

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

I. Small-molecule metabolism

A. Degradation

1. Carbon compounds

Rv0186	<i>bglS</i>	β-glucosidase
Rv2202c	<i>cbhK</i>	carbohydrate kinase
Rv0727c	<i>fucA</i>	L-fucose phosphate aldolase
Rv1731	<i>gabD1</i>	succinate-semialdehyde dehydrogenase
Rv0234c	<i>gabD2</i>	succinate-semialdehyde dehydrogenase
Rv0501	<i>galE1</i>	UDP-glucose 4-epimerase
Rv0536	<i>galE2</i>	UDP-glucose 4-epimerase
Rv0620	<i>galK</i>	galactokinase
Rv0619	<i>galT</i>	galactose-1-phosphate uridylyltransferase C-term
Rv0618	<i>galT'</i>	galactose-1-phosphate uridylyltransferase N-term
Rv0993	<i>galU</i>	UTP-glucose-1-phosphate uridylyltransferase
Rv3696c	<i>glpK</i>	ATP:glycerol 3-phosphotransferase
Rv3255c	<i>manA</i>	mannose-6-phosphate isomerase
Rv3441c	<i>mrsA</i>	phosphoglucosyltransferase or phosphomannomutase
Rv0118c	<i>oxcA</i>	oxalyl-CoA decarboxylase
Rv3068c	<i>pgmA</i>	phosphoglucosyltransferase
Rv3257c	<i>pmmA</i>	phosphomannomutase
Rv3308	<i>pmmB</i>	phosphomannomutase
Rv2702	<i>ppgK</i>	polyphosphate glucokinase
Rv0408	<i>pta</i>	phosphate acetyltransferase
Rv0729	<i>xyfB</i>	xylulose kinase
Rv1096	-	carbohydrate degrading enzyme

2. Amino acids and amines

Rv1905c	<i>aao</i>	D-amino acid oxidase
Rv2531c	<i>adi</i>	ornithine/arginine decarboxylase
Rv2780	<i>ald</i>	L-alanine dehydrogenase
Rv1538c	<i>ansA</i>	L-asparaginase
Rv1001	<i>arcA</i>	arginine deiminase
Rv0753c	<i>mmsA</i>	methylmalmonate semialdehyde dehydrogenase
Rv0751c	<i>mmsB</i>	methylmalmonate semialdehyde oxidoreductase
Rv1187	<i>rocA</i>	pyrroline-5-carboxylate dehydrogenase
Rv2322c	<i>rocD1</i>	ornithine aminotransferase
Rv2321c	<i>rocD2</i>	ornithine aminotransferase
Rv1848	<i>ureA</i>	urease γ subunit
Rv1849	<i>ureB</i>	urease β subunit
Rv1850	<i>ureC</i>	urease α subunit
Rv1853	<i>ureD</i>	urease accessory protein
Rv1851	<i>ureF</i>	urease accessory protein
Rv1852	<i>ureG</i>	urease accessory protein
Rv2913c	-	probable D-amino acid aminohydrolase
Rv3551	-	possible glutaconate CoA-transferase

