	-	putative glyoxylase II	Rv3750c	-	excisionase
Rv2299c	<i>htpG</i>	heat shock protein Hsp90 family	Rv2581c	-	putative glyoxylase II	Rv3751	-	putative integrase
Rv0563	<i>htpX</i>	probable (transmembrane) heat shock protein	Rv3177	-	probable non-heme haloperoxidase	<i>C. PE and PPE families</i>		
Rv2701c	<i>suhB</i>	putative extragenic suppressor protein	<i>IV. Other</i>			1. PE family 38 members		
Rv3269	-	probable heat shock protein	<i>A. Virulence</i>			PE subfamily 61 members		
<i>C. Cell division</i>			Rv0169	<i>mce1</i>	cell invasion protein	2. PPE family 68 members		
Rv3641c	<i>fic</i>	possible cell division protein	Rv0589	<i>mce2</i>	cell invasion protein	<i>D. Antibiotic production and resistance</i>		
Rv3102c	<i>ftsE</i>	membrane protein	Rv1966	<i>mce3</i>	cell invasion protein	Rv2068c	<i>blaC</i>	class A $\beta$ -lactamase
Rv3610c	<i>ftsH</i>	inner membrane protein, chaperone	Rv3499c	<i>mce4</i>	cell invasion protein	Rv3290c	<i>lat</i>	lysine-e aminotransferase
Rv2748c	<i>ftsK</i>	chromosome partitioning	Rv3100c	<i>smfB</i>	probable small protein b	Rv2043c	<i>pncA</i>	pyrazinamide resistance/sensitivity
Rv2151c	<i>ftsQ</i>	ingrowth of wall at septum	Rv1694	<i>tlyA</i>	cytotoxin/hemolysin homologue	Rv0133	-	possible puromycin N-acetyltransferase
Rv2154c	<i>ftsW</i>	membrane protein (shape determination)	Rv0024	-	putative p60 homologue	Rv0262c	-	aminoglycoside 2'-N-acetyltransferase
Rv3101c	<i>ftsX</i>	membrane protein	Rv0167	-	part of <i>mce1</i> operon	Rv0802c	-	acetyltransferase
Rv2921c	<i>ftsY</i>	cell division protein FtsY	Rv0168	-	part of <i>mce1</i> operon	Rv1082	-	similar to <i>S. lincolnensis</i> <i>lmbE</i>
Rv2150c	<i>ftsZ</i>	circumferential ring, GTPase	Rv0170	-	part of <i>mce1</i> operon	Rv1170	-	similar to <i>S. lincolnensis</i> <i>lmbE</i>
Rv3919c	<i>gid</i>	glucose inhibited division protein B	Rv0171	-	part of <i>mce1</i> operon	Rv1347c	-	possible aminoglycoside 6'-N-acetyltransferase
Rv3625c	<i>mesJ</i>	probable cell cycle protein	Rv0172	-	part of <i>mce1</i> operon	Rv2036	-	similar to lincomycin production genes
Rv3917c	<i>parA</i>	chromosome partitioning; DNA binding	Rv0174	-	part of <i>mce1</i> operon	Rv2303c	-	similar to <i>S. griseus</i> macrotretolide resistance protein
Rv3918c	<i>parB</i>	possibly involved in chromosome partitioning	Rv0587	-	part of <i>mce2</i> operon	Rv3225c	-	probable aminoglycoside 3'-phosphotransferases
Rv2922c	<i>smc</i>	member of Smc1/Cut3/Cut14 family	Rv0588	-	part of <i>mce2</i> operon	Rv3700c	-	probable acetyltransferase
Rv0012	-	possible cell division protein	Rv0589	-	part of <i>mce2</i> operon	Rv3817	-	probable aminoglycoside 3'-phosphotransferase
Rv0435c	-	ATPase of AAA-family	Rv0591	-	part of <i>mce2</i> operon	<i>E. Bacteriocin-like proteins</i> 3		
Rv2115c	-	ATPase of AAA-family	Rv0592	-	part of <i>mce2</i> operon	<i>F. Cytochrome P450 enzymes</i> 22		
Rv3213c	-	possible role in chromosome segregation	Rv0594	-	part of <i>mce2</i> operon	<i>G. Coenzyme F420-dependent enzymes</i> 3		
Rv1708	-	possible role in chromosome partitioning	Rv1085c	-	possible hemolysin	<i>H. Miscellaneous transferases</i> 61		
<i>D. Protein and peptide secretion</i>			Rv1477	-	putative exported p60 protein homologue	<i>I. Miscellaneous phosphatases, lyases, and hydrolases</i> 18		
Rv2916c	<i>ifn</i>	signal recognition particle protein	Rv1478	-	putative exported p60 protein homologue	<i>J. Cyclases</i> 6		
Rv2903c	<i>lepB</i>	signal peptidase I	Rv1964	-	part of <i>mce3</i> operon	<i>K. Chelatases</i> 2		
Rv1614	<i>lgt</i>	prolipoprotein diacylglycerol transferase	Rv1965	-	part of <i>mce3</i> operon	<i>V. Conserved hypotheticals</i> 912		
Rv1539	<i>lspA</i>	lipoprotein signal peptidase	Rv1967	-	part of <i>mce3</i> operon	<i>VI. Unknowns</i> 606		
Rv0379	<i>sec</i>	probable transport protein	Rv1968	-	part of <i>mce3</i> operon	TOTAL 3924		
Rv3240c	<i>secA</i>	SecA, preprotein translocase sub-	Rv1969	-	part of <i>mce3</i> operon			
			Rv1971	-	part of <i>mce3</i> operon			
			Rv2190c	-	putative p60 homologue			
			Rv3494c	-	part of <i>mce4</i> operon			
			Rv3496c	-	part of <i>mce4</i> operon			
			Rv3497c	-	part of <i>mce4</i> operon			
			Rv3498c	-	part of <i>mce4</i> operon			