3. Fatty acids

Rv2501c	<i>accA1</i>	acetylpropionyl-CoA carboxylase, α subunit
Rv0973c	<i>accA2</i>	acetylpropionyl-CoA carboxylase, α subunit
Rv2502c	<i>accD1</i>	acetylpropionyl-CoA carboxylase, β subunit
Rv0974c	<i>accD2</i>	acetylpropionyl-CoA carboxylase, β subunit
Rv3667	<i>acs</i>	acetyl-CoA synthase
Rv3409c	<i>choD</i>	cholesterol oxidase
Rv0222	<i>echA1</i>	enoyl-CoA hydratase/isomerase superfamily
Rv0456c	<i>echA2</i>	enoyl-CoA hydratase/isomerase superfamily
Rv0632c	<i>echA3</i>	enoyl-CoA hydratase/isomerase superfamily
Rv0673	<i>echA4</i>	enoyl-CoA hydratase/isomerase superfamily
Rv0675	<i>echA5</i>	enoyl-CoA hydratase/isomerase superfamily
Rv0905	<i>echA6</i>	enoyl-CoA hydratase/isomerase superfamily (aka <i>echH</i>)
Rv0971c	<i>echA7</i>	enoyl-CoA hydratase/isomerase superfamily
Rv1070c	<i>echA8</i>	enoyl-CoA hydratase/isomerase superfamily
Rv1071c	<i>echA9</i>	enoyl-CoA hydratase/isomerase superfamily
Rv1142c	<i>echA10</i>	enoyl-CoA hydratase/isomerase superfamily
Rv1141c	<i>echA11</i>	enoyl-CoA hydratase/isomerase superfamily
Rv1472	<i>echA12</i>	enoyl-CoA hydratase/isomerase superfamily
Rv1935c	<i>echA13</i>	enoyl-CoA hydratase/isomerase superfamily
Rv2486	<i>echA14</i>	enoyl-CoA hydratase/isomerase superfamily
Rv2679	<i>echA15</i>	enoyl-CoA hydratase/isomerase

Rv2831	<i>echA16</i>	superfamily enoyl-CoA hydratase/isomerase
Rv3039c	<i>echA17</i>	enoyl-CoA hydratase/isomerase superfamily
Rv3373	<i>echA18</i>	enoyl-CoA hydratase/isomerase superfamily, N-term
Rv3374	<i>echA18'</i>	enoyl-CoA hydratase/isomerase superfamily, C-term
Rv3516	<i>echA19</i>	enoyl-CoA hydratase/isomerase superfamily
Rv3550	<i>echA20</i>	enoyl-CoA hydratase/isomerase superfamily
Rv3774	<i>echA21</i>	enoyl-CoA hydratase/isomerase superfamily
Rv0859	<i>fadA</i>	β oxidation complex, β subunit (acetyl-CoA C-acetyltransferase)
Rv0243	<i>fadA2</i>	acetyl-CoA C-acetyltransferase
Rv1074c	<i>fadA3</i>	acetyl-CoA C-acetyltransferase
Rv1323	<i>fadA4</i>	acetyl-CoA C-acetyltransferase (aka <i>thiL</i>)
Rv3546	<i>fadA5</i>	acetyl-CoA C-acetyltransferase
Rv3556c	<i>fadA6</i>	acetyl-CoA C-acetyltransferase
Rv0860	<i>fadB</i>	β oxidation complex, α subunit (multiple activities)
Rv0468	<i>fadB2</i>	3-hydroxyacyl-CoA dehydrogenase
Rv1715	<i>fadB3</i>	3-hydroxyacyl-CoA dehydrogenase
Rv3141	<i>fadB4</i>	3-hydroxyacyl-CoA dehydrogenase
Rv1912c	<i>fadB5</i>	3-hydroxyacyl-CoA dehydrogenase
Rv1750c	<i>fadD1</i>	acyl-CoA synthase
Rv0270	<i>fadD2</i>	acyl-CoA synthase
Rv3561	<i>fadD3</i>	acyl-CoA synthase
Rv0214	<i>fadD4</i>	acyl-CoA synthase
Rv0166	<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

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>air</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>	probable deoxyguanosine triphosphate hydrolase	Rv2404c	<i>lepA</i>	GTP-binding protein LepA	8. Thiamine		
<i>E. Polyamine synthesis</i>			Rv2727c	<i>miaA</i>	tRNA δ(2)-isopentenylpyrophosphate transferase	Rv0422c	<i>thiD</i>	phosphomethylpyrimidine kinase
Rv2601	<i>speE</i>	spermidine synthase	Rv2445c	<i>ndkA</i>	nucleoside diphosphate kinase	Rv0414c	<i>thiE</i>	thiamine synthesis, thiazole moiety
<i>F. Purines, pyrimidines, nucleosides and nucleotides</i>			Rv2440c	<i>obg</i>	Obg GTP-binding protein	Rv0417	<i>thiG</i>	thiamine synthesis, thiazole moiety
1. Purine ribonucleotide biosynthesis			Rv2583c	<i>relA</i>	(p)ppGpp synthase I	Rv2977c	<i>thiL</i>	probable thiamine-monophosphate kinase
Rv1389	<i>gmK</i>	putative guanylate kinase	<i>G. Biosynthesis of cofactors, prosthetic groups and carriers</i>			9. Riboflavin		
Rv3396c	<i>guaA</i>	GMP synthase	1. Biotin			Rv1940	<i>ribA</i>	GTP cyclohydrolyase II
Rv1843c	<i>guaB1</i>	inosine-5'-monophosphate dehydrogenase	Rv1568	<i>bioA</i>	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	Rv1415	<i>ribA2</i>	probable GTP cyclohydrolyase II
Rv3411c	<i>guaB2</i>	inosine-5'-monophosphate dehydrogenase	Rv1589	<i>bioB</i>	biotin synthase	Rv1412	<i>ribC</i>	molybdopterin synthase α chain
Rv3410c	<i>guaB3</i>	inosine-5'-monophosphate dehydrogenase	Rv1570	<i>bioD</i>	dethiobiotin synthase	Rv2671	<i>ribD</i>	probable riboflavin deaminase
Rv1017c	<i>prsA</i>	ribose-phosphate pyrophosphokinase	Rv1569	<i>bioF</i>	8-amino-7-oxononanoate synthase	Rv2786c	<i>ribF</i>	riboflavin kinase
Rv0357c	<i>purA</i>	adenylosuccinate synthase	Rv0032	<i>bioF2</i>	C-terminal similar to <i>B. subtilis</i> BioF	Rv1409	<i>ribG</i>	riboflavin biosynthesis
Rv0777	<i>purB</i>	adenylosuccinate lyase	Rv3279c	<i>birA</i>	biotin apo-protein ligase	Rv1416	<i>ribH</i>	riboflavin synthase β chain
Rv0780	<i>purC</i>	phosphoribosylaminoimidazole-succinocarboxamide synthase	Rv1442	<i>bisC</i>	biotin sulfoxide reductase	Rv3300c	-	probable deaminase, riboflavin synthesis
Rv0772	<i>purD</i>	phosphoribosylamine-glycine ligase	Rv0089	-	possible <i>bioC</i> biotin synthesis gene	10. Thioredoxin, glutaredoxin and mycothiol		
Rv3275c	<i>purE</i>	phosphoribosylaminoimidazole carboxylase	2. Folic acid			Rv0773c	<i>ggtA</i>	putative γ-glutamyl transpeptidase
Rv0808	<i>purF</i>	amidophosphoribosyltransferase-phosphoribosylaminoimidazole-carboxamide formyltransferase	Rv2763c	<i>dfra</i>	dihydrofolate reductase	Rv2394	<i>ggtB</i>	γ-glutamyl transpeptidase precursor
Rv0957	<i>purH</i>	phosphoribosylaminoimidazole-carboxamide formyltransferase	Rv2447c	<i>folC</i>	folypolyglutamate synthase	Rv2855	<i>gorA</i>	glutathione reductase homologue
Rv3276c	<i>purK</i>	phosphoribosylaminoimidazole-carboxylase ATPase subunit	Rv3356c	<i>folD</i>	methylenetetrahydrofolate dehydrogenase	Rv0816c	<i>thiX</i>	equivalent to <i>M. leprae</i> ThiX
Rv0803	<i>purL</i>	phosphoribosylformylglycinamide synthase II	Rv3609c	<i>folE</i>	GTP cyclohydrolyase I	Rv1470	<i>trxA</i>	thioredoxin
Rv0809	<i>purM</i>	5'-phosphoribosyl-5-aminoimidazole synthase	Rv3606c	<i>folK</i>	7,8-dihydro-6-hydroxymethylpterin pyrophosphokinase	Rv1471	<i>trxB</i>	thioredoxin reductase
Rv0956	<i>purN</i>	phosphoribosylglycinamide formyltransferase I	Rv3608c	<i>folP</i>	dihydropterolate synthase	Rv3913	<i>trxB2</i>	thioredoxin reductase
Rv0788	<i>purQ</i>	phosphoribosylformylglycinamide synthase I	Rv1207	<i>folP2</i>	dihydropterolate synthase	Rv3914	<i>trxC</i>	thioredoxin
Rv0389	<i>purT</i>	phosphoribosylglycinamide formyltransferase II	Rv3607c	<i>folX</i>	may be involved in folate biosynthesis	11. Menaquinone, PQQ, ubiquinone and other terpenoids		
Rv2964	<i>purU</i>	formyltetrahydrofolate deformylase	Rv0013	<i>pabA</i>	p-aminobenzoate synthase glutamine amidotransferase	Rv2682c	<i>dxs</i>	1-deoxy-D-xylulose 5-phosphate synthase
2. Pyrimidine ribonucleotide biosynthesis			Rv1005c	<i>pabB</i>	p-aminobenzoate synthase	Rv0562	<i>grcC1</i>	heptaprenyl diphosphate synthase II
Rv1383	<i>carA</i>	carbamoyl-phosphate synthase subunit	Rv0812	<i>pabC</i>	aminodeoxychorismate lyase	Rv0989c	<i>grcC2</i>	heptaprenyl diphosphate synthase II
Rv1384	<i>carB</i>	carbamoyl-phosphate synthase subunit	3. Lipoate			Rv3398c	<i>idsA</i>	geranylgeranyl pyrophosphate synthase
Rv1380	<i>pyrB</i>	aspartate carbamoyltransferase	Rv2218	<i>lipA</i>	lipoate biosynthesis protein A	Rv2173	<i>idsA2</i>	geranylgeranyl pyrophosphate synthase
Rv1381	<i>pyrC</i>	dihydroorotate	Rv2217	<i>lipB</i>	lipoate biosynthesis protein B	Rv3383c	<i>idsB</i>	transfergeranyl, similar geranyl pyrophosphate synthase
Rv2139	<i>pyrD</i>	dihydroorotate dehydrogenase	4. Molybdopterin			Rv0534c	<i>menA</i>	pyrophosphate synthase
Rv1385	<i>pyrF</i>	orotidine 5'-phosphate decarboxylase	Rv3109	<i>moaA</i>	molybdenum cofactor biosynthesis, protein A	Rv0548c	<i>menB</i>	4-dihydroxy-2-naphthoate octaprenyltransferase
Rv1699	<i>pyrG</i>	CTP synthase	Rv0869c	<i>moaA2</i>	molybdenum cofactor biosynthesis, protein A	Rv0553	<i>menC</i>	naphthoate synthase
Rv2883c	<i>pyrH</i>	uridylate kinase	Rv0438c	<i>moaA3</i>	molybdenum cofactor biosynthesis, protein A	Rv0555	<i>menD</i>	o-succinylbenzoate-CoA synthase
Rv0382c	<i>umpA</i>	probable uridine 5'-monophosphate synthase	Rv3110	<i>moaB</i>	molybdenum cofactor biosynthesis, protein B	Rv0542c	<i>menE</i>	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase
3. 2'-deoxyribonucleotide metabolism			Rv0984	<i>moaB2</i>	molybdenum cofactor biosynthesis, protein B	Rv3853	<i>menG</i>	o-succinylbenzoic acid-CoA ligase
Rv0321	<i>dcd</i>	deoxycytidine triphosphate deaminase	Rv3111	<i>moaC</i>	molybdenum cofactor biosynthesis, protein B	Rv3397c	<i>phyA</i>	2-demethylmenaquinone phytoene synthase
Rv2697c	<i>dut</i>	deoxyuridine triphosphatase	Rv0864	<i>moaC2</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)	Rv3324c	<i>moaC3</i>	molybdenum cofactor biosynthesis, protein C	Rv0558	<i>ubiE</i>	ubiquinone/menaquinone biosynthesis methyltransferase
Rv3051c	<i>nrdE</i>	ribonucleoside diphosphate reductase α chain	Rv3112	<i>moaD</i>	molybdopterin converting factor subunit 1	12. Heme and porphyrin		
Rv1981c	<i>nrdF</i>	ribonucleotide reductase small	Rv0868c	<i>moaD2</i>	molybdopterin converting factor	Rv0509	<i>hemA</i>	glutamyl-tRNA reductase
						Rv0512	<i>hemB</i>	δ-aminolevulinic acid dehydratase
						Rv0510	<i>hemC</i>	porphobilinogen deaminase
						Rv2678c	<i>hemE</i>	uroporphyrinogen decarboxylase

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	II. Macromolecule metabolism		
Rv0894	-	putative transcriptional regulator	Rv3208	-	transcriptional regulator (TetR/AcrR family)	A. Synthesis and modification of macromolecules		
Rv1019	-	transcriptional regulator (TetR/AcrR family)	Rv3249c	-	transcriptional regulator (TetR/AcrR family)	1. Ribosomal protein synthesis and modification		
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	2. Two component systems			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)	3. Serine-threonine protein kinases and phosphoprotein phosphatases			Rv0717	<i>rpsN</i>	30S ribosomal protein S14
Rv2877	-	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,	2. Ribosome modification and maturation		
						Rv1010	<i>ksgA</i>	16S rRNA dimethyltransferase
						Rv2838c	<i>rbfA</i>	ribosome-binding factor A
						Rv2907c	<i>rimM</i>	16S rRNA processing protein
						3. Aminoacyl tRNA synthases and their modification		
						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 α subunit

Rv1650	<i>pheT</i>	phenylalanyl-tRNA synthase β 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>	probable 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, α 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 α 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, β subunit	Rv2889c	<i>tsf</i>	elongation factor EF-Ts	Rv2109c	<i>prcA</i>	proteasome α -type subunit 1
Rv3711c	<i>dnaQ</i>	DNA polymerase III ϵ chain	Rv0685	<i>tuf</i>	elongation factor EF-Tu	Rv2110c	<i>prcB</i>	proteasome β -type subunit 2
Rv3721c	<i>dnaZX</i>	DNA polymerase III, γ (dnaZ) and τ (dnaX)	7. RNA synthesis, RNA modification and DNA transcription			Rv0782	<i>ptrBa</i>	protease II, α subunit
Rv2924c	<i>fpg</i>	formamidopyrimidine-DNA glycosylase	Rv1253	<i>deaD</i>	ATP-dependent DNA/RNA helicase	Rv0781	<i>ptrBb</i>	protease II, β 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>rhIE</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>	α subunit of RNA polymerase	Rv3883c	-	probable serine protease
Rv3731	<i>ligC</i>	probable DNA ligase	Rv0667	<i>rpoB</i>	β subunit of RNA polymerase	Rv3886c	-	probable protease
Rv1020	<i>mid</i>	restriction-repair coupling factor	Rv0668	<i>rpoC</i>	β' 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 M γ A, RpoV)	Rv0315	-	probable β -1,3-glucanase
Rv0413	<i>mutT3</i>	MutT homologue	Rv2710	<i>sigB</i>	RNA polymerase sigma factor (aka M γ S β)	Rv1090	-	probable inactivated cellulase/endoglucanase
Rv3589	<i>mutY</i>	probable DNA glycosylase	Rv2069	<i>sigC</i>	ECF subfamily sigma factor	Rv1327c	-	probable glycosyl hydrolase, α -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- α -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 α -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- α -glucanotransferase	Rv1076	<i>lipU</i>	probable esterase
Rv1633	<i>uvrB</i>	excinuclease ABC subunit B	Rv2471	-	probable maltase α -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-aminoheptanoate-dimer hydro-

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 α,α -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 β -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			